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(54) Title: AGENTS AND METHODS FOR DIAGNOSING STRESS

(57) Abstract: The present invention discloses molecules and assays for qualitatively or quantitatively determining the effect of stress on the immune system, the susceptibility to developing disease or illness through immune system dysfunction as a result of stress, and for monitoring the ability of an animal to cope with stress. The invention is useful inter alia in measuring response to immunomodulatory therapies, and monitoring the immune response to natural disease under stressful conditions.

TITLE OF THE INVENTION

"AGENTS AND METHODS FOR DIAGNOSING STRESS"

FIELD OF THE INVENTION

[0001] This invention relates generally to methods and agents for determining the status of the immune system. More particularly, the present invention relates to molecules and assays for qualitatively or quantitatively determining the effect of stress on the immune system, the susceptibility to developing disease or illness through immune system dysfunction as a result of stress, and for monitoring the ability of an animal to cope with stress. The invention is useful *inter alia* in measuring response to immunomodulatory therapies, and monitoring the immune response to natural disease under stressful conditions. In certain embodiments, the invention is useful for monitoring animals in athletic training, for measuring the effects of aging on ability to respond to stress and external stressors, and for enabling better treatment and management decisions to be made in animals at risk of exposure to disease, or susceptible to disease through the effects of stress.

BACKGROUND OF THE INVENTION

[0002] The immune system functions to protect an organism from foreign invasion and insults. The host immune system of mammals can be functionally divided into adaptive and innate components. Innate immunity is often the first line of defense to external insults and consists of natural barriers, such as keratinous surfaces, secretions and chemicals, for example skin, mucous, lysozyme and acute phase proteins. The innate immune system can be found in most organisms, is non-specific, and many defense molecules that are part of the innate immune system are evolutionally conserved across a broad range of species (e.g., complement components appear early in evolution in invertebrates).

[0003] The adaptive immune system produces a specific response and "remembers" an infectious or invading agent to enable the host to engender an anamnestic response upon a subsequent challenge. The adaptive immune system can also be functionally divided into humoral and cellular components. The humoral component consists of soluble factors, and in mammals this consists of antibodies. Cells of the immune system of higher organisms consist of the lymphoid or myeloid lines. Lymphoid cells differentiate in the thymus (T cells) or bone marrow (B cells). B cells and T cells are morphologically identical. Myeloid cells are phagocytes and other cells such as platelets and mast cells. Phagocytes are either monocytes or polymorphonuclear cells. [For a general review of the immune system and its cellular and humoral components, see "Essential Immunology," 10th edition, Roitt and Delves, Blackwell Publishing 2001; and "Immunobiology. The Immune system in Health and Disease," 4th edition, Janeway *et al.*, Garland Publishing 1999].

[0004] Functional studies of the immune system of mammals constitute a vast body of literature and there are numerous tests available to measure the functional capabilities of the immune system. The humoral immune system is more amenable to functional testing as compared to the cellular immune system. For example, antibodies bind specifically to their target molecules and can be measured directly in tests such as antibody diffusion and precipitation assays, enzyme-linked immunosorbent assays, or used to detect the presence of invading organisms in antigen capture assays.

[0005] The function of the cellular immune system is more difficult to measure and often involves simple counting of the numbers of various subpopulations of cells using stains or specific antibodies to cell surface proteins. For example, one of the most common blood tests in medicine is a complete blood count (CBC) that measures red and white blood cell and platelet numbers. A differential white cell count uses Wright stain to enable the enumeration of lymphocytes, neutrophils, basophils, eosinophils and monocytes. Infection with bacteria often results in increased numbers of neutrophils in peripheral blood samples, and parasitic infections often results in increased numbers of eosinophils. However, counting the numbers of white blood cell types in a peripheral blood sample is often a poor indicator of the functional capabilities of the immune system, it is non-specific (not capable of determining the nature of infection or insult) and lymphocytes of the B and T cell lineage cannot be distinguished.

[0006] B lymphocytes produce antibodies and T lymphocytes are one of the main regulators and effectors of the immune system. Various subpopulations of B and T cells can be distinguished on the basis of different proteins (markers) on their cell surface. B cells express immunoglobulin (antibody) proteins on their cell surface and T cells express various markers depending upon their stage of development and function. Many different reagents (often antibodies) have been developed to differentiate subpopulations of T and B cells in humans and experimental animal species and many can be bought commercially from companies such as Alexis Corporation (www.alexis-corp.com). Again, simply counting the numbers of B and T cells (including subpopulations) is not informative on the functional capabilities of the cells. The preparation of reagents for detecting cell surface markers is also laborious and a highly specialized activity.

[0007] There are more direct methods of measuring immune cell function, including; plaque forming, chemotaxis, random migration, superoxide anion release, concentration of ATP in circulating $CD4^+$ cells following *in vitro* stimulation with phytohemagglutinin, and release of fluorescent dye from target cells assays. Many of these tests are laborious, require prior cell preparation and purification methods (often affecting the results of subsequent assays), and only measure the function of one particular subset of cells.

[0008] In summary, there currently exists a need for more effective modalities for measuring the functional capabilities of the immune system, and particularly the cellular immune system.

[0009] Athletic performance animals are unable to communicate their well-being to human owners or trainers. In addition, human athletes are often unaware of their well-being (due to heavy training) or are unable to communicate this effectively to trainers or medical practitioners. Therefore, there is also a need for more effective methods for monitoring the functional capabilities of the cellular immune system, especially in athletic performance animals.

[0010] It is almost 70 years since it was first recognized that stress can activate a physiological response that may be beneficial or damaging to the body (Seyle H. 1936, *Nature* **138**:32). Stress is a physical, chemical or emotional factor that causes bodily or mental tension and may be a factor in disease causation. A publication by Pedersen *et al.* (1994, *Inter J. Sports Med.* **15**:5116-5121) provides a review of work conducted in the area of stress and disease.

[0011] In recent years, rapid advances in the field of immunology have generated intense interest in the interaction between stress induced by psychosocial, nutritional and physical factors and the immune system. A major premise of this work is that stress may enhance vulnerability to disease by exerting an immunosuppressive effect. This may especially be true of diseases intimately connected with immunologic mechanisms such as infection, malignancy and autoimmune disease.

[0012] Studies demonstrating immune alterations in stress encompass a number of models in which most types of experimental and naturally occurring stresses have been associated with alteration of the components of the immune system. Some of the earliest work was conducted by the United States National Aeronautic Space Administration (NASA). The NASA studies showed that white blood cells and T-lymphocytes were elevated during the splash-down phase of space flight. However, there was impairment in the lymphoproliferative response to mitogenic stimulation during the first three (3) days after return to earth. A slight decrease in the stimulation response of lymphocytes was also observed prior to launch, possibly due to anticipation. A general overview of stress and immune function can be found in "Stress, Immunity and Illness--A Review", authored by Dorian and Garfinkel, Psychological Medicine, 17:393-407 (1987).

[0013] Physical activity and exercise are also known to produce a variety of alterations to the immune system. The effects of vigorous exercise appear to depress immune function and may compromise host defenses against upper respiratory tract infections. Epidemiological studies have generally shown a greater risk of upper respiratory tract infections with vigorous levels of exercise. See Heath *et al.*, 1992 *Sports Medicine* **14**(6) 353-365.

[0014] In addition to physical activity and exercise, stress can be evinced by external factors such as trauma (physical), major life events, physical health status and lifestyle. The way in which these external factors are perceived and the way in which the body adjusts influence the ultimate physiological response. The body's response to stress is handled by an allostatic system (adaptive) consisting primarily of the sympathetic nervous system and the hypothalamic, pituitary, adrenal axis (HPA axis) (McEwen B. 1998, *New England Journal of Medicine*, **338**:171-179). The term "allostatic load" refers to the amount of physiological response resulting from the balance between the initiation of a complex response and the shutting down of this response. Allostatic load can result from frequent stress, lack of adaptation to stress, inability to turn off an allostatic response, and lack of allostatic response in one system resulting in an increased response in another.

[0015] There is strong evidence to suggest that allostatic load leads to increased susceptibility to disease, risk of contracting disease and increased disease incidence. For example, stress induced increases in blood pressure can trigger myocardial infarction in humans and atherosclerosis in primates (Muller *et al.*, 1989 *Circulation* **79**:733-743, and Kaplan *et al.*, 1991 *Circulation*, **84** Suppl VI:VI-23-VI-32,). Intense athletic training increases allostatic load resulting in weight loss, amenorrhoea and anorexia nervosa (Boyar *et al.*, 1977 *New Engl J Med.* 296:190-193, and Loucks *et al.*, 1989 *J Clin. Endocrinol. Metabol.* **68**:402-411). Repeated social defeat (stressor) in mice is associated with (amongst other findings) increased plasma concentrations of corticosterone, which is a known immunosuppressant (Stark *et al.*, *Am. J. Physiol. Regul. Integrr. Comp. Physiol.* **280**: R1799-R1805). Age is correlated with the ability to turn off the HPA axis, and prolonged stimulation of physiological systems through the HPA axis can result in hippocampus damage and consequent cognitive deficits (Lupien *et al.*, 1994 *J Neurosci.* **14**:2893-2903). In Lewis rats, genetically determined to have hyporesponsiveness of the HPA axis, increased inflammatory responses result in an increased incidence of autoimmune and inflammatory disturbances (Sternburg *et al.*, 1989 *Proc. Natl. Acad. Sci (USA)* **86**: 4771-4775). Low HPA responsiveness is also considered to be involved in human fibromyalgia (Crofford *et al.*, 1994 *Arthritis Rheum.* **37**:1583-1592), chronic fatigue syndrome (Poteliakhoff A. 1981 *J Psychosom. Res.* **25**:91-95), infant atopic dermatitis (Buske-Kirschbaum *et al.*, 1997 *Psychosom med.* **59**:419-426) and post-traumatic stress disorder (Yehuda *et al.*, 1991 *Bio. Psychiatry* **30**:1031-1048).

[0016] Approximating allostatic load has been attempted by using measures of metabolic and cardiovascular physiology including, systolic blood pressure, overnight urinary cortisol and catecholamine excretion, ratio of waist to hip measurement, glycosylated hemoglobin value, ratio of serum high density lipoprotein in the total serum cholesterol concentration, serum concentration of dehydroepiandrosterone sulfate, and serum concentration of high density lipoprotein cholesterol. Patients with a lower allostatic score from measuring

these parameters had higher physical and mental functioning and a lower incidence of cardiovascular disease, hypertension and diabetes (Seeman *et al.*, 1997 *Arch. Intern. Med.* **157**:2259-2268). High serum fibrinogen concentrations have also been correlated to increased risk of coronary heart disease (Markowe *et al.*, 1985 *British Med. J.* **291**:1312-1314). In addition it has been noted that stress induces atrophy of the pyramidal neurones in the CA3 region of the hippocampus that can be detected using magnetic resonance imaging (Sapolsky R. M. 1996 *Science* **273**:749-750.). These measures require multiple separate assays, are expensive and often laborious, and only provide an approximation of allostatic load.

[0017] In summary there is a need for more effective processes for measuring allostatic load.

[0018] It is well known that stress affects the immune system (Hawkley and Cacioppo, 2004 *Brain Behav. Imm.* **18**:114-119; Engler *et al.*, 2004 *J Neuroimm.* **148**:106-115; Woods *et al.*, 2003 *Brain Behav. Imm.* **17**: 384-392; Mars *et al.*, 1998 *Biochem Biophys. Res. Comm.* **249**: 366-370; Bierhaus *et al.*, 2003 *Proc. Natl. Acad. Sci (USA)* **100**(4):1920-1925; Horohov *et al.*, 1996 *Vet Immunol. Immunopath.* **53**:221-233). Stress acts on the immune system mainly through the sympathetic nervous system and HPA axis causing the release of catecholamines, corticotrophin and cortisol (an example of a steroid). These molecules have known immunomodulatory effects but their mechanism of action is not fully understood. For example, glucocorticoids (steroids) such as cortisol bind to steroid receptors on the outside of cells and are then transported directly to the cell nucleus. Once inside the nucleus, steroid hormones can modulate gene expression, and hence immune function, through steroid responsive elements upstream of gene coding regions (Geng and Vedeckis, 2004 *Mol. Endocrinol.* **18**(4):912-924). For the purposes of its effects on the immune system, stress can be classified into acute (once over a period of less than say two days) and chronic forms (persistent stress over a period of several days or months). Acute stress has been demonstrated to enhance the immune system by redistributing white blood cells from blood to various body compartments such as the skin, lymph nodes and bone marrow (Dhabhar *et al.*, 1995 *J. Immunol.* **154**:5511-5527) the effect of which is partly due to release of endogenous glucocorticoids. The affect of acute stress has been reported to last for 3-5 days (Dhabhar *et al.*, 1996 *J Immunol.* **157**:1638-1644.). On the other hand, chronic stress elicits the HPA axis and the autonomic nervous system and reduces cellular immune responses and increases susceptibility to disease (McEwen *et al.*, 1997 *Brain Res. Rev.* **23**:79-113; Cohen *et al.*, 1992 *Psychol. Sci.* **3**:301-304; Cohen *et al.*, 1993 *JAMA*, **277**:1940-1944; Peijie *et al.*, 2003 *Life Sciences* **72**:2255-2262).

[0019] In summary, there is a need for better modalities for measuring and monitoring the effects of allostatic load on the function of the immune system.

SUMMARY OF THE INVENTION

[0020] The present invention represents a significant advance over current technologies for quantifying allostatic load and for measuring and monitoring immune function. It is predicated in part on measuring the level of certain functional markers in cells, especially circulating leukocytes, of the host. More particularly, the present invention relates to molecules and assays, which are useful in screening and monitoring animals for the presence or risk of developing disease or illness through immune system dysfunction as a result of stress, in determining the ability of an animal to cope with, or adapt to, external stressors, and in monitoring immune function when administering immune-modulating drugs. The invention has practical use in monitoring animals under stress, especially those in athletic training, in measuring the effects of aging on the ability to respond to external stressors, and in enabling better treatment and management decisions to be made in animals at risk of exposure to disease, or susceptible to disease through the effects of stress. In certain embodiments, the invention has practical applications in measuring the response to vaccination or immune-modifying therapies, for example, in animals under stress, which may not develop an appropriate protective response to vaccination or therapy. In other embodiments, the invention has practical use in monitoring the immune response to natural disease when an animal is subject to stressful conditions or at risk due to inappropriate response to stress. This represents a significant and unexpected advance in the screening, monitoring and management of animals under stress.

[0021] Thus, the present invention addresses the problem of detecting the presence, absence or degree of a physiological stress response or of assessing well being including the function of the immune system by detecting, for example, a differential gene expression pattern that may be measured in host cells. Advantageous embodiments involve monitoring the expression of certain genes in peripheral leukocytes of the immune system, which may be reflected in changing patterns of RNA levels or protein production that correlate with allostatic stress load or with an immune-modulating event.

[0022] Accordingly, in one aspect, the present invention provides methods for determining the presence or degree of a physiological response to stress or a related condition in a test subject. These methods generally comprise detecting in the subject aberrant expression of at least one gene (also referred to herein as a "stress marker gene") selected from the group consisting of: (a) a gene comprising a nucleotide sequence that shares at least 50% (and at least 51% to at least 99% and all integer percentages in between) sequence identity with the sequence set forth in any one of SEQ ID NO: 1, 3, 4, 5, 7, 9, 11, 13, 15, 16, 17, 19, 21, 23, 24, 25, 26, 28, 29, 30, 32, 33, 34, 35, 37, 38, 39, 40, 41, 42, 44, 46, 48, 50, 51, 52, 54, 55, 56, 57, 59, 62, 63, 64, 66, 68, 70, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 90, 91, 92, 93, 95, 96, 97, 99, 101, 103, 105, 107, 108, 109, 111, 113, 115, 117, 118, 119, 121, 123, 125, 126, 127, 129, 130, 131, 133,

135, 137, 139, 141, 143, 144, 145, 147, 148, 150, 151, 153, 155, 156, 158, 160, 161, 163, 164, 165, 167, 169, 170, 171, 173, 175, 176, 178, 180, 182, 184, 185, 186, 187, 188, 190, 192, 194, 195, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 233, 234, 236, 238, 239, 240, 241, 242, 243, 244, 246 or 248, or a complement thereof; (b) a gene comprising a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in any one of SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249; (c) a gene comprising a nucleotide sequence that encodes a polypeptide that shares at least 50% (and at least 51% to at least 99% and all integer percentages in between) sequence similarity with at least a portion of the sequence set forth in SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249, wherein the portion comprises at least 15 contiguous amino acid residues of that sequence; and (d) a gene comprising a nucleotide sequence that hybridizes to the sequence of (a), (b), (c) or a complement thereof, under at least low, medium or high stringency conditions. In accordance with the present invention, these stress marker genes are aberrantly expressed in animals with a physiological response to stress or with an allostatic load. Suitably, the related condition is immunodepression.

[0023] Suitably, the presence of the physiological response to stress or related condition is associated with psychological stress or physical stress (e.g., physical duress such as athletic training and physical trauma). Illustrative psychological conditions include depression, generalized anxiety disorder, post traumatic stress disorder, panic, chronic fatigue, myalgic encephalopathy, stress through restraint, sleep deprivation, overeating and behavioral (operant) conditioning. Other psychological conditions, especially relating to veterinary applications, include, but are not limited to, stress related to confinement, sheering, shipping or human-animal interaction. Illustrative examples of physical stress include physical duress such as athletic training and physical trauma.

[0024] As used herein, polynucleotide expression products of stress marker genes are referred to as "stress marker polynucleotides." Polypeptide expression products of the stress marker genes are referred to herein as "stress marker polypeptides."

[0025] Thus, in some embodiments, the methods comprise detecting aberrant expression of a stress marker polynucleotide selected from the group consisting of (a) a polynucleotide comprising a nucleotide sequence that shares at least 50% (and at least 51% to at least 99% and all integer percentages in between) sequence identity with the sequence set forth in any one of SEQ ID NO: 1, 3, 4, 5, 7, 9, 11, 13, 15, 16, 17, 19, 21, 23, 24, 25, 26, 28, 29, 30, 32, 33, 34, 35, 37, 38, 39, 40, 41, 42, 44, 46, 48, 50, 51, 52, 54, 55, 56, 57, 59, 62, 63, 64, 66, 68, 70, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 90, 91, 92, 93, 95, 96, 97, 99, 101, 103, 105, 107, 108, 109, 111, 113, 115, 117, 118, 119, 121, 123, 125, 126, 127, 129, 130, 131, 133, 135, 137, 139, 141, 143, 144, 145, 147, 148, 150, 151, 153, 155, 156, 158, 160, 161, 163, 164, 165, 167, 169, 170, 171, 173, 175, 176, 178, 180, 182, 184, 185, 186, 187, 188, 190, 192, 194, 195, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 233, 234, 236, 238, 239, 240, 241, 242, 243, 244, 246 or 248, or a complement thereof; (b) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in any one of SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249; (c) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide that shares at least 50% (and at least 51% to at least 99% and all integer percentages in between) sequence similarity with at least a portion of the sequence set forth in SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249, wherein the portion comprises at least 15 contiguous amino acid residues of that sequence; and (d) a polynucleotide comprising a nucleotide sequence that hybridizes to the sequence of (a), (b), (c) or a complement thereof, under at least low stringency conditions.

[0026] In other embodiments, the methods comprise detecting aberrant expression of a stress marker polypeptide selected from the group consisting of: (i) a polypeptide comprising an amino acid sequence that shares at least 50% (and at least 51% to at least 99% and all integer percentages in between) sequence similarity with the sequence set forth in any one of SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249; (ii) a polypeptide comprising a

portion of the sequence set forth in any one of SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249, wherein the portion comprises at least 5 contiguous amino acid residues of that sequence; (iii) a polypeptide comprising an amino acid sequence that shares at least 30% (and at least 31% to at least 99% and all integer percentages in between) similarity with at least 15 contiguous amino acid residues of the sequence set forth in any one of SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249; and (iv) a polypeptide comprising a portion of the sequence set forth in any one of SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249, wherein the portion comprises at least 5 contiguous amino acid residues of that sequence and is immuno-interactive with an antigen-binding molecule that is immuno-interactive with a sequence of (i), (ii) or (iii).

[0027] Typically, aberrant expression of a stress marker gene is detected by: (1) measuring in a biological sample obtained from the subject the level or functional activity of an expression product of at least one stress marker gene and (2) comparing the measured level or functional activity of each expression product to the level or functional activity of a corresponding expression product in a reference sample obtained from one or more normal subjects or from one or more subjects not under stress, wherein a difference in the level or functional activity of the expression product in the biological sample as compared to the level or functional activity of the corresponding expression product in the reference sample is indicative of the presence of a physiological response to stress. In some embodiments, the method further comprises determining the degree of stress response (or stress level) or the degree of immunomodulation when the measured level or functional activity of the or each expression product is different than the measured level or functional activity of the or each corresponding expression product. In these embodiments, the difference typically represents an at least about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80% or 90%, or even an at least about 100%, 200%, 300%, 400%, 500%, 600%, 700%, 800%, 900% or 1000% increase, or an at least about 10%, 20%, 30% 40%, 50%, 60%, 70%, 80%, 90%, 92%, 94%, 96%, 97%, 98% or 99%, or even an at

least about 99.5%, 99.9%, 99.95%, 99.99%, 99.995% or 99.999% decrease in the level or functional activity of an individual expression product as compared to the level or function activity of an individual corresponding expression product. , which is hereafter referred to as "aberrant expression." In illustrative examples of this type, the presence of a physiological response to stress is determined by detecting a decrease in the level or functional activity of at least one stress marker polynucleotide selected from (a) a polynucleotide comprising a nucleotide sequence that shares at least 50% (and at least 51% to at least 99% and all integer percentages in between) sequence identity with the sequence set forth in any one of SEQ ID NO: 1, 3, 4, 7, 9, 11, 19, 21, 24, 25, 33, 34, 38, 39, 40, 41, 42, 50, 51, 56, 57, 59, 62, 63, 66, 70, 71, 73, 75, 79, 81, 83, 89, 90, 91, 92, 93, 97, 99, 105, 107, 108, 111, 119, 121, 122, 123, 129, 130, 137, 139, 140, 141, 142, 143 or 185, or a complement thereof; (b) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in any one of SEQ ID NO: 2, 8, 10, 12, 20, 22, 43, 58, 60, 67, 71, 72, 74, 76, 80, 82, 84, 94, 98, 100, 106, 112, 120, 122, 123, 124 or 138; (c) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide that shares at least 50% (and at least 51% to at least 99% and all integer percentages in between) sequence similarity with at least a portion of the sequence set forth in SEQ ID NO: 2, 8, 10, 12, 20, 22, 43, 58, 60, 67, 71, 72, 74, 76, 80, 82, 84, 94, 98, 100, 106, 112, 120, 122, 123, 124 or 138, wherein the portion comprises at least 15 contiguous amino acid residues of that sequence; and (d) a polynucleotide comprising a nucleotide sequence that hybridizes to the sequence of (a), (b), (c) or a complement thereof, under at least low, medium, or high stringency conditions.

[0028] In other illustrative examples, the presence of a physiological response to stress is determined by detecting an increase in the level or functional activity of at least one stress marker polynucleotide selected from (a) a polynucleotide comprising a nucleotide sequence that shares at least 50% (and at least 51% to at least 99% and all integer percentages in between) sequence identity with the sequence set forth in any one of SEQ ID NO: 5, 13, 15, 16, 17, 23, 26, 28, 29, 30, 32, 35, 37, 44, 46, 48, 52, 54, 55, 64, 68, 77, 85, 87, 95, 96, 101, 103, 113, 115, 117, 118, 125, 126, 131, 133, 135, 144, 145, 147, 148, 150, 151, 153, 155, 156, 158, 160, 161, 163, 164, 165, 167, 169, 170, 171, 173, 175, 176, 178, 180, 182, 183, 184, 186, 187, 188, 190, 192, 194, 195, 196, 198, 200, 202, 204, 206 or 210, or a complement thereof; (b) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in any one of SEQ ID NO: 6, 14, 18, 27, 31, 36, 45, 47, 49, 53, 65, 69, 78, 86, 88, 102, 104, 114, 116, 132, 134, 136, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 189, 191, 193, 197, 199, 201, 203, 205, 207 or 211; (c) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide that shares at least 50% (and at least 51% to at least 99% and all integer percentages in between) sequence similarity with at least a portion of the sequence set forth in SEQ ID NO: 6, 14, 18, 27, 31, 36,

45, 47, 49, 53, 65, 69, 78, 86, 88, 102, 104, 114, 116, 132, 134, 136, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 189, 191, 193, 197, 199, 201, 203, 205, 207 or 211, wherein the portion comprises at least 15 contiguous amino acid residues of that sequence; and (d) a polynucleotide comprising a nucleotide sequence that hybridizes to the sequence of (a), (b), (c) or a complement thereof, under at least low, medium, or high stringency conditions.

[0029] In some embodiments, the method further comprises determining the absence of a physiological response to stress when the measured level or functional activity of the or each expression product is the same as or similar to the measured level or functional activity of the or each corresponding expression product. In these embodiments, the measured level or functional activity of an individual expression product varies from the measured level or functional activity of an individual corresponding expression product by no more than about 20%, 18%, 16%, 14%, 12%, 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1% or 0.1%, which is hereafter referred to as "normal expression."

[0030] In some embodiments, the methods comprise measuring the level or functional activity of individual expression products of at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44 or 45 stress marker genes. For example, the methods may comprise measuring the level or functional activity of a stress marker polynucleotide either alone or in combination with as much as 44, 43, 42, 41, 40, 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 other stress marker polynucleotide(s). In another example, the methods may comprise measuring the level or functional activity of a stress marker polypeptide either alone or in combination with as much as 44, 43, 42, 41, 40, 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 other stress marker polypeptides(s). In illustrative examples of this type, the methods comprise measuring the level or functional activity of individual expression products of at least 1, 2, 3, 4, 5 or 6 stress marker genes that have a very high correlation with the presence or risk of a physiological response to stress (hereafter referred to as "level one correlation stress marker genes"), representative examples of which include, but are not limited to, (a) a polynucleotide comprising a nucleotide sequence that shares at least 50% (and at least 51% to at least 99% and all integer percentages in between) sequence identity with the sequence set forth in any one of SEQ ID NO: 89, 90, 103, 125, 126, 163, 178, 182, 184 or 190, or a complement thereof; (b) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in any one of SEQ ID NO: 104, 179, 183 or 189; (c) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide that shares at least 50% (and at least 51% to at least 99% and all integer percentages in between) sequence similarity with at least a portion of the sequence set forth in SEQ ID NO: 104, 179, 183 or 189,

wherein the portion comprises at least 15 contiguous amino acid residues of that sequence; and (d) a polynucleotide comprising a nucleotide sequence that hybridizes to the sequence of (a), (b), (c) or a complement thereof, under at least low, medium, or high stringency conditions.

[0031] In other illustrative examples, the methods comprise measuring the level or functional activity of individual expression products of at least 1, 2, 3, 4, 5, 6, 7 or 8 stress marker genes that have a high correlation with the presence or risk of a physiological response to stress (hereafter referred to as "level two correlation stress marker genes"), representative examples of which include, but are not limited to, (a) a polynucleotide comprising a nucleotide sequence that shares at least 50% (and at least 51% to at least 99% and all integer percentages in between) sequence identity with the sequence set forth in any one of SEQ ID NO: 17, 23, 44, 52, 133, 135, 144, 147, 148, 151, 155, 192, 196, 202 or 206, or a complement thereof; (b) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in any one of SEQ ID NO: 18, 20, 45, 53, 134, 136, 149, 152, 193, 197 or 207; (c) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide that shares at least 50% (and at least 51% to at least 99% and all integer percentages in between) sequence similarity with at least a portion of the sequence set forth in SEQ ID NO: 18, 20, 45, 53, 134, 136, 149, 152, 193, 197 or 207, wherein the portion comprises at least 15 contiguous amino acid residues of that sequence; and (d) a polynucleotide comprising a nucleotide sequence that hybridizes to the sequence of (a), (b), (c) or a complement thereof, under at least low, medium, or high stringency conditions.

[0032] In still other illustrative examples, the methods comprise measuring the level or functional activity of individual expression products of at least 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 stress marker genes that have a medium correlation with the presence or risk of a physiological response to stress (hereafter referred to as "level three correlation stress marker genes"), representative examples of which include, but are not limited to, (a) a polynucleotide comprising a nucleotide sequence that shares at least 50% (and at least 51% to at least 99% and all integer percentages in between) sequence identity with the sequence set forth in any one of SEQ ID NO: 5, 30, 37, 48, 54, 55, 64, 66, 70, 77, 79, 85, 91, 92, 95, 96, 101, 115, 117, 118, 121, 150, 153, 158, 164, 170, 180, 186 or198, or a complement thereof; (b) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in any one of SEQ ID NO: 6, 31, 49, 65, 67, 78, 80, 86, 102, 116, 122, 154, 159, 181 or 199; (c) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide that shares at least 50% (and at least 51% to at least 99% and all integer percentages in between) sequence similarity with at least a portion of the sequence set forth in SEQ ID NO: 6, 31, 49, 65, 67, 78, 80, 86, 102, 116, 122, 154, 159, 181 or 199, wherein the portion comprises at least 15 contiguous amino acid residues of that sequence; and (d) a polynucleotide

comprising a nucleotide sequence that hybridizes to the sequence of (a), (b), (c) or a complement thereof, under at least low, medium, or high stringency conditions.

[0033] In still other illustrative examples, the methods comprise measuring the level or functional activity of individual expression products of at least 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 stress marker genes that have a moderate correlation with the presence or risk of a physiological response to stress (hereafter referred to as "level four correlation stress marker genes"), representative examples of which include, but are not limited to, (a) a polynucleotide comprising a nucleotide sequence that shares at least 50% (and at least 51% to at least 99% and all integer percentages in between) sequence identity with the sequence set forth in any one of SEQ ID NO: 7, 15, 16, 19, 21, 24, 25, 26, 28, 35, 38, 39, 42, 46, 57, 68, 73, 81, 83, 97, 99, 107, 113, 123, 160, 165, 175, 187, 188, 194, 195 or 200, or a complement thereof; (b) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in any one of SEQ ID NO: 20, 22, 27, 29, 36, 42, 43, 58, 69, 74, 82, 84, 98, 100, 108, 114, 124, 166, 189 or 201; (c) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide that shares at least 50% (and at least 51% to at least 99% and all integer percentages in between) sequence similarity with at least a portion of the sequence set forth in SEQ ID NO: 20, 22, 27, 29, 36, 42, 43, 58, 69, 74, 82, 84, 98, 100, 108, 114, 124, 166, 189 or 201, wherein the portion comprises at least 15 contiguous amino acid residues of that sequence; and (d) a polynucleotide comprising a nucleotide sequence that hybridizes to the sequence of (a), (b), (c) or a complement thereof, under at least low, medium, or high stringency conditions.

[0034] In still other illustrative examples, the methods comprise measuring the level or functional activity of individual expression products of at least 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 stress marker genes that have a lower correlation with the presence or risk of a physiological response to stress (hereafter referred to as "level five correlation stress marker genes"), representative examples of which include, but are not limited to, (a) a polynucleotide comprising a nucleotide sequence that shares at least 50% (and at least 51% to at least 99% and all integer percentages in between) sequence identity with the sequence set forth in any one of SEQ ID NO: 1, 3, 9, 11, 13, 32, 33, 34, 40, 41, 50, 51, 56, 59, 62, 63, 71, 75, 87, 93, 105, 111, 119, 127, 129, 130, 131, 137, 139, 141, 143, 145, 156, 161, 167, 169, 171, 173, 176, 185, 204 or 210, or a complement thereof; (b) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in any one of SEQ ID NO: 2, 4, 12, 14, 60, 61, 72, 76, 88, 94, 106, 112, 120, 128, 132, 138, 140, 142, 146, 157, 162, 168, 172, 174, 177, 205 or 211; (c) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide that shares at least 50% (and at least 51% to at least 99% and all integer percentages in between) sequence similarity with at least a portion of the sequence set forth in SEQ ID NO: 2, 4, 12, 14, 60, 61, 72, 76, 88, 94, 106, 112, 120, 128, 132, 138, 140, 142, 146, 157, 162, 168,

172, 174, 177, 205 or 211, wherein the portion comprises at least 15 contiguous amino acid residues of that sequence; and (d) a polynucleotide comprising a nucleotide sequence that hybridizes to the sequence of (a), (b), (c) or a complement thereof, under at least low, medium, or high stringency conditions.

[0035] In some embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level one correlation stress marker gene. In other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 2 level one correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level one correlation stress marker gene and the level or functional activity of an expression product of at least 1 level two stress marker gene. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 2 level one correlation stress marker genes and the level or functional activity of an expression product of at least 1 level two correlation stress marker gene. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level one correlation stress marker gene and the level or functional activity of an expression product of at least 2 level two correlation stress marker genes.

[0036] In some embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level one correlation stress marker gene and the level or functional activity of an expression product of at least 1 level three correlation stress marker gene. In other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 2 level one correlation stress marker genes and the level or functional activity of an expression product of at least 1 level three correlation stress marker gene. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level one correlation stress marker gene and the level or functional activity of an expression product of at least 2 level three correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level one correlation stress marker gene and the level or functional activity of an expression product of at least 3 level three correlation stress marker genes.

[0037] In some embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level one correlation stress marker gene and the level or functional activity of an expression product of at least 1 level four correlation stress marker gene. In other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 2 level one correlation stress marker genes and the level or functional activity of an expression product of at least 1 level four

correlation stress marker gene. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level one correlation stress marker gene and the level or functional activity of an expression product of at least 2 level four correlation stress marker gene. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level one correlation stress marker gene and the level or functional activity of an expression product of at least 3 level four correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level one correlation stress marker gene and the level or functional activity of an expression product of at least 4 level four correlation stress marker genes.

[0038] In some embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level one correlation stress marker gene and the level or functional activity of an expression product of at least 1 level five correlation stress marker gene. In other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 2 level one correlation stress marker genes and the level or functional activity of an expression product of at least 1 level five correlation stress marker gene. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level one correlation stress marker gene and the level or functional activity of an expression product of at least 2 level five correlation stress marker gene. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level one correlation stress marker gene and the level or functional activity of an expression product of at least 3 level five correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level one correlation stress marker gene and the level or functional activity of an expression product of at least 4 level five correlation stress marker genes.

[0039] In some embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level two correlation stress marker gene. In other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 2 level two correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level two correlation stress marker gene and the level or functional activity of an expression product of at least 1 level three correlation stress marker gene. In other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 2 level two correlation stress marker genes and the level or functional activity of an expression product of at least 1 level three correlation stress marker gene. In still other embodiments, the methods comprise measuring the level or functional activity of an expression

product of at least 1 level two correlation stress marker gene and the level or functional activity of an expression product of at least 2 level three correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level two correlation stress marker gene and the level or functional activity of an expression product of at least 3 level three correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level two correlation stress marker gene and the level or functional activity of an expression product of at least 4 level three correlation stress marker genes.

[0040] In some embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level two correlation stress marker gene and the level or functional activity of an expression product of at least 1 level four correlation stress marker gene. In other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 2 level two correlation stress marker genes and the level or functional activity of an expression product of at least 1 level four correlation stress marker gene. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level two correlation stress marker gene and the level or functional activity of an expression product of at least 2 level four correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level two correlation stress marker gene and the level or functional activity of an expression product of at least 3 level four correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level two correlation stress marker gene and the level or functional activity of an expression product of at least 4 level four correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level two correlation stress marker gene and the level or functional activity of an expression product of at least 5 level four correlation stress marker genes.

[0041] In some embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level two correlation stress marker gene. In other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 2 level two correlation stress marker gene. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level two correlation stress marker gene and the level or functional activity of an expression product of at least 1 level five correlation stress marker gene. In other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 2 level two correlation stress marker genes and the level or functional activity of an expression product of at least 1 level five correlation stress marker gene. In still other

embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level two correlation stress marker gene and the level or functional activity of an expression product of at least 2 level five correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level two correlation stress marker gene and the level or functional activity of an expression product of at least 3 level five correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level two correlation stress marker gene and the level or functional activity of an expression product of at least 4 level five correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level two correlation stress marker gene and the level or functional activity of an expression product of at least 5 level five correlation stress marker genes.

[0042] In some embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level three correlation stress marker gene. In other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 2 level three correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level three correlation stress marker gene and the level or functional activity of an expression product of at least 1 level four correlation stress marker gene. In other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 2 level three correlation stress marker genes and the level or functional activity of an expression product of at least 1 level four correlation stress marker gene. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level three correlation stress marker gene and the level or functional activity of an expression product of at least 2 level four correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level three correlation stress marker gene and the level or functional activity of an expression product of at least 3 level four correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level three correlation stress marker gene and the level or functional activity of an expression product of at least 4 level four correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level three correlation stress marker gene and the level or functional activity of an expression product of at least 5 level four correlation stress marker genes.

[0043] In some embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level three correlation stress marker

gene and the level or functional activity of an expression product of at least 1 level five correlation stress marker gene. In other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 2 level three correlation stress marker genes and the level or functional activity of an expression product of at least 1 level five correlation stress marker gene. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level three correlation stress marker gene and the level or functional activity of an expression product of at least 2 level five correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level three correlation stress marker gene and the level or functional activity of an expression product of at least 3 level five correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level three correlation stress marker gene and the level or functional activity of an expression product of at least 4 level five correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level three correlation stress marker gene and the level or functional activity of an expression product of at least 5 level five correlation stress marker genes.

[0044] In some embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level four correlation stress marker gene. In other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 2 level four correlation stress marker genes. In other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 3 level four correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 3 level four correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 4 level four correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 5 level four correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 6 level four correlation stress marker genes.

[0045] In some embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level four correlation stress marker gene and the level or functional activity of an expression product of at least 1 level five correlation stress marker gene. In other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 2 level four correlation stress marker genes and the level or functional activity of an expression product of at least 1 level five

correlation stress marker gene. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level four correlation stress marker gene and the level or functional activity of an expression product of at least 2 level five correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level four correlation stress marker gene and the level or functional activity of an expression product of at least 3 level five correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level four correlation stress marker gene and the level or functional activity of an expression product of at least 4 level five correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level four correlation stress marker gene and the level or functional activity of an expression product of at least 5 level five correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level four correlation stress marker gene and the level or functional activity of an expression product of at least 6 level five correlation stress marker genes.

[0046] In some embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level five correlation stress marker gene. In other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 2 level five correlation stress marker genes. In other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 3 level five correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 3 level five correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 4 level five correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 5 level five correlation stress marker genes. In still other embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 6 level five correlation stress marker genes.

[0047] Advantageously, the biological sample comprises blood, especially peripheral blood, which typically includes leukocytes. Suitably, the expression product is selected from a RNA molecule or a polypeptide. In some embodiments, the expression product is the same as the corresponding expression product. In other embodiments, the expression product is a variant (e.g., an allelic variant) of the corresponding expression product.

[0048] In certain embodiments, the expression product or corresponding expression product is a target RNA (e.g., mRNA) or a DNA copy of the target RNA whose level is measured using at least one nucleic acid probe that hybridises under at least low stringency conditions to the target RNA or to the DNA copy, wherein the nucleic acid probe comprises at least 15 contiguous nucleotides of a stress marker gene. In these embodiments, the measured level or abundance of the target RNA or its DNA copy is normalised to the level or abundance of a reference RNA or a DNA copy of the reference RNA that is present in the same sample. Suitably, the nucleic acid probe is immobilized on a solid or semi-solid support. In illustrative examples of this type, the nucleic acid probe forms part of a spatial array of nucleic acid probes. In some embodiments, the level of nucleic acid probe that is bound to the target RNA or to the DNA copy is measured by hybridization (e.g., using a nucleic acid array). In other embodiments, the level of nucleic acid probe that is bound to the target RNA or to the DNA copy is measured by nucleic acid amplification (e.g., using a polymerase chain reaction (PCR)). In still other embodiments, the level of nucleic acid probe that is bound to the target RNA or to the DNA copy is measured by nuclease protection assay.

[0049] In other embodiments, the expression product or corresponding expression product is a target polypeptide whose level is measured using at least one antigen-binding molecule that is immuno-interactive with the target polypeptide. In these embodiments, the measured level of the target polypeptide is normalized to the level of a reference polypeptide that is present in the same sample. Suitably, the antigen-binding molecule is immobilized on a solid or semi-solid support. In illustrative examples of this type, the antigen-binding molecule forms part of a spatial array of antigen-binding molecule. In some embodiments, the level of antigen-binding molecule that is bound to the target polypeptide is measured by immunoassay (e.g., using an ELISA).

[0050] In still other embodiments, the expression product or corresponding expression product is a target polypeptide whose level is measured using at least one substrate for the target polypeptide with which it reacts to produce a reaction product. In these embodiments, the measured functional activity of the target polypeptide is normalized to the functional activity of a reference polypeptide that is present in the same sample.

[0051] In some embodiments, a system is used to perform the method, which suitably comprises at least one end station coupled to a base station. The base station is suitably caused (a) to receive subject data from the end station *via* a communications network, wherein the subject data represents parameter values corresponding to the measured or normalized level or functional activity of at least one expression product in the biological sample, and (b) to compare the subject data with predetermined data representing the measured or normalized level or functional activity of at least one corresponding expression product in the reference sample to

thereby determine any difference in the level or functional activity of the expression product in the biological sample as compared to the level or functional activity of the corresponding expression product in the reference sample. Desirably, the base station is further caused to provide a diagnosis for the presence, absence, degree, or risk of development, of a stress response. In these embodiments, the base station may be further caused to transfer an indication of the diagnosis to the end station *via* the communications network.

[0052] In another aspect, the invention provides methods for determining the presence or degree of immunosuppression in a test subject. These methods generally comprise detecting in the subject aberrant expression of at least one stress marker gene as broadly described above.

[0053] In yet another aspect, the present invention provides methods for treating or preventing the development of stress or a related condition in a test subject. These methods generally comprise detecting aberrant expression of at least one stress marker gene in the subject, and managing the environment of the subject to prevent or minimize exposure of the subject to a causative stressor and/or administering to the subject an effective amount of an agent that treats or ameliorates the symptoms or reverses or inhibits the development of stress in the subject. In certain embodiments, the related condition is immunosuppression.

[0054] Accordingly, in a related aspect, the present invention provides methods for treating or preventing the development of immunosuppression in a test subject. These methods generally comprise detecting aberrant expression of at least one stress marker gene in the subject, and managing the environment of the subject to prevent or minimize exposure of the subject to a causative stressor and/or administering to the subject an effective amount of an agent that treats or ameliorates the symptoms or reverses or inhibits the development of stress in the subject.

[0055] In still another aspect, the present invention provides methods for assessing the capacity of a subject's immune system to produce an immunogenic response to a selected antigen. These methods generally comprise determining whether at least one stress marker gene as broadly described above is normally or aberrantly expressed in the subject, whereby normal expression of the or each stress marker gene is indicative of a normal capacity to produce the immunogenic response and whereby aberrant expression of the or each stress marker gene is indicative of an impaired capacity to produce the immunogenic response.

[0056] In a further aspect, the present invention provides methods for eliciting an immune response to a selected antigen in a test subject *via* administration of a composition comprising the antigen. These methods generally comprise detecting normal expression of at least one stress marker gene as broadly described above in the subject and administering the composition to the subject.

[0057] In some embodiments, the methods further comprise detecting in the subject aberrant expression of at least one stress marker gene as broadly described above and managing the environment of the subject to prevent or minimize exposure of the subject to a causative stressor and/or administering to the subject an effective amount of an agent that reverses or inhibits the development of stress in the subject, and administering the composition to the subject. In some embodiments, the composition is administered to the subject when the or each stress marker gene is normally expressed in the subject.

[0058] In a related aspect, the invention provides methods for improving an immune response to a selected antigen in a test subject to whom/which has been administered a composition comprising the antigen. These methods generally comprise detecting aberrant expression of at least one stress marker gene as broadly described above in the subject and managing the environment of the subject to prevent or minimize exposure of the subject to a causative stressor and/or administering to the subject an effective amount of an agent that reverses or inhibits the development of stress in the subject, whereby the management or administration leads to normal expression of the or each stress marker gene in the subject.

[0059] In another aspect, the present invention provides isolated polynucleotides, referred to herein as "stress marker polynucleotides," which are generally selected from: (a) a polynucleotide comprising a nucleotide sequence that shares at least 50% (and at least 51% to at least 99% and all integer percentages in between) sequence identity with the sequence set forth in any one of SEQ ID NO: 15, 16, 23, 24, 25, 28, 29, 32, 33, 34, 37, 38, 39, 40, 41, 50, 51, 54, 55, 62, 63, 89, 90, 91, 92, 95, 96, 107, 108, 117, 118, 125, 126, 129, 130, 143, 144, 147, 150, 155, 163, 164, 169, 170, 175, 184, 185, 186, 187, 194, 195, 232, 233, 238, 239, 240, 241, 242 or 243, or a complement thereof; (b) a polynucleotide comprising a portion of the sequence set forth in any one of SEQ ID NO: 15, 16, 23, 24, 25, 28, 29, 32, 33, 34, 37, 38, 39, 40, 41, 50, 51, 54, 55, 62, 63, 89, 90, 91, 92, 95, 96, 107, 108, 117, 118, 125, 126, 129, 130, 143, 144, 147, 150, 155, 163, 164, 169, 170, 175, 184, 185, 186, 187, 194, 195, 232, 233, 238, 239, 240, 241, 242 or 243, or a complement thereof, wherein the portion comprises at least 15 contiguous nucleotides of that sequence or complement; (c) a polynucleotide that hybridizes to the sequence of (a) or (b) or a complement thereof, under at least low, medium or high stringency conditions; and (d) a polynucleotide comprising a portion of any one of SEQ ID NO: 15, 16, 23, 24, 25, 28, 29, 32, 33, 34, 37, 38, 39, 40, 41, 50, 51, 54, 55, 62, 63, 89, 90, 91, 92, 95, 96, 107, 108, 117, 118, 125, 126, 129, 130, 143, 144, 147, 150, 155, 163, 164, 169, 170, 175, 184, 185, 186, 187, 194, 195, 232, 233, 238, 239, 240, 241, 242 or 243, or a complement thereof, wherein the portion comprises at least 15 contiguous nucleotides of that sequence or complement and hybridizes to a sequence of (a), (b) or (c), or a complement thereof, under at least low, medium or high stringency conditions.

[0060] In another aspect, the present invention provides a nucleic acid construct comprising a polynucleotide as broadly described above in operable connection with a regulatory element, which is operable in a host cell. In certain embodiments, the construct is in the form of a vector, especially an expression vector.

[0061] In yet another aspect, the present invention provides isolated host cells containing a nucleic acid construct or vector as broadly described above. In certain advantageous embodiments, the host cells are selected from bacterial cells, yeast cells and insect cells.

[0062] In still another aspect, the present invention provides probes for interrogating nucleic acid for the presence of a polynucleotide as broadly described above. These probes generally comprise a nucleotide sequence that hybridizes under at least low stringency conditions to a polynucleotide as broadly described above. In some embodiments, the probes consist essentially of a nucleic acid sequence which corresponds or is complementary to at least a portion of a nucleotide sequence encoding the amino acid sequence set forth in any one of SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249, wherein the portion is at least 15 nucleotides in length. In other embodiments, the probes comprise a nucleotide sequence which is capable of hybridizing to at least a portion of a nucleotide sequence encoding the amino acid sequence set forth in any one of SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249 under at least low stringency conditions, wherein the portion is at least 15 nucleotides in length. In still other embodiment, the probes comprise a nucleotide sequence that is capable of hybridizing to at least a portion of any one of SEQ ID NO: 1, 3, 4, 5, 7, 9, 11, 13, 15, 16, 17, 19, 21, 23, 24, 25, 26, 28, 29, 30, 32, 33, 34, 35, 37, 38, 39, 40, 41, 42, 44, 46, 48, 50, 51, 52, 54, 55, 56, 57, 59, 62, 63, 64, 66, 68, 70, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 90, 91, 92, 93, 95, 96, 97, 99, 101, 103, 105, 107, 108, 109, 111, 113, 115, 117, 118, 119, 121, 123, 125, 126, 127, 129, 130, 131, 133, 135, 137, 139, 141, 143, 144, 145, 147, 148, 150, 151, 153, 155, 156, 158, 160, 161, 163, 164, 165, 167, 169, 170, 171, 173, 175, 176, 178, 180, 182, 184, 185, 186, 187, 188, 190, 192, 194, 195, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 233, 234, 236, 238, 239, 240, 241, 242, 243, 244, 246 or 248 under at least low stringency conditions, wherein the portion is at least 15 nucleotides in length. Representative

probes for detecting the stress marker polynucleotides according to the resent invention are set forth in SEQ ID NO: 250-1807 (see Table 2).

[0063] In a related aspect, the invention provides a solid or semi-solid support comprising at least one nucleic acid probe as broadly described above immobilized thereon. In some embodiments, the solid or semi-solid support comprises a spatial array of nucleic acid probes immobilized thereon.

[0064] In a further aspect, the present invention provides isolated polypeptides, referred to herein as "stress marker polypeptides," which are generally selected from: (i) a polypeptide comprising an amino acid sequence that shares at least 50% (and at least 51% to at least 99% and all integer percentages in between) sequence similarity with a polypeptide expression product of a stress marker gene as broadly described above, for example, especially a stress marker gene that comprises a nucleotide sequence that shares at least 50% (and at least 51% to at least 99% and all integer percentages in between) sequence identity with the sequence set forth in any one of SEQ ID NO: 15, 16, 23, 24, 25, 28, 29, 32, 33, 34, 37, 38, 39, 40, 41, 50, 51, 54, 55, 62, 63, 89, 90, 91, 92, 95, 96, 107, 108, 117, 118, 125, 126, 129, 130, 143, 144, 147, 150, 155, 163, 164, 169, 170, 175, 184, 185, 186, 187, 194, 195, 232, 233, 238, 239, 240, 241, 242 or 243; (ii) a portion of the polypeptide according to (i) wherein the portion comprises at least 5 contiguous amino acid residues of that polypeptide; (iii) a polypeptide comprising an amino acid sequence that shares at least 30% similarity (and at least 31% to at least 99% and all integer percentages in between) with at least 15 contiguous amino acid residues of the polypeptide according to (i); and (iv) a polypeptide comprising an amino acid sequence that is immuno-interactive with an antigen-binding molecule that is immuno-interactive with a sequence of (i), (ii) or (iii).

[0065] Still a further aspect of the present invention provides an antigen-binding molecule that is immuno-interactive with a stress marker polypeptide as broadly described above.

[0066] In a related aspect, the invention provides a solid or semi-solid support comprising at least one antigen-binding molecule as broadly described above immobilized thereon. In some embodiments, the solid or semi-solid support comprises a spatial array of antigen-binding molecules immobilized thereon.

[0067] Still another aspect of the invention provides the use of one or more stress marker polynucleotides as broadly described above, or the use of one or more probes as broadly described above, or the use of one or more stress marker polypeptides as broadly described above, or the use of one or more antigen-binding molecules as broadly described above, in the manufacture of a kit for assessing the physiological response to stress or immune function in a subject.

BRIEF DESCRIPTION OF THE DRAWINGS

[0068] Figure 1 is a graphical representation of a receiver operating curve (ROC) for comparison of gene expression at 28 days after stressor to Day 0 (Day 0 is following 2 days of road transport). ROC curves are based on cross validated components discriminant function scores.

[0069] Figure 2 is a graphical representation of a receiver operating curve (ROC) for comparison of gene expression at 28 days after stressor to Day 2 (Day 0 is following 2 days of road transport). ROC curves are based on cross validated components discriminant function scores.

[0070] Figure 3 is a graphical representation of a receiver operating curve (ROC) for comparison of gene expression at 28 days after stressor to Day 4 (Day 0 is following 2 days of road transport). ROC curves are based on cross validated components discriminant function scores.

[0071] Figure 4 is a graphical representation of a receiver operating curve (ROC) for comparison of gene expression at 28 days after stressor to Day 7 (Day 0 is following 2 days of road transport). ROC curves are based on cross validated components discriminant function scores.

[0072] Figure 5 is a graphical representation of a receiver operating curve (ROC) for comparison of gene expression at 28 days after stressor to Day 9 (Day 0 is following 2 days of road transport). ROC curves are based on cross validated components discriminant function scores.

[0073] Figure 6 is a graphical representation of a receiver operating curve (ROC) for comparison of gene expression at 28 days after stressor to Day 11 (Day 0 is following 2 days of road transport). ROC curves are based on cross validated components discriminant function scores.

[0074] Figure 7 is a graphical representation of a receiver operating curve (ROC) for comparison of gene expression at 28 days after stressor to Day 14 (Day 0 is following 2 days of road transport). ROC curves are based on cross validated components discriminant function scores.

[0075] Figure 8 is a graphical representation of a receiver operating curve (ROC) for comparison of gene expression at 28 days after stressor to Day 17 (Day 0 is following 2 days of road transport). ROC curves are based on cross validated components discriminant function scores.

[0076] Figure 9 is a graphical representation of a receiver operating curve (ROC) for comparison of gene expression at 28 days after stressor to Day 21 (Day 0 is following 2 days of road transport). ROC curves are based on cross validated components discriminant function scores.

[0077] Figure 10 is a graphical representation of a receiver operating curve (ROC) for comparison of gene expression at 28 days after stressor to Day 24 (Day 0 is following 2 days of road transport). ROC curves are based on cross validated components discriminant function scores.

DETAILED DESCRIPTION OF THE INVENTION

1. Definitions

[0078] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by those of ordinary skill in the art to which the invention belongs. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, preferred methods and materials are described. For the purposes of the present invention, the following terms are defined below.

[0079] The articles "a" and "an" are used herein to refer to one or to more than one (i.e. to at least one) of the grammatical object of the article. By way of example, "an element" means one element or more than one element.

[0080] The term "aberrant expression," as used herein to describe the expression of a stress marker gene, refers to the overexpression or underexpression of a stress marker gene relative to the level of expression of the stress marker gene or variant thereof in cells obtained from a healthy subject or from a subject free of stress, and/or to a higher or lower level of a stress marker gene product (e.g., transcript or polypeptide) in a tissue sample or body fluid obtained from a healthy subject or from a subject not under stress. In particular, a stress marker gene is aberrantly expressed if the level of expression of the stress marker gene is higher by at least about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80% or 90%, or even an at least about 100%, 200%, 300%, 400%, 500%, 600%, 700%, 800%, 900% or 1000%, or lower by at least about 10%, 20%, 30% 40%, 50%, 60%, 70%, 80%, 90%, 92%, 94%, 96%, 97%, 98% or 99%, or even an at least about 99.5%, 99.9%, 99.95%, 99.99%, 99.995% or 99.999% that the level of expression of the stress marker gene by cells obtained from a healthy subject or from a subject not under stress, and/or relative to the level of expression of the stress marker gene in a tissue sample or body fluid obtained from a healthy subject or from a subject not under stress.

[0081] By "about" is meant a quantity, level, value, number, frequency, percentage, dimension, size, amount, weight or length that varies by as much as 30, 25, 20, 25, 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 % to a reference quantity, level, value, number, frequency, percentage, dimension, size, amount, weight or length.

[0082] The term "amplicon" refers to a target sequence for amplification, and/or the amplification products of a target sequence for amplification. In certain other embodiments an "amplicon" may include the sequence of probes or primers used in amplification.

[0083] By "antigen-binding molecule" is meant a molecule that has binding affinity for a target antigen. It will be understood that this term extends to immunoglobulins,

immunoglobulin fragments and non-immunoglobulin derived protein frameworks that exhibit antigen-binding activity.

[0084] As used herein, the term "binds specifically," "specifically immuno-interactive" and the like when referring to an antigen-binding molecule refers to a binding reaction which is determinative of the presence of an antigen in the presence of a heterogeneous population of proteins and other biologics. Thus, under designated immunoassay conditions, the specified antigen-binding molecules bind to a particular antigen and do not bind in a significant amount to other proteins or antigens present in the sample. Specific binding to an antigen under such conditions may require an antigen-binding molecule that is selected for its specificity for a particular antigen. For example, antigen-binding molecules can be raised to a selected protein antigen, which bind to that antigen but not to other proteins present in a sample. A variety of immunoassay formats may be used to select antigen-binding molecules specifically immuno-interactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select monoclonal antibodies specifically immuno-interactive with a protein. See Harlow and Lane (1988) "Antibodies, A Laboratory Manual," Cold Spring Harbor Publications, New York, for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity.

[0085] By "biologically active portion" is meant a portion of a full-length parent peptide or polypeptide which portion retains an activity of the parent molecule. As used herein, the term "biologically active portion" includes deletion mutants and peptides, for example of at least about 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 40, 50, 60, 70, 80, 90, 100, 120, 150, 300, 400, 500, 600, 700, 800, 900, 1000 contiguous amino acids, which comprise an activity of a parent molecule. Portions of this type may be obtained through the application of standard recombinant nucleic acid techniques or synthesized using conventional liquid or solid phase synthesis techniques. For example, reference may be made to solution synthesis or solid phase synthesis as described, for example, in Chapter 9 entitled "Peptide Synthesis" by Atherton and Shephard which is included in a publication entitled "Synthetic Vaccines" edited by Nicholson and published by Blackwell Scientific Publications. Alternatively, peptides can be produced by digestion of a peptide or polypeptide of the invention with proteinases such as endoLys-C, endoArg-C, endoGlu-C and staphylococcus V8-protease. The digested fragments can be purified by, for example, high performance liquid chromatographic (HPLC) techniques. Recombinant nucleic acid techniques can also be used to produce such portions.

[0086] The term "biological sample" as used herein refers to a sample that may be extracted, untreated, treated, diluted or concentrated from an animal. The biological sample may include a biological fluid such as whole blood, serum, plasma, saliva, urine, sweat, ascitic fluid,

peritoneal fluid, synovial fluid, amniotic fluid, cerebrospinal fluid, tissue biopsy, and the like. In certain embodiments, the biological sample is blood, especially peripheral blood.

[0087] As used herein, the term "*cis*-acting sequence", "*cis*-acting element" or "cis-regulatory region" or "regulatory region" or similar term shall be taken to mean any sequence of nucleotides, which when positioned appropriately relative to an expressible genetic sequence, is capable of regulating, at least in part, the expression of the genetic sequence. Those skilled in the art will be aware that a cis-regulatory region may be capable of activating, silencing, enhancing, repressing or otherwise altering the level of expression and/or cell-type-specificity and/or developmental specificity of a gene sequence at the transcriptional or post-transcriptional level. In certain embodiments of the present invention, the cis-acting sequence is an activator sequence that enhances or stimulates the expression of an expressible genetic sequence.

[0088] Throughout this specification, unless the context requires otherwise, the words "comprise," "comprises" and "comprising" will be understood to imply the inclusion of a stated step or element or group of steps or elements but not the exclusion of any other step or element or group of steps or elements.

[0089] By "corresponds to" or "corresponding to" is meant a polynucleotide (a) having a nucleotide sequence that is substantially identical or complementary to all or a portion of a reference polynucleotide sequence or (b) encoding an amino acid sequence identical to an amino acid sequence in a peptide or protein. This phrase also includes within its scope a peptide or polypeptide having an amino acid sequence that is substantially identical to a sequence of amino acids in a reference peptide or protein.

[0090] By "effective amount", in the context of treating or preventing a condition, is meant the administration of that amount of active to an individual in need of such treatment or prophylaxis, either in a single dose or as part of a series, that is effective for the prevention of incurring a symptom, holding in check such symptoms, and/or treating existing symptoms, of that condition. The effective amount will vary depending upon the health and physical condition of the individual to be treated, the taxonomic group of individual to be treated, the formulation of the composition, the assessment of the medical situation, and other relevant factors. It is expected that the amount will fall in a relatively broad range that can be determined through routine trials.

[0091] The terms "expression" or "gene expression" refer to either production of RNA message or translation of RNA message into proteins or polypeptides. Detection of either types of gene expression in use of any of the methods described herein are part of the invention.

[0092] By "expression vector" is meant any autonomous genetic element capable of directing the transcription of a polynucleotide contained within the vector and suitably the

synthesis of a peptide or polypeptide encoded by the polynucleotide. Such expression vectors are known to practitioners in the art.

[0093] The term "gene" as used herein refers to any and all discrete coding regions of the cell's genome, as well as associated non-coding and regulatory regions. The gene is also intended to mean the open reading frame encoding specific polypeptides, introns, and adjacent 5' and 3' non-coding nucleotide sequences involved in the regulation of expression. In this regard, the gene may further comprise control signals such as promoters, enhancers, termination and/or polyadenylation signals that are naturally associated with a given gene, or heterologous control signals. The DNA sequences may be cDNA or genomic DNA or a fragment thereof. The gene may be introduced into an appropriate vector for extrachromosomal maintenance or for integration into the host.

[0094] By "high density polynucleotide arrays" and the like is meant those arrays that contain at least 400 different features per cm^2.

[0095] The phrase "high discrimination hybridization conditions" refers to hybridization conditions in which single base mismatch may be determined.

[0096] "Hybridization" is used herein to denote the pairing of complementary nucleotide sequences to produce a DNA-DNA hybrid or a DNA-RNA hybrid. Complementary base sequences are those sequences that are related by the base-pairing rules. In DNA, A pairs with T and C pairs with G. In RNA U pairs with A and C pairs with G. In this regard, the terms "match" and "mismatch" as used herein refer to the hybridization potential of paired nucleotides in complementary nucleic acid strands. Matched nucleotides hybridize efficiently, such as the classical A-T and G-C base pair mentioned above. Mismatches are other combinations of nucleotides that do not hybridize efficiently.

[0097] The phrase "hybridizing specifically to" and the like refer to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent conditions when that sequence is present in a complex mixture (e.g., total cellular) DNA or RNA.

[0098] Reference herein to "immuno-interactive" includes reference to any interaction, reaction, or other form of association between molecules and in particular where one of the molecules is, or mimics, a component of the immune system.

[0099] "Immune function" or "immunoreactivity" refers to the ability of the immune system to respond to foreign antigen as measured by standard assays well known in the art.

[0100] The term "immunosuppression" refers to a decrease in the overall immunoreactivity of the immune system resulting from stress or the physiological response to

stress. Suitably, the decrease is by at least 20-40%, or by at least 50-75%, or even by at least 80% relative to the immunoreactivity in the absence of stress. Additionally, the term "immunosuppression" includes within its scope a delay in the occurrence of the immune response as compared to a subject not under stress. A delay in the occurrence of an immune response can be a short delay, for example 1 hr-10 days, i.e., 1 hr, 2, 5 or 10 days. A delay in the occurrence of an immune response can also be a long delay, for example, 10 days-10 years (i.e., 30 days, 60 days, 90 days, 180 days, 1, 2, 5 or 10 years). "Immunosuppression" according to the invention can also mean a decrease in the intensity of an immune response, e.g., a reduced intensity such that it is 5-100%, 25-100% or 75 -100% less than the intensity of the immune response of a subject not compromised by stress.

[0101] By "isolated" is meant material that is substantially or essentially free from components that normally accompany it in its native state. For example, an "isolated polynucleotide", as used herein, refers to a polynucleotide, which has been purified from the sequences which flank it in a naturally-occurring state, e.g., a DNA fragment which has been removed from the sequences that are normally adjacent to the fragment. Alternatively, an "isolated peptide" or an "isolated polypeptide" and the like, as used herein, refer to in vitro isolation and/or purification of a peptide or polypeptide molecule from its natural cellular environment, and from association with other components of the cell, i.e., it is not associated with in vivo substances.

[0102] By "marker gene" is meant a gene that imparts a distinct phenotype to cells expressing the marker gene and thus allows such transformed cells to be distinguished from cells that do not have the marker. A selectable marker gene confers a trait for which one can 'select' based on resistance to a selective agent (e.g., a herbicide, antibiotic, radiation, heat, or other treatment damaging to untransformed cells). A screenable marker gene (or reporter gene) confers a trait that one can identify through observation or testing, i.e., by 'screening' (e.g. β-glucuronidase, luciferase, or other enzyme activity not present in untransformed cells).

[0103] As used herein, a "naturally-occurring" nucleic acid molecule refers to a RNA or DNA molecule having a nucleotide sequence that occurs in nature. For example a naturally-occurring nucleic acid molecule can encode a protein that occurs in nature.

[0104] By "obtained from" is meant that a sample such as, for example, a cell extract or nucleic acid or polypeptide extract is isolated from, or derived from, a particular source. For instance, the extract may be isolated directly from biological fluid or tissue of the subject.

[0105] The term "oligonucleotide" as used herein refers to a polymer composed of a multiplicity of nucleotide residues (deoxyribonucleotides or ribonucleotides, or related structural variants or synthetic analogues thereof, including nucleotides with modified or

substituted sugar groups and the like) linked via phosphodiester bonds (or related structural variants or synthetic analogues thereof). Thus, while the term "oligonucleotide" typically refers to a nucleotide polymer in which the nucleotide residues and linkages between them are naturally-occurring, it will be understood that the term also includes within its scope various analogues including, but not restricted to, peptide nucleic acids (PNAs), phosphorothioate, phosphorodithioate, phophoroselenoate, phosphorodiselenoate, phosphoroanilothioate, phosphoraniladate, phosphoroamidate, methyl phosphonates, 2-O-methyl ribonucleic acids, and the like. The exact size of the molecule can vary depending on the particular application. Oligonucleotides are a polynucleotide subset with 200 bases or fewer in length. Preferably, oligonucleotides are 10 to 60 bases in length and most preferably 12, 13, 14, 15, 16, 17, 18, 19, or 20 to 40 bases in length. Oligonucleotides are usually single stranded, e.g., for probes; although oligonucleotides may be double stranded, e.g., for use in the construction of a variant nucleic acid sequence. Oligonucleotides of the invention can be either sense or antisense oligonucleotides.

[0106] The term "oligonucleotide array" refers to a substrate having oligonucleotide probes with different known sequences deposited at discrete known locations associated with its surface. For example, the substrate can be in the form of a two dimensional substrate as described in U.S. Patent No. 5,424,186. Such substrate may be used to synthesize two-dimensional spatially addressed oligonucleotide (matrix) arrays. Alternatively, the substrate may be characterized in that it forms a tubular array in which a two dimensional planar sheet is rolled into a three-dimensional tubular configuration. The substrate may also be in the form of a microsphere or bead connected to the surface of an optic fibre as, for example, disclosed by Chee *et al.* in WO 00/39587. Oligonucleotide arrays have at least two different features and a density of at least 400 features per cm^2. In certain embodiments, the arrays can have a density of about 500, at least one thousand, at least 10 thousand, at least 100 thousand, at least one million or at least 10 million features per cm^2. For example, the substrate may be silicon or glass and can have the thickness of a glass microscope slide or a glass cover slip, or may be composed of other synthetic polymers. Substrates that are transparent to light are useful when the method of performing an assay on the substrate involves optical detection. The term also refers to a probe array and the substrate to which it is attached that form part of a wafer.

[0107] The term "operably connected" or "operably linked" as used herein means placing a structural gene under the regulatory control of a promoter, which then controls the transcription and optionally translation of the gene. In the construction of heterologous promoter/structural gene combinations, it is generally preferred to position the genetic sequence or promoter at a distance from the gene transcription start site that is approximately the same as the distance between that genetic sequence or promoter and the gene it controls in its natural setting; i.e., the gene from which the genetic sequence or promoter is derived. As is known in

the art, some variation in this distance can be accommodated without loss of function. Similarly, the preferred positioning of a regulatory sequence element with respect to a heterologous gene to be placed under its control is defined by the positioning of the element in its natural setting; i.e., the genes from which it is derived.

[0108] The term "polynucleotide" or "nucleic acid" as used herein designates mRNA, RNA, cRNA, cDNA or DNA. The term typically refers to polymeric form of nucleotides of at least 10 bases in length, either ribonucleotides or deoxynucleotides or a modified form of either type of nucleotide. The term includes single and double stranded forms of DNA.

[0109] The terms "polynucleotide variant" and "variant" refer to polynucleotides displaying substantial sequence identity with a reference polynucleotide sequence or polynucleotides that hybridize with a reference sequence under stringent conditions that are defined hereinafter. These terms also encompass polynucleotides in which one or more nucleotides have been added or deleted, or replaced with different nucleotides. In this regard, it is well understood in the art that certain alterations inclusive of mutations, additions, deletions and substitutions can be made to a reference polynucleotide whereby the altered polynucleotide retains a biological function or activity of the reference polynucleotide. The terms "polynucleotide variant" and "variant" also include naturally-occurring allelic variants.

[0110] "Polypeptide", "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues and to variants and synthetic analogues of the same. Thus, these terms apply to amino acid polymers in which one or more amino acid residues is a synthetic non-naturally-occurring amino acid, such as a chemical analogue of a corresponding naturally-occurring amino acid, as well as to naturally-occurring amino acid polymers.

[0111] The term "polypeptide variant" refers to polypeptides which are distinguished from a reference polypeptide by the addition, deletion or substitution of at least one amino acid residue. In certain embodiments, one or more amino acid residues of a reference polypeptide are replaced by different amino acids. It is well understood in the art that some amino acids may be changed to others with broadly similar properties without changing the nature of the activity of the polypeptide (conservative substitutions) as described hereinafter.

[0112] By "primer" is meant an oligonucleotide which, when paired with a strand of DNA, is capable of initiating the synthesis of a primer extension product in the presence of a suitable polymerizing agent. The primer is preferably single-stranded for maximum efficiency in amplification but can alternatively be double-stranded. A primer must be sufficiently long to prime the synthesis of extension products in the presence of the polymerization agent. The length of the primer depends on many factors, including application, temperature to be employed, template reaction conditions, other reagents, and source of primers. For example,

depending on the complexity of the target sequence, the primer may be at least about 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, 500, to one base shorter in length than the template sequence at the 3' end of the primer to allow extension of a nucleic acid chain, though the 5' end of the primer may extend in length beyond the 3' end of the template sequence. In certain embodiments, primers can be large polynucleotides, such as from about 35 nucleotides to several kilobases or more. Primers can be selected to be "substantially complementary" to the sequence on the template to which it is designed to hybridise and serve as a site for the initiation of synthesis. By "substantially complementary", it is meant that the primer is sufficiently complementary to hybridise with a target polynucleotide. Desirably, the primer contains no mismatches with the template to which it is designed to hybridise but this is not essential. For example, non-complementary nucleotide residues can be attached to the 5' end of the primer, with the remainder of the primer sequence being complementary to the template. Alternatively, non-complementary nucleotide residues or a stretch of non-complementary nucleotide residues can be interspersed into a primer, provided that the primer sequence has sufficient complementarity with the sequence of the template to hybridise therewith and thereby form a template for synthesis of the extension product of the primer.

[0113] "Probe" refers to a molecule that binds to a specific sequence or sub-sequence or other moiety of another molecule. Unless otherwise indicated, the term "probe" typically refers to a polynucleotide probe that binds to another polynucleotide, often called the "target polynucleotide", through complementary base pairing. Probes can bind target polynucleotides lacking complete sequence complementarity with the probe, depending on the stringency of the hybridization conditions. Probes can be labeled directly or indirectly and include primers within their scope.

[0114] The term "recombinant polynucleotide" as used herein refers to a polynucleotide formed in vitro by the manipulation of nucleic acid into a form not normally found in nature. For example, the recombinant polynucleotide may be in the form of an expression vector. Generally, such expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleotide sequence.

[0115] By "recombinant polypeptide" is meant a polypeptide made using recombinant techniques, i.e., through the expression of a recombinant or synthetic polynucleotide.

[0116] By "regulatory element" or "regulatory sequence" is meant nucleic acid sequences (e.g., DNA) necessary for expression of an operably linked coding sequence in a particular host cell. The regulatory sequences that are suitable for prokaryotic cells for example, include a promoter, and optionally a cis-acting sequence such as an operator sequence and a

ribosome binding site. Control sequences that are suitable for eukaryotic cells include promoters, polyadenylation signals, transcriptional enhancers, translational enhancers, leader or trailing sequences that modulate mRNA stability, as well as targeting sequences that target a product encoded by a transcribed polynucleotide to an intracellular compartment within a cell or to the extracellular environment.

[0117] The term "sequence identity" as used herein refers to the extent that sequences are identical on a nucleotide-by-nucleotide basis or an amino acid-by-amino acid basis over a window of comparison. Thus, a "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over the window of comparison, determining the number of positions at which the identical nucleic acid base (e.g., A, T, C, G, I) or the identical amino acid residue (e.g., Ala, Pro, Ser, Thr, Gly, Val, Leu, Ile, Phe, Tyr, Trp, Lys, Arg, His, Asp, Glu, Asn, Gln, Cys and Met) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison (i.e., the window size), and multiplying the result by 100 to yield the percentage of sequence identity. For the purposes of the present invention, "sequence identity" will be understood to mean the "match percentage" calculated by the DNASIS computer program (Version 2.5 for windows; available from Hitachi Software engineering Co., Ltd., South San Francisco, California, USA) using standard defaults as used in the reference manual accompanying the software.

[0118] "Similarity" refers to the percentage number of amino acids that are identical or constitute conservative substitutions as defined in Table 3 *infra*. Similarity may be determined using sequence comparison programs such as GAP (Deveraux *et al.* 1984, Nucleic Acids Research **12**, 387-395). In this way, sequences of a similar or substantially different length to those cited herein might be compared by insertion of gaps into the alignment, such gaps being determined, for example, by the comparison algorithm used by GAP.

[0119] Terms used to describe sequence relationships between two or more polynucleotides or polypeptides include "reference sequence," "comparison window," "sequence identity," "percentage of sequence identity" and "substantial identity". A "reference sequence" is at least 12 but frequently 15 to 18 and often at least 25 monomer units, inclusive of nucleotides and amino acid residues, in length. Because two polynucleotides may each comprise (1) a sequence (i.e., only a portion of the complete polynucleotide sequence) that is similar between the two polynucleotides, and (2) a sequence that is divergent between the two polynucleotides, sequence comparisons between two (or more) polynucleotides are typically performed by comparing sequences of the two polynucleotides over a "comparison window" to identify and compare local regions of sequence similarity. A "comparison window" refers to a conceptual segment of at least 6 contiguous positions, usually about 50 to about 100, more

usually about 100 to about 150 in which a sequence is compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. The comparison window may comprise additions or deletions (i.e., gaps) of about 20% or less as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. Optimal alignment of sequences for aligning a comparison window may be conducted by computerized implementations of algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package Release 7.0, Genetics Computer Group, 575 Science Drive Madison, WI, USA) or by inspection and the best alignment (i.e., resulting in the highest percentage homology over the comparison window) generated by any of the various methods selected. Reference also may be made to the BLAST family of programs as for example disclosed by Altschul *et al.*, 1997, Nucl. Acids Res. **25**:3389. A detailed discussion of sequence analysis can be found in Unit 19.3 of Ausubel *et al.*, "Current Protocols in Molecular Biology", John Wiley & Sons Inc, 1994-1998, Chapter 15.

[0120] The terms "subject" or "individual" or "patient", used interchangeably herein, refer to any subject, particularly a vertebrate subject, and even more particularly a mammalian subject, for whom therapy or prophylaxis is desired. Suitable vertebrate animals that fall within the scope of the invention include, but are not restricted to, primates, avians, livestock animals (e.g., sheep, cows, horses, donkeys, pigs), laboratory test animals (e.g., rabbits, mice, rats, guinea pigs, hamsters), companion animals (e.g., cats, dogs) and captive wild animals (e.g., foxes, deer, dingoes). A preferred subject is an equine animal in need of treatment or prophylaxis for stress. However, it will be understood that the aforementioned terms do not imply that symptoms are present.

[0121] The phrase "substantially similar affinities" refers herein to target sequences having similar strengths of detectable hybridization to their complementary or substantially complementary oligonucleotide probes under a chosen set of stringent conditions.

[0122] The term "template" as used herein refers to a nucleic acid that is used in the creation of a complementary nucleic acid strand to the "template" strand. The template may be either RNA and/or DNA, and the complementary strand may also be RNA and/or DNA. In certain embodiments, the complementary strand may comprise all or part of the complementary sequence to the "template," and/or may include mutations so that it is not an exact, complementary strand to the "template". Strands that are not exactly complementary to the template strand may hybridise specifically to the template strand in detection assays described here, as well as other assays known in the art, and such complementary strands that can be used in detection assays are part of the invention.

[0123] The term "transformation" means alteration of the genotype of an organism, for example a bacterium, yeast, mammal, avian, reptile, fish or plant, by the introduction of a foreign or endogenous nucleic acid.

[0124] By "vector" is meant a polynucleotide molecule, suitably a DNA molecule derived, for example, from a plasmid, bacteriophage, yeast, virus, mammal, avian, reptile or fish into which a polynucleotide can be inserted or cloned. A vector preferably contains one or more unique restriction sites and can be capable of autonomous replication in a defined host cell including a target cell or tissue or a progenitor cell or tissue thereof, or be integrable with the genome of the defined host such that the cloned sequence is reproducible. Accordingly, the vector can be an autonomously replicating vector, i.e., a vector that exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, e.g., a linear or closed circular plasmid, an extrachromosomal element, a minichromosome, or an artificial chromosome. The vector can contain any means for assuring self-replication. Alternatively, the vector can be one which, when introduced into the host cell, is integrated into the genome and replicated together with the chromosome(s) into which it has been integrated. A vector system can comprise a single vector or plasmid, two or more vectors or plasmids, which together contain the total DNA to be introduced into the genome of the host cell, or a transposon. The choice of the vector will typically depend on the compatibility of the vector with the host cell into which the vector is to be introduced. The vector can also include a selection marker such as an antibiotic resistance gene that can be used for selection of suitable transformants. Examples of such resistance genes are known to those of skill in the art.

[0125] The terms "wild-type" and "normal" are used interchangeably to refer to the phenotype that is characteristic of most of the members of the species occurring naturally and contrast for example with the phenotype of a mutant.

2. Abbreviations

[0126] The following abbreviations are used throughout the application:

nt =nucleotide
nts =nucleotides
aa =amino acid(s)
kb =kilobase(s) or kilobase pair(s)
kDa =kilodalton(s)
d =day
h =hour
s =seconds

3. Markers of stress and uses therefor

[0127] The present invention concerns measuring the stress level or physiological response to stress in a subject of interest. Markers of stress, in the form of RNA molecules of specified sequences, or polypeptides expressed from these RNA molecules in cells, especially in blood cells, and more especially in peripheral blood cells, of subjects subjected to stress or perceived to be under stressful conditions, are disclosed. These markers are indicators of stress and, when differentially expressed, are diagnostic for a physiological response to stress in tested subjects. Such markers provide considerable advantages over the prior art in this field. In certain advantageous embodiments where peripheral blood is used for the analysis, it is possible to monitor the reaction to stress, and in addition, the drawing of a blood sample is minimally invasive and relatively inexpensive. The detection methods disclosed herein are thus suitable for widespread screening of subjects.

[0128] It will be apparent that the nucleic acid sequences disclosed herein will find utility in a variety of applications in assessing the response to stress, as well as managing and treating stress. Examples of such applications within the scope of the present disclosure include amplification of stress markers using specific primers, detection of stress markers by hybridisation with oligonucleotide probes, incorporation of isolated nucleic acids into vectors, expression of vector-incorporated nucleic acids as RNA and protein, and development of immunological reagents corresponding to marker encoded products.

[0129] The identified stress markers may in turn be used to design specific oligonucleotide probes and primers. Such probes and primers may be of any length that would specifically hybridize to the identified marker gene sequences and may be at least about 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, 500 nucleotides in length and in the case of probes, up to the full length of the sequences of the marker genes identified herein. Probes may also include additional sequence at their 5' and/or 3' ends so that they extent beyond the target sequence with which they hybridize.

[0130] When used in combination with nucleic acid amplification procedures, these probes and primers enable the rapid analysis of biological samples (e.g., peripheral blood samples) for detecting or quantifying marker gene transcripts. Such procedures include any method or technique known in the art or described herein for duplicating or increasing the number of copies or amount of a target nucleic acid or its complement.

[0131] The identified markers may also be used to identify and isolate full-length gene sequences, including regulatory elements for gene expression, from genomic DNA libraries, which are suitably but not exclusively of equine origin. The cDNA sequences identified in the present disclosure may be used as hybridization probes to screen genomic DNA libraries by conventional techniques. Once partial genomic clones have been identified, full-

length genes may be isolated by "chromosomal walking" (also called "overlap hybridization") using, for example, the method disclosed by Chinault & Carbon (1979, *Gene* **5**: 111-126). Once a partial genomic clone has been isolated using a cDNA hybridization probe, non-repetitive segments at or near the ends of the partial genomic clone may be used as hybridization probes in further genomic library screening, ultimately allowing isolation of entire gene sequences for the stress markers of interest. It will be recognized that full-length genes may be obtained using the partial cDNA sequences or short expressed sequence tags (ESTs) described in this disclosure using standard techniques as disclosed for example by Sambrook, *et al.* (MOLECULAR CLONING. A LABORATORY MANUAL (Cold Spring Harbor Press, 1989) and Ausubel *et al.*, (CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, Inc. 1994). In addition, the disclosed sequences may be used to identify and isolate full-length cDNA sequences using standard techniques as disclosed, for example, in the above-referenced texts. Sequences identified and isolated by such means may be useful in the detection of the stress marker genes using the detection methods described herein, and are part of the invention.

[0132] One of ordinary skill in the art could select segments from the identified marker genes for use in determining susceptibility, the different detection, diagnostic, or prognostic methods, vector constructs, antigen-binding molecule production, kit, and/or any of the embodiments described herein as part of the present invention. Marker gene sequences that are desirable for use in the invention are those set fort in SEQ ID NO: 1, 3, 4, 5, 7, 9, 11, 13, 15, 16, 17, 19, 21, 23, 24, 25, 26, 28, 29, 30, 32, 33, 34, 35, 37, 38, 39, 40, 41, 42, 44, 46, 48, 50, 51, 52, 54, 55, 56, 57, 59, 62, 63, 64, 66, 68, 70, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 90, 91, 92, 93, 95, 96, 97, 99, 101, 103, 105, 107, 108, 109, 111, 113, 115, 117, 118, 119, 121, 123, 125, 126, 127, 129, 130, 131, 133, 135, 137, 139, 141, 143, 144, 145, 147, 148, 150, 151, 153, 155, 156, 158, 160, 161, 163, 164, 165, 167, 169, 170, 171, 173, 175, 176, 178, 180, 182, 184, 185, 186, 187, 188, 190, 192, 194, 195, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 233, 234, 236, 238, 239, 240, 241, 242, 243, 244, 246 or 248 (see Table 1).

4. Nucleic acid molecules of the invention

[0133] As described in the Examples and in Table 1, the present disclosure provides 134 markers of stress (i.e., 134 stress marker genes), identified by GeneChip™ analysis of blood obtained from normal horses and from horses subjected to stress. Of the 134 marker genes, 96 have full-length or substantially full-length coding sequences and the remaining 38 have partial sequence information at one or both of their 5' and 3' ends. The identified stress marker genes include 38 previously uncharacterised equine genes.

[0134] In accordance with the present invention, the sequences of isolated nucleic acids disclosed herein find utility *inter alia* as hybridization probes or amplification primers.

These nucleic acids may be used, for example, in diagnostic evaluation of biological samples or employed to clone full-length cDNAs or genomic clones corresponding thereto. In certain embodiments, these probes and primers represent oligonucleotides, which are of sufficient length to provide specific hybridization to a RNA or DNA sample extracted from the biological sample. The sequences typically will be about 10-20 nucleotides, but may be longer. Longer sequences, e.g., of about 30, 40, 50, 100, 500 and even up to full-length, are desirable for certain embodiments.

[0135] Nucleic acid molecules having contiguous stretches of about 10, 15, 17, 20, 30, 40, 50, 60, 75 or 100 or 500 nucleotides of a sequence set forth in any one of SEQ ID NO: 1, 3, 4, 5, 7, 9, 11, 13, 15, 16, 17, 19, 21, 23, 24, 25, 26, 28, 29, 30, 32, 33, 34, 35, 37, 38, 39, 40, 41, 42, 44, 46, 48, 50, 51, 52, 54, 55, 56, 57, 59, 62, 63, 64, 66, 68, 70, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 90, 91, 92, 93, 95, 96, 97, 99, 101, 103, 105, 107, 108, 109, 111, 113, 115, 117, 118, 119, 121, 123, 125, 126, 127, 129, 130, 131, 133, 135, 137, 139, 141, 143, 144, 145, 147, 148, 150, 151, 153, 155, 156, 158, 160, 161, 163, 164, 165, 167, 169, 170, 171, 173, 175, 176, 178, 180, 182, 184, 185, 186, 187, 188, 190, 192, 194, 195, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 233, 234, 236, 238, 239, 240, 241, 242, 243, 244, 246 or 248 are contemplated. Molecules that are complementary to the above mentioned sequences and that bind to these sequences under high stringency conditions are also contemplated. These probes are useful in a variety of hybridization embodiments, such as Southern and northern blotting. In some cases, it is contemplated that probes may be used that hybridize to multiple target sequences without compromising their ability to effectively measure a stress response. In general, it is contemplated that the hybridization probes described herein are useful both as reagents in solution hybridization, as in PCR, for detection of expression of corresponding genes, as well as in embodiments employing a solid phase.

[0136] Various probes and primers may be designed around the disclosed nucleotide sequences. For example, in certain embodiments, the sequences used to design probes and primers may include repetitive stretches of adenine nucleotides (poly-A tails) normally attached at the ends of the RNA for the identified marker genes. In other embodiments, probes and primers may be specifically designed to not include these or other segments from the identified marker genes, as one of ordinary skilled in the art may deem certain segments more suitable for use in the detection methods disclosed. In any event, the choice of primer or probe sequences for a selected application is within the realm of the ordinary skilled practitioner. Illustrative probe sequences for detection of stress marker genes are presented in Table 2.

[0137] Primers may be provided in double-stranded or single-stranded form, although the single-stranded form is desirable. Probes, while perhaps capable of priming, are

designed to bind to a target DNA or RNA and need not be used in an amplification process. In certain embodiments, the probes or primers are labelled with radioactive species ^{32}P, ^{14}C, ^{35}S, ^{3}H, or other label), with a fluorophore (e.g., rhodamine, fluorescein) or with a chemillumiscent label (e.g., luciferase).

[0138] The present invention provides 96 substantially full-length cDNA sequences as well as 59 EST or partial cDNA sequences that are useful as markers of stress. It will be understood, however, that the present disclosure is not limited to these disclosed sequences and is intended particularly to encompass at least isolated nucleic acids that are hybridizable to nucleic acids comprising the disclosed sequences or that are variants of these nucleic acids. For example, a nucleic acid of partial sequence may be used to identify a structurally-related gene or the full-length genomic or cDNA clone from which it is derived. Methods for generating cDNA and genomic libraries which may be used as a target for the above-described probes are known in the art (see, for example, Sambrook *et al.*, 1989, *supra* and Ausubel *et al.*, 1994, *supra*). All such nucleic acids as well as the specific nucleic acid molecules disclosed herein are collectively referred to as "*stress marker polynucleotides*." Additionally, the present invention includes within its scope isolated or purified expression products of stress marker polynucleotides (i.e., RNA transcripts and polypeptides).

[0139] Accordingly, the present invention encompasses isolated or substantially purified nucleic acid or protein compositions. An "isolated" or "purified" nucleic acid molecule or protein, or biologically active portion thereof, is substantially or essentially free from components that normally accompany or interact with the nucleic acid molecule or protein as found in its naturally occurring environment. Thus, an isolated or purified polynucleotide or polypeptide is substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. Suitably, an "isolated" polynucleotide is free of sequences (especially protein encoding sequences) that naturally flank the polynucleotide (i.e., sequences located at the 5' and 3' ends of the polynucleotide) in the genomic DNA of the organism from which the polynucleotide was derived. For example, in various embodiments, an isolated stress marker polynucleotide can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb, or 0.1 kb of nucleotide sequences that naturally flank the polynucleotide in genomic DNA of the cell from which the polynucleotide was derived. A polypeptide that is substantially free of cellular material includes preparations of protein having less than about 30%, 20%, 10%, 5%, (by dry weight) of contaminating protein. When the protein of the invention or biologically active portion thereof is recombinantly produced, culture medium suitably represents less than about 30%, 20%, 10%, or 5% (by dry weight) of chemical precursors or non-protein-of-interest chemicals.

[0140] The present invention also encompasses portions of the full-length or substantially full-length nucleotide sequences of the stress marker genes or their transcripts or DNA copies of these transcripts. Portions of a stress marker nucleotide sequence may encode polypeptide portions or segments that retain the biological activity of the native polypeptide. Alternatively, portions of a stress marker nucleotide sequence that are useful as hybridization probes generally do not encode amino acid sequences retaining such biological activity. Thus, portions of a stress marker nucleotide sequence may range from at least about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 40, 50, 60, 80, 90, 100 nucleotides, or almost up to the full-length nucleotide sequence encoding the stress marker polypeptides of the invention.

[0141] A portion of a stress marker nucleotide sequence that encodes a biologically active portion of a stress marker polypeptide of the invention may encode at least about 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 40, 50, 60, 70, 80, 90, 100, 120, 150, 300, 400, 500, 600, 700, 800, 900 or 1000, or even at least about 2000, 3000, 4000 or 5000 contiguous amino acid residues, or almost up to the total number of amino acids present in a full-length stress marker polypeptide. Portions of a stress marker nucleotide sequence that are useful as hybridization probes or PCR primers generally need not encode a biologically active portion of a stress marker polypeptide.

[0142] Thus, a portion of a stress marker nucleotide sequence may encode a biologically active portion of a stress marker polypeptide, or it may be a fragment that can be used as a hybridization probe or PCR primer using standard methods known in the art. A biologically active portion of a stress marker polypeptide can be prepared by isolating a portion of one of the stress marker nucleotide sequences of the invention, expressing the encoded portion of the stress marker polypeptide (e.g., by recombinant expression *in vitro*), and assessing the activity of the encoded portion of the stress marker polypeptide. Nucleic acid molecules that are portions of a stress marker nucleotide sequence comprise at least about 15, 16, 17, 18, 19, 20, 25, 30, 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, or 650 nucleotides, or almost up to the number of nucleotides present in a full-length stress marker nucleotide sequence.

[0143] The invention also contemplates variants of the stress marker nucleotide sequences. Nucleic acid variants can be naturally-occurring, such as allelic variants (same locus), homologues (different locus), and orthologues (different organism) or can be non naturally-occurring. Naturally occurring variants such as these can be identified with the use of well-known molecular biology techniques, as, for example, with polymerase chain reaction (PCR) and hybridization techniques as known in the art. Non-naturally occurring variants can be made by mutagenesis techniques, including those applied to polynucleotides, cells, or organisms. The variants can contain nucleotide substitutions, deletions, inversions and insertions. Variation can

occur in either or both the coding and non-coding regions. The variations can produce both conservative and non-conservative amino acid substitutions (as compared in the encoded product). For nucleotide sequences, conservative variants include those sequences that, because of the degeneracy of the genetic code, encode the amino acid sequence of one of the stress marker polypeptides of the invention. Variant nucleotide sequences also include synthetically derived nucleotide sequences, such as those generated, for example, by using site-directed mutagenesis but which still encode a stress marker polypeptide of the invention. Generally, variants of a particular nucleotide sequence of the invention will have at least about 30%, 40% 50%, 55%, 60%, 65%, 70%, generally at least about 75%, 80%, 85%, desirably about 90% to 95% or more, and more suitably about 98% or more sequence identity to that particular nucleotide sequence as determined by sequence alignment programs described elsewhere herein using default parameters.

[0144] The stress marker nucleotide sequences of the invention can be used to isolate corresponding sequences and alleles from other organisms, particularly other mammals, especially other equine species. Methods are readily available in the art for the hybridization of nucleic acid sequences. Coding sequences from other organisms may be isolated according to well known techniques based on their sequence identity with the coding sequences set forth herein. In these techniques all or part of the known coding sequence is used as a probe which selectively hybridizes to other stress marker coding sequences present in a population of cloned genomic DNA fragments or cDNA fragments (i.e., genomic or cDNA libraries) from a chosen organism. Accordingly, the present invention also contemplates polynucleotides that hybridize to the stress marker gene nucleotide sequences, or to their complements, under stringency conditions described below. As used herein, the term "hybridizes under low stringency, medium stringency, high stringency, or very high stringency conditions" describes conditions for hybridization and washing. Guidance for performing hybridization reactions can be found in Ausubel *et al.*, (1998, *supra*), Sections 6.3.1-6.3.6. Aqueous and non-aqueous methods are described in that reference and either can be used. Reference herein to low stringency conditions include and encompass from at least about 1% v/v to at least about 15% v/v formamide and from at least about 1 M to at least about 2 M salt for hybridization at 42° C, and at least about 1 M to at least about 2 M salt for washing at 42° C. Low stringency conditions also may include 1% Bovine Serum Albumin (BSA), 1 mM EDTA, 0.5 M $NaHPO_4$ (pH 7.2), 7% SDS for hybridization at 65° C, and (i) 2 × SSC, 0.1% SDS; or (ii) 0.5% BSA, 1 mM EDTA, 40 mM $NaHPO_4$ (pH 7.2), 5% SDS for washing at room temperature. One embodiment of low stringency conditions includes hybridization in 6 × sodium chloride/sodium citrate (SSC) at about 45° C, followed by two washes in 0.2 × SSC, 0.1% SDS at least at 50° C (the temperature of the washes can be increased to 55° C for low stringency conditions). Medium stringency

conditions include and encompass from at least about 16% v/v to at least about 30% v/v formamide and from at least about 0.5 M to at least about 0.9 M salt for hybridization at 42° C, and at least about 0.1 M to at least about 0.2 M salt for washing at 55° C. Medium stringency conditions also may include 1% Bovine Serum Albumin (BSA), 1 mM EDTA, 0.5 M $NaHPO_4$ (pH 7.2), 7% SDS for hybridization at 65° C, and (i) 2 × SSC, 0.1% SDS; or (ii) 0.5% BSA, 1 mM EDTA, 40 mM $NaHPO_4$ (pH 7.2), 5% SDS for washing at 60-65° C. One embodiment of medium stringency conditions includes hybridizing in 6 × SSC at about 45° C, followed by one or more washes in 0.2 × SSC, 0.1% SDS at 60° C. High stringency conditions include and encompass from at least about 31% v/v to at least about 50% v/v formamide and from about 0.01 M to about 0.15 M salt for hybridization at 42° C, and about 0.01 M to about 0.02 M salt for washing at 55° C. High stringency conditions also may include 1% BSA, 1 mM EDTA, 0.5 M $NaHPO_4$ (pH 7.2), 7% SDS for hybridization at 65° C, and (i) 0.2 × SSC, 0.1% SDS; or (ii) 0.5% BSA, 1 mM EDTA, 40 mM $NaHPO_4$ (pH 7.2), 1% SDS for washing at a temperature in excess of 65° C. One embodiment of high stringency conditions includes hybridizing in 6 × SSC at about 45° C, followed by one or more washes in 0.2 × SSC, 0.1% SDS at 65° C.

[0145] In certain embodiments, a stress marker polynucleotide of the invention hybridises to a disclosed nucleotide sequence under very high stringency conditions. One embodiment of very high stringency conditions includes hybridising in 0.5 M sodium phosphate, 7% SDS at 65° C, followed by one or more washes at 0.2 × SSC, 1% SDS at 65° C.

[0146] Other stringency conditions are well known in the art and a skilled person will recognize that various factors can be manipulated to optimize the specificity of the hybridization. Optimization of the stringency of the final washes can serve to ensure a high degree of hybridization. For detailed examples, see Ausubel *et al.*, *supra* at pages 2.10.1 to 2.10.16 and Sambrook *et al.* (1989, *supra*) at sections 1.101 to 1.104.

[0147] While stringent washes are typically carried out at temperatures from about 42° C to 68° C, one skilled in the art will appreciate that other temperatures may be suitable for stringent conditions. Maximum hybridization rate typically occurs at about 20° C to 25° C below the T_m for formation of a DNA-DNA hybrid. It is well known in the art that the T_m is the melting temperature, or temperature at which two complementary polynucleotide sequences dissociate. Methods for estimating T_m are well known in the art (see Ausubel *et al.*, *supra* at page 2.10.8). In general, the T_m of a perfectly matched duplex of DNA may be predicted as an approximation by the formula:

[0148] $T_m = 81.5 + 16.6 (\log_{10} M) + 0.41 (\%G+C) - 0.63 (\%\text{ formamide}) - (600/\text{length})$

[0149] wherein: M is the concentration of Na^+, preferably in the range of 0.01 molar to 0.4 molar; %G+C is the sum of guanosine and cytosine bases as a percentage of the total number of bases, within the range between 30% and 75% G+C; % formamide is the percent formamide concentration by volume; length is the number of base pairs in the DNA duplex. The T_m of a duplex DNA decreases by approximately 1° C with every increase of 1% in the number of randomly mismatched base pairs. Washing is generally carried out at $T_m - 15°$ C for high stringency, or $T_m - 30°$ C for moderate stringency.

[0150] In one example of a hybridization procedure, a membrane (e.g., a nitrocellulose membrane or a nylon membrane) containing immobilized DNA is hybridized overnight at 42° C in a hybridization buffer (50% deionised formamide, 5 × SSC, 5 × Denhardt's solution (0.1% ficoll, 0.1% polyvinylpyrollidone and 0.1% bovine serum albumin), 0.1% SDS and 200 mg/mL denatured salmon sperm DNA) containing labeled probe. The membrane is then subjected to two sequential medium stringency washes (i.e., 2 × SSC, 0.1% SDS for 15 min at 45° C, followed by 2 × SSC, 0.1% SDS for 15 min at 50° C), followed by two sequential higher stringency washes (i.e., 0.2 × SSC, 0.1% SDS for 12 min at 55° C followed by 0.2 × SSC and 0.1%SDS solution for 12 min at 65-68° C.

5. Polypeptides of the invention

[0151] The present invention also contemplates full-length polypeptides encoded by the stress marker genes of the invention as well as the biologically active portions of those polypeptides, which are referred to collectively herein as "stress marker polypeptides". Biologically active portions of full-length stress marker polypeptides include portions with immuno-interactive activity of at least about 6, 8, 10, 12, 14, 16, 18, 20, 25, 30, 40, 50, 60 amino acid residues in length. For example, immuno-interactive fragments contemplated by the present invention are at least 6 and desirably at least 8 amino acid residues in length, which can elicit an immune response in an animal for the production of antigen-binding molecules that are immuno-interactive with a stress marker polypeptide of the invention. Such antigen-binding molecules can be used to screen other mammals, especially equine mammals, for structurally and/or functionally related stress marker polypeptides. Typically, portions of a full-length stress marker polypeptide may participate in an interaction, for example, an intramolecular or an inter-molecular interaction. An inter-molecular interaction can be a specific binding interaction or an enzymatic interaction (e.g., the interaction can be transient and a covalent bond is formed or broken). Biologically active portions of a full-length stress marker polypeptide include peptides comprising amino acid sequences sufficiently similar to or derived from the amino acid sequences of a (putative) full-length stress marker polypeptide, for example, the amino acid sequences shown in SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53,

58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249, which include less amino acids than a full-length stress marker polypeptide, and exhibit at least one activity of that polypeptide. Typically, biologically active portions comprise a domain or motif with at least one activity of a full-length stress marker polypeptide. A biologically active portion of a full-length stress marker polypeptide can be a polypeptide which is, for example, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 40, 50, 60, 70, 80, 90, 100, 120, 150, 300, 400, 500, 600, 700, 800, 900 or 1000, or even at least about 2000, 3000, 4000 or 5000, or more amino acid residues in length. Suitably, the portion is a "biologically-active portion" having no less than about 1%, 10%, 25% 50% of the activity of the full-length polypeptide from which it is derived.

[0152] The present invention also contemplates variant stress marker polypeptides. "Variant" polypeptides include proteins derived from the native protein by deletion (so-called truncation) or addition of one or more amino acids to the N-terminal and/or C-terminal end of the native protein; deletion or addition of one or more amino acids at one or more sites in the native protein; or substitution of one or more amino acids at one or more sites in the native protein. Variant proteins encompassed by the present invention are biologically active, that is, they continue to possess the desired biological activity of the native protein. Such variants may result from, for example, genetic polymorphism or from human manipulation. Biologically active variants of a native stress marker protein of the invention will have at least 40%, 50%, 60%, 70%, generally at least 75%, 80%, 85%, preferably about 90% to 95% or more, and more preferably about 98% or more sequence similarity with the amino acid sequence for the native protein as determined by sequence alignment programs described elsewhere herein using default parameters. A biologically active variant of a protein of the invention may differ from that protein generally by as much 1000, 500, 400, 300, 200, 100, 50 or 20 amino acid residues or suitably by as few as 1-15 amino acid residues, as few as 1-10, such as 6-10, as few as 5, as few as 4, 3, 2, or even 1 amino acid residue.

[0153] A stress marker polypeptide of the invention may be altered in various ways including amino acid substitutions, deletions, truncations, and insertions. Methods for such manipulations are generally known in the art. For example, amino acid sequence variants of a stress marker protein can be prepared by mutations in the DNA. Methods for mutagenesis and nucleotide sequence alterations are well known in the art. See, for example, Kunkel (1985, *Proc. Natl. Acad. Sci. USA* **82**:488-492), Kunkel *et al.* (1987, *Methods in Enzymol.* **154**:367-382), U.S. Pat. No. 4,873,192, Watson, J. D. *et al.* ("Molecular Biology of the Gene", Fourth Edition, Benjamin/Cummings, Menlo Park, Calif., 1987) and the references cited therein.

Guidance as to appropriate amino acid substitutions that do not affect biological activity of the protein of interest may be found in the model of Dayhoff *et al.* (1978) Atlas of Protein Sequence and Structure (Natl. Biomed. Res. Found., Washington, D.C.). Methods for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property are known in the art. Such methods are adaptable for rapid screening of the gene libraries generated by combinatorial mutagenesis of stress marker polypeptides. Recursive ensemble mutagenesis (REM), a technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify stress marker polypeptide variants (Arkin and Yourvan (1992) *Proc. Natl. Acad. Sci. USA* 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6:327-331). Conservative substitutions, such as exchanging one amino acid with another having similar properties, may be desirable as discussed in more detail below.

[0154] Variant stress marker polypeptides may contain conservative amino acid substitutions at various locations along their sequence, as compared to the parent stress marker amino acid sequence. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art, which can be generally sub-classified as follows:

[0155] Acidic: The residue has a negative charge due to loss of H ion at physiological pH and the residue is attracted by aqueous solution so as to seek the surface positions in the conformation of a peptide in which it is contained when the peptide is in aqueous medium at physiological pH. Amino acids having an acidic side chain include glutamic acid and aspartic acid.

[0156] Basic: The residue has a positive charge due to association with H ion at physiological pH or within one or two pH units thereof (e.g., histidine) and the residue is attracted by aqueous solution so as to seek the surface positions in the conformation of a peptide in which it is contained when the peptide is in aqueous medium at physiological pH. Amino acids having a basic side chain include arginine, lysine and histidine.

[0157] Charged: The residues are charged at physiological pH and, therefore, include amino acids having acidic or basic side chains (i.e., glutamic acid, aspartic acid, arginine, lysine and histidine).

[0158] Hydrophobic: The residues are not charged at physiological pH and the residue is repelled by aqueous solution so as to seek the inner positions in the conformation of a peptide in which it is contained when the peptide is in aqueous medium. Amino acids having a hydrophobic side chain include tyrosine, valine, isoleucine, leucine, methionine, phenylalanine and tryptophan.

[0159] Neutral/polar: The residues are not charged at physiological pH, but the residue is not sufficiently repelled by aqueous solutions so that it would seek inner positions in the conformation of a peptide in which it is contained when the peptide is in aqueous medium. Amino acids having a neutral/polar side chain include asparagine, glutamine, cysteine, histidine, serine and threonine.

[0160] This description also characterizes certain amino acids as "small" since their side chains are not sufficiently large, even if polar groups are lacking, to confer hydrophobicity. With the exception of proline, "small" amino acids are those with four carbons or less when at least one polar group is on the side chain and three carbons or less when not. Amino acids having a small side chain include glycine, serine, alanine and threonine. The gene-encoded secondary amino acid proline is a special case due to its known effects on the secondary conformation of peptide chains. The structure of proline differs from all the other naturally-occurring amino acids in that its side chain is bonded to the nitrogen of the α-amino group, as well as the α-carbon. Several amino acid similarity matrices (e.g., PAM120 matrix and PAM250 matrix as disclosed for example by Dayhoff *et al.* (1978) A model of evolutionary change in proteins. Matrices for determining distance relationships *In* M. O. Dayhoff, (ed.), Atlas of protein sequence and structure, Vol. 5, pp. 345-358, National Biomedical Research Foundation, Washington DC; and by Gonnet *et al.*, 1992, *Science* **256**(5062): 144301445), however, include proline in the same group as glycine, serine, alanine and threonine. Accordingly, for the purposes of the present invention, proline is classified as a "small" amino acid.

[0161] The degree of attraction or repulsion required for classification as polar or nonpolar is arbitrary and, therefore, amino acids specifically contemplated by the invention have been classified as one or the other. Most amino acids not specifically named can be classified on the basis of known behavior.

[0162] Amino acid residues can be further sub-classified as cyclic or noncyclic, and aromatic or nonaromatic, self-explanatory classifications with respect to the side-chain substituent groups of the residues, and as small or large. The residue is considered small if it contains a total of four carbon atoms or less, inclusive of the carboxyl carbon, provided an additional polar substituent is present; three or less if not. Small residues are, of course, always nonaromatic. Dependent on their structural properties, amino acid residues may fall in two or more classes. For the naturally-occurring protein amino acids, sub-classification according to the this scheme is presented in the Table 3.

[0163] Conservative amino acid substitution also includes groupings based on side chains. For example, a group of amino acids having aliphatic side chains is glycine, alanine, valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of amino acids having amide-containing side chains is asparagine

and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine, and tryptophan; a group of amino acids having basic side chains is lysine, arginine, and histidine; and a group of amino acids having sulfur-containing side chains is cysteine and methionine. For example, it is reasonable to expect that replacement of a leucine with an isoleucine or valine, an aspartate with a glutamate, a threonine with a serine, or a similar replacement of an amino acid with a structurally related amino acid will not have a major effect on the properties of the resulting variant polypeptide. Whether an amino acid change results in a functional stress marker polypeptide can readily be determined by assaying its activity. Conservative substitutions are shown in Table 4 under the heading of exemplary substitutions. More preferred substitutions are shown under the heading of preferred substitutions. Amino acid substitutions falling within the scope of the invention, are, in general, accomplished by selecting substitutions that do not differ significantly in their effect on maintaining (a) the structure of the peptide backbone in the area of the substitution, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. After the substitutions are introduced, the variants are screened for biological activity.

[0164] Alternatively, similar amino acids for making conservative substitutions can be grouped into three categories based on the identity of the side chains. The first group includes glutamic acid, aspartic acid, arginine, lysine, histidine, which all have charged side chains; the second group includes glycine, serine, threonine, cysteine, tyrosine, glutamine, asparagine; and the third group includes leucine, isoleucine, valine, alanine, proline, phenylalanine, tryptophan, methionine, as described in Zubay, G., *Biochemistry*, third edition, Wm.C. Brown Publishers (1993).

[0165] Thus, a predicted non-essential amino acid residue in a stress marker polypeptide is typically replaced with another amino acid residue from the same side chain family. Alternatively, mutations can be introduced randomly along all or part of a stress marker gene coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an activity of the parent polypeptide to identify mutants which retain that activity. Following mutagenesis of the coding sequences, the encoded peptide can be expressed recombinantly and the activity of the peptide can be determined.

[0166] Accordingly, the present invention also contemplates variants of the naturally-occurring stress marker polypeptide sequences or their biologically-active fragments, wherein the variants are distinguished from the naturally-occurring sequence by the addition, deletion, or substitution of one or more amino acid residues. In general, variants will display at least about 30, 40, 50, 55, 60, 65, 70, 75, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 % similarity to a parent stress marker polypeptide sequence as, for example, set forth in any one of SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69,

72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249. Desirably, variants will have at least 30, 40, 50, 55, 60, 65, 70, 75, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 % sequence identity to a parent stress marker polypeptide sequence as, for example, set forth in any one of SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249. Moreover, sequences differing from the native or parent sequences by the addition, deletion, or substitution of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 30, 40, 50, 60 ,70, 80 ,90, 100, 150, 200, 300, 500 or more amino acids but which retain the properties of the parent stress marker polypeptide are contemplated. stress marker polypeptides also include polypeptides that are encoded by polynucleotides that hybridise under stringency conditions as defined herein, especially high stringency conditions, to the stress marker polynucleotide sequences of the invention, or the non-coding strand thereof, as described above.

[0167] In one embodiment, variant polypeptides differ from a stress marker sequence by at least one but by less than 50, 40, 30, 20, 15, 10, 8, 6, 5, 4, 3 or 2 amino acid residue(s). In another, variant polypeptides differ from the corresponding sequence in any one of SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249 by at least 1% but less than 20%, 15%, 10% or 5% of the residues. (If this comparison requires alignment the sequences should be aligned for maximum similarity. "Looped" out sequences from deletions or insertions, or mismatches, are considered differences.) The differences are, suitably, differences or changes at a non-essential residue or a conservative substitution.

[0168] A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of an embodiment polypeptide without abolishing or substantially altering one or more of its activities. Suitably, the alteration does not substantially alter one of these activities, for example, the activity is at least 20%, 40%, 60%, 70% or 80% of wild-type. An "essential" amino acid residue is a residue that, when altered from the wild-type sequence of a stress marker polypeptide of the invention, results in abolition of an activity of the parent molecule such that less than 20% of the wild-type activity is present.

[0169] In other embodiments, a variant polypeptide includes an amino acid sequence having at least about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97%, 98% or more similarity to a corresponding sequence of a stress marker polypeptide as, for example, set forth in any one of SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249, and has the activity of that stress marker polypeptide.

[0170] Stress marker polypeptides of the invention may be prepared by any suitable procedure known to those of skill in the art. For example, the polypeptides may be prepared by a procedure including the steps of: (a) preparing a chimeric construct comprising a nucleotide sequence that encodes at least a portion of a stress marker polynucleotide and that is operably linked to a regulatory element; (b) introducing the chimeric construct into a host cell; (c) culturing the host cell to express the stress marker polypeptide; and (d) isolating the stress marker polypeptide from the host cell. In illustrative examples, the nucleotide sequence encodes at least a portion of the sequence set forth in any one of SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249, or a variant thereof.

[0171] The chimeric construct is typically in the form of an expression vector, which is suitably selected from self-replicating extra-chromosomal vectors (e.g., plasmids) and vectors that integrate into a host genome.

[0172] The regulatory element will generally be appropriate for the host cell employed for expression of the stress marker polynucleotide. Numerous types of expression vectors and regulatory elements are known in the art for a variety of host cells. Illustrative elements of this type include, but are not restricted to, promoter sequences (e.g., constitutive or inducible promoters which may be naturally occurring or combine elements of more than one promoter), leader or signal sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and termination sequences, and enhancer or activator sequences.

[0173] In some embodiments, the expression vector comprises a selectable marker gene to permit the selection of transformed host cells. Selectable marker genes are well known in the art and will vary with the host cell employed.

[0174] The expression vector may also include a fusion partner (typically provided by the expression vector) so that the stress marker polypeptide is produced as a fusion polypeptide with the fusion partner. The main advantage of fusion partners is that they assist identification and/or purification of the fusion polypeptide. In order to produce the fusion polypeptide, it is necessary to ligate the stress marker polynucleotide into an expression vector so that the translational reading frames of the fusion partner and the stress marker polynucleotide coincide. Well known examples of fusion partners include, but are not limited to, glutathione-S-transferase (GST), Fc potion of human IgG, maltose binding protein (MBP) and hexahistidine (HIS_6), which are particularly useful for isolation of the fusion polypeptide by affinity chromatography. In some embodiments, fusion polypeptides are purified by affinity chromatography using matrices to which the fusion partners bind such as but not limited to glutathione-, amylose-, and nickel- or cobalt-conjugated resins. Many such matrices are available in "kit" form, such as the QIAexpress™ system (Qiagen) useful with (HIS_6) fusion partners and the Pharmacia GST purification system. Other fusion partners known in the art are light-emitting proteins such as green fluorescent protein (GFP) and luciferase, which serve as fluorescent "tags" that permit the identification and/or isolation of fusion polypeptides by fluorescence microscopy or by flow cytometry. Flow cytometric methods such as fluorescence activated cell sorting (FACS) are particularly useful in this latter application.

[0175] Desirably, the fusion partners also possess protease cleavage sites, such as for Factor X_a or Thrombin, which permit the relevant protease to partially digest the fusion polypeptide and thereby liberate the stress marker polypeptide from the fusion construct. The liberated polypeptide can then be isolated from the fusion partner by subsequent chromatographic separation.

[0176] Fusion partners also include within their scope "epitope tags," which are usually short peptide sequences for which a specific antibody is available. Well known examples of epitope tags for which specific monoclonal antibodies are readily available include c-Myc, influenza virus, hemagglutinin and FLAG tags.

[0177] The chimeric constructs of the invention are introduced into a host by any suitable means including "transduction" and "transfection," which are art recognized as meaning the introduction of a nucleic acid, for example, an expression vector, into a recipient cell by nucleic acid-mediated gene transfer. "Transformation," however, refers to a process in which a host's genotype is changed as a result of the cellular uptake of exogenous DNA or RNA, and, for example, the transformed cell comprises the expression system of the invention. There are many methods for introducing chimeric constructs into cells. Typically, the method employed will depend on the choice of host cell. Technology for introduction of chimeric constructs into host cells is well known to those of skill in the art. Four general classes of

methods for delivering nucleic acid molecules into cells have been described: (1) chemical methods such as calcium phosphate precipitation, polyethylene glycol (PEG)-mediate precipitation and lipofection; (2) physical methods such as microinjection, electroporation, acceleration methods and vacuum infiltration; (3) vector based methods such as bacterial and viral vector-mediated transformation; and (4) receptor-mediated. Transformation techniques that fall within these and other classes are well known to workers in the art, and new techniques are continually becoming known. The particular choice of a transformation technology will be determined by its efficiency to transform certain host species as well as the experience and preference of the person practising the invention with a particular methodology of choice. It will be apparent to the skilled person that the particular choice of a transformation system to introduce a chimeric construct into cells is not essential to or a limitation of the invention, provided it achieves an acceptable level of nucleic acid transfer.

[0178] Recombinant stress marker polypeptides may be produced by culturing a host cell transformed with a chimeric construct. The conditions appropriate for expression of the stress marker polynucleotide will vary with the choice of expression vector and the host cell and are easily ascertained by one skilled in the art through routine experimentation. Suitable host cells for expression may be prokaryotic or eukaryotic. An illustrative host cell for expression of a polypeptide of the invention is a bacterium. The bacterium used may be *Escherichia coli*. Alternatively, the host cell may be a yeast cell or an insect cell such as, for example, *SF9* cells that may be utilized with a baculovirus expression system.

[0179] Recombinant stress marker polypeptides can be conveniently prepared using standard protocols as described for example in Sambrook, *et al.*, (1989, *supra*), in particular Sections 16 and 17; Ausubel *et al.*, (1994, *supra*), in particular Chapters 10 and 16; and Coligan *et al.*, CURRENT PROTOCOLS IN PROTEIN SCIENCE (John Wiley & Sons, Inc. 1995-1997), in particular Chapters 1, 5 and 6. Alternatively, the stress marker polypeptides may be synthesized by chemical synthesis, e.g., using solution synthesis or solid phase synthesis as described, for example, in Chapter 9 of Atherton and Shephard (*supra*) and in Roberge *et al* (1995, *Science* **269**: 202).

6. Antigen-binding molecules

[0180] The invention also provides antigen-binding molecules that are specifically immuno-interactive with a stress marker polypeptide of the invention. In one embodiment, the antigen-binding molecule comprise whole polyclonal antibodies. Such antibodies may be prepared, for example, by injecting a stress marker polypeptide of the invention into a production species, which may include mice or rabbits, to obtain polyclonal antisera. Methods of producing polyclonal antibodies are well known to those skilled in the art. Exemplary protocols which may be used are described for example in Coligan *et al.*, CURRENT

PROTOCOLS IN IMMUNOLOGY, (John Wiley & Sons, Inc, 1991), and Ausubel *et al.*, (1994-1998, *supra*), in particular Section III of Chapter 11.

[0181] In lieu of polyclonal antisera obtained in a production species, monoclonal antibodies may be produced using the standard method as described, for example, by Köhler and Milstein (1975, *Nature* **256**, 495-497), or by more recent modifications thereof as described, for example, in Coligan *et al.*, (1991, *supra*) by immortalizing spleen or other antibody producing cells derived from a production species which has been inoculated with one or more of the stress marker polypeptides of the invention.

[0182] The invention also contemplates as antigen-binding molecules Fv, Fab, Fab' and $F(ab')_2$ immunoglobulin fragments. Alternatively, the antigen-binding molecule may comprise a synthetic stabilized Fv fragment. Exemplary fragments of this type include single chain Fv fragments (sFv, frequently termed scFv) in which a peptide linker is used to bridge the N terminus or C terminus of a V_H domain with the C terminus or N-terminus, respectively, of a V_L domain. ScFv lack all constant parts of whole antibodies and are not able to activate complement. ScFvs may be prepared, for example, in accordance with methods outlined in Kreber *et al* (Kreber *et al.* 1997, *J. Immunol. Methods*; **201(1)**: 35-55). Alternatively, they may be prepared by methods described in U.S. Patent No 5,091,513, European Patent No 239,400 or the articles by Winter and Milstein (1991, *Nature* **349**:293) and Plückthun *et al* (1996, In *Antibody engineering: A practical approach*. 203-252). In another embodiment, the synthetic stabilised Fv fragment comprises a disulphide stabilised Fv (dsFv) in which cysteine residues are introduced into the V_H and V_L domains such that in the fully folded Fv molecule the two residues will form a disulphide bond between them. Suitable methods of producing dsFv are described for example in (Glockscuther *et al. Biochem.* **29**: 1363-1367; Reiter *et al.* 1994, *J. Biol. Chem.* **269**: 18327-18331; Reiter *et al.* 1994, *Biochem. 33*: 5451-5459; Reiter *et al.* 1994. *Cancer Res.* **54**: 2714-2718; Webber *et al.* 1995, *Mol. Immunol.* **32**: 249-258).

[0183] Phage display and combinatorial methods for generating anti-stress marker polypeptide antigen-binding molecules are known in the art (as described in, e.g., Ladner *et al.* U.S. Patent No. 5,223,409; Kang *et al.* International Publication No. WO 92/18619; Dower *et al.* International Publication No. WO 91/17271; Winter *et al.* International Publication WO 92/20791; Markland *et al.* International Publication No. WO 92/15679; Breitling *et al.* International Publication WO 93/01288; McCafferty *et al.* International Publication No. WO 92/01047; Garrard *et al.* International Publication No. WO 92/09690; Ladner *et al.* International Publication No. WO 90/02809; Fuchs *et al.* (1991) *Bio/Technology* 9:1370-1372; Hay *et al.* (1992) *Hum Antibod Hybridomas* 3:81-85; Huse *et al.* (1989) *Science* 246:1275-1281; Griffths *et al.* (1993) *EMBO J* 12:725-734; Hawkins *et al.* (1992) *J Mol Biol* 226:889-896; Clackson *et al.* (1991) *Nature* 352:624-628; Gram *et al.* (1992) *PNAS* 89:3576-3580; Garrad *et al.* (1991)

Bio/Technology 9:1373-1377; Hoogenboom *et al.* (1991) *Nuc Acid Res* 19:4133-4137; and Barbas *et al.* (1991) *PNAS* 88:7978-7982). The antigen-binding molecules can be used to screen expression libraries for variant stress marker polypeptides. They can also be used to detect and/or isolate the stress marker polypeptides of the invention. Thus, the invention also contemplates the use of antigen-binding molecules to isolate stress marker polypeptides using , for example, any suitable immunoaffinity based method including, but not limited to, immunochromatography and immunoprecipitation. A suitable method utilises solid phase adsorption in which anti- stress marker polypeptide antigen-binding molecules are attached to a suitable resin, the resin is contacted with a sample suspected of containing a stress marker polypeptide, and the stress marker polypeptide, if any, is subsequently eluted from the resin. Illustrative resins include: Sepharose® (Pharmacia), Poros® resins (Roche Molecular Biochemicals, Indianapolis), Actigel Superflow™ resins (Sterogene Bioseparations Inc., Carlsbad Calif.), and Dynabeads™ (Dynal Inc., Lake Success, N.Y.).

[0184] The antigen-binding molecule can be coupled to a compound, e.g., a label such as a radioactive nucleus, or imaging agent, e.g. a radioactive, enzymatic, or other, e.g., imaging agent, e.g., a NMR contrast agent. Labels which produce detectable radioactive emissions or fluorescence are preferred. An anti- stress marker polypeptide antigen-binding molecule (e.g., monoclonal antibody) can be used to detect stress marker polypeptides (e.g., in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the protein. In certain advantageous application in accordance with the present invention, such antigen-binding molecules can be used to monitor stress marker polypeptides levels in biological samples (including whole cells and fluids) for diagnosing the presence, absence, degree, of stress or risk of development of disease as a consequences of stress. Detection can be facilitated by coupling (i.e., physically linking) the antibody to a detectable substance (i.e., antibody labeling). Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I, ^{131}I, ^{35}S or ^{3}H. The label may be selected from a group including a chromogen, a catalyst, an enzyme, a fluorophore, a chemiluminescent molecule, a lanthanide ion such as Europium (Eu^{34}), a radioisotope and a direct visual label. In the case of a direct visual label, use may be made of a colloidal metallic or non-metallic particle,

a dye particle, an enzyme or a substrate, an organic polymer, a latex particle, a liposome, or other vesicle containing a signal producing substance and the like.

[0185] A large number of enzymes useful as labels is disclosed in United States Patent Specifications U.S. 4,366,241, U.S. 4,843,000, and U.S. 4,849,338. Enzyme labels useful in the present invention include alkaline phosphatase, horseradish peroxidase, luciferase, β-galactosidase, glucose oxidase, lysozyme, malate dehydrogenase and the like. The enzyme label may be used alone or in combination with a second enzyme in solution.

7. Methods of detecting aberrant stress marker gene expression or alleles

[0186] The present invention is predicated in part on the discovery that horses subjected to stress have aberrant expression of certain genes or certain alleles of genes, referred to herein as stress marker genes, as compared to horses not subjected to stress. It is proposed that aberrant expression of these genes or their homologues or orthologues will be found in other animals under stress. Accordingly, the present invention features a method for assessing stress or for diagnosing stress or a stress-related condition (stress sequelae) in a subject, which is suitably a mammal, by detecting aberrant expression of a stress marker gene in a biological sample obtained from the subject. According to some embodiments, the related condition is characterized by elevated levels of corticosteroids or their modulators (e.g., corticotropin releasing factor). Illustrative examples of such related conditions include: physical stress such as athletic training and physical trauma; mood disorders such as depression, including major depression, single episode depression, recurrent depression, child abuse induced depression, seasonal affective disorder, postpartum depression, dysthemia, bipolar disorders, and cyclothymia; anxiety disorders including panic, phobias, obsessive-compulsive disorder; post-traumatic stress disorder; and sleep disorders induced by stress; inflammation; pain; chronic fatigue syndrome; stress-induced headache; cancer; human immunodeficiency virus (HIV) infections; neurodegenerative diseases such as Alzheimer's disease, Parkinson's disease and Huntington's disease; gastrointestinal diseases such as ulcers, irritable bowel syndrome, Crohn's disease, spastic colon, diarrhea, and post operative ileus, and colonic hypersensitivity associated by psychopathological disturbances or stress; eating disorders such as anorexia and bulimia nervosa; supranuclear palsy; amyotrophic lateral sclerosis; a decrease in immune function or immunosuppression; hemorrhagic stress; stress-induced psychotic episodes; euthyroid sick syndrome; syndrome of inappropriate antidiarrhetic hormone (ADH); overeating or obesity; infertility; head traumas; spinal cord trauma; ischemic neuronal damage (e.g., cerebral ischemia such as cerebral hippocampal ischemia); excitotoxic neuronal damage; epilepsy; cardiovascular disorders including hypertension, tachycardia and congestive heart failure; stroke; immune dysfunctions including stress-induced immune dysfunctions (e.g., stress induced fevers, porcine stress syndrome, bovine shipping fever, equine paroxysmal fibrillation,

and dysfunctions induced by confinement in chickens, sheering stress in sheep or human-animal interaction related stress in dogs); restraint; behavioral (operant) conditioning; muscular spasms; urinary incontinence; senile dementia of the Alzheimer's type; multiinfarct dementia; amyotrophic lateral sclerosis; chemical dependencies and addictions (e.g., dependencies on alcohol, cocaine, heroin, benzodiazepines, or other drugs); drug and alcohol withdrawal symptoms; osteoporosis; psychosocial dwarfism; hypoglycemia; hair loss; abnormal circadian rhythm; and disorders related to abnormal circadian rhythm such as time zone change syndrome, seasonal affective disorder, sleep deprivation, irregular sleep-wake pattern, delayed sleep phase syndrome, advanced sleep phase syndrome, non-24 hour sleep wake disorder, light-induced clock resetting, REM sleep disorder, hypersomnia, parasomnia, narcolepsy, nocturnal enuresis, restless legs syndrome, sleep apnea, dysthymia, and abnormal circadian rhythm associated with chronic administration and withdrawal of antidepressant agents.

[0187] In order to make the assessment or the diagnosis, it will be desirable to qualitatively or quantitatively determine the levels of stress marker gene transcripts, or the presence of levels of particular alleles of a stress marker gene, or the level or functional activity of stress marker polypeptides. In some embodiments, the presence, degree or stage of stress or risk of development of stress sequelae is diagnosed when a stress marker gene product is present at a detectably lower level in the biological sample as compared to the level at which that gene is present in a reference sample obtained from normal subjects or from subjects not under stress. In other embodiments, the presence, degree or stage of stress or risk of development of stress sequelae is diagnosed when a stress marker gene product is present at a detectably higher level in the biological sample as compared to the level at which that gene is present in a reference sample obtained from normal subjects or from subjects free of stress. Generally, such diagnoses are made when the level or functional activity of a stress marker gene product in the biological sample varies from the level or functional activity of a corresponding stress marker gene product in the reference sample by at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 92%, 94%, 96%, 97%, 98% or 99%, or even by at least about 99.5%, 99.9%, 99.95%, 99.99%, 99.995% or 99.999%, or even by at least about 100%, 200%, 300%, 400%, 500%, 600%, 700%, 800%, 900% or 1000%. Illustrative increases or decreases in the expression level of representative stress marker genes are shown in Table 6.

[0188] The corresponding gene product is generally selected from the same gene product that is present in the biological sample, a gene product expressed from a variant gene (e.g., an homologous or orthologous gene) including an allelic variant, or a splice variant or protein product thereof. In some embodiments, the method comprises measuring the level or functional activity of individual expression products of at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or 30 stress marker genes.

[0189] Generally, the biological sample contains blood, especially peripheral blood, or a fraction or extract thereof. Typically, the biological sample comprises blood cells such as mature, immature and developing leukocytes, including lymphocytes, polymorphonuclear leukocytes, neutrophils, monocytes, reticulocytes, basophils, coelomocytes, hemocytes, eosinophils, megakaryocytes, macrophages, dendritic cells natural killer cells, or fraction of such cells (e.g., a nucleic acid or protein fraction). In specific embodiments, the biological sample comprises leukocytes including peripheral blood mononuclear cells (PBMC).

7.1 Nucleic acid-based diagnostics

[0190] Nucleic acid used in polynucleotide-based assays can be isolated from cells contained in the biological sample, according to standard methodologies (Sambrook, *et al.*, 1989, *supra*; and Ausubel *et al.*, 1994, *supra*). The nucleic acid is typically fractionated (e.g., poly A^+ RNA) or whole cell RNA. Where RNA is used as the subject of detection, it may be desired to convert the RNA to a complementary DNA. In some embodiments, the nucleic acid is amplified by a template-dependent nucleic acid amplification technique. A number of template dependent processes are available to amplify the stress marker sequences present in a given template sample. An exemplary nucleic acid amplification technique is the polymerase chain reaction (referred to as PCR) which is described in detail in U.S. Pat. Nos. 4,683,195, 4,683,202 and 4,800,159, Ausubel *et al.* (*supra*), and in Innis *et al.*, ("PCR Protocols", Academic Press, Inc., San Diego Calif., 1990). Briefly, in PCR, two primer sequences are prepared that are complementary to regions on opposite complementary strands of the marker sequence. An excess of deoxynucleoside triphosphates are added to a reaction mixture along with a DNA polymerase, e.g., *Taq* polymerase. If a cognate stress marker sequence is present in a sample, the primers will bind to the marker and the polymerase will cause the primers to be extended along the marker sequence by adding on nucleotides. By raising and lowering the temperature of the reaction mixture, the extended primers will dissociate from the marker to form reaction products, excess primers will bind to the marker and to the reaction products and the process is repeated. A reverse transcriptase PCR amplification procedure may be performed in order to quantify the amount of mRNA amplified. Methods of reverse transcribing RNA into cDNA are well known and described in Sambrook *et al.*, 1989, *supra*. Alternative methods for reverse transcription utilize thermostable, RNA-dependent DNA polymerases. These methods are described in WO 90/07641. Polymerase chain reaction methodologies are well known in the art.

[0191] In certain advantageous embodiments, the template-dependent amplification involves the quantification of transcripts in real-time. For example, RNA or DNA may be quantified using the Real-Time PCR technique (Higuchi, 1992, *et al.*, *Biotechnology* 10: 413-417). By determining the concentration of the amplified products of the target DNA in PCR reactions that have completed the same number of cycles and are in their linear ranges, it is

possible to determine the relative concentrations of the specific target sequence in the original DNA mixture. If the DNA mixtures are cDNAs synthesized from RNAs isolated from different tissues or cells, the relative abundance of the specific mRNA from which the target sequence was derived can be determined for the respective tissues or cells. This direct proportionality between the concentration of the PCR products and the relative mRNA abundance is only true in the linear range of the PCR reaction. The final concentration of the target DNA in the plateau portion of the curve is determined by the availability of reagents in the reaction mix and is independent of the original concentration of target DNA.

[0192] Another method for amplification is the ligase chain reaction ("LCR"), disclosed in EPO No. 320 308. In LCR, two complementary probe pairs are prepared, and in the presence of the target sequence, each pair will bind to opposite complementary strands of the target such that they abut. In the presence of a ligase, the two probe pairs will link to form a single unit. By temperature cycling, as in PCR, bound ligated units dissociate from the target and then serve as "target sequences" for ligation of excess probe pairs. U.S. Pat. No. 4,883,750 describes a method similar to LCR for binding probe pairs to a target sequence.

[0193] Qβ Replicase, described in PCT Application No. PCT/US87/00880, may also be used. In this method, a replicative sequence of RNA that has a region complementary to that of a target is added to a sample in the presence of an RNA polymerase. The polymerase will copy the replicative sequence that can then be detected.

[0194] An isothermal amplification method, in which restriction endonucleases and ligases are used to achieve the amplification of target molecules that contain nucleotide 5'α-thio-triphosphates in one strand of a restriction site may also be useful in the amplification of nucleic acids in the present invention, Walker *et al.*, (1992, *Proc. Natl. Acad. Sci. U.S.A* **89**: 392-396).

[0195] Strand Displacement Amplification (SDA) is another method of carrying out isothermal amplification of nucleic acids which involves multiple rounds of strand displacement and synthesis, i.e., nick translation. A similar method, called Repair Chain Reaction (RCR), involves annealing several probes throughout a region targeted for amplification, followed by a repair reaction in which only two of the four bases are present. The other two bases can be added as biotinylated derivatives for easy detection. A similar approach is used in SDA. Target specific sequences can also be detected using a cyclic probe reaction (CPR). In CPR, a probe having 3' and 5' sequences of non-specific DNA and a middle sequence of specific RNA is hybridized to DNA that is present in a sample. Upon hybridization, the reaction is treated with RNase H, and the products of the probe identified as distinctive products that are released after digestion. The original template is annealed to another cycling probe and the reaction is repeated.

[0196] Still another amplification method described in GB Application No. 2 202 328, and in PCT Application No. PCT/US89/01025, may be used. In the former application, "modified" primers are used in a PCR-like, template- and enzyme-dependent synthesis. The primers may be modified by labeling with a capture moiety (e.g., biotin) and/or a detector moiety (e.g., enzyme). In the latter application, an excess of labeled probes are added to a sample. In the presence of the target sequence, the probe binds and is cleaved catalytically. After cleavage, the target sequence is released intact to be bound by excess probe. Cleavage of the labeled probe signals the presence of the target sequence.

[0197] Other nucleic acid amplification procedures include transcription-based amplification systems (TAS), including nucleic acid sequence based amplification (NASBA) and 3SR (Kwoh *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.*, **86**: 1173; Gingeras *et al.*, PCT Application WO 88/10315). In NASBA, the nucleic acids can be prepared for amplification by standard phenol/chloroform extraction, heat denaturation of a clinical sample, treatment with lysis buffer and minispin columns for isolation of DNA and RNA or guanidinium chloride extraction of RNA. These amplification techniques involve annealing a primer which has target specific sequences. Following polymerization, DNA/RNA hybrids are digested with RNase H while double stranded DNA molecules are heat denatured again. In either case the single stranded DNA is made fully double stranded by addition of second target specific primer, followed by polymerization. The double-stranded DNA molecules are then multiply transcribed by an RNA polymerase such as T7 or SP6. In an isothermal cyclic reaction, the RNAs are reverse transcribed into single stranded DNA, which is then converted to double stranded DNA, and then transcribed once again with an RNA polymerase such as T7 or SP6. The resulting products, whether truncated or complete, indicate target specific sequences.

[0198] Davey *et al.*, EPO No. 329 822 disclose a nucleic acid amplification process involving cyclically synthesizing single-stranded RNA ("ssRNA"), ssDNA, and double-stranded DNA (dsDNA), which may be used in accordance with the present invention. The ssRNA is a template for a first primer oligonucleotide, which is elongated by reverse transcriptase (RNA-dependent DNA polymerase). The RNA is then removed from the resulting DNA:RNA duplex by the action of ribonuclease H (RNase H, an RNase specific for RNA in duplex with either DNA or RNA). The resultant ssDNA is a template for a second primer, which also includes the sequences of an RNA polymerase promoter (exemplified by T7 RNA polymerase) 5' to its homology to the template. This primer is then extended by DNA polymerase (exemplified by the large "Klenow" fragment of E. coli DNA polymerase I), resulting in a double-stranded DNA ("dsDNA") molecule, having a sequence identical to that of the original RNA between the primers and having additionally, at one end, a promoter sequence. This promoter sequence can be used by the appropriate RNA polymerase to make many RNA copies of the DNA. These copies can then re-enter the cycle leading to very swift amplification.

With proper choice of enzymes, this amplification can be done isothermally without addition of enzymes at each cycle. Because of the cyclical nature of this process, the starting sequence can be chosen to be in the form of either DNA or RNA.

[0199] Miller *et al.* in PCT Application WO 89/06700 disclose a nucleic acid sequence amplification scheme based on the hybridization of a promoter/primer sequence to a target single-stranded DNA ("ssDNA") followed by transcription of many RNA copies of the sequence. This scheme is not cyclic, *i.e.*, new templates are not produced from the resultant RNA transcripts. Other amplification methods include "RACE" and "one-sided PCR" (Frohman, M. A., In: "PCR Protocols: A Guide to Methods and Applications", Academic Press, N.Y., 1990; Ohara *et al.*, 1989, *Proc. Natl Acad. Sci. U.S.A.*, **86**: 5673-567).

[0200] Methods based on ligation of two (or more) oligonucleotides in the presence of nucleic acid having the sequence of the resulting "di-oligonucleotide", thereby amplifying the di-oligonucleotide, may also be used for amplifying target nucleic acid sequences. Wu *et al.*, (1989, *Genomics* **4**: 560).

[0201] Depending on the format, the stress marker nucleic acid of interest is identified in the sample directly using a template-dependent amplification as described, for example, above, or with a second, known nucleic acid following amplification. Next, the identified product is detected. In certain applications, the detection may be performed by visual means (e.g., ethidium bromide staining of a gel). Alternatively, the detection may involve indirect identification of the product *via* chemiluminescence, radioactive scintigraphy of radiolabel or fluorescent label or even via a system using electrical or thermal impulse signals (Affymax Technology; Bellus, 1994, *J Macromol. Sci. Pure, Appl. Chem.*, **A31**(1): 1355-1376).

[0202] In some embodiments, amplification products or "amplicons" are visualized in order to confirm amplification of the stress marker sequences. One typical visualization method involves staining of a gel with ethidium bromide and visualization under UV light. Alternatively, if the amplification products are integrally labeled with radio- or fluorometrically-labeled nucleotides, the amplification products can then be exposed to x-ray film or visualized under the appropriate stimulating spectra, following separation. In some embodiments, visualization is achieved indirectly. Following separation of amplification products, a labeled nucleic acid probe is brought into contact with the amplified stress marker sequence. The probe is suitably conjugated to a chromophore but may be radiolabeled. Alternatively, the probe is conjugated to a binding partner, such as an antigen-binding molecule, or biotin, and the other member of the binding pair carries a detectable moiety or reporter molecule. The techniques involved are well known to those of skill in the art and can be found in many standard texts on molecular protocols (e.g., see Sambrook *et al.*, 1989, *supra* and Ausubel *et al.* 1994, *supra*). For

example, chromophore or radiolabel probes or primers identify the target during or following amplification.

[0203] In certain embodiments, target nucleic acids are quantified using blotting techniques, which are well known to those of skill in the art. Southern blotting involves the use of DNA as a target, whereas Northern blotting involves the use of RNA as a target. Each provide different types of information, although cDNA blotting is analogous, in many aspects, to blotting or RNA species. Briefly, a probe is used to target a DNA or RNA species that has been immobilized on a suitable matrix, often a filter of nitrocellulose. The different species should be spatially separated to facilitate analysis. This often is accomplished by gel electrophoresis of nucleic acid species followed by "blotting" on to the filter. Subsequently, the blotted target is incubated with a probe (usually labeled) under conditions that promote denaturation and rehybridisation. Because the probe is designed to base pair with the target, the probe will bind a portion of the target sequence under renaturing conditions. Unbound probe is then removed, and detection is accomplished as described above.

[0204] Following detection/quantification, one may compare the results seen in a given subject with a control reaction or a statistically significant reference group of normal subjects or of subjects free of stress. In this way, it is possible to correlate the amount of a stress marker nucleic acid detected with the progression or severity of the disease.

[0205] Also contemplated are genotyping methods and allelic discrimination methods and technologies such as those described by Kristensen *et al.* (Biotechniques **30**(2): 318-322), including the use of single nucleotide polymorphism analysis, high performance liquid chromatography, TaqMan™, liquid chromatography, and mass spectrometry.

[0206] Also contemplated are biochip-based technologies such as those described by Hacia *et al.* (1996, *Nature Genetics* **14**: 441-447) and Shoemaker *et al.* (1996, *Nature Genetics* **14**: 450-456). Briefly, these techniques involve quantitative methods for analyzing large numbers of genes rapidly and accurately. By tagging genes with oligonucleotides or using fixed probe arrays, one can employ biochip technology to segregate target molecules as high density arrays and screen these molecules on the basis of hybridization. See also Pease *et al.* (1994, *Proc. Natl. Acad. Sci. U.S.A.* **91**: 5022-5026); Fodor *et al.* (1991, *Science* **251**: 767-773). Briefly, nucleic acid probes to stress marker polynucleotides are made and attached to biochips to be used in screening and diagnostic methods, as outlined herein. The nucleic acid probes attached to the biochip are designed to be substantially complementary to specific expressed stress marker nucleic acids, i.e., the target sequence (either the target sequence of the sample or to other probe sequences, for example in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. This complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with

hybridization between the target sequence and the nucleic acid probes of the present invention. However, if the number of mismatches is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. In certain embodiments, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being desirable, are used to build in a redundancy for a particular target. The probes can be overlapping (i.e. have some sequence in common), or separate.

[0207] As will be appreciated by those of ordinary skill in the art, nucleic acids can be attached to or immobilized on a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of either electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

[0208] In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

[0209] The biochip comprises a suitable solid or semi-solid substrate or solid support. By "substrate" or "solid support" is meant any material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by practitioners in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon™, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials

including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluorescese.

[0210] Generally the substrate is planar, although as will be appreciated by those of skill in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

[0211] In certain embodiments, oligonucleotides probes are synthesized on the substrate, as is known in the art. For example, photoactivation techniques utilizing photopolymerisation compounds and techniques can be used. In an illustrative example, the nucleic acids are synthesized *in situ*, using well known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Pat. Nos. 5,700,637 and 5,445,934; and references cited within; these methods of attachment form the basis of the Affymetrix GeneChip™ technology.

[0212] In an illustrative biochip analysis, oligonucleotide probes on the biochip are exposed to or contacted with a nucleic acid sample suspected of containing one or more stress polynucleotides under conditions favoring specific hybridization. Sample extracts of DNA or RNA, either single or double-stranded, may be prepared from fluid suspensions of biological materials, or by grinding biological materials, or following a cell lysis step which includes, but is not limited to, lysis effected by treatment with SDS (or other detergents), osmotic shock, guanidinium isothiocyanate and lysozyme. Suitable DNA, which may be used in the method of the invention, includes cDNA. Such DNA may be prepared by any one of a number of commonly used protocols as for example described in Ausubel, *et al.*, 1994, *supra*, and Sambrook, *et al.*, *et al.*, 1989, *supra.*

[0213] Suitable RNA, which may be used in the method of the invention, includes messenger RNA, complementary RNA transcribed from DNA (cRNA) or genomic or subgenomic RNA. Such RNA may be prepared using standard protocols as for example described in the relevant sections of Ausubel, *et al.* 1994, *supra* and Sambrook, *et al.* 1989, *supra*).

[0214] cDNA may be fragmented, for example, by sonication or by treatment with restriction endonucleases. Suitably, cDNA is fragmented such that resultant DNA fragments are of a length greater than the length of the immobilized oligonucleotide probe(s) but small enough to allow rapid access thereto under suitable hybridization conditions. Alternatively, fragments of cDNA may be selected and amplified using a suitable nucleotide amplification technique, as described for example above, involving appropriate random or specific primers.

[0215] Usually the target stress marker polynucleotides are detectably labeled so that their hybridization to individual probes can be determined. The target polynucleotides are typically detectably labeled with a reporter molecule illustrative examples of which include chromogens, catalysts, enzymes, fluorochromes, chemiluminescent molecules, bioluminescent molecules, lanthanide ions (e.g., Eu^{34}), a radioisotope and a direct visual label. In the case of a direct visual label, use may be made of a colloidal metallic or non-metallic particle, a dye particle, an enzyme or a substrate, an organic polymer, a latex particle, a liposome, or other vesicle containing a signal producing substance and the like. Illustrative labels of this type include large colloids, for example, metal colloids such as those from gold, selenium, silver, tin and titanium oxide. In some embodiments in which an enzyme is used as a direct visual label, biotinylated bases are incorporated into a target polynucleotide. Hybridization is detected by incubation with streptavidin-reporter molecules.

[0216] Suitable fluorochromes include, but are not limited to, fluorescein isothiocyanate (FITC), tetramethylrhodamine isothiocyanate (TRITC), R-Phycoerythrin (RPE), and Texas Red. Other exemplary fluorochromes include those discussed by Dower *et al.* (International Publication WO 93/06121). Reference also may be made to the fluorochromes described in U.S. Patents 5,573,909 (Singer *et al*), 5,326,692 (Brinkley *et al*). Alternatively, reference may be made to the fluorochromes described in U.S. Patent Nos. 5,227,487, 5,274,113, 5,405,975, 5,433,896, 5,442,045, 5,451,663, 5,453,517, 5,459,276, 5,516,864, 5,648,270 and 5,723,218. Commercially available fluorescent labels include, for example, fluorescein phosphoramidites such as Fluoreprime™ (Pharmacia), Fluoredite™ (Millipore) and FAM (Applied Biosystems International)

[0217] Radioactive reporter molecules include, for example, ^{32}P, which can be detected by an X-ray or phosphoimager techniques.

[0218] The hybrid-forming step can be performed under suitable conditions for hybridizing oligonucleotide probes to test nucleic acid including DNA or RNA. In this regard, reference may be made, for example, to NUCLEIC ACID HYBRIDIZATION, A PRACTICAL APPROACH (Homes and Higgins, eds.) (IRL press, Washington D.C., 1985). In general, whether hybridization takes place is influenced by the length of the oligonucleotide probe and the polynucleotide sequence under test, the pH, the temperature, the concentration of mono- and divalent cations, the proportion of G and C nucleotides in the hybrid-forming region, the viscosity of the medium and the possible presence of denaturants. Such variables also influence the time required for hybridization. The preferred conditions will therefore depend upon the particular application. Such empirical conditions, however, can be routinely determined without undue experimentation.

[0219] In certain advantageous embodiments, high discrimination hybridization conditions are used. For example, reference may be made to Wallace *et al.* (1979, *Nucl. Acids Res.* **6**: 3543) who describe conditions that differentiate the hybridization of 11 to 17 base long oligonucleotide probes that match perfectly and are completely homologous to a target sequence as compared to similar oligonucleotide probes that contain a single internal base pair mismatch. Reference also may be made to Wood *et al.* (1985, *Proc. Natl. Acid. Sci. USA* **82**: 1585) who describe conditions for hybridization of 11 to 20 base long oligonucleotides using 3M tetramethyl ammonium chloride wherein the melting point of the hybrid depends only on the length of the oligonucleotide probe, regardless of its GC content. In addition, Drmanac *et al.* (*supra*) describe hybridization conditions that allow stringent hybridization of 6-10 nucleotide long oligomers, and similar conditions may be obtained most readily by using nucleotide analogues such as 'locked nucleic acids (Christensen *et al.*, 2001 *Biochem J* **354**: 481-4).

[0220] Generally, a hybridization reaction can be performed in the presence of a hybridization buffer that optionally includes a hybridization optimizing agent, such as an isostabilising agent, a denaturing agent and/or a renaturation accelerant. Examples of isostabilising agents include, but are not restricted to, betaines and lower tetraalkyl ammonium salts. Denaturing agents are compositions that lower the melting temperature of double stranded nucleic acid molecules by interfering with hydrogen bonding between bases in a double stranded nucleic acid or the hydration of nucleic acid molecules. Denaturing agents include, but are not restricted to, formamide, formaldehyde, dimethylsulfoxide, tetraethyl acetate, urea, guanidium isothiocyanate, glycerol and chaotropic salts. Hybridization accelerants include heterogeneous nuclear ribonucleoprotein (hnRP) A1 and cationic detergents such as cetyltrimethylammonium bromide (CTAB) and dodecyl trimethylammonium bromide (DTAB), polylysine, spermine, spermidine, single stranded binding protein (SSB), phage T4 gene 32 protein and a mixture of ammonium acetate and ethanol. Hybridization buffers may include target polynucleotides at a concentration between about 0.005 nM and about 50 nM, preferably between about 0.5 nM and 5 nM, more preferably between about 1 nM and 2 nM.

[0221] A hybridization mixture containing the target stress marker polynucleotides is placed in contact with the array of probes and incubated at a temperature and for a time appropriate to permit hybridization between the target sequences in the target polynucleotides and any complementary probes. Contact can take place in any suitable container, for example, a dish or a cell designed to hold the solid support on which the probes are bound. Generally, incubation will be at temperatures normally used for hybridization of nucleic acids, for example, between about 20° C and about 75° C, example, about 25° C, about 30° C, about 35° C, about 40° C, about 45° C, about 50° C, about 55° C, about 60° C, or about 65° C. For probes longer than 14 nucleotides, 20° C to 50° C is desirable. For shorter probes, lower temperatures are

preferred. A sample of target polynucleotides is incubated with the probes for a time sufficient to allow the desired level of hybridization between the target sequences in the target polynucleotides and any complementary probes. For example, the hybridization may be carried out at about 45° C +/-10° C in formamide for 1-2 days.

[0222] After the hybrid-forming step, the probes are washed to remove any unbound nucleic acid with a hybridization buffer, which can typically comprise a hybridization optimising agent in the same range of concentrations as for the hybridization step. This washing step leaves only bound target polynucleotides. The probes are then examined to identify which probes have hybridized to a target polynucleotide.

[0223] The hybridization reactions are then detected to determine which of the probes has hybridized to a corresponding target sequence. Depending on the nature of the reporter molecule associated with a target polynucleotide, a signal may be instrumentally detected by irradiating a fluorescent label with light and detecting fluorescence in a fluorimeter; by providing for an enzyme system to produce a dye which could be detected using a spectrophotometer; or detection of a dye particle or a colored colloidal metallic or non metallic particle using a reflectometer; in the case of using a radioactive label or chemiluminescent molecule employing a radiation counter or autoradiography. Accordingly, a detection means may be adapted to detect or scan light associated with the label which light may include fluorescent, luminescent, focussed beam or laser light. In such a case, a charge couple device (CCD) or a photocell can be used to scan for emission of light from a probe:target polynucleotide hybrid from each location in the micro-array and record the data directly in a digital computer. In some cases, electronic detection of the signal may not be necessary. For example, with enzymatically generated colour spots associated with nucleic acid array format, visual examination of the array will allow interpretation of the pattern on the array. In the case of a nucleic acid array, the detection means is suitably interfaced with pattern recognition software to convert the pattern of signals from the array into a plain language genetic profile. In certain embodiments, oligonucleotide probes specific for different stress marker gene products are in the form of a nucleic acid array and detection of a signal generated from a reporter molecule on the array is performed using a 'chip reader'. A detection system that can be used by a 'chip reader' is described for example by Pirrung *et al* (U.S. Patent No. 5,143,854). The chip reader will typically also incorporate some signal processing to determine whether the signal at a particular array position or feature is a true positive or maybe a spurious signal. Exemplary chip readers are described for example by Fodor *et al* (U.S. Patent No., 5,925,525). Alternatively, when the array is made using a mixture of individually addressable kinds of labeled microbeads, the reaction may be detected using flow cytometry.

7.2 Protein-based diagnostics

[0224] Consistent with the present invention, the presence of an aberrant concentration of a stress marker protein is indicative of the presence, degree or stage of stress or risk of development of stress sequelae. Stress marker protein levels in biological samples can be assayed using any suitable method known in the art. For example, when a stress marker protein is an enzyme, the protein can be quantified based upon its catalytic activity or based upon the number of molecules of the protein contained in a sample. Antibody-based techniques may be employed, such as, for example, immunohistological and immunohistochemical methods for measuring the level of a protein of interest in a tissue sample. For example, specific recognition is provided by a primary antibody (polyclonal or monoclonal) and a secondary detection system is used to detect presence (or binding) of the primary antibody. Detectable labels can be conjugated to the secondary antibody, such as a fluorescent label, a radiolabel, or an enzyme (e.g., alkaline phosphatase, horseradish peroxidase) which produces a quantifiable, e.g., colored, product. In another suitable method, the primary antibody itself can be detectably labeled. As a result, immunohistological labeling of a tissue section is provided. In some embodiments, a protein extract is produced from a biological sample (e.g., tissue, cells) for analysis. Such an extract (e.g., a detergent extract) can be subjected to western-blot or dot/slot assay of the level of the protein of interest, using routine immunoblotting methods (Jalkanen *et al.*, 1985, *J. Cell. Biol.* **101**: 976-985; Jalkanen *et al.*, 1987, *J. Cell. Biol.* **105**: 3087-3096).

[0225] Other useful antibody-based methods include immunoassays, such as the enzyme-linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). For example, a protein-specific monoclonal antibody, can be used both as an immunoadsorbent and as an enzyme-labeled probe to detect and quantify a stress marker protein of interest. The amount of such protein present in a sample can be calculated by reference to the amount present in a standard preparation using a linear regression computer algorithm (see Lacobilli *et al.*, 1988, *Breast Cancer Research and Treatment* **11**: 19-30). In other embodiments, two different monoclonal antibodies to the protein of interest can be employed, one as the immunoadsorbent and the other as an enzyme-labeled probe.

[0226] Additionally, recent developments in the field of protein capture arrays permit the simultaneous detection and/or quantification of a large number of proteins. For example, low-density protein arrays on filter membranes, such as the universal protein array system (Ge, 2000 *Nucleic Acids Res.* 28(2):e3) allow imaging of arrayed antigens using standard ELISA techniques and a scanning charge-coupled device (CCD) detector. Immuno-sensor arrays have also been developed that enable the simultaneous detection of clinical analytes. It is now possible using protein arrays, to profile protein expression in bodily fluids,

such as in sera of healthy or diseased subjects, as well as in subjects pre- and post-drug treatment.

[0227] Protein capture arrays typically comprise a plurality of protein-capture agents each of which defines a spatially distinct feature of the array. The protein-capture agent can be any molecule or complex of molecules which has the ability to bind a protein and immobilize it to the site of the protein-capture agent on the array. The protein-capture agent may be a protein whose natural function in a cell is to specifically bind another protein, such as an antibody or a receptor. Alternatively, the protein-capture agent may instead be a partially or wholly synthetic or recombinant protein which specifically binds a protein. Alternatively, the protein-capture agent may be a protein which has been selected *in vitro* from a mutagenized, randomized, or completely random and synthetic library by its binding affinity to a specific protein or peptide target. The selection method used may optionally have been a display method such as ribosome display or phage display, as known in the art. Alternatively, the protein-capture agent obtained *via in vitro* selection may be a DNA or RNA aptamer which specifically binds a protein target (see, e.g., Potyrailo *et al.*, 1998 *Anal. Chem.* 70:3419-3425; Cohen *et al.*, 1998, *Proc. Natl. Acad. Sci. USA* 95:14272-14277; Fukuda, *et al.*, 1997 *Nucleic Acids Symp. Ser.* 37:237-238; available from SomaLogic). For example, aptamers are selected from libraries of oligonucleotides by the Selex™ process and their interaction with protein can be enhanced by covalent attachment, through incorporation of brominated deoxyuridine and UV-activated crosslinking (photoaptamers). Aptamers have the advantages of ease of production by automated oligonucleotide synthesis and the stability and robustness of DNA; universal fluorescent protein stains can be used to detect binding. Alternatively, the *in vitro* selected protein-capture agent may be a polypeptide (e.g., an antigen) (see, e.g., Roberts and Szostak, 1997 *Proc. Natl. Acad. Sci. USA*, 94:12297-12302).

[0228] An alternative to an array of capture molecules is one made through 'molecular imprinting' technology, in which peptides (e.g., from the C-terminal regions of proteins) are used as templates to generate structurally complementary, sequence-specific cavities in a polymerizable matrix; the cavities can then specifically capture (denatured) proteins which have the appropriate primary amino acid sequence (e.g., available from ProteinPrint™ and Aspira Biosystems).

[0229] Exemplary protein capture arrays include arrays comprising spatially addressed antigen-binding molecules, commonly referred to as antibody arrays, which can facilitate extensive parallel analysis of numerous proteins defining a proteome or subproteome. Antibody arrays have been shown to have the required properties of specificity and acceptable background, and some are available commercially (e.g., BD Biosciences, Clontech, BioRad and Sigma). Various methods for the preparation of antibody arrays have been reported (see, e.g.,

Lopez *et al.*, 2003 *J. Chromatogr. B* 787:19-27; Cahill, 2000 *Trends in Biotechnology* 7:47-51; U.S. Pat. App. Pub. 2002/0055186; U.S. Pat. App. Pub. 2003/0003599; PCT publication WO 03/062444; PCT publication WO 03/077851; PCT publication WO 02/59601; PCT publication WO 02/39120; PCT publication WO 01/79849; PCT publication WO 99/39210). The antigen-binding molecules of such arrays may recognize at least a subset of proteins expressed by a cell or population of cells, illustrative examples of which include growth factor receptors, hormone receptors, neurotransmitter receptors, catecholamine receptors, amino acid derivative receptors, cytokine receptors, extracellular matrix receptors, antibodies, lectins, cytokines, serpins, proteases, kinases, phosphatases, ras-like GTPases, hydrolases, steroid hormone receptors, transcription factors, heat-shock transcription factors, DNA-binding proteins, zinc-finger proteins, leucine-zipper proteins, homeodomain proteins, intracellular signal transduction modulators and effectors, apoptosis-related factors, DNA synthesis factors, DNA repair factors, DNA recombination factors, cell-surface antigens, hepatitis C virus (HCV) proteases and HIV proteases.

[0230] Antigen-binding molecules for antibody arrays are made either by conventional immunization (e.g., polyclonal sera and hybridomas), or as recombinant fragments, usually expressed in *E. coli*, after selection from phage display or ribosome display libraries (e.g., available from Cambridge Antibody Technology, BioInvent, Affitech and Biosite). Alternatively, 'combibodies' comprising non-covalent associations of VH and VL domains, can be produced in a matrix format created from combinations of diabody-producing bacterial clones (e.g., available from Domantis). Exemplary antigen-binding molecules for use as protein-capture agents include monoclonal antibodies, polyclonal antibodies, Fv, Fab, Fab' and $F(ab')_2$ immunoglobulin fragments, synthetic stabilized Fv fragments, e.g., single chain Fv fragments (scFv), disulfide stabilized Fv fragments (dsFv), single variable region domains (dAbs) minibodies, combibodies and multivalent antibodies such as diabodies and multi-scFv, single domains from camelids or engineered human equivalents.

[0231] Individual spatially distinct protein-capture agents are typically attached to a support surface, which is generally planar or contoured. Common physical supports include glass slides, silicon, microwells, nitrocellulose or PVDF membranes, and magnetic and other microbeads.

[0232] While microdrops of protein delivered onto planar surfaces are widely used, related alternative architectures include CD centrifugation devices based on developments in microfluidics (e.g., available from Gyros) and specialized chip designs, such as engineered microchannels in a plate (e.g., The Living Chip™, available from Biotrove) and tiny 3D posts on a silicon surface (e.g., available from Zyomyx).

[0233] Particles in suspension can also be used as the basis of arrays, providing they are coded for identification; systems include color-coding for microbeads (e.g., available from Luminex, Bio-Rad and Nanomics Biosystems) and semiconductor nanocrystals (e.g., Qdots™, available from Quantum Dots), and barcoding for beads (UltraPlex™, available from Smartbeads) and multimetal microrods (Nanobarcodes™ particles, available from Surromed). Beads can also be assembled into planar arrays on semiconductor chips (e.g., available from LEAPS technology and BioArray Solutions). Where particles are used, individual protein-capture agents are typically attached to an individual particle to provide the spatial definition or separation of the array. The particles may then be assayed separately, but in parallel, in a compartmentalized way, for example in the wells of a microtiter plate or in separate test tubes.

[0234] In operation, a protein sample, which is optionally fragmented to form peptide fragments (see, e.g., U.S. Pat. App. Pub. 2002/0055186), is delivered to a protein-capture array under conditions suitable for protein or peptide binding, and the array is washed to remove unbound or non-specifically bound components of the sample from the array. Next, the presence or amount of protein or peptide bound to each feature of the array is detected using a suitable detection system. The amount of protein bound to a feature of the array may be determined relative to the amount of a second protein bound to a second feature of the array. In certain embodiments, the amount of the second protein in the sample is already known or known to be invariant.

[0235] For analyzing differential expression of proteins between two cells or cell populations, a protein sample of a first cell or population of cells is delivered to the array under conditions suitable for protein binding. In an analogous manner, a protein sample of a second cell or population of cells to a second array, is delivered to a second array which is identical to the first array. Both arrays are then washed to remove unbound or non-specifically bound components of the sample from the arrays. In a final step, the amounts of protein remaining bound to the features of the first array are compared to the amounts of protein remaining bound to the corresponding features of the second array. To determine the differential protein expression pattern of the two cells or populations of cells, the amount of protein bound to individual features of the first array is subtracted from the amount of protein bound to the corresponding features of the second array.

[0236] In an illustrative example, fluorescence labeling can be used for detecting protein bound to the array. The same instrumentation as used for reading DNA microarrays is applicable to protein-capture arrays. For differential display, capture arrays (e.g. antibody arrays) can be probed with fluorescently labeled proteins from two different cell states, in which cell lysates are labeled with different fluorophores (e.g., Cy-3 and Cy-5) and mixed, such that the color acts as a readout for changes in target abundance. Fluorescent readout sensitivity can

be amplified 10-100 fold by tyramide signal amplification (TSA) (e.g., available from PerkinElmer Lifesciences). Planar waveguide technology (e.g., available from Zeptosens) enables ultrasensitive fluorescence detection, with the additional advantage of no washing procedures. High sensitivity can also be achieved with suspension beads and particles, using phycoerythrin as label (e.g., available from Luminex) or the properties of semiconductor nanocrystals (e.g., available from Quantum Dot). Fluorescence resonance energy transfer has been adapted to detect binding of unlabelled ligands, which may be useful on arrays (e.g., available from Affibody). Several alternative readouts have been developed, including adaptations of surface plasmon resonance (e.g., available from HTS Biosystems and Intrinsic Bioprobes), rolling circle DNA amplification (e.g., available from Molecular Staging), mass spectrometry (e.g., available from Sense Proteomic, Ciphergen, Intrinsic and Bioprobes), resonance light scattering (e.g., available from Genicon Sciences) and atomic force microscopy (e.g., available from BioForce Laboratories). A microfluidics system for automated sample incubation with arrays on glass slides and washing has been co-developed by NextGen and Perkin Elmer Life Sciences.

[0237] In certain embodiments, the techniques used for detection of stress marker expression products will include internal or external standards to permit quantitative or semi-quantitative determination of those products, to thereby enable a valid comparison of the level or functional activity of these expression products in a biological sample with the corresponding expression products in a reference sample or samples. Such standards can be determined by the skilled practitioner using standard protocols. In specific examples, absolute values for the level or functional activity of individual expression products are determined.

[0238] In specific embodiments, the diagnostic method is implemented using a system as disclosed, for example, in International Publication No. WO 02/090579 and in copending PCT Application No. PCT/AU03/01517 filed November 14, 2003, comprising at least one end station coupled to a base station. The base station is typically coupled to one or more databases comprising predetermined data from a number of individuals representing the level or functional activity of stress marker expression products, together with indications of the actual status of the individuals (e.g., presence, absence, degree, stage of stress or risk of development of stress sequelae) when the predetermined data was collected. In operation, the base station is adapted to receive from the end station, typically *via* a communications network, subject data representing a measured or normalized level or functional activity of at least one expression product in a biological sample obtained from a test subject and to compare the subject data to the predetermined data stored in the database(s). Comparing the subject and predetermined data allows the base station to determine the status of the subject in accordance with the results of the comparison. Thus, the base station attempts to identify individuals having

similar parameter values to the test subject and once the status has been determined on the basis of that identification, the base station provides an indication of the diagnosis to the end station.

7.3 Kits

[0239] All the essential materials and reagents required for detecting and quantifying stress marker gene expression products may be assembled together in a kit. The kits may also optionally include appropriate reagents for detection of labels, positive and negative controls, washing solutions, blotting membranes, microtiter plates dilution buffers and the like. For example, a nucleic acid-based detection kit may include (i) a stress marker polynucleotide (which may be used as a positive control), (ii) a primer or probe that specifically hybridizes to a stress marker polynucleotide. Also included may be enzymes suitable for amplifying nucleic acids including various polymerases (Reverse Transcriptase, Taq, Sequenase™ DNA ligase etc. depending on the nucleic acid amplification technique employed), deoxynucleotides and buffers to provide the necessary reaction mixture for amplification. Such kits also generally will comprise, in suitable means, distinct containers for each individual reagent and enzyme as well as for each primer or probe. Alternatively, a protein-based detection kit may include (i) a stress marker polypeptide (which may be used as a positive control), (ii) an antigen-binding molecule that is immuno-interactive with a stress marker polynucleotide. The kit can also feature various devices and reagents for performing one of the assays described herein; and/or printed instructions for using the kit to quantify the expression of a stress marker gene.

7.4 Monitoring immune function

[0240] The present invention also provides methods for monitoring immune function by measuring the level or functional activity of an expression product of one or more stress marker genes in a subject. When the measured level or functional activity is the same as or similar to the measured level or functional activity of a corresponding expression product in a reference sample obtained from one or more normal subjects or from one or more subjects not under stress, this generally indicates that the subject is not under stress and has normal immune function. Conversely, when the measured level or functional activity is different than the measured level or functional activity of the corresponding expression product, this generally indicates that the subject is under stress and consequently has reduced immune function (or immunosuppression).

[0241] The normalcy of immune function is important to the effective combat of disease and ultimate protection to natural challenge. In addition, it is vital to obtain an effective immune response to vaccination, and, in this regard, the identified stress markers can also be used to monitor the immune system of individuals so that vaccination can be timed to produce an immune response that leads to the best level of protection. For instance, in the context of

athletic performance animals such as human athletes and racehorses, monitoring the immune system in this fashion allows the performance animal or his/her/its trainer to reduce potential stressors that may lead to an inappropriate or non-protective immune response to vaccination. When the performance animal's immune system has recovered, as determined by monitoring using the identified stress markers, vaccination can be performed.

[0242] Also, the identified stress markers can be used to assess the immune system's response to vaccine preparations. An inappropriate immune response to an initial vaccination may lead to a decision to revaccinate, or to modify the vaccination regimen, or to delay a vaccination regimen until potential stressors (that affect immune function) are removed and the animal's immune system has recovered.

[0243] By way of example, there are known vaccine preparations available for Equine Herpes Virus. It is widely used in the veterinary field, especially in pregnant mares so that foals will be afforded some protection through transfer of milk antibodies (colostrum). Pregnancy and the puerperal periods are times of high stress and immune modulation. Immune function can be monitored during these periods using the identified stress markers, to time vaccination so that appropriate and protective vaccine responses are generated. Alternatively, stress marker levels could be used to modify the vaccination regimen depending upon the monitored immune response to vaccination.

8. Methods of treatment or prophylaxis

[0244] The present invention also extends to the treatment or prevention of stress in subjects following positive diagnosis for the risk of development of stress sequelae in the subjects. Generally, the treatment will include administering to a positively diagnosed subject an effective amount of an agent or therapy that ameliorates the symptoms or reverses the development of stress or that reduces or abrogates a stress-related condition as described for example above, or that reduces potential of the subject to developing a stress-related condition. Current agents suitable for treating stress include, but are not limited to corticotropin-releasing factor antagonists as described, for example, in U.S. Patent Nos. 6,723,721, 6,670,371, 6,664,261, 6,586,456, 6,548,509, 6,323,312, 6,255,310; glucocorticoid receptor antagonists as disclosed in U.S. Patent Application Publication No. 20020169152; adenosine compounds as described, for example, in U.S. Patent No. 6,642,209; nitric oxide donors as described, for example in U.S. Patent No. 6,455,542; nutritional compositions as described for example in U.S. Patent Nos. 6,444,700, 6,391,332 and 6,218,420; herbal extracts as disclosed, for example, in U.S. Patent No. 6,416,795; NK-1 receptor antagonists as disclosed, for example, in U.S. Patent No. 6,087,348; fatty acid-based compositions as described, for example, in U.S. Patent No. 6,077,867; peptide derivatives from yeast as disclosed, for example, in U.S. Patent

Application Publication No. 20040101934; and zinc ionophores as described, for example, in U.S. Patent Application No. 20020183300;

[0245] Alternatively, the subject may be treated using stress-relieving processes known in the art including for example: removing or decreasing the level of stressor in the subject's environment; and altering ion flux across cell membranes with electric fields as described in U.S. Patent Application Publication No. 20030233124.

[0246] However, it will be understood that the present invention encompasses any agent or process that is useful for treating or preventing stress and is not limited to the aforementioned illustrative compounds and formulations.

[0247] Typically, stress-relieving agents will be administered in pharmaceutical (or veterinary) compositions together with a pharmaceutically acceptable carrier and in an effective amount to achieve their intended purpose. The dose of active compounds administered to a subject should be sufficient to achieve a beneficial response in the subject over time such as a reduction in, or relief from, the symptoms of stress. The quantity of the pharmaceutically active compounds(s) to be administered may depend on the subject to be treated inclusive of the age, sex, weight and general health condition thereof. In this regard, precise amounts of the active compound(s) for administration will depend on the judgement of the practitioner. In determining the effective amount of the active compound(s) to be administered in the treatment or prevention of stress, the physician or veterinarian may evaluate severity of any symptom associated with the presence of stress including symptoms related to stress sequelae as mentioned above. In any event, those of skill in the art may readily determine suitable dosages of the stress relieving agents and suitable treatment regimens without undue experimentation.

[0248] The stress relieving agents may be administered in concert with adjunctive therapies to reduce an aberrant immune response in the subject. Illustrative examples of such adjunctive therapies include but are not limited to, removal of the stressor, yoga, meditation, acupuncture, massage, mild exercise and breathing exercises.

[0249] In order that the invention may be readily understood and put into practical effect, particular preferred embodiments will now be described by way of the following non-limiting examples.

EXAMPLES

EXAMPLE 1

IDENTIFICATION OF SPECIFIC DIAGNOSTIC GENES FOR STRESS

[0250] Blood samples obtained from 20 animals exposed to transport stress over 48 hours were analyzed using GeneChips™ (method of use is described below in detail in "Generation of Gene Expression Data") containing thousands of genes expressed in white blood cells of horses. Analysis of these data (see "Identification of Responding Genes and Demonstration of Diagnostic Potential" below) reveals specific genes that are expressed differentially at day 0 through to day 28. It is possible to design an assay that measures the RNA level in the sample using at least one and desirably at least two stress marker genes representative sequences of which are set forth in SEQ ID NO: 1, 3, 4, 5, 7, 9, 11, 13, 15, 16, 17, 19, 21, 23, 24, 25, 26, 28, 29, 30, 32, 33, 34, 35, 37, 38, 39, 40, 41, 42, 44, 46, 48, 50, 51, 52, 54, 55, 56, 57, 59, 62, 63, 64, 66, 68, 70, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 90, 91, 92, 93, 95, 96, 97, 99, 101, 103, 105, 107, 108, 109, 111, 113, 115, 117, 118, 119, 121, 123, 125, 126, 127, 129, 130, 131, 133, 135, 137, 139, 141, 143, 144, 145, 147, 148, 150, 151, 153, 155, 156, 158, 160, 161, 163, 164, 165, 167, 169, 170, 171, 173, 175, 176, 178, 180, 182, 184, 185, 186, 187, 188, 190, 192, 194, 195, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 233, 234, 236, 238, 239, 240, 241, 242, 243, 244, 246 or 248.

Materials and Methods

Blood Collection

[0251] Blood is collected from a horse (in a non-agitated state) for the purpose of extraction of high quality RNA or protein. Suitable blood collection tubes for the collection, preservation, transport and isolation of RNA include PAXgene™ tubes (PreAnalytix Inc., Valencia, CA, USA). Alternatively, blood can be collected into tubes containing solutions designed for the preservation of nucleic acids (available from Roche, Ambion, Invitrogen and ABI). For the determination of protein levels, 50 mL of blood is prevented from clotting by collection into a tube containing 4 mL of 4% sodium citrate. White blood cells and plasma are isolated and stored frozen for later analysis and detection of specific proteins. PAXgene tubes can be kept at room temperature prior to RNA extraction. Clinical signs are recorded in a standard format.

Total RNA Extraction

[0252] A kit available from Qiagen Inc (Valencia, CA, USA) has the reagents and instructions for the isolation of total RNA from 2.5 mL blood collected in the PAXgene Blood RNA Tube. Isolation begins with a centrifugation step to pellet nucleic acids in the PAXgene

blood RNA tube. The pellet is washed and resuspended and incubated in optimized buffers together with Proteinase K to bring about protein digestion. An additional centrifugation is carried out to remove residual cell debris and the supernatant is transferred to a fresh microcentrifuge tube. Ethanol is added to adjust binding conditions, and the lysate is applied to the PAXgene RNA spin column. During brief centrifugation, RNA is selectively bound to the silica-gel membrane as contaminants pass through. Remaining contaminants are removed in three efficient wash steps and RNA is then eluted in Buffer BR5.

[0253] Determination of RNA quantity and quality is necessary prior to proceeding and can be achieved using an Agilent Bioanalyzer and Absorbance 260/280 ratio using a spectrophotometer.

DNA Extraction

[0254] A kit available from Qiagen Inc (Valencia, CA, USA) has the reagents and instructions for the isolation of total DNA from 8.5 mL blood collected in the PAXgene Blood DNA Tube. Isolation begins with the addition of additional lysis solution followed by a centrifugation step. The pellet is washed and resuspended and incubated in optimized buffers together with Proteinase K to bring about protein digestion. DNA is precipitated using alcohol and an additional centrifugation is carried out to pellet the nucleic acid. Remaining contaminants are removed in a wash step and the DNA is then resuspended in Buffer BG4.

[0255] Determination of DNA quantity and quality is necessary prior to proceeding and can be achieved using a spectrophotometer or agarose gel electrophoresis.

Generation of Gene Expression Data

Choice of Method

[0256] Measurement of specific RNA levels in a tissue sample can be achieved using a variety of technologies. Two common and readily available technologies that are well known in the art are:

[0257] GeneChip® analysis using Affymetrix technology.

[0258] Real-Time Polymerase Chain Reaction (TaqMan™ from Applied Biosystems for example).

[0259] GeneChips® quantitate RNA by detection of labeled cRNA hybridized to short oligonucleotides built on a silicon substrate. Details on the technology and methodology can be found at www.affymetrix.com.

[0260] Real-Time Polymerase Chain Reaction (RT-PCR) quantitates RNA using two PCR primers, a labeled probe and a thermostable DNA polymerase. As PCR product is

generated a dye is released into solution and detected. Internal controls such as 18S RNA probes are often used to determine starting levels of total RNA in the sample. Each gene and the internal control are run separately. Details on the technology and methods can be found at www.appliedbiosytems.com or www.qiagen.com or www.biorad..com. Applied Biosystems offer a service whereby the customer provides DNA sequence information and payment and is supplied in return all of the reagents required to perform RT-PCR analysis on individual genes.

[0261] GeneChip® analysis has the advantage of being able to analyze thousands of genes at a time. However it is expensive and takes over 3 days to perform a single assay. RT-PCR generally only analyses one gene at a time, but is inexpensive and can be completed within a single day.

[0262] RT-PCR is the method of choice for gene expression analysis if the number of specific genes to be analyzed is less than 20. GeneChip® or other gene expression analysis technologies (such as Illumina Bead Arrays) are the method of choice when many genes need to be analysed simultaneously.

[0263] The methodology for GeneChip® data generation and analysis and Real Time PCR is presented below in brief.

GeneChip® Data Generation

cDNA & cRNA Generation:

[0264] The following method for cDNA and cRNA generation from total RNA has been adapted from the protocol provided and recommended by Affymetrix (www.affymetrix.com).

[0265] The steps are:

[0266] • A total of 3 μg of total RNA is used as a template to generate double stranded cDNA.

[0267] • cRNA is generated and labeled using biotinylated Uracil (dUTP).

[0268] • biotin-labeled cRNA is cleaned and the quantity determined using a spectrophotometer and MOPS gel analysis.

[0269] • labeled cRNA is fragmented to ~ 300bp in size.

[0270] • RNA quantity is determined on an Agilent "Lab-on-a-Chip" system (Agilent Technologies).

Hybridization, Washing & Staining:

[0271] The steps are:

[0272] • A hybridization cocktail is prepared containing 0.05 μg/μL of labeled and fragmented cRNA, spike-in positive hybridization controls, and the Affymetrix oligonucleotides B2, bioB, bioC, bioD and cre.

[0273] • The final volume (80 μL) of the hybridization cocktail is added to the GeneChip™ cartridge.

[0274] • The cartridge is placed in a hybridization oven at constant rotation for 16 hours.

[0275] • The fluid is removed from the GeneChip™ and stored.

[0276] • The GeneChip™ is placed in the fluidics station.

[0277] • The experimental conditions for each GeneChip™ are recorded as an .EXP file.

[0278] • All washing and staining procedures are carried out by the Affymetrix fluidics station with an attendant providing the appropriate solutions.

[0279] • The GeneChip™ is washed, stained with steptavidin-phycoerythin dye and then washed again using low salt solutions.

[0280] • After the wash protocols are completed, the dye on the probe array is 'excited' by laser and the image captured by a CCD camera using an Affymetrix Scanner (manufactured by Agilent).

Scanning & Data File Generation:

[0281] The scanner and MAS 5 software generates an image file from a single GeneChip™ called a .DAT file (see figure overleaf).

[0282] The .DAT file is then pre-processed prior to any statistical analysis.

[0283] Data pre-processing steps (prior to any statistical analysis) include:

[0284] • .DAT File Quality Control (QC).

[0285] • .CEL File Generation.

[0286] • Scaling and Normalization.

.DAT File Quality Control

[0287] The .DAT file is an image. The image is inspected manually for artifacts (e.g. high/low intensity spots, scratches, high regional or overall background). (The B2 oligonucleotide hybridization performance is easily identified by an alternating pattern of intensities creating a border and array name.) The MAS 5 software used the B2 oligonucleotide border to align a grid over the image so that each square of oligonucleotides was centered and identified.

[0288] The other spiked hybridization controls (bioB, bioC, bioD and cre) are used to evaluate sample hybridization efficiency by reading "present" gene detection calls with increasing signal values, reflecting their relative concentrations. (If the .DAT file is of suitable quality it is converted to an intensity data file (.CEL file) by Affymetrix MAS 5 software).

.CEL File Generation

[0289] The .CEL files generated by the MAS 5 software from .DAT files contain calculated raw intensities for the probe sets. Gene expression data is obtained by subtracting a calculated background from each cell value. To eliminate negative intensity values, a noise correction fraction based from a local noise value from the standard deviation of the lowest 2% of the background is applied.

[0290] All .CEL files generated from the GeneChip™ are subjected to specific quality metrics parameters.

[0291] Some metrics are routinely recommended by Affymetrix and can be determined from Affymetrix internal controls provided as part of the GeneChip™. Other metrics are based on experience and the processing of many GeneChip™.

Analysis of GeneChip® Data

[0292] Three illustrative approaches to normalizing data might be used:

[0293] • Affymetrix MAS 5 Algorithm.

[0294] • Robust Multi-chip Analysis (RMA) algorithm of Irizarry (Irizarray *et al.*, 2002, *Biostatistics* (in print)).

[0295] • Robust Multi-chip Analysis Saved model (RMAS).

[0296] Those of skill in the art will recognize that many other approaches might be adopted, without materially affecting the invention.

Affymetrix MAS 5 Algorithm

[0297] .CEL files are used by Affymetrix MAS 5 software to normalize or scale the data. Scaled data from one chip are compared to similarly scaled data from other chips.

[0298] Affymetrix MAS 5 normalization is achieved by applying the default "Global Scaling" option of the MAS 5 algorithm to the .CEL files. This procedure subtracts a robust estimate of the center of the distribution of probe values, and divides by a robust estimate of the probe variability. This produces a set of chips with common location and scale at the probe level.

[0299] Gene expression indices are generated by a robust averaging procedure on all the probe pairs for a given gene. The results are constrained to be non-negative.

[0300] Given that scaling takes place at the level of the probe, rather than at the level of the gene, it is possible that even after normalization there may be chip-to-chip differences in overall gene expression level. Following standard MAS5 normalization, values for each gene were de-trended with respect to median chip intensity. That is, values for each gene were regressed on the median chip intensity, and residuals were calculated. These residuals were taken as the de-trended estimates of expression for each gene

[0301] Median chip intensity was calculated using the Affymetrix MAS5 algorithm, but with a scale factor fixed at one.

RMAS Analysis

[0302] This method is identical to the RMA method, with the exception that probe weights and target quantiles are established using a long term library of chip .cel files, and are not re-calculated for these specific chips. Again, normalization occurs at the probe level.

Real-Time PCR Data Generation

[0303] Background information for conducting Real-time PCR may be obtained, for example, at http://dorakmt.tripod.com/genetics/realtime.html and in a review by Bustin SA (2000, *J Mol Endocrinol* 25:169-193).

TaqMan™ Primer and Probe Design Guidelines:

[0304] 1. The Primer Express™ (ABI) software designs primers with a melting temperature (Tm) of 58-60° C, and probes with a Tm value of 10° C higher. The Tm of both primers should be equal;

[0305] 2. Primers should be 15-30 bases in length;

[0306] 3. The G+C content should ideally be 30-80%. If a higher G+C content is unavoidable, the use of high annealing and melting temperatures, cosolvents such as glycerol, DMSO, or 7-deaza-dGTP may be necessary;

[0307] 4. The run of an identical nucleotide should be avoided. This is especially true for G, where runs of four or more Gs is not allowed;

[0308] 5. The total number of Gs and Cs in the last five nucleotides at the 3' end of the primer should not exceed two (the newer version of the software has an option to do this automatically). This helps to introduce relative instability to the 3' end of primers to reduce non-specific priming. The primer conditions are the same for SYBR Green assays;

[0309] 6. Maximum amplicon size should not exceed 400 bp (ideally 50-150 bases). Smaller amplicons give more consistent results because PCR is more efficient and more tolerant of reaction conditions (the short length requirement has nothing to do with the efficiency of 5' nuclease activity);

[0310] 7. The probes should not have runs of identical nucleotides (especially four or more consecutive Gs), G+C content should be 30-80%, there should be more Cs than Gs, and not a G at the 5' end. The higher number of Cs produces a higher ΔRn. The choice of probe should be made first;

[0311] 8. To avoid false-positive results due to amplification of contaminating genomic DNA in the cDNA preparation, it is preferable to have primers spanning exon-exon junctions. This way, genomic DNA will not be amplified (the PDAR kit for human GAPDH amplification has such primers);

[0312] 9. If a TaqMan™ probe is designed for allelic discrimination, the mismatching nucleotide (the polymorphic site) should be in the middle of the probe rather than at the ends;

[0313] 10. Use primers that contain dA nucleotides near the 3' ends so that any primer-dimer generated is efficiently degraded by AmpErase™ UNG (mentioned in p.9 of the manual for EZ RT-PCR kit; P/N 402877). If primers cannot be selected with dA nucleotides near the ends, the use of primers with 3' terminal dU-nucleotides should be considered.

[0314] (See also the general principles of PCR Primer Design by Invitrogen.)

General Method:

[0315] 1. Reverse transcription of total RNA to cDNA should be done with random hexamers (not with oligo-dT). If oligo-dT has to be used long mRNA transcripts or amplicons greater than two kilobases upstream should be avoided, and 18S RNA cannot be used as normaliser;

[0316] 2. Multiplex PCR will only work properly if the control primers are limiting (ABI control reagents do not have their primers limited);

[0317] 3. The range of target cDNA used is 10 ng to 1 μg. If DNA is used (mainly for allelic discrimination studies), the optimum amount is 100 ng to 1 μg;

[0318] 4. It is ideal to treat each RNA preparation with RNAse free DNAse to avoid genomic DNA contamination. Even the best RNA extraction methods yield some genomic DNA. Of course, it is ideal to have primers not amplifying genomic DNA at all but sometimes this may not be possible;

[0319] 5. For optimal results, the reagents (before the preparation of the PCR mix) and the PCR mixture itself (before loading) should be vortexed and mixed well. Otherwise there may be shifting Rn value during the early (0 - 5) cycles of PCR. It is also important to add probe to the buffer component and allow it to equilibrate at room temperature prior to reagent mix formulation.

TaqMan™ Primers and Probes:

[0320] The TaqMan™ probes ordered from ABI at midi-scale arrive already resuspended at 100 μM. If a 1/20 dilution is made, this gives a 5 μM solution. This stock solution should be aliquoted, frozen and kept in the dark. Using 1 μL of this in a 50 μL reaction gives the recommended 100 nM final concentration.

[0321] The primers arrive lyophilized with the amount given on the tube in pmols (such as 150.000 pmol which is equal to 150 nmol). If X nmol of primer is resuspended in X μL of H_2O, the resulting solution is 1 mM. It is best to freeze this stock solution in aliquots. When the 1 mM stock solution is diluted 1/100, the resulting working solution will be 10 μM. To get the recommended 50 - 900 nM final primer concentration in 50 μL reaction volume, 0.25 - 4.50 μL should be used per reaction (2.5 μL for 500 nM final concentration).

[0322] The PDAR primers and probes are supplied as a mix in one tube. They have to be used 2.5 μL in a 50 μL reaction volume.

Setting up One-step TaqMan™ Reaction:

[0323] One-step real-time PCR uses RNA (as opposed to cDNA) as a template. This is the preferred method if the RNA solution has a low concentration but only if singleplex reactions are run. The disadvantage is that RNA carryover prevention enzyme AmpErase cannot be used in one-step reaction format. In this method, both reverse transcriptase and real-time PCR take place in the same tube. The downstream PCR primer also acts as the primer for reverse transcriptase (random hexamers or oligo-dT cannot be used for reverse transcription in

one-step RT-PCR). One-step reaction requires higher dNTP concentration (greater than or equal to 300 mM vs 200 mM) as it combines two reactions needing dNTPs in one. A typical reaction mix for one-step PCR by Gold RT-PCR kit is as follows:

Reagents	Volume
H_2O + RNA :	20.5 µL [24 µL if PDAR is used]
10X TaqMan buffer :	5.0 µL
$MgCl_2$ (25 mM) :	11.0 µL
dATP (10mM) :	1.5 µL [for final concentration of 300 µM]
dCTP (10mM) :	1.5 µL [for final concentration of 300 µM]
dGTP (10mM) :	1.5 µL [for final concentration of 300 µM]
dUTP (20mM) :	1.5 µL [for final concentration of 600 µM]
Primer F (10 µM) * :	2.5 µL [for final concentration of 500 nM]
Primer R (10 µM) * :	2.5 µL [for final concentration of 500 nM]
TaqMan Probe * :	1.0 µL [for final concentration of 100 nM]
AmpliTaq Gold :	0.25 µL [can be increased for higher efficiency]
Reverse Transcriptase :	0.25 µL
RNAse inhibitor :	1.00 µL

[0324] If a PDAR is used, 2.5 µL of primer + probe mix used.

[0325] Ideally 10 pg - 100 ng RNA should be used in this reaction. Note that decreasing the amount of template from 100 ng to 50 ng will increase the C_T value by 1. To decrease a C_T value by 3, the initial amount of template should be increased 8-fold. ABI claims that 2 picograms of RNA can be detected by this system and the maximum amount of RNA that can be used is 1 microgram. For routine analysis, 10 pg - 100 ng RNA and 100 pg - 1 µg genomic DNA can be used.

Cycling Parameters for One-step PCR:

[0326] Reverse transcription (by MuLV) 48° C for 30 min.

[0327] AmpliTaq activation 95° C for 10 min.

[0328] PCR: denaturation 95° C for 15 sec and annealing/extension 60° C for 1 min (repeated 40 times) (On ABI 7700, minimum holding time is 15 seconds.)

[0329] The recently introduced EZ one-step™ RT-PCR kit allows the use of UNG as the incubation time for reverse transcription is 60° C thanks to the use of a thermostable

reverse transcriptase. This temperature also a better option to avoid primer dimers and non-specific bindings at 48° C.

Operating the ABI 7700:

[0330] Make sure the following before starting a run:

[0331] 1. Cycle parameters are correct for the run;

[0332] 2. Choice of spectral compensation is correct (*off* for singleplex, *on* for multiplex reactions);

[0333] 3. Choice of "Number of PCR Stages" is correct in the Analysis Options box (Analysis/Options). This may have to be manually assigned after a run if the data is absent in the amplification plot but visible in the plate view, and the X-axis of the amplification is displaying a range of 0-1 cycles;

[0334] 4. No Template Control is labeled as such (for accurate ΔRn calculations);

[0335] 5. The choice of dye component should be made correctly before data analysis;

[0336] 6. You must save the run before it starts by giving it a name (not leaving as untitled);

[0337] 7. Also at the end of the run, first save the data before starting to analyze.

[0338] The ABI software requires extreme caution. Do not attempt to stop a run after clicking on the Run button. You will have problems and if you need to switch off and on the machine, you have to wait for at least an hour to restart the run.

[0339] When analyzing the data, remember that the default setting for baseline is 3 - 15. If any C_T value is <15, the baseline should be changed accordingly (the baseline stop value should be 1-2 smaller than the smallest C_T value). For a useful discussion of this matter, see the ABI Tutorial on Setting Baselines and Thresholds. (Interestingly, this issue is best discussed in the manual for TaqMan™ Human Endogenous Control Plate.)

[0340] If the results do not make sense, check the raw spectra for a possible CDC camera saturation during the run. Saturation of CDC camera may be prevented by using optical caps rather than optical adhesive cover. It is also more likely to happen when SYBR Green I is used, when multiplexing and when a high concentration of probe is used.

Interpretation of Results:

[0341] At the end of each reaction, the recorded fluorescence intensity is used for the following calculations:

[0342] Rn^+ is the Rn value of a reaction containing all components, Rn^- is the Rn value of an unreacted sample (baseline value or the value detected in NTC). ΔRn is the difference between Rn^+ and Rn^-. It is an indicator of the magnitude of the signal generated by the PCR.

[0343] There are three illustrative methods to quantitate the amount of template:

[0344] 1. Absolute standard method: In this method, a known amount of standard such as in vitro translated RNA (cRNA) is used;

[0345] 2. Relative standard: Known amounts of the target nucleic acid are included in the assay design in each run;

[0346] 3. Comparative C_T method: This method uses no known amount of standard but compares the relative amount of the target sequence to any of the reference values chosen and the result is given as relative to the reference value (such as the expression level of resting lymphocytes or a standard cell line).

The Comparative CT Method (ΔΔCT) for Relative Quantitation of Gene Expression:

[0347] This method enables relative quantitation of template and increases sample throughput by eliminating the need for standard curves when looking at expression levels relative to an active reference control (normaliser). For this method to be successful, the dynamic range of both the target and reference should be similar. A sensitive method to control this is to look at how ΔC_T (the difference between the two CT values of two PCRs for the same initial template amount) varies with template dilution. If the efficiencies of the two amplicons are approximately equal, the plot of log input amount versus ΔC_T will have a nearly horizontal line (a slope of <0.10). This means that both PCRs perform equally efficiently across the range of initial template amounts. If the plot shows unequal efficiency, the standard curve method should be used for quantitation of gene expression. The dynamic range should be determined for both (1) minimum and maximum concentrations of the targets for which the results are accurate and (2) minimum and maximum ratios of two gene quantities for which the results are accurate. In conventional competitive RT-PCR, the dynamic range is limited to a target-to-competitor ratio of about 10:1 to 1:10 (the best accuracy is obtained for 1:1 ratio). The real-time PCR is able to achieve a much wider dynamic range.

[0348] Running the target and endogenous control amplifications in separate tubes and using the standard curve method requires the least amount of optimization and validation. The advantage of using the comparative C_T method is that the need for a standard curve is eliminated (more wells are available for samples). It also eliminates the adverse effect of any dilution errors made in creating the standard curve samples.

[0349] As long as the target and normaliser have similar dynamic ranges, the comparative C_T method ($\Delta\Delta C_T$ method) is the most practical method. It is expected that the normaliser will have a higher expression level than the target (thus, a smaller C_T value). The calculations for the quantitation start with getting the difference (ΔC_T) between the C_T values of the target and the normaliser:

[0350] $\Delta C_T = C_T$ (target) - C_T (normaliser)

[0351] This value is calculated for each sample to be quantitated (unless, the target is expressed at a higher level than the normaliser, this should be a positive value. It is no harm if it is negative). One of these samples should be chosen as the reference (baseline) for each comparison to be made. The comparative $\Delta\Delta C_T$ calculation involves finding the difference between each sample's ΔC_T and the baseline's ΔC_T. If the baseline value is representing the minimum level of expression, the $\Delta\Delta C_T$ values are expected to be negative (because the ΔC_T for the baseline sample will be the largest as it will have the greatest C_T value). If the expression is increased in some samples and decreased in others, the $\Delta\Delta C_T$ values will be a mixture of negative and positive ones. The last step in quantitation is to transform these values to absolute values. The formula for this is:

[0352] comparative expression level = $2^{-\Delta\Delta CT}$

[0353] For expressions increased compared to the baseline level this will be something like $2^3 = 8$ times increase, and for decreased expression it will be something like $2^{-3} =$ 1/8 of the reference level. Microsoft Excel can be used to do these calculations by simply entering the C_T values (there is an online ABI tutorial at http://www.appliedbiosystems.com/support/tutorials/7700amp/ on the use of spread sheet programs to produce amplification plots; the TaqMan™ Human Endogenous Control Plate protocol also contains detailed instructions on using MS Excel for real-time PCR data analysis).

[0354] The other (absolute) quantification methods are outlined in the ABI User Bulletins (http://docs.appliedbiosystems.com/search.taf?_UserReference=A8658327189850A13A0C598E). The Bulletins #2 and #5 are most useful for the general understanding of real-time PCR and quantification.

Recommendations on Procedures:

[0355] 1. Use positive-displacement pipettes to avoid inaccuracies in pipetting;

[0356] 2. The sensitivity of real-time PCR allows detection of the target in 2 pg of total RNA. The number of copies of total RNA used in the reaction should ideally be enough to

give a signal by 25-30 cycles (preferably less than 100 ng). The amount used should be decreased or increased to achieve this;

[0357] 3. The optimal concentrations of the reagents are as follows;

[0358] i. Magnesium chloride concentration should be between 4 and 7 mM. It is optimized as 5.5 mM for the primers/probes designed using the Primer Express software;

[0359] ii. Concentrations of dNTPs should be balanced with the exception of dUTP (if used). Substitution of dUTP for dTTP for control of PCR product carryover requires twice dUTP that of other dNTPs. While the optimal range for dNTPs is 500 μM to 1 mM (for one-step RT-PCR), for a typical TaqMan reaction (PCR only), 200 μM of each dNTP (400 μM of dUTP) is used;

[0360] iii. Typically 0.25 μL (1.25 U) AmpliTaq DNA Polymerase (5.0 U/μL) is added into each 50 μL reaction. This is the minimum requirement. If necessary, optimization can be done by increasing this amount by 0.25 U increments;

[0361] iv. The optimal probe concentration is 50-200 nM, and the primer concentration is 100-900 nM. Ideally, each primer pair should be optimised at three different temperatures (58, 60 and 62^0 C for TaqMan primers) and at each combination of three concentrations (50, 300, 900 nM). This means setting up three different sets (for three temperatures) with nine reactions in each (50/50 mM, 50/300 mM, 50/900, 300/50, 300/300, 300/900, 900/50, 900/300, 900/900 mM) using a fixed amount of target template. If necessary, a second round of optimization may improve the results. Optimal performance is achieved by selecting the primer concentrations that provide the lowest C_T and highest ΔRn. Similarly, the probe concentration should be optimized for 25-225 nM;

[0362] 4. If AmpliTaq Gold DNA Polymerase is being used, there has to be a 9-12 min pre-PCR heat step at 92 - 95^0 C to activate it. If AmpliTaq Gold DNA Polymerase is used, there is no need to set up the reaction on ice. A typical TaqMan reaction consists of 2 min at 50^0 C for UNG (see below) incubation, 10 min at 95^0 C for Polymerase activation, and 40 cycles of 15 sec at 95^0 C (denaturation) and 1 min at 60^0 C (annealing and extension). A typical reverse transcription cycle (for cDNA synthesis), which should precede the TaqMan reaction if the starting material is total RNA, consists of 10 min at 25^0 C (primer incubation), 30 min at 48^0 C (reverse transcription with conventional reverse transcriptase) and 5 min at 95^0 C (reverse transcriptase inactivation);

[0363] 5. AmpErase uracil-N-glycosylase (UNG) is added in the reaction to prevent the reamplification of carry-over PCR products by removing any uracil incorporated into amplicons. This is why dUTP is used rather than dTTP in PCR reaction. UNG does not function above 55 ^{0}C and does not cut single-stranded DNA with terminal dU nucleotides. UNG-

containing master mix should not be used with one-step RT-PCR unless r*Tth* DNA polymerase is being used for reverse transcription and PCR (TaqMan EZ RT-PCR kit);

[0364] 6. It is necessary to include at least three No Amplification Controls (NAC) as well as three No Template Controls (NTC) in each reaction plate (to achieve a 99.7% confidence level in the definition of +/- thresholds for the target amplification, six replicates of NTCs must be run). NAC former contains sample and no enzyme. It is necessary to rule out the presence of fluorescence contaminants in the sample or in the heat block of the thermal cycler (these would cause false positives). If the absolute fluorescence of the NAC is greater than that of the NTC after PCR, fluorescent contaminants may be present in the sample or in the heating block of the thermal cycler;

[0365] 7. The dynamic range of a primer/probe system and its normaliser should be examined if the $\Delta\Delta C_T$ method is going to be used for relative quantitation. This is done by running (in triplicate) reactions of five RNA concentrations (for example, 0, 80 pg/μL, 400 pg/μL, 2 ng/μL and 50 ng/μL). The resulting plot of log of the initial amount vs C_T values (standard curve) should be a (near) straight line for both the target and normaliser real-time RT-PCRs for the same range of total RNA concentrations;

[0366] 8. The passive reference is a dye (ROX) included in the reaction (present in the TaqMan universal PCR master mix). It does not participate in the 5' nuclease reaction. It provides an internal reference for background fluorescence emission. This is used to normalize the reporter-dye signal. This normalization is for non-PCR-related fluorescence fluctuations occurring well-to-well (concentration or volume differences) or over time and different from the normalization for the amount of cDNA or efficiency of the PCR. Normalization is achieved by dividing the emission intensity of reporter dye by the emission intensity of the passive reference. This gives the ratio defined as Rn;

[0367] 9. If multiplexing is done, the more abundant of the targets will use up all the ingredients of the reaction before the other target gets a chance to amplify. To avoid this, the primer concentrations for the more abundant target should be limited;

[0368] 10. TaqMan Universal PCR master mix should be stored at 2 to 8° C (not at –20° C);

[0369] 11. The GAPDH probe supplied with the TaqMan Gold RT-PCR kit is labeled with a JOE reporter dye, the same probe provided within the Pre-Developed TaqMan™ Assay Reagents (PDAR) kit is labeled with VIC. Primers for these human GAPDH assays are designed not to amplify genomic DNA;

[0370] 12. The carryover prevention enzyme, AmpErase UNG, cannot be used with one-step RT-PCR which requires incubation at 48° C but may be used with the EZ RT-PCR kit;

[0371] 13. One-step RT-PCR can only be used for singleplex reactions, and the only choice for reverse transcription is the downstream primer (not random hexamers or oligo-dT);

[0372] 14. It is ideal to run duplicates to control pipetting errors but this inevitably increases the cost;

[0373] 15. If multiplexing, the spectral compensation option (in Advanced Options) should be checked before the run;

[0374] 16. Normalization for the fluorescent fluctuation by using a passive reference (ROX) in the reaction and for the amount of cDNA/PCR efficiency by using an endogenous control (such as GAPDH, active reference) are different processes;

[0375] 17. ABI 7700 can be used not only for quantitative RT-PCR but also end-point PCR. The latter includes presence/absence assays or allelic discrimination assays (such as SNP typing);

[0376] 18. Shifting Rn values during the early cycles (cycle 0-5) of PCR means initial disequilibrium of the reaction components and does not affect the final results as long as the lower value of baseline range is reset;

[0377] 19. If an abnormal amplification plot has been noted (C_T value <15 cycles with amplification signal detected in early cycles), the upper value of the baseline range should be lowered and the samples should be diluted to increase the C_T value (a high C_T value may also be due to contamination);

[0378] 20. A small ΔRn value (or greater than expected C_T value) indicates either poor PCR efficiency or low copy number of the target;

[0379] 21. A standard deviation >0.16 for C_T value indicates inaccurate pipetting;

[0380] 22. SYBR Green entry in the Pure Dye Setup should be abbreviated as "SYBR" in capitals. Any other abbreviation or lower case letters will cause problems;

[0381] 23. The SDS software for ABI 7700 have conflicts with the Macintosh Operating System version 8.1. The data should not be analyzed on such computers;

[0382] 24. The ABI 7700 should not be deactivated for extended periods of time. If it has ever been shutdown, it should be allowed to warm up for at least one hour before a run. Leaving the instrument on all times is recommended and is beneficial for the laser. If the machine has been switched on just before a run, an error box stating a firmware version conflict may appear. If this happens, choose the "Auto Download" option;

[0383] 25. The ABI 7700 is only one of the real-time PCR systems available, others include systems from BioRad, Cepheid, Corbett Research, Roche and Stratagene.

Genotyping Analysis

[0384] Many methods are available to genotype DNA. A review of allelic discrimination methods can be found in Kristensen *et al.* (Biotechniques 30(2): 318-322 (2001). Only one method, allele-specific PCR is described here.

Primer Design

[0385] Upstream and downstream PCR primers specific for particular alleles can be designed using freely available computer programs, such as Primer3 (http://frodo.wi.mit.edu/primer3/primer3_code.html). Alternatively the DNA sequences of the various alleles can be aligned using a program such as ClustalW (http://www.ebi.ac.uk/clustalw/) and specific primers designed to areas where DNA sequence differences exist but retaining enough specificity to ensure amplification of the correct amplicon. Preferably a PCR amplicon is designed to have a restriction enzyme site in one allele but not the other. Primers are generally 18-25 base pairs in length with similar melting temperatures.

PCR Amplification

[0386] The composition of PCR reactions has been described elsewhere (Clinical Applications of PCR, Dennis Lo (Editor), Blackwell Publishing, 1998). Briefly, a reaction contains primers, DNA, buffers and a thermostable polymerase enzyme. The reaction is cycled (up to 50 times) through temperature steps of denaturation, hybridization and DNA extension on a thermocycler such as the MJ Research Thermocycler model PTC-96V.

DNA Analysis

[0387] PCR products can be analyzed using a variety of methods including size differentiation using mass spectrometry, capillary gel electrophoresis and agarose gel electrophoresis. If the PCR amplicons have been designed to contain differential restriction enzyme sites, the DNA in the PCR reaction is purified using DNA-binding columns or precipitation and re-suspended in water, and then restricted using the appropriate restriction enzyme. The restricted DNA can then be run on an agarose gel where DNA is separated by size using electric current. Various alleles of a gene will have different sizes depending on whether they contain restriction sites.

EXAMPLE 2

IDENTIFICATION OF GENES AND PRIORITY RANKING OF GENES

[0388] Significant genes were ranked according to an Empirical Bayes approach (Lonnstedt and Speed, 2002, *Statistica Sinica* **12**: 31–46), based on a comparison of all animals

at Day 28 compared to animals on days 0, 2, 4, 7, 9, 11, 14, 17, 21, and 24. The empirical Bayes approach was used to provide a shrinkage estimator of the within groups variance for each gene.

[0389] Individual p values were based on a t Test using this shrinkage estimator. The p values of the t test were adjusted using Holms method to maintain strong control of the family wise type I error rate.

[0390] The genes listed in Table 5 were generated from a total of 783 genes that were significant ($p<0.05$) across the various days. This gene list was trimmed by eliminating those genes that were significant for less than two days and where $p>0.001$. The remaining genes were then ranked in increasing order of their p value..

[0391] It should be noted that this gene list is not inclusive of the genes that can act as diagnostics for stress (see also the minimally predictive set and gene ontology).

[0392] The genes listed in Table 6 are ranked in order of their t statistic or value - which may be interpreted as a signal-to-noise ratio. The tabulation also displays the log 2 fold change (M value), and the adjusted p values. Genes with a negative t value (and hence a negative M value) are down regulated. Genes with positive t and M values are up-regulated. The priority ranking of genes is based on increasing value of t value for the first day each gene is significant ($p<0.001$) following stress induction, and for genes that were significant for at least three sampling times.

EXAMPLE 3

DEMONSTRATION OF DIAGNOSTIC POTENTIAL TO DETERMINE STRESS RESPONSE

[0393] The diagnostic potential of the entire set of genes was assessed using discriminant analysis (Venables and Ripley, 2002, Modern Applied Statistics in S, Springer) on the principal component scores (Jolliffe, I.T. Principal components analysis, Springer-Verlag, 1986) calculated from gene expression. Comparisons were made between samples taken immediately after the stressor, and at 2, 4, 7, 9, 11, 14, 17, 21, 24 and 28 days after the stressor.

[0394] The entire process was cross-validated. Sensitivity and specificity were calculated for a uniform prior. This may be interpreted as a form of shrinkage regularization, where the estimates are shrunken to lie in a reduced space.

[0395] Cross validated estimates of discriminant function scores were then used to construct an ROC curve (Lloyd C.J., 1998, The use of smoothed ROC curves to summarize and compare diagnostic systems, *Journal of the American Statistical Association* **93**:1356-1364). The ROC curves were based both on empirical cumulative distribution functions, and on kernel density estimates with a smoothing window chosen using Lloyd's method (*loc. cit*).

[0396] ROC curves for the comparison of each day with Day 28 are shown in Figures 1 to 10, respectively.

[0397] Changes in gene expression following transport stress are of sufficient magnitude to produce excellent diagnostic potential.

EXAMPLE 4

MINIMALLY PREDICTIVE GENE SETS

[0398] Although a large number of genes has been identified as having diagnostic potential, a much fewer number are generally required for acceptable diagnostic performance.

[0399] Table 7 shows the cross-validated classification success, sensitivity and specificity obtained from a linear discriminant analysis, based on two genes selected from the set of potential diagnostic genes. The pairs presented are those producing the highest prediction success, many other pairs of genes produce acceptable classification success. The identification of alternate pairs of genes would be readily apparent to those skilled in the art. Techniques for identifying pairs include (but are not limited to) forward variable selection (Venables W.N. and Ripley B.D. Modern Applied Statistics in S 4th Edition 2002. Springer), best subsets selection, backwards elimination (Venables W.N. and Ripley B.D., 2002, *supra*), stepwise selection (Venables W.N. and Ripley B.D., 2002, *supra*) and stochastic variable elimination (Figuerado M.A. Adaptive Sparseness for Supervised Learning).

[0400] Table 8 shows the cross-validated classification success obtained from a linear discriminant analysis based on three genes selected from the diagnostic set. Only twenty sets of three genes are presented. It will be readily apparent to those of skill in the art that other suitable diagnostic selections based on three stress marker genes can be made.

[0401] Table 9 shows the cross-validated classification success obtained from a linear discriminant analysis based on four genes selected from the diagnostic set. Only twenty sets of four genes are presented. It will be readily apparent to practitioners in the art that other suitable diagnostic selections based on four stress marker genes can be made.

[0402] Table 10 shows the cross-validated classification success obtained from a linear discriminant analysis based on five genes selected from the diagnostic set. Only twenty sets of five genes are presented. It will be readily apparent to practitioners in the art that other suitable diagnostic selections based on five stress marker genes can be made.

[0403] Table 11 shows the cross-validated classification success obtained from a linear discriminant analysis based on six genes selected from the diagnostic set. Only twenty sets of six genes are presented. It will be readily apparent to practitioners in the art that other suitable diagnostic selections based on six stress marker genes can be made.

[0404] Table 12 shows the cross-validated classification success obtained from a linear discriminant analysis based on seven genes selected from the diagnostic set. Only twenty sets of seven genes are presented. It will be readily apparent to practitioners in the art that other suitable diagnostic selections based on seven stress marker genes can be made.

[0405] Table 13 shows the cross-validated classification success obtained from a linear discriminant analysis based on eight genes selected from the diagnostic set. Only twenty sets of eight genes are presented. It will be readily apparent to practitioners in the art that other suitable diagnostic selections based on eight stress marker genes can be made.

[0406] Table 14 shows the cross-validated classification success obtained from a linear discriminant analysis based on nine genes selected from the diagnostic set. Only twenty sets of nine genes are presented. It will be readily apparent to practitioners in the art that other suitable diagnostic selections based on nine stress marker genes can be made.

[0407] Table 15 shows the cross-validated classification success obtained from a linear discriminant analysis based on ten genes selected from the diagnostic set. Only twenty sets of ten genes are presented. It will be readily apparent to practitioners in the art that other suitable diagnostic selections based on ten stress marker genes can be made.

[0408] Table 16 shows the cross-validated classification success obtained from a linear discriminant analysis based on 20 genes selected from the diagnostic set. Only 20 sets of twenty genes are presented. It will be readily apparent to practitioners in the art that other suitable diagnostic selections based on twenty stress marker genes can be made.

EXAMPLE 5

DEMONSTRATION OF SPECIFICITY

[0409] The specificity of a stress gene signature is difficult to define because the test is an assessment rather than a diagnostic.

[0410] Nonetheless, the entire set of "stress genes" were used as a training set against a gene expression database of over 850 GeneChip™. Gene expression results in the database were obtained from samples from horses with various diseases and conditions including; chronic and acute induced EPM, clinical cases of EPM, herpes virus infection, degenerative osteoarthritis, Rhodococcus infection, endotoxemia, laminitis, gastric ulcer syndrome, animals in athletic training and clinically normal animals. The stress status of these animals was not known *a priori*.

[0411] A stress index score was calculated for each GeneChip™, using the genes in the training set. The score was calculated from a regularized discriminant function, so that large

values would be associated with high probability of stress, and the variance of the score should be approximately 1. GeneChip™ were ranked on this score, from the largest to the smallest.

[0412] Specificity was investigated by varying a threshold value for a positive diagnosis. At each value of the threshold, specificity was defined as the proportion of positive results (i.e. GeneChip™ index score greater than the threshold) which were true positives. A threshold value of two (i.e. two standard deviations) was adopted.

[0413] 59 animals from the database that were not part of the induced stress trial were identified as having immune modification associated with stress and were two standard deviations above zero on discriminant function when using four principal components and the entire gene set (3105). Of these 59 animals, 10 were in a laminitis trial, 14 had R. equi infection and nine had gastritis. Thirteen animals were "controls," and of these, three had been recently transported, two were in a trial, three were not clinically normal and five were foals with exposure to R. equi. Twelve animals deemed to be clinically normal were identified by the signature as stressed. Based on this information, it can be stated that the specificity of the stress signature is over 90% when used against a database of over 850 samples.

[0414] 79 animals from the database that were not part of the induced stress trial were identified as having immune modification associated with stress and were two standard deviations above zero on discriminant function when using four principal components and the unique stress signature genes listed in Table 1. Of these 79 animals, 15 were in a laminitis trial, 8 had R. equi infection and 24 had gastritis. Twenty-one were "controls", and of these, 12 were in a trial, and three were not clinically normal. Nine animals deemed to be clinically normal were identified by the signature as stressed. Based on this information, it can be stated that the specificity of the stress signature is over 90% when used against a database of over 850 samples.

EXAMPLE 7

GENE ONTOLOGY

[0415] Gene sequences were compared against the GenBank database using the BLAST algorithm (Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment search tool." *J. Mol. Biol.* **215**:403-410), and gene homology and gene ontology searches were performed in order to group genes based on function, metabolic processes or cellular component (using UniProt and GenBank). Table 17 lists and groups the genes based on these criteria and information available at the time. See also Table 1, which contains sequence information for each gene.

[0416] The disclosure of every patent, patent application, and publication cited herein is hereby incorporated herein by reference in its entirety.

[0417] The citation of any reference herein should not be construed as an admission that such reference is available as "Prior Art" to the instant application.

[0418] Throughout the specification the aim has been to describe the preferred embodiments of the invention without limiting the invention to any one embodiment or specific collection of features. Those of skill in the art will therefore appreciate that, in light of the instant disclosure, various modifications and changes can be made in the particular embodiments exemplified without departing from the scope of the present invention. All such modifications and changes are intended to be included within the scope of the appended claims.

TABLE 1

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
WBC590	Zinc Finger Protein 198	1 CGAAGGGGGGTGGGCCGGGGGAGGGGAGGTTCGTTCCGCGGAGCGCAGCCAGAACCGGGA 61 CCAAGAATCGCCTTCAGCCCTGTCTGGTGCATCCTTGGCAGAAAGTGAGGAGGAAAACAC 121 CCCCATTGTTAGATGAGGTCTTAATCATGGAACATTTGAAGTCACGTAAAGAAGGTTCTT 181 TGGCATGGACACAAGTTCAGTGGGAGGATTAGAATTGACTGATCAGACTCCTGTTTTATT 241 AGGGAGTACGGCCATGGCAACTAGTCTCACGAATGTAGGAAACTCATTTAGTGGTCCAGC 301 TAATCCTTTAGTGTCTAGATCTAATAAGTTTCAGAACTCGTCAGTGGAAGATGATGATGA 361 TGTTGTTTTTATCGAACCTGTACAACCTCCCCCACCTTCTGTACCAGTGGTAGCTGATCA 421 AAGAACCATAACATTTACATCATCAAAAAATGAAGAACTACAAGGAAATGATTCCAAAAT 481 TACTCCTTCCTCAAAAGAGTTGGCATCTCAGAAGGGAAGTGTAAGTGAGACAATTGTCAT 541 TGATGATGAAGAGGACATGGAAACAAATCAAGGGCAAGAGAAAAATTCCTCCAATTTTAT 601 TGAACGAAGACCTCCTGAGACTAAAAACAGAACCAATGATGTGGATTTCTCCACTTCCAG 661 TTTTTCAAGAAGTAAGGTAAATGCAGGAATGGGTAATAGTGGTATCACCACAGAACCAGA 721 CTCTGAAATTCAGATTGCTAATGTTACAACTTTAGAAACAGGTGTAAGCTCTGTGAATGA 781 TGGCCAATTAGAAAATACTGACGGGCGAGATATGAACTTAATGATTACACATGTAACATC 841 ACTGCAGAATACCAACTTGGGAGATGTCTCTAACGGACTGCAGTCAAGTAATTTTGGTGT 901 TAATATACAAACATACACCCCATCTTTAACTTCACAGACCAAGACTGGAGTAGGACCTTT 961 TAATCCTGGTAGAATGAATGTGGCAGGAGACGTTTTTCAGAATGGAGAATCTGCAACTCA 1021 TCATAATCCTGATTCTTGGATCTCCCAGTCAGCTTCATTTCCCCGTAATCAGAAACAACC 1081 AGGGGTGGACTCTTTATCACCAGTGGCCTCACTTCCTAAACAGATTTTCCAGCCGTCTGT 1141 CCAACAGCAGCCTACTAAACCAGTTAAAGTCACTTGTGCAAACTGCAAAAAACCTTTACA 1201 GAAGGGCCAGACAGCTTATCAACGAAAAGGATCAGCTCACCTCTTTTGTTCTACCACCTG 1261 CCTTTCTTCCTTCTCCCACAAGCCTGCTCCAAAGAAACTCTGTGTTATGTGTAAAAAAGA 1321 TATAACTACAATGAAAGGAACCATTGTTGCTCAAGTGGATTCAAGTGAGTCCTTCCAGGA 1381 ATTCTGTAGTACATCTTGTTTATCTCTCTATGAAGACAAACAGAATCCTACTAAAGGAGC 1441 TCTAAATAAATCAAGATGTACAATCTGTGGTAAACTAACTGAGATTCGCCATGAAGTCAG 1501 CTTTAAAAATATGACTCATAAGCTGTGCAGTGACCACTGCTTTAATAGATATAGAATGGC 1561 CAATGGTTTAATAATGAATTGCTGTGAACAGTGTGGAGAGTACTTGCCCAGTAAAGGTGC 1621 TGGAAATAATGTTCTGGTGATTGATGGTCAACAGAAAAGATTTTGCTGTCAAAGTTGTGT 1681 CAGTGAATACAAACAGGTAGGTAGCCATCCAAGCTTCCTGAAGGAGGTTCGAGATCACAT 1741 GCAGGACTCTTTCTTAATGCAGCCTGAGAAATATGGAAAACTGACAACTTGTACTGGTTG 1801 CCGAACACAGTGCAGGTTTTTTGATATGACTCAGTGTATAGGTCCTAATGGATATATGGA 1861 GCCATATTGTTCAACTGCTTGTATGAACAGTCACAAGACAAAATATGCAAAATCACAAAG 1921 TTTGGGAATTATTTGCCATTTTTGTAAGCGAAACTCTTTACCTCAATACCAAGCCACAAT 1981 GCCTGATGCAAAACTGTACAACTTTTGCAATTCCAGTTGTGTGGCTAAATTTCAGGCTCT 2041 AAGTATGCAGTCATCTCCAAATGGCCAGTTTGTAGCGCCAAGTGATATTCAGTTGAAATG 2101 CAACTACTGCAAAAATTCCTTTTGTTCAAAACCAGAAATCCTGGAATGGGAGAACAAAGT 2161 GCATCAGTTCTGCAGCAAAACTTGTTCAGATGACTATAAGAAGTTGCATTGCATAGTTAC 2221 ATATTGCGAATACTGTCAAGAGGAGAAGACTCTTCATGAAACAGTAAATTTCTCTGGCGT 2281 TAAGAGACCTTTCTGTAGTGAAGGCTGCAAATTATTATACAAACAGGATTTTGCCAGACG 2341 TTTAGGATTGAGATGTGTTACTTGCAACTATTGTTCTCAGCTATGTAAGAAGGGAGCAAC 2401 TAAAGAACTCGATGGTGTTGTGAGAGATTTCTGCAGTGAAGATTGCTGTAAAAAATTTCA 2461 GGATTGGTACTACAAGGCTGCAAGGTGTGACTGTTGTAAATCTCAAGGAACTCTTAAAGA	SEQ ID NO:1

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2521 GCGAGTTCAGTGGCGTGGGGAAATGAAACATTCTGTGATCAACATTGCTTACTGCGTTT	
		2581 CTACTGTCAACAAAATGAGCCCAACATGACAACTCAGAAAGGACCTGAAAACTTACATTA	
		2641 TGATCAGGGTTGTCAGACATCTCGAACCAAATGACAGGTTCAGCACCACCCCTTCTCC	
		2701 AACACCTAACAAAGAGATGAAGAACAAAGCAGTTCTTTGCAAACCTTTAACAATGACAAA	
		2761 AGCTACTTACTGTAAACCTCACATGCAGACCAAATCTTGTCAGACAGATGATACTTGGAG	
		2821 GACAGAATATGTTCCAGTGCCTATCCCTGTGTATATCCCAGTTCCTATGCACAT	
		2881 GTACAGTCAGAATATTCCTGTTCCTACTACAGTTCCTGTTCCTGTCCAGTTCCTGTTTT	
		2941 TCTGCCTGCTCCCATTGGACAGCAGTGAGAAGATTCCTGCAGCAATTGAGGAGCTAAAAAG	
		3001 CAAGGTTTCTTCAGATGCTCTTGATACAGAGTTGCTTACAATGACGGATATGATGAGTGA	
		3061 AGACGAGGGCGAAAACAGACAACCAACATCACAGTGTAATTATTGAAACAGATATAAT	
		3121 TGGTTCAGACCTTTTGAAGAACTCTGACCCAGAGACACAGTCCAGCATGCCTGATGTACC	
		3181 ATATGAACCAGATTTGGATATCGAAATAGATTTTCCCAGAGCTGCTGAGGAGCTTGATAT	
		3241 GGAAAATGAATTTTTATATTACCACCTGTTTTTGGCGAAGAATATGAGGAACAGCCCAGACC	
		3301 TCGATCTAAAAAAAAAGGGAGCCAAGAGAAAGGCTGTATCAGGATACCAGTCTCATGATGA	
		3361 TAGTTCTGACAATTCAGAATGCAGCTTTCCTTCAAATATACGTATGGCGTAAATGCATG	
		3421 GAAACACTGGGTCAAAACTAGGCAACTTGATGAAGATCTTCTGGTATTAGATGAGTTAAA	
		3481 ATCTTCTAAATCAGTAAAGTTAAAAGAGGATCTACTCTCTCACACCACAGCTGAGCTTAA	
		3541 CTATGGGTTAGCTCATTTTGTCAATGAGATCCGACGGCCAAATGGAGAGGAATTATGCACC	
		3601 TGACAGCATCTATTACCTTTGCCTTGGAATACAGGAGTATTTGTGTGGAAGTAATCGAAA	
		3661 AGACAACATATTTATTGATCCTGGATACCAAACATTTGAGCAAGAATTGAATAAAATACT	
		3721 GCGAAGCTGGCAACCAAGCATACTTCCAGATGGGTCAATATTCTCTCGAGTTGAAGAAGA	
		3781 CTATCTCTGGAGGATAAAACAACTAGGATCACACTCTCCAGTAGCTCTTCTCGAATACACT	
		3841 GTTCTACTTTAACACTAAGTATTTTGGCCTGAAAACAGTGGAACAACACTTAAGACTTTC	
		3901 CTTTGGCACTGTGTTTAGGCATTGGAAAAAAAAATCCTTTACGATGGAAAACAAAGCGTG	
		3961 TCTTCGATACCAAGTGTCTTCCTTGTGTGGAACAGATAATGAAGATAAAATTACTACTGG	
		4021 AAAAAGAAAACATGAAGATGATGAGCCAGTATTTGAACAAATTGAAAACACACCCAATCC	
		4081 TTCCAGATGTCCTGTGAAAATGTTTGAATGCTACTTGTCTAAAAGTCCACAGAATCTTAA	
		4141 TCAGAGGATGGATGTTTTTTATTTGCAACCAGAATGCTCTAGTTCTACAGATAGCCCTGT	
		4201 CTGGTATACGTCTACTTCACTGGACCGAAACACCTTGGAAAAATATGCTTGTACGGGTTCT	
		4261 TCTAGTAAAAGATATTTATGATAAAGACACAATTATCAACTGGATGAAGACACAGACTAAAA	
		4321 AGGAACGTTGCAGAAGCAATCGGGATAAAACAGCATTAGATAGTCATGCTGCTAGATCTT	
		4381 TATTATGGAAAACATTTCAAGTTTACTCCTTCTGTTTTGAGTTTTGTAGCAGTGTACCCA	
		4441 CGCTGGGTATTACCATGTAAATAATCTGTGAGTGAAAGTTGCCATTATTCTATGTAGTGG	
		4501 TTTTAGGATACTTAACAAATACATTCAAATTCTTTTTTATTATTATTTATTGATTAGG	
		4561 TATGTTTGTAACTTTTTACATTACAGAATATGAATGAGAATGTGCCATGTATAATTTTTT	
		4621 TCTTGTAGTAAGAAACATCCATATTGCACAACTCTACTGTTGCAAAGCTTCCTTGGAAGG	
		4681 GGGCTCTTTTACTGGGTTCTTAACCAGATGGTTGTGTATGGGTAGCACTACTAAAAGTTT	
		4741 AGAACTTGCAGTGTCTTTCGGAATTTTTAAATAAACTGTAAACTAATAGGCTGGGGTTT	
		4801 TTGTTTTGTTTTGGGGTTTTGTTTTGTTTACATTTTAGTTACTGAAGCCCTTACA	
		4861 AGGTTATGTAGAGAGATACCATCTTCTGTACCAAAAATAGACAAGAGAATGCTGTCAATA	
		4921 TTGGTGTACTGTAATGTGAATCTATGCTGGTGAAAACAATTTTTTGTTCCCCTTATTAAA	
		4981 ACCTTAGTGTCCTTTTCTCATTTGTGGCTTTCTGCATCACCCAATCAATAAAAAACAAAT	
		5041 ATATATATGT	
		1 M D T S S V G G L E L T D Q T P V L L G	SEQ ID NO:2
		1 ATGGACACAAGTTCAGTGGGAGGATTAGAATTGACTGATCAGACTCCTGTTTTATTAGGG	
		21 S T A M A T S L T N V G N S F S G P A N	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		61 AGTACGGCCATGGCAACTAGTCTCACGAATGTAGGAAACTCATTTAGTGGTCCAGCTAAT	
		41 P L V S R S N K F Q N S S V E D D D D V	
		121 CCTTTAGTGTCTAGATCTAATAAGTTTCAGAACTCGTCAGTGGAAGATGATGATGTT	
		61 V F I E P V Q P P P P S V P V V A D Q R	
		181 GTTTTTATCGAACCTGTACAACCTCCCCCACCTTCTGTACCAGTGGTAGCTGATCAAAGA	
		81 T I T F T S S K N E E L Q G N D S K I T	
		241 ACCATAACATTTACATCATCAAAAAATGAAGAACTACAAGGAAATGATTCCAAAATTACT	
		101 P S S K E L A S Q K G S V S E T I V I D	
		301 CCTTCCTCAAAAGAGTTGGCATCTCAGAAGGGAAGTGTAAGTGAGACAATTGTCATTGAT	
		121 D E E D M E T N Q G Q E K N S S N F I E	
		361 GATGAAGAGGACATGGAAACAAATCAAGGCAAGAGAAAAATTCCTCCAATTTTATTGAA	
		141 R R P P E T K N R T N D V D F S T S S F	
		421 CGAAGACCTCCTGAGACTAAAAACAGAACCAATGATGTGGATTTCTCCACTTCCAGTTTT	
		161 S R S K V N A G M G N S G I T T E P D S	
		481 TCAAGAAGTAAGGTAAATGCAGGAATGGGTAATAGTGGTATCACCACAGAACCAGACTCT	
		181 E I Q I A N V T T L E T G V S S V N D G	
		541 GAAATTCAGATTGCTAATGTTACAACTTTAGAAACAGGTGTAAGCTCTGTGAATGATGGC	
		201 Q L E N T D G R D M N L M I T H V T S L	
		601 CAATTAGAAAATACTGACGGCGAGATATGAACTTAATGATTACACATGTAACATCACTG	
		221 Q N T N L G D V S N G L Q S S N F G V N	
		661 CAGAATACCAACTTGGGAGATGTCTCTAACGGACTGCAGTCAAGTAATTTTGGTGTTAAT	
		241 I Q T Y T P S L T S Q T K T G V G P F N	
		721 ATACAAACATACACCCCATCTTTAACTTCACAGACCAAGACTGGAGTAGGACCTTTTAAT	
		261 P G R M N V A G D V F Q N G E S A T H H	
		781 CCTGGTAGAATGAATGTGGCAGGAGACGTTTTTCAGAATGGAGAATCTGCAACTCATCAT	
		281 N P D S W I S Q S A S F P R N Q K Q P G	
		841 AATCCTGATTCTTGGATCTCCCAGTCAGCTTCATTTCCCCGTAATCAGAAACAACCAGGG	
		301 V D S L S P V A S L P K Q I F Q P S V Q	
		901 GTGGACTCTTTATCACCAGTGGCCTCACTTCCTAAACAGATTTTCCAGCCGTCTGTCCAA	
		321 Q Q P T K P V K V T C A N C K K P L Q K	
		961 CAGCAGCCTACTAAACCAGTTAAAGTCACTTGTGCAAACTGCAAAAAACCTTTACAGAAG	
		341 G Q T A Y Q R K G S A H L F C S T T C L	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1021 GGCCAGACAGCTTATCAACGAAAAGGATCAGCTCACCTCTTTGTTCTACCACCTGCCTT	
		361 S S F S H K P A P K K L C V M C K K D I	
		1081 TCTTCCTTCTCCCACAAGCCTGCTCCAAAGAAACTCTGTGTTATGTGTAAAAAAGATATA	
		381 T T M K G T I V A Q V D S S E S F Q E F	
		1141 ACTACAATGAAAGGAACCATTGTTGCTCAAGTGGATTCAAGTGAGTCCTTCCAGGAATTC	
		401 C S T S C L S L Y E D K Q N P T K G A L	
		1201 TGTAGTACATCTTGTTTATCTCTCTATGAAGACAAACAGAATCCTACTAAAGGAGCTCTA	
		421 N K S R C T I C G K L T E I R H E V S F	
		1261 AATAAATCAAGATGTACAATCTGTGGTAAACTAACTGAGATTCGCCATGAAGTCAGCTTT	
		441 K N M T H K L C S D H C F N R Y R M A N	
		1321 AAAAATATGACTCATAAGCTGTGCAGTGACCACTGCTTTAATAGATATAGAATGGCCAAT	
		461 G L I M N C C E Q C G E Y L P S K G A G	
		1381 GGTTTAATAATGAATTGCTGTGAACAGTGTGGAGAGTACTTGCCCAGTAAAGGTGCTGGA	
		481 N N V L V I D G Q Q K R F C C Q S C V S	
		1441 AATAATGTTCTGGTGATTGATGGTCAACAGAAAAGATTTTGCTGTCCAAAGTTGTCTCAGT	
		501 E Y K Q V G S H P S F L K E V R D H M Q	
		1501 GAATACAAACAGGTAGGTAGCCATCCAAGCTTCCTGAAGGAGGTTCGAGATCACATGCAG	
		521 D S F L M Q P E K Y G K L T T C T G C R	
		1561 GACTCTTTCTTAATGCAGCCTGAGAAATATGGAAAACTGACAACTTGTACTGGTTGCCGA	
		541 T Q C R F F D M T Q C I G P N G Y M E P	
		1621 ACACAGTGCAGGTTTTTTGATATGACTCAGTGTATAGGTCCTAATGGATATATGGAGCCA	
		561 Y C S T A C M N S H K T K Y A K S Q S L	
		1681 TATTGTTCAACTGCTTGTATGAACAGTCACAAGACAAAATATGCAAAATCACAAAGTTTG	
		581 G I I C H F C K R N S L P Q Y Q A T M P	
		1741 GGAATTATTTGCCATTTTTGTAAGCGAAACTCTTTACCTCAATACCAAGCCACAATGCCT	
		601 D G K L Y N F C N S S C V A K F Q A L S	
		1801 GATGGAAAACTGTACAACTTTGCAATTCCAGTTGTGTGGCTAAATTTCAGGCTCTAAGT	
		621 M Q S S P N G Q F V A P S D I Q L K C N	
		1861 ATGCAGTCATCTCCAAATGGCCAGTTTGTAGCGCCAAGTGATATTCAGTTGAAATGCAAC	
		641 Y C K N S F C S K P E I L E W E N K V H	
		1921 TACTGCAAAAATTCCTTTGTTCAAAACCAGAAATCCTGGAATGGGAGAACAAAGTGCAT	
		661 Q F C S K T C S D D Y K K L H C I V T Y	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1981 CAGTTCTGCAGCAAAACTTGTTCAGATGACTATAAGAAGTTGCATTGCATAGTTACATAT	
		681 C E Y Y C Q E E K T L H E T V N F S G V K	
		2041 TGCGAATACTGTCAAGAGGAGAAGACTCTTCATGAAACAGTAAATTTCTCTGGCGTTAAG	
		701 R P F C S E G C K L L Y K Q D F A R R L	
		2101 AGACCTTTCTGTAGTGAAGGCTGCAAATTATTATACAAACAGGATTTTGCCAGACGTTTA	
		721 G L R C V T C N Y C S Q L C K K G A T K	
		2161 GGATTGAGATGTGTTACTTGCAACTATTGTTCTCAGCTATGTAAGAAGGGAGCAACTAAA	
		741 E L D G V V R D F C S E D C C K K F Q D	
		2221 GAACTCGATGGTGTTGTCAGAGATTTCTGCAGTGAAGATTGCTGTAAAAAATTTCAGGAT	
		761 W Y Y K A A R C D C C K S Q G T L K E R	
		2281 TGGTACTACAAGGCTGCAAGGTGTGACTGTTGTAAATCTCAAGGAACTCTTAAAGAGCGA	
		781 V Q W R G E M K H F C D Q H C L L R F Y	
		2341 GTTCAGTGGCGTGGGGAAATGAAACATTTCTGTGATCAACATTGCTTACTGCGTTTCTAC	
		801 C Q Q N E P N M T T Q K G P E N L H Y D	
		2401 TGTCAACAAAATGAGCCCAACATGACAACTCAGAAAGGACCTGAAAACTTACATTATGAT	
		821 Q G C Q T S R T K M T G S A P P P S P T	
		2461 CAGGGTTGTCAGACATCTCGAACCAAAATGACAGGTTCAGCACCACCCCCTTCTCCAACA	
		841 P N K E M K N K A V L C K P L T M T K A	
		2521 CCTAACAAAGAGATGAAGAACAAAGCAGTTCTTTGCAAACCTTTAACAATGACAAAAGCT	
		861 T Y C K P H M Q T K S C Q T D D T W R T	
		2581 ACTTACTGTAAACCTCACATGCAGACCAAATCTTGTCAGACAGATGATACTTGGAGGACA	
		881 E Y V P V P I P V P V Y I P V P M H M Y	
		2641 GAATATGTTCCAGTGCCTATCCCTGTGCCTGTGTATATCCCAGTTCCTATGCACATGTAC	
		901 S Q N I P V P T T V P P V P V P V F L	
		2701 AGTCAGAATATTCCTGTTCCTACTACAGTTCCTGTTCCTGTGCCAGTTCCTGTTTTCTG	
		921 P A P L D S S E K I P A A I E E L K S K	
		2761 CCTGCTCCATTGGACAGCAGTGAGAAGATTCCTGCAGCAATTGAGGAGCTAAAAAGCAAG	
		941 V S S D A L D T E L L T M T D M M S E D	
		2821 GTTTCTTCAGATGCTCTTGATACAGAGTTGCTTACAATGACGGATATGAGTGAAGAC	
		961 E G K T E T T N I N S V I I E T D I I G	
		2881 GAGGGGAAAACAGAGACAACCAACATCAACAGTGTAATTATTGAAACAGATATAATGGT	
		981 S D L L K N S D P E T Q S S M P D V P Y	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2941 TCAGACCTTTGAAGAACTCTGACCCAGAGACACAGTCCAGCATGCCTGATGTACCATAT	
		1001 E P D L D I E I D F P R A A E E L D M E	
		3001 GAACCAGATTTGGATATCGAAATAGATTTCCCAGAGCTGCTGAGGAGCCTTGATATGGAA	
		1021 N E F L L P P V F G E E Y E E Q P R P R	
		3061 AATGAATTTTTATTACCACCTGTTTTTGGCGAAGAATATGAGGAACAGCCCAGACCTCGA	
		1041 S K K K G A K R K A V S G Y Q S H D D S	
		3121 TCTAAAAAAAAGGGAGCCAAGAGAAAGGCTGTATCAGGATACCAGTCTCATGATGATAGT	
		1061 S D N S E C S F P F K Y T Y G V N A W K	
		3181 TCTGACAATTCAGAATGCAGCTTTCCTTTCAAATATACGTATGGCGTAAATGCATGGAAA	
		1081 H W V K T R Q L D E D L L V L D E L K S	
		3241 CACTGGGTCAAAACTAGGCAACTTGATGAAGATCTTCTGGTATTAGATGAGTTAAAATCT	
		1101 S K S V K L K E D L L S H T T A E L N Y	
		3301 TCTAAATCAGTAAAGTTAAAAGAGGATCTACTCTCTCACACCACAGCTGAGCTTAACTAT	
		1121 G L A H F V N E I R R P N G E N Y A P D	
		3361 GGGTTAGCTCATTTTGTCAATGAGATCCGACGGCCAAATGGAGAGAATTATGCACCTGAC	
		1141 S I Y Y L C L G I Q E Y L C G S N R K D	
		3421 AGCATCTATTACCTTGCCTTGGAATACAGGAGTATTTGTGTGGAAGTAATCGAAAAGAC	
		1161 N I F I D P G Y Q T F E Q E L N K I L R	
		3481 AACATATTTATTGATCCTCGATACCAAACATTTGAGCAAGAATTGAATAAAATACTGCGA	
		1181 S W Q P S I L P D G S I F S R V E E D Y	
		3541 AGCTGGCAACCAAGCATACTTCCAGATGGGTCAATATTCTCTCGAGTTGAAGAAGACTAT	
		1201 L W R I K Q L G S H S P V A L L N T L F	
		3601 CTCTGGAGGATAAAACAACTAGGATCACACTCTCCAGTAGCTCTTCTGAATACACTGTTC	
		1221 Y F N T K Y F G L K T V E Q H L R L S F	
		3661 TACTTTAACACTAAGTATTTTGGCCTGAAAACAGTGGAACAACACTTAAGACTTTCCTTT	
		1241 G T V F R H W K K N P L T M E N K A C L	
		3721 GGCACTGTGTTTAGGCATTGGAAAAAAAATCCTTTAACGATGGAAAACAAAGCGTGTCTT	
		1261 R Y Q V S S L C G T D N E D K I T T G K	
		3781 CGATACCAAGTGTCTTCCTTGTGTGGAACAGATAATGAAGATAAAATTACTACTGGAAAA	
		1281 R K H E D D E P V F E Q I E N T A N P S	
		3841 AGAAAACATGAAGATGATGAGCCAGTATTTGAACAAATTGAAAACACAGCCAATCCTTCC	
		1301 R C P V K M F E C Y L S K S P Q N L N Q	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		3901 AGATGTCCTGTGAAAATGTTTGAATGCTACTTGTCTAAAAGTCCACAGAATCTTAATCAG 1321 R M D V F Y L Q P E C S S S T D S P V W 3961 AGGATGGATGTTTTTTATTTGCAACCAGAATGCTCTAGTTCTACAGATAGCCCTGTCTGG 1341 Y T S T S L D R N T L E N M L V R V L L 4021 TATACGTCTACTTCACTGGACCGAAACACCTTGGAAAATATGCTTGTACGGGTTCTTCTA 1361 V K D I Y D K D N Y E L D E D T D - 4081 GTAAAAGATATTTATGATAAAGACAATTATGAACTGGATGAAGACACAGACTAA	
WBC493	Homo sapiens mRNA; cDNA DKFZp667N084	1 TCTGCCTTTGTTTCATCTAGCTTGAACTGTGAGTGTTTGGGTCGGCCGATCACATTGATC 61 AGGCACTAAAGCCAAATGCTTTGTAGTTTGATATGTATGTATCCCTTAAAAATCATGGAG 121 TGTGATCTTTCCATTTTAATTTAGGGTACATTTCTGCCTTCTCTTAGTTTGTCATATGAC 181 CAGAACAAGAGAAGCCTTAACCTGTATTTGCTCCAATTCTAAATCCTCATTTTTTTTTTG 241 TTTTTATTTTATATATTTATACCTTTGACAAAGAGACCAGTGCCCACATCCCACCACAAC 301 TCTGAATCTATCAGGACTGTTGAAGCAGTAAATCCTCAGTGCAAACTTTTGCCAAATAAT 361 AAGTATCAACAAAATAATCTCTTCGTAATGAAAGGTTCAGAGAATTAGTAAATCTAATAT 421 ATACTTCCATAAAAGTTTATTGTAATTAATAGGTTTTTACTTCTTCCAAATGATTACTTT 481 CAATATGATCTTCAGGGAGAAAAAAACTTAAATGGTTTTCATGAGGGTGATAAGTCACAA 541 TGTCATCATGTGCATGACCTCCTCGAGAATCTCTCCCAGGCTGGAAATGTGGCAGTAATC 601 ATGGGAGTTTTCAAGAAGAAACCTACTTTTTATAAAGTGTTGTCTCCCCTACAAAAAGAT 661 GGGGAGAAAGTTTCCTTGTATATTTAAAACAATGATTATTCTAATATATTTTGTTTCTAA 721 AAATGTGATATTAAAGTAGATATATCCCTTTAGCATTACCTTAAAGGCTAGAACAAAGGG 781 GTAAATCTTCAGAAAAGTGTCACAGTACATTTTCAAGTTTAGACTTGAATCCCAGTTCAT 841 CTTTACCTTTCGTTGTGCTTTTTTAACGCTTCTTTATTTTTGATACACAGACTGCAGTCG 901 TACTTGATTTTTTAAAAATTAAA	SEQ ID NO:3
		1 GATTATTCTAATATATTTTGTTTCTAAAAATGTGATATTAAAGTAGATATATCCCTTTAG 61 CATTACCTTAAAGGCTAGAACAAAGGGGTAAATCTTCAGAAAAGTGTCACAGTACATTTT 121 CAAGTTTAGACTTGAATCCCAGTTCATCTTTAGCTTTCGTTGTGCTTTTTTAACGCTTCT 181 TTATTTTTGATACACAGACTGCAGTCGTACTTGATTTTTTTAAAAATTAAAACATGAGCTT 241 ATCAGCAAAAGACAAAAACAGAACTGCACAGTCCTAATAATCAAATAGCAATTATACTGC 301 ACAATTCAGTGATTGTAAAGTATCCTGTAACAAGCAATGTTTGTTTCCTATTTTTTGATA 361 CCTCTTAAACTTATGTCTTTTAGAAAGACAGTGCCTCTGTATGCTTTTTGTATTTTTACT 421 GAGTGTAAATATTTGTTATATTTTTGGTTAAGAGAATGTAAAAGTACCATTATTATTAGC 481 ATATCTACTAATACATTGGTGGAATCAATAAAGAATCTACAATAAAAAAAAAAAAAAAAA 541 AAAA	SEQ ID NO:4
WBC434	CGG triplet repeat binding protein 1 (CGGBP1),	1 gcaggcggac ggggcgcggc gggggacacg gcggccgccg cggggctcga tcgggcaacg 61 gcggcgacgg cggcagcgac ggatcctcct cctcccttat tcccttgctc ctctttcttc 121 cttttctttt cctttccggc cgggcctcgt ccactttccc taacggcggc ctcgatccta 181 cgtaaaggca tgacttcctg gcaccacagg gaaaatcggg tgcaagccca gaaactattt 241 ccccaccacc acttgttgaa aaactgattt gaaggcatct ccggggttga acaaacggaa	SEQ ID NO:5

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		301 agtgccagga tttgatgcgt ctctggtttc gctctggaga ccatccctg ctaagtatca	
		361 agacgaaaaa aactggaaac taatccgaac catatttatt tagagtcaga atggagcgat	
		421 ttgtagtaac agcaccacct gctcgaaacc gttctaagac tgcttttgtat gtgactcccc	
		481 tggatcgagt cactgagttt ggaggtgagc tgcatgaaga tggaggaaaa ctcttctgca	
		541 ctctttgcaa tgtggttctg aatcatgttc gcaagtctgc cattagtgac cacctcaagt	
		601 caaagactca taccaagagg aaggcagaat ttgaagagca gaatgtgaga aagaagcaga	
		661 ggcccctaac tgcatctctt cagtgcaaca gtactgcgca aacagagaaa gtcagtgtta	
		721 tccaggactt tgtgaaaatg tgcctggaag ccaacatccc acttgagaag gctgatcacc	
		781 cagcagtccg tgctttccta tctcgccatg tgaagaatgg aggctccata cctaagtcag	
		841 accagctacg gagggcatat cttcctgatg gatatgagaa tgagaatcaa ctcctcaact	
		901 cacaagattg ttgactagga ggttaccacc attgtgatca agataaatgt ggagtattaa	
		961 agttatgtgt tgattgtgtg gttcattttt gtatttattt catttaaaat catgtgacgc	
		1021 agaatagttt tgcaatgtgt atatagttgc aggcaaaaaa aaaaccacct cactgcaaaa	
		1081 cttattgtta attttagtca ccaatggtat aaagcaaaac ctaggtttag agtgtgctag	
		1141 gatacctgaa acctgatggt tatctttaaa attaatggtt tttcctctga aatgtttgtg	
		1201 catggaagaa ctgccctgct tttttaccct gttgccatgt atgattattc cttgtgagat	
		1261 tacttaatta cttggattga agactagcct attgaagctg ctgccaggca acaccactta	
		1321 acagtaactt aaaggaatta ttttctttag aggatcctct tcaaaaagga agggagatag	
		1381 tggaaaactg ttcttatatc ttcagatccc tagcagaaat gactgtttat ttcaaactat	
		1441 gttttacttg tatatgatgt agtcaccttа actatctttc aattccatac ttccccgcc	
		1501 ccatttttaa aggcttattg ttgtatttg tagcagcttc aagtgaccaa aagactaaaa	
		1561 tctttcaacg tcaatgccaa aagccaaggg gaatttgca gtgacaggat tttagtctct	
		1621 tactatgaat actaatttcg aaccatagct ttcattttaa gcatcatctt gaattttctaa	
		1681 actttttct atgtcttggt gttaaaagat ttcaagattg gcatttttac ttaaacagac	
		1741 atttatggt tgagtttct ctttattata gagaattagt aatttttttt tggctgacag	
		1801 atcagataaa attacttttct attcattaat ttttctctac aactttatga gtttatttag	
		1861 gtgatagtc tagactagaa acaagtttac tttatctgct ttgcctctgg tggtacaagg	
		1921 ttttaacat ggatggtaaa caattgtcta gaaattctgg caggtttttt gtattggaga	
		1981 tctggcagta tcctgcataa ctttgggtga ggaaattgtt ctcttaaaga tcagccatgt	
		2041 tcaggaaatg atctctgttt gaacctcact atcctgtaag gttatccaag tagcttagcc	
		2101 cagctaagtt ctatcagaga cccaaattat atttttaaaa aatttaacag ctggaaactt	
		2161 ggactagagc tttaataaaa aatcttaaat tctttgaaat tcaagttaaa aatacttata	
		2221 tatttctatt acaaagcagt gacaaatgat gccctgtgtg acttggagtt atctttgact	
		2281 ttaccacaa atcttcattt ataaaagaaa aagccaaagt gaaaaaagt tagattgtgt	
		2341 attttcagt aacagcttc catgtcttaa gatttttta cagacttaag tttctaattc	
		2401 aggttgtcaa actggccatt tgacttcaga gatttgtttt cattaaaaaa taagcctgcc	
		2461 gccaaaataa atcacttatc aaaatgtgaa ctgttttcct catgttcagt tatgttaaag	
		2521 tagtatgata aatgcatgcc tagagtagtg ctctcgttga tgaagcacat gtatgaggag	
		2581 accagcagca aaacataacc atatgtgttt tgcgtttact tcctctagaa aagaatttgc	
		2641 aggcaaccat gtttaatttg aactatctaa gatggtagat tttagaagct aggaataatt	
		2701 gagttttata gcactatttt cagaatacga aaagatacac aatcattctg tttttgaaa	
		2761 ttccatgtga ttcaaactgc tccctattat ttgggtatta atttgcacta atagcaaaat	
		2821 gtaatggcag atcagctttg agagtggtcc taagcagtaa actggatgat gttgcattag	
		2881 aaaaacatca ataattcata tttaagtttt agtagttact actgatttga taatcactta	
		2941 aatttttat atcttaatgt aattttttcag actcctaatt aattcccaca ttcactgtaa	
		3001 ctagggcat agtccattct gttaggatta tatcctctcc ttagaaatgt tttccatcct	
		3061 gttgtgggga tttggtatta atgtttcttc attgattatg gaacttttgt tccctgaagc	
		3121 tagttaactg tgtctaaagt taaataaata cagcagaatg attgttttag cctgctcgaa	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		3181 ctgatacaaa tccctgaaac catgattggc atatgttaga taacaaatga ggatgtctaa 3241 gaggcatatg ctgctttgga ggtgtagtga acgtgtgtac agaagttttc aatcttaact 3301 atatagtgtt agtgtgatgc tatactattg gaaaaatagc agctttttc tattttataa 3361 gttgtatgca taaacataag atttgtaatg tttcatttat aaactgcctt cttcaacaca 3421 tgttaatagt gttttctcaa agtattgata gtatgtcttc cagaatttca caatatgctt 3481 acagtaaata tttcctagct tgttgaaatg ttcaattctt tgttggcttt cttcttgatt 3541 ctgtgggggt gtataacaag cctgaaggac attgtaatca tttcttacaa ggtgaaaatt 3601 aagaaagatt gtgtatgaga gcctatatag ttgttttatc cattatcatc tttgattaag 3661 actttaaaaa aatgctattt ccagttaatg catttggccc tattgaattt tcagggacca 3721 gaaaacatta aaaagttctg catcttataa tggtaaccaa ttaagcttga gattgttctg 3781 aaagtatcaa ttgctttaaa actgttgtaa gtacagttgg caagatctcc aagctgaaac 3841 ttccacgtta aaacttttgc ctgtaagaat ttgcacatga atgttaatgg aaaacacaaa 3901 acttaagatg gcccaaaaca aaagccacaa acagttcatc atttggtgct tagtctttgt 3961 aagggctctc tgtggtttga cttaccccag ctaccgttaa atgaggacaa atcaccttaa 4021 aacatgttca tttgattcat aacaaggaaa attgggtcta tgatttttg ccaatcttag 4081 cctaaaagaa attgctttag cttctggtca gcactgatta aaatgtgaat agtgaagtgg 4141 ctatcctaaa ctggtttatc tccacccaca ctatcataga tttcttaggt aaatacaatt 4201 cttatctagt ggtattctac ttgtattcag aatactgtat taaaatttta ctatttcatt 4261 tttgtattct gtgcttattt tttttgctca cgcatgtatg cttagtataa atgtgtcact 4321 tctaaagttt tgtctctgac ttttagaaat aaatttcaga aaaattgttt caaaagattt 4381 tgaaagcaca ttttgttttg tgagtcaatg acaaatatat ttcctgatta caaaacaaaa 4441 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4501 aaaaaa 1 M E R F V V T A P P A R N R S K T A L Y 1 ATGGAGCGATTTGTAGTAACAGCACCACCTGCTCGAAACCGTTCTAAGACTGCTTTGTAT 21 V T P L D R V T E F G G E L H E D G G K 61 GTGACTCCCCTGGATCGAGTCACTGAGTTTGGAGGTGAGCTGCATGAAGATGGAGGAAAA 41 L F C T S C N V V L N H V R K S A I S D 121 CTCTTCTGCACTTCTTGCAATGTGGTTCTGAATCATGTTCGCAAGTCTGCCATTAGTGAC 61 H L K S K T H T K R K A E F E E Q N V R 181 CACCTCAAGTCAAAGACTCATACCAAGAGGAAGGCAGAATTTGAAGAGCAGAATGTGAGA 81 K K Q R P L T A S L Q C N S T A Q T E K 241 AAGAAGCAGAGGCCCCTAACTGCATCTCTTCAGTGCAACAGTACTGCGCAAACAGAGAAA 101 V S V I Q D F V K M C L E A N I P L E K 301 GTCAGTGTTATCCAGGACTTTGTGAAAATGTGCCTGGAAGCCAACATCCCACTTGAGAAG 121 A D H P A V R A F L S R H V K N G G S I 361 GCTGATCACCCAGCAGTCCGTGCTTTCCTATCTCGCCATGTGAAGAATGGAGGCTCCATA 141 P K S D Q L R R A Y L P D G Y E N E N Q 421 CCTAAGTCAGACCAGCTACGGAGGGCATATCTTCCTGATGGATATGAGAATGAGAATCAA	SEQ ID NO:6

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		161 L L N S Q D C - 481 CTCCTCAACTCACAAGATTGTTGA	
WBC166	Mst3 and SOK1-related kinase (MASK)	1 ggcatcactc gagcccaggt cccagtcatc accactcaca gcgctcggcg ttcaggaaga 61 ggagcaccag cggagcgcgg ctgcttcagc ggcgggcggg cgccagaaag gcccgcatcg 121 aaaagcctgg gagggcgccc gaactacccc cggagggagg agccagtccg aacccaaggc 181 gccaccgccg cagaagcgga gcgaggcagc attcgcctcc atggcccact cgccgtggcc 241 tgtccaagtg cctggatgc agaataacat agctgatcca gaagaactgt tcacaaaatt 301 agagcgcatt gggaaaggct catttgggga agttttcaaa ggaattgata accgtaccca 361 gcaagtcgtt gctattaaaa tcatagacct tgaggaagcc gaagatgaaa tagaagacat 421 tcagcaagaa ataactgtct tgagtcaatg tgacagctca tatgtaacaa aatactatgg 481 gtcatattta aagggtctta aattatggat aataatggaa tacctgggcg gtggttcagc 541 actggatctt cttcgagctg gtccatttga tgagttccag attgctacca tgctaaagga 601 aattttaaaa ggtctggact atctgcattc agaaaagaaa attcaccgag acataaaagc 661 tgccaatgtc ttgctctcag aacaaggaga tgttaaactt gctgattttg gagttgctgg 721 tcagctgaca gatacacaga ttaaaagaaa tacctttgtg ggaactccat ttggatggc 781 tcctgaagtt attcaacagt cagcttatga ctcaaaagct gacatttggt cattgggaat 841 tactgctatt gaactagcca agggagagcc acctaactcc gatatgcatc caatgagagt 901 tctgtttctt attcccaaaa acaatcctcc aactcttgtt ggagacttta ctaagtcttt 961 taaggagttt attgatgctt gcctgaacaa agatccatca tttcgtccta cagcaaaaga 1021 acttctgaaa cacaaattca ttgtaaaaaa ttcaaagaag acttcttatc tgactgaact 1081 gatagatcgt tttaagagat ggaaggcaga aggacacagt gatgatgaat ctgattccga 1141 gggctctgat tcggaatcta ccagcaggga aaacaatact catcctgaat ggagctttac 1201 caccgtacga aagaagcctg atccaaagaa agtacagaat gggcagagc aagatcttgt 1261 gcaaaccctg agttgtttgt ctatgataat cacacctgca tttgctgaac ttaaacagca 1321 ggacgagaat aacgctagca ggaatcaggc gattgaagaa ctcgagaaaa gtattgctgt 1381 ggctgaagcc gcctgtcccg gcatcacaga taaaatggtg aagaaactaa ttgaaaaatt 1441 tcaaaagtgt tcagcagacg aatcccccta agaaacttat tattggcttc tgtttcatat 1501 ggacccagag agccccacca aacctacgtc aagattaaca atgcttaacc catgagctcc 1561 atgtgccttt tggatctttg caacactgaa gatttggaag aagctattaa actatttgt 1621 gatggcgttt atcatttcat atttgaaag gatattttg taaggaataa ctttaatac 1681 tatagtttca cctgtattct agtaaatgtt gagacaccgt ttgctttta agtatcccta 1741 ttcttaagt tacgaggatg aatacctttc acatttgat ctttagttga ctctacagtc 1801 atgaaacata caggtctttc aaagtcattc tcaatattca gcttttgtaa attatcaagc 1861 ttcaaaaagc ttttttttta aaaaaaaaaa catgcatatt ctaaaaatga ctattggtgg 1921 ggaggtgtaa ataagtcata ccttcttaaa acagaaaatt taagtaaagt cttttaaatg 1981 aaacctgtaa aagtattgac tcttctacca agttggtatg atattccagg cagctcaatg 2041 attatcacat ttgagaccct gtgtttgaag cattacagg caatgtacag caacagaggt 2101 acctcttggt gtatagtatt tacattctct tttaggtaga agaggcaatt ttacccttat 2161 ttcacatggt tagaaatttg aagcaagatc atttacccaa ggataggtgt ttggtaatgt 2221 tgaaggagtt agtctggctt catgtttcac atcttcaact aaaatcccat actatctgct 2281 tggatttgga gagccaaaaa ataaagctga ttgtcatgtg attaaatatc tgatcaacag 2341 gtatgaatat aacttaaatc agcatatttt tgccatggta ataaattgtc gttttaaacta 2401 tttatatatt tttgttcttc atattatca ctaataagca tcagtttgtt gttttaaaa 2461 ggatatttaa gtgagcattt tctagttcat atgaaaataa ccatagtaca ggatgatttc	SEQ ID NO:7

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2521 tgtccacaca aaggttaaat tagattgcac agttaatttt cacttatatt tatggtacta 2581 ttatgtgggt gatgccttct tcttttaagc ccagtacata tattatgcct gcctaagttc 2641 tgaactgggg ctgtatttca gtagttgtag aattattgat atttagtttt gatagctaat 2701 gtttaattgt ttggatctgc acagtttggt ttttgcacaa aagtcattta aaaaaatctg 2761 agtaattgtc aaatattaaa agaaagatat tcttcctgta aggaatacag tttttagtca 2821 aagtggccat tacatccctct ttttaattta cataatacag atacttgaga aagttgttgt 2881 ggtgttgtat gccaagaaaa ttcttttttat tggtgcctat attgtaacaa ttatttttaa 2941 tgcattgtat tttgaagtaa cggttcagtt aaatttttca cctgctgtgt aactgaagca 3001 caattacagt ttataaatcat ctgtagaagt ctggagataa tttgcaact catgttatgg 3061 gttaaatgaa tatttttgta aaagtaaaag caacaaattt ataaattgat tatttgaaac 3121 ttacaacac aattgcatcc caaatacaaa ttgtattgct tattcattat agctattcgt 3181 cctgtaatct gtttctaggt gaagcatact ccagtgtttt agggggtttg aaaataaata 3241 tttaaatttc acagtcaaaa aaa 1 M A H S P V A V Q V P G M Q N N I A D P 1 ATGGCCCACTCGCCGGTGGCTGTCCAAGTGCCTGGGATGCAGAATAACATAGCTGATCCA 21 E E L F T K L E R I G K G S F G E V F K 61 GAAGAACTGTTCACAAAATTAGAGCGCATTGGGAAAGGCTCATTTGGGGAAGTTTTCAAA 41 G I D N R T Q Q V V A I K I I D L E E A 121 GGAATTGATAACCGTACCCAGCAAGTCGTTGCTATTAAAATCATAGACCTTGAGGAAGCC 61 E D E I E D I Q Q E I T V L S Q C D S S 181 GAAGATGAAATAGAAGACATTCAGCAAGAAATAACTGTCTTGAGTCAATGTGACAGCTCA 81 Y V T K Y Y G S Y L K G S K L W I I M E 241 TATGTAACAAAATACTATGGGTCATATTTAAAGGGGTCTAAATTATGGATAATAATGGAA 101 Y L G G G S A L D L L R A G P F D E F Q 301 TACCTGGGCGGTGGTTCAGCACTGGATCTTCTTCGAGCTGGTCCATTTGATGAGTTCCAG 121 I A T M L K E I L K G L D Y L H S E K K 361 ATTGCTACCATGCTAAAGGAAATTTTAAAAGGTCTGGACTATCTGCATTCAGAAAAGAAA 141 I H R D I K A A N V L L S E Q G D V K L 421 ATTCACCGAGACATAAAAGCTGCCAATGTCTTGCTCTCAGAACAAGGAGATGTTAAACTT 161 A D F G V A G Q L T D T Q I K R N T F V 481 GCTGATTTTGGAGTTGCTGGTCAGCTGACAGATACACAGATTAAAAGAAATACCTTTGTG 181 G T P F W M A P E V I Q Q S A Y D S K A 541 GGAACTCCATTTTGGATGGCTCCTGAAGTTATTCAACAGTCAGCTTATGACTCAAAGCT 201 D I W S L G I T A I E L A K G E P P N S 601 GACATTTGGTCATTGGGAATTACTGCTATTGAACTAGCCAAGGGAGAGCCACCTAACTCC	SEQ ID NO:8

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		221 D M H P M R V L F L I P K N N P P T L V 661 GATATGCATCCAATGAGAGTTCTGTTTCTTATTCCCAAAACAATCCTCCAACTCTTGTT 241 G D F T K S F K E F I D A C L N K D P S 721 GGAGACTTTACTAAGTCTTTTAAGGAGTTTATTGATGCTTGCCTGAACAAAGATCCATCA 261 F R P T A K E L L K H K F I V K N S K K 781 TTTCGTCCTACAGCAAAAGAACTTCTGAAACACAAATTCATTGTAAAAAATTCAAAGAAG 281 T S Y L T E L I D R F K R W K A E G H S 841 ACTTCTTATCTGACTGAACTGATAGATCGTTTTAAGAGATGGAAGGCAGAAGGACACAGT 301 D D E S D S E G S D S E S T S R E N N T 901 GATGATGAATCTGATTCCGAGGGCTCTGATTCGGAATCTACCAGCAGGGAAAACAATACT 321 H P E W S F T T V R K K P D P K K V Q N 961 CATCCTGAATGGAGCTTTACCACCGTACGAAGAAGCCTGATCCAAAGAAAGTACAGAAT 341 G A E Q D L V Q T L S C L S M I I T P A 1021 GGGGCAGAGCAAGATCTTGTGCAAACCCTGAGTTGTTTGTCTATGATAATCACACCTGCA 361 F A E L K Q Q D E N N A S R N Q A I E E 1081 TTTGCTGAACTTAAACAGCAGGACGAGAATAACGCTAGCAGGAATCAGGCGATTGAAGAA 381 L E K S I A V A E A A C P G I T D K M V 1141 CTCGAGAAAAGTATTGCTGTGGCTGAAGCCGCCTGTCCCGGCATCACAGATAAAATGGTG 401 K K L I E K F Q K C S A D E S P - 1201 AAGAAACTAATTGAAAAATTTCAAAAGTGTTCAGCAGACGAATCCCCCTAA	
WBC043G11.bFSP_20021401.esd	Homo sapiens high mobility group nucleosomal binding domain 4, mRNA	1 TCTGTCTTAGGGCTGGTGCTGGCCCTGCCCACGCCTAGGGCTCCGGCGCGTCACGGCCT 61 CAGCTGGGATTCCCGCGCCCCTCGGACGGCCACGAGACTCGGACATCTTTCCAGGAACAG 121 CGTGAGGAGGACAGAAGCACCCAACAGGACTGCTCAAGCCACCTGCGACACACTGCTCTA 181 CCATGCCCAAGAGAAAGGCAAAAGGAGATGCTAAAGGTGATAAAGCAAAGGTGAAGGATG 241 AGCCACAGAGGAGATCAGCTCGGTTGTCTGCTAAACCAGCTCCTCCAAAACCAGAGCCCA 301 GGCCTAAAAAGAGCCCCTGCAAGAAGGGAGAAGCTACCCAAAGGGAGAAAGGGGAAA 361 GCAGAATAGTGGCAAGGATGGGAACACACCCTGCGAAAAACCGAGATGCCACCACAGTCCA 421 GTCACAGAAAGCGGAAGGCAGCGGGGATGCCAAGTGAAGTGTGCTATTTTGATAGCTCTG 481 TACTTGTAGTGACTCTGCTGTTTGAAATACTATTTTTTTAAATCAAGTTTTATAAAAGTG 541 TAGAATTTTGGCTTTTTTAGTATATTGTTAGCACACAGGACACTTTGTTGTCTTTTGT 601 GGAAAGGGCAAATACCACTAACAGAGTGTTTCAGAAGCTGGATTAAAATGGAGGAAAATA 661 GTATTTTCTGTCCTCATTTTTGAAGATTATTCTTGATTCCCTTGATTCCCAGGAGACATT 721 CTCTGACATTCACACACGAGTCAGTCACTTTGGCTCAGACGCCTTACAGTGTGTGGAAGC 781 AAAACTTCATGTCTCCTCTTTCCCCGATGCCATCAGCATAGACTTGACTTCCTTAACCG 841 AGAGTTTTGATGTGGCCTTGGCAACCCTAAAATCAGCTGTGTTGGGTAATAATCCTCAGG 901 CCTTCTGATGAAGACATCGACATGGTGTTGCTCAAAAGAGCCAAGATTCCTGTTTGCAAT	SEQ ID NO:9

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		961 TTGTGGATTCATCCTGCTGGTTTTACTTTAGTCCCTCCATGTCAAAGTGGGCCTGTGAAA 1021 AGCTCTTACATGCCTCATGTGAAATATCCCACCCTCTCTGAAAATCTTTCTTGTTCCAAAAC 1081 AGCAACGACATATCTTGTTAACTTTACGGTGACTTTTGGAGGAGGGGAGTTTGGAAATT 1141 GTAAAATGTTATAGATTGTTGCCTATTTCCTGCTGAAAGTAAATGTTTTTTAAAAGTATC 1201 ATATAAAGCTGAATACAAATTGGTTTGGGGGGAGATCCTTTCCTACCCAAAGTCATAAAT 1261 ATATTCTTTACTGCCTTGTGGAAATTTTATAGTTTGCCTTTCACATTTGTCTTTAGTCT 1321 GTCCTGAACTGATTTTTGTGCAAAATTATAGATTAGAAATTCAACTTAACATTTTTCATAT 1381 TCGAAGTGGTTGTTGCAGCACCATTTTCTGAAAAGTTCATCCTTTCCTCACTGACCTGTA 1441 ACACTGTCTCTTTCATAAATCAAGTTTGTGTTTGTGGTCTCTTGATGGTTTCTGT 1501 TCTGACTCACTGGTCAATTTGTCTAACCTGTGGCAGTACTATACAATCCTGAGTATGACA 1561 ACTTTAGAAAAAGGCTCTGATAAAAACCAAGATGCCCTCCACATTTTGTCATAATTGTAACC 1621 AATTTCACCTCTGTCTCCAGTATCATCACCAAATTTTTCTTCCTTGAGAGTATCTTGGCT 1681 ATTTTTAGCCACTGTTCCTCCATATTACTTCTAGAATTAGACCAACAATTTATAAATCAA 1741 ACAAACCCAAGAGCATTGAAATTTTGATTGGATTTGTATTGAATTTATAGATTAATCTGG 1801 TAAACCATGTCATCTTTACAATGTTGTCTTCCAATACTATGAATATGGTACAGCTCTTCAT 1861 TTATTTAGGCTTTTTAAATGTCTTTCAATAAAGTTTTATAATTTTCTCCAAAAAAAAAA 1921 AAAAA 1 M P K R R K A K G D A K G D K A K V K D E 1 ATGCCCAAGAGAAAGGCAAAAGGAGATGCTAAAGGTCATAAAGCAAAGGTGAAGGATGAG 21 P Q R R S A R L S A K P A P P K P E P R 61 CCACAGAGGAGATCAGCTCGGTTGTCTGCTAAACCAGCTCCTCCAAAACCAGAGCCCAGG 41 P K K S P C K E G R E A T Q R E K G E S 121 CCTAAAAAGAGCCCCTGCAAAGAAGGGAGAGGAAGCTACCCAAAGGGAGAAAGGGCAAAGC 61 R I V A R M G T T L R K T E M P P Q S S 181 AGAATAGTGGCAAGGATGGGAACAACCCTGCGAAAAACCGAGATGCCACCACACGTCCAGT 81 H R K R K A A G M P S E V C Y F D S S V 241 CACAGAAAGCGGAAGGCAGCGGGGATGCCAAGTGAAGTGTGCTATTTTGATAGCTCTGTA 101 L V V T L L F E I L F F - 301 CTTGTAGTGACTCTGCTGTTTGAAATACTATTTTTTTAA	SEQ ID NO:10
WBC041B05	ARP3 actin-related protein 3 homolog (yeast)	1 atcttggctt cccgggggaaa ggcggcgtga gggaagaaag ttgtagggtg ggggcaggag 61 tgaggaggag ggaagagaga gggggaggag gccgcggcgg ggcagggcgg ggactgcctg 121 cctgcctggg ttgcggaagt gatagccgcc gaccgagcct gctgctttct tgctactgct 181 tcggcttccc ggctacccgc cggacggtga aggcggccca gctgtggatg gtcagatagc 241 ccttgtttcc cgccgcccaat ctctggccca tagcagcacg gagcagacgg cggcagcagc 301 agcagcaggc gaggaggaag atggcgggac ggctgccggc ctgtgtggtg gactgtggca 361 cggggtatac aaaactagga tatgctggaa atacagaacc acagtttatc atcccttcct 421 gtattgctat taaggagtca gcaaaagtgg gtgatcaagc tcaaaggagg gtgatgaaag 481 gtgttgatga cctagacttc ttcattggtg atgaagcaat agaaaaacct acatatgcaa 541 caaagtggcc aatccgccat ggtatagttg aagatggga cttaatggaa aggtttatgg	SEQ ID NO:11

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		601 agcaagtgat ctttaaatat ttaagggcag aacctgaaga ccattatttt cttttgactg 661 aacctccatt gaatactcca gaaaacaggg aatatactgc tgaaataatg tttgagtcct 721 tcaatgttcc aggcttgtac attgctgtgc aggctgttct tgccttagct gcatcttgga 781 cctcaagaca agtaggagaa cggacgttga ccggtacggt aatagacagt ggagatggtg 841 tcactcatgt cattcctgtg gctgaagggt atgtgattgg cagctgtatt aaacacattc 901 caatcgcagg acgagatata acatatttta ttcagcaact gctgagagac cgagaagtag 961 gaatccctcc agaacaatcc ttggaaactg ctaaggcagt aaaggagcgc tatagttatg 1021 tctgcccaga tttagtaaaa gaatttaaca agtatgatac agatgggtca aaatggatta 1081 aacagtatac tggaatcaat gctatctcaa agaaagagtt ttctatcgat gttggttatg 1141 agagattttt gggacctgaa atctttttttc atccagagtt tgctaatcca gactttacac 1201 aacctatctc agaagttgta gatgaagtaa ttcagaattg tcctattgat gtcagacgtc 1261 ctctctacaa gaatattgtc ctctctggag gttcaaccat gttcagggac tttggacgtc 1321 gcttgcaaag agatttgaaa agaactgtag atgcccggct gaaattaagt gaggaattga 1381 gtggtggtag attgaagcca aaacctattg atgtacaagt cattacacac cacatgcagc 1441 gatatgcagt ttggtttgga ggatcaatgc tggcttccac gcctgagttc taccaagtat 1501 gccacaccaa aaaggattat gaagaaattg gacctagcat ttgtcgtcac aatccagtgt 1561 ttggagtcat gtcgtaaaat tggcttcata gttattgggg ttagggaggt ggggaagaga 1621 taatctttct gattacctgt tttgtctgga tggctggttt tgaggtttta aacctgactt 1681 gaaatagtaa caccaaacat gattatacag gaatatttta ataagtgtat caccatgcag 1741 atgtagaaga gagcgaaagt gattgtgttt ttctttagat tgaatatttg aatcttatgt 1801 gtaacaaaaa gaagtgggtt ttagttcttt ctgtgccctg atattttgta tattaatgaa 1861 ttatccaaga ttcgatggga tttatcagtg tgtagatagc tctataatgc ttgaattgta 1921 cacttctaag tgtgcagtgc aagagcttgt ttatatttca tacttttttat actttgagga 1981 aaaaaagtca aagaaaaatt gtatttgagg gaaaaaacca tgaccaagta aaggataaat 2041 tcaaaaaata gcctcatgag acttggcata cacactcgtg ggattccagt tattatggag 2101 tgcttccatc cctctccacc ccttcccccc aaaaggtttt ctttgcaagt gcttttggaa 2161 ctaagagcta gtatcttgga ttaactgatg cctgctagtg ctttctgatt actcgcattc 2221 tgtttcttgc tttaaaagaa gagtaaagac aagagtgttg gaccagtatt gcagttctgt 2281 agtgtcattt cttataaaaa acaaaacaac aacaataatt tatcaaaatt ggcatattta 2341 aagcctaaca ttctaataaa ggcacaaatt tctttttaat acttgtttca gcctctttaa 2401 tctctttata agttaactaa taaatctatt ttcttcagac ttctgcaata gttctttaaa 2461 atcacaacag ttagcaagct gacttttgta atgtgctcaa tacaaatact tgtgaacttt 2521 taatatgttg agtgctttca ttttgataac tggatctcca tttgatattt tcatttgtat 2581 aactcatttg cagtctgaaa attttttttta gtgccagtcc ctgaacatat cattgaaagt 2641 taattttctt tgcattttaa aatatctgga ttatgaagaa aaagtgatga aaataaatta 2701 aaactgaatt acaaaaaaaa aaaaaaaa 1 M A G R L P A C V V D C G T G Y T K L G 1 ATGGCGGGACGGCTGCCGGCCTGTGTGGTGGACTGTGGCACGGGGTATACAAAACTAGGA 21 Y A G N T E P Q F I I P S C I A I K E S 61 TATGCTGGAAATACAGAACCACAGTTTATCATCCCTTCCTGTATTGCTATTAAGGAGTCA 41 A K V G D Q A Q R R V M K G V D D L D F 121 GCAAAAGTGGGTGATCAAGCTCAAAGGAGGGTGATGAAAGGTGTTGATGACCTAGACTTC 61 F I G D E A I E K P T Y A T K W P I R H	SEQ ID NO:12

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		181 TTCATTGGTGATGAAGCAATAGAAAAACCTACATATGCAACAAAGTGGCCAATCCGCCAT	
		81 G I V E D W D L M E R F M E Q V I F K Y	
		241 GGTATAGTTGAAGATTGGGACTTAATGGAAAGGTTTATGGAGCAAGTGATCTTTAAATAT	
		101 L R A E P E D H Y F L L T E P P L N T P	
		301 TTAAGGGCAGAACCTGAAGACCATTATTTTCTTTTGACTGAACCTCCATTGAATACTCCA	
		121 E N R E Y T A E I M F E S F N V P G L Y	
		361 GAAAACAGGGAATATACTGCTGAAATAATGTTTGAGTCCTTCAATGTTCCAGGCTTGTAC	
		141 I A V Q A V L A L A A S W T S R Q V G E	
		421 ATTGCTGTGCAGGCTGTTCTTGCCTTAGCTGCATCTTGGACCTCAAGACAAGTAGGAGAA	
		161 R T L T G T V I D S G D G V T H V I P V	
		481 CGGACGTTGACCGCTACGGTAATAGACAGTGGAGATGGTGTCACTCATGTCATTCCTGTG	
		181 A E G Y Y V I G S C I K H I P I A G R D I	
		541 GCTGAAGGGTATGTGATTGGCAGCTGTATTAAACACATTCCAATCGCAGGACGAGATATA	
		201 T Y F I Q Q L L R D R E V G I P P E Q S	
		601 ACATATTTTATTCAGCAACTGCTGAGACCGAGAAGTAGGAATCCCTCCAGAACAATCC	
		221 L E T A K A V K E R Y S Y V C P D L V K	
		661 TTGGAAACTGCTAAGGCAGTAAAGGAGCGCTATAGTTATGTCTGCCCAGATTTAGTAAAA	
		241 E F N K Y D T D G S K W I K Q Y T G I N	
		721 GAATTTAACAAGTATGATACAGATGGGTCAAAATGGATTAAACAGTATACTGGAATCAAT	
		261 A I S K K E F S I D V G Y E R F L G P E	
		781 GCTATCTCAAAGAAAGAGTTTTCTATCGATGTTGGTTATGAGAGATTTTTGGGACCTGAA	
		281 I F F H P E F A N P D F T Q P I S E V V	
		841 ATCTTTTTTCATCCAGAGTTTGCTAATCCAGACTTTACACAACCTATCTCAGAAGTTGTA	
		301 D E V I Q N C P I D V R R P L Y K N I V	
		901 GATGAAGTAATTCAGAATTGTCCTATTGATGTCAGACGTCCTCTCTACAAGAATATTGTC	
		321 L S G G S T M F R D F G R R L Q R D L K	
		961 CTCTCTGGAGGTTCAACCATGTTCAGGGACTTTGGACGTCGCTTGCAAAGAGATTTGAAA	
		341 R T V D A R L K L S E E L S G G R L K P	
		1021 AGAACTGTAGATGCCCGGCTGAAATTAAGTGAGGAATTGAGTGGTGGTAGATTGAAGCCA	
		361 K P I D V Q V I T H H M Q R Y A V W F G	
		1081 AAACCTATTGATGTACAAGTCATTACACACCACATGCAGCGATATGCAGTTTGGTTTGGA	
		381 G S M L A S T P E F Y Q V C H T K K D Y	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1141 GGATCAATGCTGGCTTCCACGCCTGAGTTCTACCAAGTATGCCACACCAAAAAGGATTAT 401 E E I G P S I C R H N P V F G V M S - 1201 GAAGAAATTGGACCTAGCATTTGTCGTCACAATCCAGTGTTTGGAGTCATGTCGTAA	
WBC039F12	Leu-8 pan leukocyte antigen	1 ctccctttgg gcaaggacct gagaccctg tgctaagtca agaggctcaa tgggctgcag 61 aagaactaga gaaggaccaa gcaaagccat gatatttcca tggaaatgtc agagcaccca 121 gagggactta tggaacatct tcaagttgtg gggtggaca atgctctgtt gtgatttcct 181 ggcacatcat ggaaccgact gctggactta ccattattct gaaaaaccca tgaactggca 241 aagggctaga agattctgcc gagacaatta cacagattta gttgccatac aaaacaaggc 301 ggaaattgag tatctggaga agactctgcc tttcagtcgt tcttactact ggataggaat 361 ccggaagata ggaggaatat ggacgtgggt gggaaccaac aaatctctca ctgaagaagc 421 agagaactgg ggagatggtg agcccaacaa caagaagaac aaggaggact gcgtggagat 481 ctatatcaag agaaacaaag atgcaggcaa atggaacgat gacgcctgcc acaaactaaa 541 ggcagccctc tgttacacag ctctttgcca gccctggtca tgcagtggcc atggagaatg 601 tgtagaaatc atcaataatt acacctgcaa ctgtgatgtg gggtactatg ggcccccagtg 661 tcagtttgtg attcagtgtg agcctttgga ggccccagag ctgggtacca tggactgtac 721 tcactctttg ggaaacttca gcttcagctc acagtgtgcc ttcagctgct ctgaaggaac 781 aaacttaact gggattgaag aaaccacctg tggaccattt ggaaactggt catctccaga 841 accaacctgt caagtgattc agtgtgagcc tctatcagca ccagatttgg ggatcatgaa 901 ctgtagccat ccctggcca gcttcagctt tacctctgca tgtaccttca tctgctcaga 961 aggaactgag ttaattggga agaagaaaac cattgtgaa tcatctggaa tctggtcaaa 1021 tcctagtcca atatgtcaaa aattggacaa aagtttctca atgattaagg agggtgatta 1081 taacccctc ttcattccag tggcagtcat ggttactgca ttctctgggt tggcatttat 1141 catttggctg gcaaggagat taaaaaaagg caagaaatcc aagagaagta tgaatgaccc 1201 atattaaatc gccttggtg aaagaaaatt cttggaatac taaaaatcat gagatccttt 1261 aaatccttcc atgaaacgtt ttgtgtggtg gcacctccta cgtcaaacat gaagtgtgtt 1321 tccttcagtg catctgggaa gatttctacc tgaccaacag ttccttcagc ttccatttcg 1381 ccctcatatt atccctcaac ccccagccca caggtgttta tacagctcag cttttgtcct 1441 tttctgagga gaaacaaata agaccataaa gggaaaggat tcatgtggaa tataaagatg 1501 gctgactttg ctctttcttg actctttgttt tcagtttcaa ttcagtgctg tacttgatga 1561 cagacactic taaatgaagt gcaaatttga tacatatgtg aatatggact cagttttctt 1621 gcagatcaaa tttcacgtcg tcttctgtat actgtggagg tacactctta tagaaagttc 1681 aaaaagtcta cgctctcctt tctttctaac tccagtgaag taatggggtc ctgctcaagt 1741 tgaaagagtc ctatttgcac tgtagcctcg ccgtctgtga attggaccat cctatttaac 1801 tggcttcagc ctccccacct tcttcagcca cctctctttt tcagttggct gacttccaca 1861 cctagcatct catgagtgcc aagcaaaagg agagaagaga gaaatagcct gcgctgtttt 1921 ttagtttggg ggttttgctg tttcctttta tgagacccat tcctatttct tatagtcaat 1981 gtttcttta tcacgatatt attagtaaga aaacatcact gaaatgctag ctgcaagtga 2041 catctctttg atgtcatatg gaagagttaa aacaggtgga gaaattcctt gattcacaat 2101 gaaatgctct ctttccctt gccccagac ctttatccg acttacctag atctacata 2161 ttctttaaat ttcatctcag gcctccctca acccaccac ttctttata actagtcctt 2221 tactaatcca acccatgatg agctcctctt cctggcttct tactgaaagg ttaccctgta 2281 acatgcaatt ttgcattiga ataaagcctg cttttaagt gtt	SEQ ID NO:13

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1 M G C R R T T R E G P S K A M I F P W K C 1 ATGGGCTGCAGAAGACTAGAGAAGGACCAAGCAAAGCCATGATATTTCCATGGAAATGT 21 Q S T Q R D L W N I F K L W G W T M L C 61 CAGAGCACCCAGAGGGACTTATGGAACATCTTCAAGTTGTGGGGGTGGACAATGCTCTGT 41 C D F L A H H G T D C W T Y H Y S E K P 121 TGTGATTTCCTGGCACATCATGGAACCGACTGCTGCACTTACCATTATTCTGAAAAACCC 61 M N W Q R A R R F C R D N Y T D L V A I 181 ATGAACTGGCAAAGGGCTAGAAGATTCTGCCGAGACAATTACACAGATTTAGTTGCCATA 81 Q N K A E I E Y L E K T L P F S R S Y Y 241 CAAAACAAGGCGGAAATTGAGTATCTGGAGAAGACTCTGCCTTTCAGTCGTTCTTACTAC 101 W I G I R K I G G I W T W V G T N K S L 301 TGGATAGGAATCCGGAAGATAGGAGGAATATGGACGTGGGTGGCAACCAACAAATCTCTC 121 T E E A E N W G D G E P N N K K N K E D 361 ACTGAAGAAGCAGAGAACTGGGGAGATGGTGAGCCCAACAACAAGAAGAACAAGGAGAC 141 C V E I Y I K R N K D A G K W N D D A C 421 TGCGTGGAGATCTATATCAAGAGAAACAAAGATGCAGGCAAATGGAACGATGACGCCTGC 161 H K L K A A L C Y T A S C Q P W S C S G 481 CACAAACTAAAGGCAGCCCCTCTGTTACACAGCTTCTTGCCAGCCCTGGTCATGCAGTGGC 181 H G E C V E I I N N Y T C N C D V G Y Y 541 CATGGAGAATGTGTAGAAATCATCAATAATTACACCTGCAACTGTGATGTGGGTACTAT 201 G P Q C Q F V I Q C E P L E A P E L G T 601 GGGCCCCAGTGTCAGTTTGTGATTCAGTGTGAGCCTTTGGAGGCCCCAGAGCTGGGTACC 221 M D C T H S L G N F S F S S Q C A F S C 661 ATGGACTGTACTCACTCTTTGGGAAACTTCAGCTTCAGCTCACAGTGTGCCTTCAGCTGC 241 S E G T N L T G I E E T T C G P F G N W 721 TCTGAAGGAACAAACTTAACTGGGATTGAAGAAACCACCTGTGGACCATTTGGAAACTGG 261 S S P E P T C Q V I Q C E P L S A P D L 781 TCATCTCCAGAACCAACCTGTCAAGTGATTCAGTGTGAGCCTCTATCAGCACCAGATTTG 281 G I M N C S H P L A S F S F T S A C T F 841 GGGATCATGAACTGTAGCCATCCCCTGGCCAGCTTCAGCTTTACCTCTGCATGTACCTTC 301 I C S E G T E L I G K K K T I C E S S G 901 ATCTGCTCAGAAGGAACTGAGTTAATTGGGAAGAAGAAAACCATTTGTGAATCATCTGGA	SEQ ID NO:14

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		321 I W S N P S P I C Q K L D K S F S M I K 961 ATCTGGTCAAATCCTAGTCCAATATGTCAAAAATTGGACAAAAGTTTCTCAATGATTAAG 341 E G D Y N P L F I P V A V M V T A F S G 1021 GAGGGTGATTATAACCCCCTCTTCATTCCAGTGGCAGTCATGGTTACTGCATTCTCTGGG 361 L A F I I W L A R R L K K G K K S K R S 1081 TTGGCATTTATCATTTGGCTGGCAAGGAGATTAAAAAAAGGCAAGAAATCCAAGAGAAGT 381 M N D P Y - 1141 ATGAATGACCCATATTAA	
WBC038G11_V1.3_at	No Homology	1 GATGCCTGCAATACCTCTTATCATCGTTGTAACATTTCTTCCAAATTAATGACCCAACC 61 CGTCCTCTCTGGGCCAGAGTTAAAGCGAGGCTTGGACAAGAAGAATCGGCCTATGCAGAC 121 TCAAAAGAGTTTATCCTGTGCCAGCACGGGAAAATTGGACCACCTAAACTGGATATCAGA 181 AAGAAAGACGACCAGATCATTATTGACATATCTCACCCTTTATTTGCTGTAAATGGATTT 241 GACCTGGAAGCCATGTATGATGATGAAAATGCTTGTTACGAATTCGTGTACAAGGTGTAT 301 GTGAAAATAAACGGAAGTGGAGAGAGCATGGAGAGAGTGTATGAATGCAGAGACGAGGAC 361 TGCAATGAGACCCACTGCCGCCTCGGCATCCCAGCGTCCTCCCTGAACTCTCAGTGCTGC 421 GCTGCAGCAGAGGGAGTCTCGGAACGATGGGAGTTCACAACTGACAAGTCCGAAGAACTC 481 TGCCTGACCGTTTTCGATGATGGCAGCCCAGAAGGTTCGGTTGGATTCCAGTTGTTGCT 541 GCTTTCCTACTCTTTCTAGTCATTCTGCTGGTTGCGTGTTGTTATTGTCGCATTAAGACG 601 AAGAATCTGTTTAAGAGAAGAAACAACCCTTTACCCAGTTCCTTGCTGTCTGTGCTAAGA 661 AGTGCCTCTTCAGAGCCAGACTCTGAATCAAAGCATATATCGCCTGTCACCTACCAGCCA 721 ATTGTCCCGGAGAACGATCACCTGTCTTCAGCAGCGGTGTCAGGGACGCAGGCTGAAGAC 781 AGTCC 1 GTGGACGAAGGTGGGAAGCAGTTCCCTGATCGGCTACAGACTGACAGCTGACTCCCAGGA 61 GTTCTCCTGAGCTCAGCCGAGGGGCCCGGCCCTGAAGGAAGGGCTCTGCCTGAGCAGTTC 121 TTCCTGAACGGCTTTGAGTTTGTGAAAAGATCTGATTTCTGGAATTGTGTCAATATTAAC 181 CACATGCAATGTCTGGTTCAGATCAAAATGTGAACTCCCTGTTGAACTTGGTCGCATTTG 241 GTCTGAAAACAGCAAACCAGTTTCAAAACCTGTCTTAGGAAACAAGCGACATCAGCACC 301 TGGGAGCCTTTCTCCCGGCACGGCCAGCTGTGACAGTGGCACTCCCTGCCACCCTCTCC 361 TGCGACAGCGGTGGCATCTGTGGCGGATGTTTCTTCTGCGCCTCCGTGTGGGATTTGG 421 TTTGGAAGTTTGTGTAGATAGTACTTTTAAATACCTCCTTTTGGAAGAAATCCTCGAAGC 481 TTTTCAAAACTGGCATTTAAAATCAGATTTGAGCCAGTGGAATTAATAGAGGGTGTAAAT 541 AGAGACGTGCATGTGTCTTCCAGGAGCATTGCACGTTGCCTGTAGAAAGTTTTAAATAAA 601 ACATTTTTAAAATTAAAAAAAAAAA	SEQ ID NO:15 SEQ ID NO:16
WBC032G05	Glycerol kinase (GK)	1 TTGAACTCCTGGAGCCCGTCACCCAGGAAACCGGCCCCAATCGCCGGCCGACCTGAAGCT 61 GGTTTCATGGCAGCCTCAAAGAAGGCAGTTTTGGGGCCATTGGTGGGGGCGGTGGACCAG 121 GGCACCAGTTCGACGCGCTTTTTGGTTTTCAATTCAAAAACAGCTGAACTACTTAGTCAT 181 CATCAAGTAGAAATAAACAAGAGTTCCCAAGAGAAGATGGGTGGAACAGGACCCTAAG 241 GAAATTCTACATTCTGTCTATGAGTGTATAGAGAAAACATGTGACAAACTTGGACAGCTC	SEQ ID NO:17

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		301 AATATTGATATTTCCAACATAAAGCTATTGGTGTCAGCAACCAGAGGGAAACCACTGTA 361 GTCTGGGACAAGATAACTGGAGAGAGCCTCTCTACAATGCTGTGGTGTGGCTTGATCTAAGA 421 ACCCAGTCTACCGTTGAGAGTCTTAGTAAAAGAATTCCAGGAAATAATACTTTGTCAAG 481 TCCAAGACAGGCCTTCCACTTACTTCAGTGCAGTGAAACTTCGTTGGCTCCTT 541 GACAATGTGAGAAAAGTTCAAAAGGCCGTTGAAGAAAACGAGCTCTTTTTGGACTATT 601 GATTCATGGCTTATTTGGAGTTTGACAGGAGGAGTCAATGGAGGTGTCCACTGTACAGAT 661 GTAACAAATGCAAGTAGGACTATGCTTTTCAACATTCATTCTCTGCAATGGGATAAAGAG 721 CTCTGCGAATTTTTTTGAAATTCCAATGAAAGTCCTTCCAAATGTCCGGAGTTCCTCTGAG 781 ATCTATGGCCTAATGAAAGCTGGGGCCTTGGAAGGTGTGCCAATATCTGGGTGTTTGGGA 841 GACCAGTCTGCTGCATTGGTGGGACAAATGTGCTTCCAGGATGGACAAGCCAAAAACACG 901 TATGGAACAGGCTGTTTCTTACTATGTAATACAGCCCGTAAGTGTGTATTTTCTGAACAC 961 GGCCTTCTGACCACAGTGGCTTATAAACTCGGCACAGATAAACCCGTATATTATGCATTG 1021 GAAGGTTCTGTAGCTATAGCTGGTGCTGTTATTCCGCTGGCTAAGACAATCTAGGAATT 1081 ATACAGACCTCAGAGGAAATTGAAAACTTGCTAAAGAAGTTGGTACTTCTTATGGCTGC 1141 TATTTCGTCCCAGCATTTTCAGGGTTATATGCGCCTTATTGGGAGCCCAGTGCAAGAGGG 1201 ATCATCTGTGGGCTCACACAGTTCACCAATAAATGCCATATTGCTTTTGCCGCATTAGAA 1261 GCTGTCTGTTTCCAAACCCGAGAGATTTTGGATGCCATGAACCGCGACTGTGGGATTCCA 1321 CTCAGTCATTTGCAGGTAGATGGAGGAATGACCAACAACAGATTCTTATGCAGCTCCAA 1381 GCTGACATTCTGTACATCCCAGTAGTGAAGCCCTCGATGCCTGAAACAACGGCTCTGGGA 1441 GCTGCCATGGCTGCAGGCGCTGCAGAAGGCGTCGGCGTCTGGAGTCTCGAACCCGAGGAT 1501 TTGTCAGCTGTCACAATGGAACGGTTTGAACCCCAGATCAATGCTGAGGAAAGTGAAATT 1561 CGTTATTCTACGTGGAAGAAAGCTGTGATGAAGTCAATGGGTTGGCTTACAACTCAGTCT 1621 TCGGAAAGTGGTATCCCGTAAATAATACCAACTCATGGATTCCAAAGATGCGACCTCTTT 1681 ATCTAATGAGAGAATCCAGTGGTTGTCTCTAAATGTGATGACACTATTCATAGACTCTGA 1741 TTTTATTTATAAGCCACTTGCTGCATGACCCTCCAAGTAGACCCGTGGCTTGAAATAAAG 1801 AAAATGCAGCAGAAAGAATGTTATAGAAATATTTGCTGGTTTTTTTTTTTTAAACATCC 1861 ACAGTTAAGGTTGGGCCAGCTACCTTTGGGGGTGACCCCCCCCATTGCCATAACATCCTG 1921 CTCCATTCCCTCTAAGATGTAGGAAGAATTCGGATCCTTACCATTGGAATCTTCCATCGA 1981 ACATACTCAAACACTTTGGGCCAGGATTTGAGTCTCTGCATGACATATACTTGATTAAA 2041 AGGTTATTACTAACCTGTTAAAAATC 1 M A A S K K A V L G P L V G A V D Q G T SEQ ID NO:18 1 ATGGCAGCCTCAAAGAAGGCAGTTTGGGGCCATTGGTGGGGGCGGTGGACCAGGGCACC 21 S S T R F L V F N S K T A E L L S H H Q 61 AGTTCGACGCGCTTTTTGGTTTTCAATTCAAAAACAGCTGAACTACTTAGTCATCATCAA 41 V E I K Q E F P R E G W V E Q D P K E I 121 GTAGAAATAAAACAAGAGTTCCCAAGAGAAGGATGGGTGGAACAGGACCCTAAGGAAATT 61 L H S V Y E C I E K T C E K L G Q L N I 181 CTACATTCTGTCTATGAGTGTATAGAGAAAACATGTGAGAAACTTGGACAGCTCAATATT 81 D I S N I K A I G V S N Q R E T T V V W 241 GATATTTCCAACATAAAGCTATTGGTGTCAGCAACCAGAGGGAAACCACTGTAGTCTGG 101 D K I T G E P L Y N A V V W L D L R T Q 301 GACAAGATAACTGGAGAGCCTCTCTACAATGCTGTGGTGTGGCTTGATCTAAGAACCCAG	

Gene Name	GenBank HomoLogy	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		121 S T V E S L S S K R I P G N N N F V K S K 361 TCTACCGTTGAGAGTCTTAGTAAAAGAATTCCAGGAAATAATAACTTTGTCAAGTCCAAG	
		141 T G L P L S T Y F S A V K L R W L L D N 421 ACAGGCCTTCCACTTAGCACTTACTTCAGTGCAGTGAAACTTCGTTGGCTCCTTGACAAT	
		161 V R K V Q K A V E E K K R A L F G T I D S 481 GTGAGAAAAGTTCAAAAGGCCGTTGAAGAAAAACGAGCTCTTTTTGGGACTATTGATTCA	
		181 W L I W S L T G G V N G G V H C T D V T 541 TGGCTTATTTTGGAGTTTGACAGGAGGAGTCAATGGAGGTGTCCACTGTACAGATGTAACA	
		201 N A S R T M L F N I H S L E W D K E L C 601 AATGCAAGTAGGACTATGCTTTTCAACATTCATTCTCTGGAATGGGATAAAGAGCTCTGC	
		221 E F F E I P M K V L P N V R S S S E I Y 661 GAATTTTTTGAAATTCCAATGAAAGTCCTTCCAAATGTCCGGAGTTCCTCTGAGATCTAT	
		241 G L M K A G A L E G V P I S G C L G D Q 721 GGCCTAATGAAAGCTGGGGCCTTGGAAGGTGTGCCAATATCTGGGTGTTTGGGAGACCAG	
		261 S A A L V G Q M C F Q D G Q A K N T Y G 781 TCTGCTGCATTGGTGGACAAATGTGCTTCCAGGATGGACAAGCCAAAACACGTATGGA	
		281 T G C F L L C N T G R K C V F S E H G L 841 ACAGGCTGTTTCTTACTATGTAATACAGGCCGTAAGTGTGTATTTTCTGAACACGGCCTT	
		301 L T T V A Y K L G R D K P V Y Y A L E G 901 CTGACCACAGTGGCTTATAAACTCGGCAGAGATAAACCCGTATATTATGCATTGGAAGGT	
		321 S V A I A G A V I R W L R D N L G I I Q 961 TCTGTAGCTATAGCTGGTGCTGTTATTCGCTGGCTAAGAGACAATCTAGGAATTATACAG	
		341 T S E E I E K L A K E V G T S Y G C Y F 1021 ACCTCAGAGGAAATTGAAAACTTGCTAAAGAAGTTGGTACTTCTTATGGCTGCTATTTC	
		361 V P A F S G L Y A P Y W E P S A R G I I 1081 GTCCCAGCATTTTCAGGGTTATATGCGCCTTATTGGGAGCCCAGTGCAAGAGGGATCATC	
		381 C G L T Q F T N K C H I A F A A L E A V 1141 TGTGGGCTCACACAGTTCACCAATAAATGCCATATTGCTTTTGCCGCATTAGAAGCTGTC	
		401 C F Q T R E I L D A M N R D C G I P L S 1201 TGTTTCCAAACCCGAGAGATTTTGGATGCCATGAACCGCGACTGTGGGATTCCACTCAGT	
		421 H L Q V D G G M T N N K I L M Q L Q A D 1261 CATTTGCAGGTAGATGGAGGAATGACCAACAACAAGATTCTTATGCAGCTCCAAGCTGAC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		441 I L Y I P V V K P S M P E T T A L G A A 1321 ATTCTGTACATCCCAGTAGTGAAGCCCTCGATGCCTGAAACACGGCTCTGGGAGCTGCC 461 M A A G A A E G V G V W S L E P E D L S 1381 ATGGCTGCAGCGCTGCAGAAGGCGTCGGCGTCTGGAGTCTCGAACCCGAGGATTTGTCA 481 A V T M E R F E P Q I N A E E S E I R Y 1441 GCTGTCACAATGGAACGGTTTGAACCCAGATCAATGCTGAGGAAAGTGAAATTCGTTAT 501 S T W K K A V M K S M G W V T T Q S S E 1501 TCTACGTGGAAGAAAGCTGTGATGAAGTCAATGGGTTGGGTTACAACTCAGTCTTCGGAA 521 S G I P - 1561 AGTGGTATCCCGTAA	
WBC032B05	DDHD domain containing 1	1 aacgcagctg cggcggctgc gggtctcgtg ggggcggagc ggtcgccgct gccgccgcag 61 ctcgggtcgg gatttgaaag attagaaact tcgggtggag agggcggcgg cgttgaatgt 121 gtggcggaag cgctgggggt cacggctccg cgcgccgccg gacagccggc ggcgtctcca 181 cagcatgaat tacccgggcc gcgggtcccc acggagcccc gagcataacg gccgaggcgg 241 cggcggcggc gcctgggagc tgggctcaga cgcgaggcca gcgttcggcg gcggcgtctg 301 ctgcttcgag cacctgcccg gcgggaccgc ggacgacggc gacgtgcccc tggccctgct 361 gcgcgggggaa cccgggctgc atttggcgcc gggcaccgac gaccacaacc accacctgcc 421 gctggacccc tgcctcagtg acgagaacta tgacttcagc tccgccgagt cgggctcctc 481 gctgcgctac tacagcgagg gtgagagcgg cggcggcggc agctccttgt cgctgcaccc 541 gccgcagcag cctccgctgg tcccgacgaa ctcgggcgcga ggcggcgcga caggagggtc 601 ccccgggggaa aggaaacgta cccggcttgg cggcccggcg gcccgcacc gctatgaggt 661 agtgacggag ctgggcccgg aggaggtacg ctggttctac aaggaggaca agaagacctg 721 gaagcccttc atcggctacg actcgctccg catcgagctc gccttccgga ccctgctgca 781 gaccacgggt gcccggcccc agggcgggga ccgggacggc gaccatgtgt gctccccgac 841 gggcccagcc tccagttccg gagaagatga cgatgaggac cgcgcctgcg gcttctgcca 901 gagtacgacg gggcacgagc cggagatggt ggagcttgtg aacatcgagc ctgtgtgcgt 961 gcgggcggc ctctacgagg tggatgtgac ccaaggagag tgctacccgg tgtactggaa 1021 ccaggctgat aaaataccag taatgcgtgg acagtggttt attgacggca cttggcagcc 1081 tctagaagag gaagaaagta atttaattga gcaagaacat ctcaattgtt ttaggggcca 1141 gcagatgcag gaaaatttcg atattgaagt gtcaaaatcc atagatggaa aagatgctgt 1201 tcatagtttc aagttgagtc gaaaccatgt ggactggcac agtgtggatg aagtatatct 1261 ttatagtgat gcaacaacat ctaaaattgc aagaacagtt acccaaaaac tgggattttc 1321 taaagcatca agtagtggta ccagacttca tagaggttat gtagaagaag ccacattaga 1381 agacaagcca tcacagacta cccatattgt atttgttgtg catggcattg ggcagaaaat 1441 ggaccaagga agaattatca aaaatacagc tatgatgaga gaagctgcaa gaaaaataga 1501 agaaaggcat ttttccaacc atgcaacaca tgttgaattt ctgcctgttg agtggcggtc 1561 aaaacttact cttgatggag acactgttga ttccattact cctgacaaag tacgaggttt 1621 aagggatatg ctgaacagca gtgcaatgga cataatgtat tatactagtc cactttatag 1681 agatgaacta gttaaaggcc ttcagcaaga gctgaatcga ttgtattccc ttttctgttc 1741 tcggaatcca gactttgaag aaaaggggg taaagtctca atagtatcac attccttggg	SEQ ID NO:19

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1801 atgtgtaatt acttatgaca taatgactgg ctggaatcca gttcggctgt atgaacagtt 1861 gctgcaaaag gaagaagagt tgcctgatga acgatggatg agctatgaag aacgacatct 1921 tcttgatgaa ctctatataa ctaaacgacg gctgaaggaa atagaagaac ggcttcacgg 1981 attgaaagca tcatctatga cacaaacacc tgccttaaaa tttaaggttg agaatttctt 2041 ctgtatggga tccccattag cagttttctt ggcgttgcgt ggcatccgcc caggaaatac 2101 tggaagtcaa gaccatattt tgcctagaga gatttgtaac cggttactaa atatttttca 2161 tcctacagat ccagtggctt atagattaga accattaata ctgaaacgct acagcaacat 2221 ttcacctgtc cagatccact ggtacaatac ttcaaatcct ttaccttatg aacatatgaa 2281 gccaagcttt ctcaaccčag ctaaagaacc tacctcagtt tcagagaatg aaggcatttc 2341 aaccatacca agccctgtga cctcaccagt tttgtcccgc cgacactatg gagaatctat 2401 aacaaatata ggcaaagcaa gcatattagg ggctgctagc attggaaagg gacttggagg 2461 aatgttgttc tcaagatttg gacgttcatc tacaacacag tcatctgaaa catcaaaaga 2521 ctcaatggaa gatgagaaga agccagttgc ctcaccttct gctaccaccg tagggacaca 2581 gacccttcca catagcagtt ctggcttcct cgattctgca ttggagttgg atcacaggat 2641 tgattttgaa ctcagagaag gccttgtgga gagccgctat tggtcagctg tcacgtcgca 2701 tactgcctat tggtcatcct tggatgttgc ccttttcttt ttaaccttca tgtataaaca 2761 tgagcacgat gatgatgcaa aacccaattt agatccaatc tgaactctct tgaaggacat 2821 gaatggccta aaactgattt ttttttttc cgttaaaatg tgtgtgtcaa gatacggaga 2881 ttcagggttt aaagtatatt tcagttttct ttagggcaac atatatttga atttaaaagc 2941 actttattta aaaaaaaaag aagttttcag ttcttgaagaa gtcatttaca gtttgcatca 3001 ttttaattat gagtctgaca aaaccttctc cagagaatca agcaagacct ggatgtgaag 3061 aaggttggg taaactgcat gtaaaggcta caaatcacaa tctgattcct cccaaatata 3121 aaggcatatg gaacataatg tattaaccaa agtatgttat aaatcaaaaa tggtcaaggt 3181 tcagcatatt ctatatgaag atcacaaggt ggtatcgttt tagatttcta tgaaggcttt 3241 catttgtaca tccctttgaa aaaatataac agatttaaaa tgttttgaat ttaacttgtt 3301 tagaaaaact aatgcttaaa acaatatttg aactactgta tttataattt attacctcta 3361 attgctttat ttcagtgtat gagacattac tgtttttaatg tttgctttga acataattta 3421 agaaccagat ttatttttcta tagtgataaa ccctttttc tcagaactcc atctttgtac 3481 tcttcagatg aatatataga cactgtggca tacatttttt ttcattaaaa acttatggct 3541 tcatacaaaa aaaaaaaaaa aaa 1 M N Y P G R G S P R S P E H N G R G G G 1 ATGAATTACCCGGGCCGCGGGTCCCCACGGAGCCCCGAGCATAACGGCCGAGGCGGCGGC 21 G G A W E L G S D A R P A F G G G G V C C 61 GGCGGCCCCTGGCAGCTGGCTCAGACGCGAGGCCAGCGTTCGGCGGCGGCGTCTGCTGC 41 F E H L P G G D P D D G D V P L A L L R 121 TTCGAGCACCTGCCCGGCGGGGACCCGGACGACGGCGACGTGCCCCTGGCCCTGCTGCGC 61 G E P G L H L A P G T D D H N H H L A L 181 GGGGAACCCGGGCTGCATTTGGCGCCGGGCACCGACGACCACACCAACCACACCTCGCGCTG 81 D P C L S D E N Y D F S S A E S G S S L 241 GACCCCTGCCTCAGTGACGAGAACTATGACTTCAGCTCCGCCGAGTCGGGCTCCTCGCTG 101 R Y Y S E G E S G G G G S S L S L H P P 301 CGCTACTACAGCGAGGGTGAGAGCGGCGGCGGCAGCTCCTTGTCGCTGCACCCGCCG	SEQ ID NO:20

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		121 Q Q P P L V P P T N S G G G G G A T G G S P 361 CAGCAGCCTCCGCTGGTCCCGACGAACTCGGGGGGGCGGCGGCGCGACAGGAGGGTCCCCC	
		141 G E R K R T R L G G G P A A R H R Y E E V V 421 GGGGAAAGGAAACGTACCCGGCTTGGCGGCCCGGCGGCCCGGCACCGCTATGAGGTAGTG	
		161 T E L G P E E V R W F Y K E D K K T W K 481 ACGGAGCTGGGCCCGGAGGAGGTACGCTGGTTCTACAAGGAGGACAAGAAGACCTGGAAG	
		181 P F I G Y D S L R I E L A F R T L L Q T 541 CCCTTCATCGGCTACGACTCGCTCCGCATCGAGCTCGCCTTCCGGACCCTGCTGCAGACC	
		201 T G A R P Q G G G D R D G D H V C S P T G 601 ACGGGTGCCCGGCCCCAGGGCGGGACCGGGACGCGACCATGTGTGCTCCCCCACGGGC	
		221 P A S S S G E D D D E D R A C G F C Q S 661 CCAGCCTCCAGTTCCGGAGAAGATGACGATGAGGACCGCGCCTGCGGCTTCTGCCAGAGT	
		241 T T G H E P P E M V E L V N I E P V C V R 721 ACGACGGGGCACGAGCCGGAGATGGTGGAGCTTGTGAACATCGAGCCTGTGTGCGTGCGG	
		261 G G L Y E V D V T Q G E C Y P V Y W N Q 781 GGCGGCCTCTACGAGGTGGATGTGACCCAAGGAGAGTGCTACCCGGTGTACTGGAACCAG	
		281 A D K I P V M R G Q W F I D G T W Q P L 841 GCTGATAAAATACCAGTAATGCGTGGACAGTGGTTTATTGACGGCACTTGGCAGCCTCTA	
		301 E E E E S N L I E Q E H L N C F R G Q Q 901 GAAGAGGAAGAAAGTAATTTAATTGAGCAAGAACATCTCAATTGTTTTAGGGGCCAGCAG	
		321 M Q E N F D I E V S K S I D G K D A V H 961 ATGCAGGAAAATTTCGATATTGAGTGTCAAAATCCATAGATGGAAAGATGCTGTTCAT	
		341 S F K L S R N H V D W H S V D E V Y L Y 1021 AGTTTCAAGTTGAGTCGAAACCATGTGGACTGGCACAGTGTGGATGAAGTATATCTTTAT	
		361 S D A T T S K I A R T V T Q K L G F S K 1081 AGTGATGCCAACAACATCTAAAATTGCAAGACAGTTACCCAAAAACTGGGATTTTCTAAA	
		381 A S S S G T R L H R G Y V E E A T L E D 1141 GCATCAAGTAGTGGTACCAGACTTCATAGAGGTTATGTAGAAGAAGCCACATTAGAAGAC	
		401 K P S Q T T H I V F V V H G I G Q K M D 1201 AAGCCATCACAGACTACCCATATTGTATTTGTTGTGCATGGCATTGGGCAGAAAATGGAC	
		421 Q G R I I K N T A M M R E A A R K I E E 1261 CAAGGAAGAATTATCAAAATACAGCTATGATGAGAGAAGCTGCAAGAAAAATAGAAGAA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		441 R H F S N H A T H V E F L P V E W R S K 1321 AGGCATTTTTCCAACCATGCAACACATGTTGAATTTCTGCCTGTTGAGTGGCGGTCAAAA	
		461 L T L D G D T V D S I T P D K V R G L R 1381 CTTACTCTTGATGGAGACACTGTTGATTCCATTACTCCTGACAAAGTACGAGGTTTAAGG	
		481 D M L N S S A M D I M Y Y T S P L Y R D 1441 GATATGCTGAACAGCAGTGCAATGGACATAATGTATTATACTAGTCCACTTTATAGAT	
		501 E L V K G L Q Q E L N R L Y S L F C S R 1501 GAACTAGTTAAAGGCCTTCAGCAAGAGCTGAATCGATTGTATTCCCTTTTCTGTTCTCGG	
		521 N P D F E E K G G K V S I V S H S L G C 1561 AATCCAGACTTTGAAGAAAAAGGGGGTAAAGTCTCAATAGTATCACATTCCTTGGCATGT	
		541 V I T Y D I M T G W N P V R L Y E Q L L 1621 GTAATTACTTATGACATAATGACTGGCTGGAATCCAGTTCGGCTGTATGACACAGTTGCTG	
		561 Q K E E E L P D E R W M S Y E E R H L L 1681 CAAAAGGAAGAGAGTTGCCTGATGAACGATGGATGAGCTATGAAGAACGACATCTTCTT	
		581 D E L Y I T K R R L K E I E E R L H G L 1741 GATGAACTCTATATAACTAAACCACGGCTGAAGGAAATAGAGAAGCGGCTTCACGGATTG	
		601 K A S S M T Q T P A L K F K V E N E F C 1801 AAAGCATCATCTATGACACAAACACCTGCCTTAAAATTTAAGGTTGAGAATTTCTTCTGT	
		621 M G S P L A V F L A L R G I R P G N T G 1861 ATGGGATCCCCATTAGCAGTTTTCTTGGCGTTGCGTGGCATCCGCCCAGGAAATACTGGA	
		641 S Q D H I L P R E I C N R L L N I F H P 1921 AGTCAAGACCATATTTTGCCTAGAGAGATTTGTAACCGGTTACTAAATATTTTTCATCCT	
		661 T D P V A Y R L E P L I L K R Y S N I S 1981 ACAGATCCAGTGGCTTATAGATTAGAACCATTAATACTGAAACGCTACAGCAACATTTCA	
		681 P V Q I H W Y N T S N P L P Y E H M K P 2041 CCTGTCCAGATCCACTGGTACAATACTTCAAATCCTTTACCTTATGAACATATGAAGCCA	
		701 S F L N P A K E P T S V S E N E G I S T 2101 AGCTTTCTCAACCCAGCTAAAGAACCTACCTCAGTTTCAGAGAATGAAGGCATTTCAACC	
		721 I P S P V T S P V L S R R H Y G E S I T 2161 ATACCAAGCCCTGTGACCTCACCAGTTTTGTCCCGCCGACACTATGGAGAATCTATAACA	
		741 N I G K A S I L G A A S I G K G L G G M 2221 AATATAGGCAAAGCAAGCATATTAGGGGCTGCTAGCATTGGAAAGGGACTTGGAGGAATG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		761 L F S R F G G R S S T T Q S S E T S K D S 2281 TTGTTCTCAAGATTTGGACGTTCATCTACAACACAGTCATCTGAAACATCAAAGACTCA 781 M E D E K K P V A S P S A T T V G T Q T 2341 ATGGAAGATGAGAAGAAGCCAGTTGCCTCACCTTCTGCTACCACCGTAGGGACACAGACC 801 L P H S S S G F L D S A L E L D H R I D 2401 CTTCCACATAGCAGTTCTGGCTTCCTCGATTCTGCATTGGAGTTGGATCACAGGATTGAT 821 F E L R E G L V E S R Y W S A V T S H T 2461 TTTGAACTCAGAGAAGGCCTTGTGGAGAGCCGCTATTGGTCAGCTGTCACGTCGCATACT 841 A Y W S S L D V A L F L L T F M Y K H E 2521 GCCTATTGGTCATCCTTGGATGTTGCCCTTTTTCTTTTAACCTTCATGTATAAACATGAG 861 H D D D A K P N L D P I - 2581 CACGATGATGATGCAAAACCCAATTTAGATCCAATCTGA	
WBC030D02	Putative membrane protein (GENX-3745 gene)	1 gggatttttaaaaaatcaaaatacaaatccaacttttgagtttttcgttgtcattgctct 61 tatctttcctgagtcacttcccatttttccaaactcagcaacccccagtttgcgagtctggt 121 ttcatgaaccttttgtaaggtgtttggtgcggtcacrgtgtatacttgccgtgtagtattt 181 gactcagcgcgatctgccttgagtcatttttaccgcggccatttactactgccgttgagcc 241 ctgtccacgccttgggagtgttgatatgttgagagttttctgtctggctgrggagggatc 301 atttagttttttgcggacgtatgttgcactgaggatttagggagagagcaagatttctgtt 361 gaggaggttcagaagtataaggaatcgggagagtagatagagtgaagcatttggcagcg 421 taaagaagcttggcttagctttaatggattgagagattgctatctagcattattaca 481 tgttattgttcttcttttgctatttttatacacctagaacaacctttccctcgggtttaacaa 541 acatcttcaacctctgtttttctgtatggctcctgactcttacctttgtttttaggaggcttc 601 cctcttcagaggaaactgggagaagccaatttccactgcttctttttttcctgtgccttttt 661 aacactcaaacccagaacacttaatcctctgcagctcgtgcaaaaattcagtctgtaatt 721 taaaatgtgtgcacggtacactgctgaccatgggcatgtcttattgtttgtatctgtaatg 781 tgtatgtccatttcagtgttgtctgtttttagtatgcagttgatagactagagaacaagac 841 ctctgtctccgtagcatcctggagcagtctgaatgccagaatggataaccgttttgctac 901 agcattgtaattgcttgtgtgctttagcctcatttccaccatctacatggcagcctccat 961 tggcacagacttctggtatgaatatcgaagtccagttcaagaaaattccagtgatttgaa 1021 taaaagcatctgggatgaattcattagtgatgaggcagatgaaaagacttataatgatgc 1081 acttttcgatacaatggcacagtgggattgtggagacggtgtatcaccatacccaaaaa 1141 catgcattgtatagcccaccagaaaggacagagtcatttgatgtggtcacaaaaatgtgt 1201 gagtttcacactaactgagcagttcatggagaaatttgttgatcccggaaaccacaatag 1261 cgggattgatctccttaggacctatctttggcgttgccagttcctttttacctttttgtgag 1321 tttaggtttgatgtgctttgggcttttgatcggacttttgtgcttgcatttgccgaagctt 1381 atatcccaccattgccacgggcattctccatctccttgcaggtctgtgtacactgggctc 1441 agtaagttgttatgttgctggaattgaactactccaccagaaaactagagctccctgacaa 1501 tgtatccggtgaatttggatggtcctttctgcctggcttgtgtctctgctccctttacagtt 1561 catggcttctgctcttcatctgggctgctccacaccaaccggaaagagtacaccttaat	SEQ ID NO:21

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1621 gaaggcatatcgtgtggcatgagcaagaaactgcctgctttacaattgccatttttattt 1681 ttttaaaataatactgatatttcccccacctctcaattgtttttaatttttattttgtgga 1741 tataccatttattatgaaaatctatttttatttatacacattcaccactaaatacacact 1801 taataccactaaaatttatgtggtttactttaagcgatgccatctttcaaataaactaat 1861 ctaggtctagacagaaagaaatggatagagacttgacacaaatttatgaaagaaaattgg 1921 gagtaggaatgtgaccgaaaacaagttgtgctaatgtctgttagacttttcagtaaaact 1981 aaagtaactgtatctgttcaactaaaaactctatattagtttctttgggaaacctctcat 2041 cgtcaaaactttatgttcactttgctgttagatagccagtcaaccagcagtattagtg 2101 ctgttttcaaagatttaagctctataaaattgggaaattatctaagatcatttccctaa 2161 gcattgacacatagcttcatctgaggtgagatatggcagctgtttgtatctgcactgtgt 2221 ctgtctacaaaagtgaaaaatacagtgtttacttgaaatttaacttgtaactgcaag 2281 aattccagttcagccgggcgaggattagtattatttttaactctccgtaagattttcagt 2341 accaccaaattgttttggatttttttctttcctcttcacataccaggttattaaaagt 2401 gtgctttctttttacattatatattacagttacaaggtaaaattcctcaactgctatttatt 2461 tattccagcccagtactatataagaacgtttccaccataatgaccctccagagctgggaaac 2521 ctaccacaagatctaaagttctggctgtccattaacctccaactatggtctttatttctt 2581 gtggtaatatgatgtgcctttcctttgcctaaatccctccttcctggtgtgtatcaacattatt 2641 taatgtcttctaattcagtcatttttttataagtatgtctatataacattgaacttttaaaa 2701 aacttatttatttattccactactgtagcaattgacagattaaaaaaaatgtaacttcata 2761 atttcttaccataacctcaatgtcttttttaaaaaaataaaattaaaaatgaaaagagaaa	
		1 M D N R F A T A F V I A C V L S L I S T 1 ATGGATAACCGTTTTGCTACAGCATTTGTAATTGCTTGTGTGCTTAGCCTCATTTCCACC	SEQ ID NO:22
		21 I Y M A A S I G T D F W Y E Y R S P V Q 61 ATCTACATGGCAGCCTCCATTGGCACAGACTTCTGGTATGAATATCGAGTCCAGTTCAA	
		41 E N S S D L N K S I W D E F I S D E A D 121 GAAAATTCCAGTGATTTGAATAAAAGCATCTGGGATGAATTCATTAGTGATCAGGCAGAT	
		61 E K T Y N D A L F R Y N G T V G L W R R 181 GAAAAGACTTATAATGATGCACTTTTTCGATACAATGGCACAGTGGGATTGTGGAGACGG	
		81 C I T T I P K N M H W Y S P P E R T E S F 241 TGTATCACCATACCCAAAAACATGCATTGGTATAGCCCACCAGAAAGGACAGAGTCATTT	
		101 D V V T K C V S F T L T E Q F M E K F V 301 GATGTGGTCACAAAATGTGTGAGTTTCACACTAACTGAGCAGTTCATGGAGAAATTTGTT	
		121 D P G N H N S G I D L L R T Y L W R C Q 361 GATCCCGGAAACCACAATAGCGGGATTGATCTCCTTAGGACCTATCTTTGGCGTTGCCAG	
		141 F L L P F V S L G L M C F G A L I G L C 421 TTCCTTTACCTTTTGTGAGTTTAGGTTTGATGTGCTTTGGGGCTTTGATCGGACTTTGT	
		161 A C I C R S L Y P T I A T G I L H L L A 481 GCTTGCATTTGCCGAAGCTTATATCCCACCATTGCCACGGGCATTCTCCATCTCCTTGCA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		181 G L C T L G S V S C Y V A G I E L L H Q 541 GGTCTGTGTACACTGGGCTCAGTAAGTTGTTATGTTGCTGGAATTGAACTACTCCACCAG 201 K L E L P D N V S G G E F G W S F C L A C 601 AAACTAGAGCTCCCTGACAATGTATCCGGTGAATTTGGATGGTCCTTCTGCCTGGCTTGT 221 V S A P L Q F M A S A L F I W A A H T N 661 GTCTCTGCTCCCTTACAGTTCATGGCTTCTGCTCTTCATCTGGGCTGCTCACACCAAC 241 R K E Y T L M K A Y R V A - 721 CGGAAAGAGTACACCTTAATGAAGGCATATCGTGTGGCATGA	
WBC030C04	No homology	1 GAAGGTTTCCCTGAGCGTCTCTAAGCTCGCCCAGCCACACCCTGTGCCCCTCCATTTG 61 TGTCCTCTGTCCCCCTTTCCTGCTTCCCTCCTTCCCCACCGTGGCTGGTCTAGGTGTCTG 121 TAATAGTCAGAATGCCAGGTTTGGCAACTTGAACAAAACTTTTAAATAACAGTGGCTTAAA 181 CCACAAAAAAAAATTGATTTCTCTGGTAATATCTAAGCACACAAGCAGGCCAGGCAATATGG 241 GGACTCCCTGGTTTTGAGATCCAGGATTCCCAGGTCTTGGCGCTACGAGGTCCACATTCT 301 AGGCCTCAAGACCAGGGAAGAAGGCAGTGAAAGGGAGCATGACCCTCCCCTTCAAGGGCA 361 CAGCTAGGAATCACCCACATCACCTCTAATTGGCTGGAATGTGGTCACACGGTCACACCT 421 AGCTGCAAGGAAGGCAGGGAAATGTAGTCTTTATTCTGACCACAACGTGCCCAGGTGAAA 481 TTTGTCACTAGAGAACCGGTGGGCAGATATGTGTAGATAATCAATAATCTCCACCTCAGG 541 GGCATTGAGGCAGCCTCTTACTTCCTCTGCGTGACACCAGAGTTCGATTCCCATCTGAAA 601 CGACCCCTCTTTGTACCACCAGCTCCACTAGGGCTGCGTAAGGGAGGGTGGTAGTTCTCA 661 AGAAGGGGAGATTTTGCCCCCACAGGGGACATTTGGCAAAGTCCAGAGACATTTTCCGTT 721 GTCACAACTTGGGGGGTGCTATCGCCATCTAGTGGGGAGAGGTCACCGATGCTGCTAAAC 781 ATCATATGATGCCCCCCACCACAATAGAGTTGTCTGCCCCAAAGCATCAGCAGAAGCCCTG 841 ATGCAGGGAAAGCGTGCGTTCCCCGGGGTCAGACACGCCTGACTTCTAACCCTGAAGCCC 901 CGCCTCCCTCCCCGTGTGGCCTTAGTGACCAATCAGTCACTTCACCCCTCGGAACATCGA 961 TGATGGTAACATGGACTTCCCTGCATTGTATGAGAACCAATTCAGGTCGTTTACTGAGGG 1021 CTTACCATGTGCTGTGTGCTCTGTGTACCCTCAGATCACGTGAACTCCCTTTCCATGCGC 1081 ACATTTACTAGCACCTACTATGCGGGGAAGTGGATTCCTCTGGATGATTTTGTTATAATA 1141 AACAGAAAAACAGCTTGAAAAAAA	SEQ ID NO:23
WBC028F05	No homology	1 GGACCACCCTCTGCCCCGTCGTGGGCCCAGCAGCCACCGACCGAGCCTTTGCCCTGTGCA 61 GACGGGAGGTTCTCACGGTCCTCTTGGGACCCTTCGCGTCAGCATTTCAGCCTTGGGAGC 121 GCCCCACCCCCATCTGAGGGGACCCGGTCCAGGCTGCCGACCCTCGGCACCTCTGTCCCC 181 GTTGCAGATCTCTCGCCCCATCAGCAGGGTGTTGTGCACCTTGAGAAGCCCCCCCAGTGC 241 TCGTGGTGCCGGCCACCGAGCTTGACCTCTGCTCTGAGGGCCACCAACCCAGAACCTCGC 301 AGGAAGGTCTCCACTCCTTTGGAAAAGACTGCGTTTATTTTCACAGTCGACCCAAGGCCG 361 ACGACGTGATGGGGCCGGCGGGCCGGCAGGCAGGCGGGCTCATGTTCAGCACCCCTCCCC 421 TCAGCTGCAACGTCAACAGAAACTGTCAGGCTCCTGGCCTATGGGCTCGGGCCGGCATGC 481 TCCGCCCCATCCCCCAGGCCCCTCCCCGCTCGGTTTCGGGCCCGACTCACACAGCACAGCGA 541 CTTGGGGGCAAGGCCCAGCAGGAAATTTAAATCGTTCCTGTGTACGATTTACTGCTAGGA	SEQ ID NO:24

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		601 GCACGACTTCTGCAGATTTGAGGGAGCAGACTTCCTTCAGTCCCACGTGATCACATCTTG 661 CTTGAGCTTGAGCTTCTTTTGCACTTTCCTGAAGTCCTCAGTCTCTGCATTAGAGTTCTG 721 CACTTTCTCAACCAGTTCAACTTTCTCATCTGAAAGTTGGTCAGGAGCCTGTCTCGCTAGA 781 GTCAGTTTCAAAGTCCTTTCCGTGACCCTCTCTGAAGATGAAAGACTTGCAGAAACAG 841 AGTCAAACCAAACTGTCCTGTAAATGACAAGGATTTCAAAATGGCAATGGACAAAGAAAT 901 TTGGTTATTT	SEQ ID NO:25
		1 CTCTTTCCCCAGAAAAGAAGAAAACTTTAAGCAAATGATCCTTTTAAGAGAGGGCAAAAA 61 CCGAAATCTAATTTGGCAACAGCTTCCCTTCGATATGAAAGTTCACTGACTTCGTTCAGT 121 TCGTTTCCATAGTAGCCAATTTGATCATGCCACAAAACTCTTTCTTTGAGTTTTTTCCCC 181 TCATACATTCTAGAACCTTCTTTTTACATTAAGAATTTGTCCTAGGGCTGCTTTCCTTTT 241 TTAGGACCCATTTATCTTTCTTACCAAAACCAACAAAGACATTTCCATTCTTTAAATTTT 301 CTTGCCTGAGAACATTCATCCTGCTTTCCTTAGCGCACAAAGATGTCTTCCTCTCAATT 361 TTGAGTAGCTTTAATCACATCTCTCCTTAGAAGTCTCAGCCTTTACAGACCTTGTTTTC 421 AGTAGAATCTAAGAAGGAAGCAATTATAAACTGTCCTTTCCATTAGCATTCTGTGGCTTT 481 ACAAATTTATAAATATATTTATAATTTCCAGAATCATACTACTTCCTAGGACACTCTTAT 541 GATAAAAACGTAAGGCATCTTTACTAATAGACCCAAAGATCTTTGGTTTCTCTGTCAAA 601 ATAAGCCTGAAGTAGATAAACCTCTGTCTAATAACTACTGTCTAATATTTTATCTTATTT 661 GGAAATGATCTAGAGACTCCCATAAATTTCTATCATTCAACTGAACTTAATAAAACTTGAA 721 GGTGTCAAGTAAAAAAAAAAAAAAAAAA	SEQ ID NO:26
WBC028E07	Homo sapiens cDNA FLJ13038 fis, clone NT2RP3001272, weakly similar to Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein	1 AAACTACAACGAAAAAAGACAGAGCTCATAATGGATGCTATCCATAAACAAAAGAGCTTA 61 CAATTCAAGAAAACCATGGATGCAAAGAAGAACTATGAGCAGAAATGCCGGGACAAAGAT 121 GAGGCAGAACAGGCCGTCAGCCGGAGTGCCAACCTGGTGAACCCAAGCAACAAGAAAAG 181 CTTTTGTGAAACTGGCAACTTCAAAGACCGCAGTAGAGGACTCAGACAAAGCATACATG 241 CTGCACATCGGCACCCTGGATAAGGTCCGAGAAGAGTGGCAGAGTGAGCACATCAAGGCC 301 TGCGAGGCATTTGAGGCTCAAGAATGTGAACGAATATAAACTTCTTTCGGAATGCATTGTGG 361 TTACACATGAATCAGCTGTCACACAATGTGTCACAAGTGACACAACATGTATGAAGAAGTC 421 CGTAAGAGTTTAGAAATGTGCAGCATTGAGAAGGACATTGAGTACTTTGTGAATCAACGT 481 AAAACTGGACAGACACCACCAGCACCCATCATGTATGAGAATTCTACAGCCCCCAGAAG 541 AATGCAGCCCCACCAGCAAAGGCGACAGGGCCTAACGTAGCAAGGAGAGGACCTCTCCCA 601 GTTCCTAAAAGCTTACCAGGTGACCCTGCATTATTCTTTGATTGGTGCACTACACGCTTGATC 661 TATCAGTAACATCAGTGAAAACAAAGCTTTTTCCAGCTGGTGCTTCTATGGCATGGAAGG 721 AGGCACTCAGAGCAGCAGGACCTATAGCCACGTTTATGTCAGCAATGAAGACTTTCAAGTG 781 AACCCTTGCTATAATTTTTTGATATTTTAAATTTATAGTAGATCGTTTAGTTCAACTTAAG 841 CTAGTAGAGTTCTGCAGTTTTTTAAGTTGACAAATTGCCCCCCGACTGAAGAATTATCCT 901 TTCCCAGTTACTCAGGTTATGAATGAATTAGGTTTTCAACATGGGAAGCATGAAATCCAC 961 TTCTGGATTTGGAGCATCCACTTGAGGAGCAGAGGTGGCAGCAGAGGATTCATGAGCCACC 1021 AACTGCAGTAGTGGCTCCTTTGGCTTTGGGCAGCATGACTATGGAATTTCCACGGCGCCA 1081 CACATTCTCAGTGGTCCAAGATTTAAAATTACCTTCCTTTTTGGCTGGAAGACTTAGAAG 1141 CCATCTGATTGCACTTTCTCATTTTACAGATGAGAAAATGAGGCCCAGATGTGTGAAATC 1201 AATTTCCTTACAGTTCTTCCAGCTGATTAGGGACAGAACTAGAGCCTGAGCCCAACCCAC 1261 ATCACTATTCTTCTAACCCTTCCTGAAGTTGTGATGCTCATGCTGAAATTTAAGATGCCA 1321 AATATTTTTGCCAGCACTTTTTCAGTTGGGAGAATCACCAGGGTTTAAATGTCAGATTTA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1381 TTTTTATGTGGATCCCTGTGTATGCTGAACTACAGAGCATGATGTTTAATCTAATTTAAG 1441 GAGCCACTGATTGTAAAACATGCCATTATTTTATGTTGCACTAAGAAGGTGGGGTCGAGG 1501 AGTTGCCAATAAACTTGGGACAGACTATTGATGGCCAAGCCCATCTGAATTTAAGATGCT 1561 AAAGTATGAAAAAAATACATCTTAGAATCAATGAAATACCATATTTTGATTCCATTCCTC 1621 AAGAGAATTTTAGAGTTAAAAAGCCAGTCCTCAATCCTGCGTCTTTGCAGAGAATCTTTC 1681 CCTTCCTAGACCCCAGAATTTTAAATGCATCCGTCTCTTACACTTTCACAAATATTTGGGTT 1741 TTCCTTTTTCACTCACAAACAGCAGGGAGGTCATGTACTTTTTGTACAACACCTGTGCAC 1801 TATGAGAAAATGGTACCTTTTAGTTATTGACAAGTTAAAATAGCACTCTCAGTTTTTCAG 1861 TATTACAGAGACGCAAATATTTTCCTGACCTGCTCTGTGCATAGCTTACCCAGAATTACGG 1921 ACAAGTTGATTGAAAGAAGATTGATTATTCCCTCATCTTTTTTTCTTTTTTTGAGGCAG 1981 AGTCTCTCTCTGTCCCCAGGCTGAAGTGCAGCGGCATGATCTCAGCTCACTGCCAACCTC 2041 TGCCTCCCGGTTCAAGTGATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGC 2101 ACCCACCACACCTGGCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTCACCATGT 2161 TGGTCAGGCTGGTCTCAAACTCCTGACCTCAGGTGATCCACCTGCCTCGGCCTCCCAAAG 2221 TGCTGGGATTACAGGCGTGAGCCACTGCGCCCGGCCTATTTCCCCACCTTTCGTGTAAGG 2281 TGCTACTGAACATGACAGCTTCTTGTTATGACAGAGAACTTGCATCAGTGGATATCCTT 2341 TTGAGAAAGTGAAGTTTACAAAGGGCCATTGACTTCCCCAAACTGAACAGGCTCAGGAAA 2401 TTTTCCTTCGAACTCAGAACATTCTGTTTTTAAGTATTTTATTATTGTTGGCACTTCCT 2461 CAGGGATTTCACTTTCTCCCTATTGGTCAGTGTGATTGATGTAAAAGTGTTTTCTGAAC 2521 CGAAAATATTTGTATTTTATTGCTCTTTCAGTTTGGTAGGTTAAATAAAGGTTCTTGGTA 2581 ATTTGGG	SEQ ID NO:27
		1 M D A I H K Q K S L Q F K K T M D A K K 1 ATGGATGCTATCCATAAACAAAAGAGCTTACAATTCAAGAAAACCATGGATGCAAAGAAG	
		21 N Y E Q K C R D K D E A E Q A V S R S A 61 AACTATGAGCAGAAATGCCGGGACAAAGATGAGGCAGAACAGGCCGTCAGCCGGAGTGCC	
		41 N L V N P K Q Q E K L F V K L A T S K T 121 AACCTGGTGAACCCGAAGCAACAAGAAAAGCTTTTGTGAAACTGGCAACTTCAAAGACC	
		61 A V E D S D K A Y M L H I G T L D K V R 181 GCAGTAGAGGACTCAGACAAAGCATACATGCTGCACATCGGCACCCTGGATAAGGTCCGA	
		81 E E W Q S E H I K A C E A F E A Q E C E 241 GAAGAGTGGCAGAGTGAGCACATCAAGGCCTGCGAGGCATTTGAGGCTCAAGAATGTGAA	
		101 R I N F F R N A L W L H M N Q L S Q Q C 301 CGAATAAACTTCTTTCGGAATGCATTGTGGTTACACATGAATCAGCTGTCACAACAATGT	
		121 V T S D N M Y E E V R K S L E M C S I E 361 GTCACAAGTGACAACATGTATGAAGAAGTCCGTAAGAGTTTAGAAATGTGCAGCATTGAG	
		141 K D I E Y F V N Q R K T G Q T P P A P I 421 AAGGACATTGAGTACTTTGTGAATCAACGTAAAACTGGACAGACACCACCAGCACCCATC	
		161 M Y E N F Y S P Q K N A A P P G K A T G 481 ATGTATGAGAATTTCTACAGCCCCCAGAAGAATGCCAGCCCCCACCAGCGGAAGGCGCACAGGG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		181 P N V A R R G P L P V P K S L P G D P D 541 CCTAACGTAGCAAGGAGAGGACCTCTCCCAGTTCCTAAAAGCTTACCAGGTGACCCTGAT 201 Y S L I G D Y S L I Y Q - 601 TATTCTTTGATTGGTGACTACAGCTTGATCTATCAGTAA	
WBC028D09	No homology	1 GACTTTATGAAATAAAGCCACTTGGAAATATTGGCCTGGTACCTTGTTTACAGGGTTCCC 61 AGCAAGCTTACTGGGTAAGTAAAGAAGGTCATTTATCTGGCAGGTGCAAGGAACCTCAAT 121 ATTTTGGGGAACCTCAAAAGAAGAGAATACCTCACCCAAATCTGTAGGCGTTACAGGTTT 181 TGTCTGATAAGTCTTTGGCTTGGCTTTCCTGGCCTCAAGAGGCCTTTAAAATTCAATCTG 241 AGATTCCTTATTAAAAGTTCCAGCAAAGCAGGTTTACAAGAGCCTATATGATCAATTGCT 301 ATTCTTGCTGCACTTATGTAAATAATTGGGCCAAATTTATTGAAACTAAACTTATTTTGT 361 GAATCAGTTAGTCTTAATTTGGCAACCTTTGGGAAAAATGAGGATGATTTTAGAGAGAAA 421 AATTATGTTTCAGTAGAAACTATAGTACACATTTGCAGATATTAGATTCTAGTTTTGTTA 481 ACTGTCTGAGTATTTTGTTTTCTGCCTGTAAATTGAACTGGATCCTGAATTCTTCTAGTC 541 TTCTGAAATATCTGGCTACAAATCTCCAAACTAATGTTTTCGATTTTTTCCCTCATTTTT 601 ATTTGAAATCATGGAGAACTAAAACCACCTTTGTTCCTGACCCCTAAAAACTAAAGCTGG 661 ACAACTAGATTTAAACTTAAGAGACATCACCACAATAACATGCCTGTTGCTATGTAAGCC 721 ACTCAGAAGGATACCTGAACACTCAATGACATCATCAGACACACTTCAAACAGCAAAAGA 781 TGCTCCGACTCTGACATCTAAAAATCTTCTTGACTGGCTGCCCCCTAGGCTCAGGAACTG 841 GA	SEQ ID NO:28
		1 CAAAGAAACCCAGGCGGCAGAGTCGGTCTCAAAGCCAGATGTCAGTGAAGAATCTCCAGG 61 GACATCGAAAATTAAGACAGGGAAGCCTGAAGAAGCCGGCCTTGATTCTAGAGAGAAGAA 121 GACCAACTCTGCTCCCAAAAGTGCAGCAACAAACGGAAGCTCTTCTGGAAAAGTCGGGAA 181 GCCTCCGTGTGGAGCCATGAAAAGGTCCATCGCCGACAGCGAAGAATCTGAAGCTTATAA 241 GTCTCTGTTCACAACTCACAGCTCCGCCAAGCGCTCCAAGGAGGAGTCGGCGCACTGGGT 301 CACCCACACGTCCTACTGCTTCTGAAGCCCACGCAGGCGCGGCTCAGGCTCCACATGGAT 361 GGGTGGCGTGGGCGCTGGCTGTGCTGGGTGTTGTGTGCCGGGCCTCTGTTTGACGGCATT 421 AGAAAGTTGTCCGCCGAGCTGGCGTGGTCACGCTGGCTGTGGGGGATGGGGGGTGACTCG 481 CAGAGGGACCGTGCTGGGCACCCGCCCCGTCACCTCTCCCGCAGGCTCGTGCTCACTTTG 541 CCTGCATTTGCTCCTCTTCTCACAGCCCGGAAAGCTCTGTTGGCTGCACTTTTTGTGTTT 601 GAAATAATTAAAGACTCCAGATTCCTCATGAAAAAAAAAAAAAAAAAACTCGAGGGGGCC 661 C	SEQ ID NO:29
WBC028C01_V1.3_at	Ras homolog gene family, member A	1 CTCGTTAGTCCACGGTCTGGTCTTCAGCTACCCGCCTTCGTCTCCGAGTTTGCGACTCGC 61 GGACCGGCGTCCCCGGCGCGAAGAGGCTGGACTCGGATTCGTTGCCTGAGCA**ATG**GCTGC 121 CATCAGGAAGAAACTCGTGATTGTTGGTGATGGAGCCTGTGGCAAGACTTGCTTGCTCAT 181 CGTCTTTAGCAAGGACCAGTTCCCAGAGGTGTATGTACCCACGGTGTTTGAGAACTATGT 241 GGCAGATATCGAAGTGGATGGGAAGCAGGTAGAGTTAGCTTTGTGGGACACAGCTGGGCA	SEQ ID NO:30

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		301 GGAAGATTATGATCGCTTGAGGCCTCTCCTACCCAGACACCGATGTTATACTCATGTG 361 TTTCTCCATTGACAGCCCTGATAGTTTAGAAAACATCCCAGAAAAATGGACTCCTGAAGT 421 CAAGCATTTCTGTCCCAACGTGCCCATCATCCTGGTTGGAAACAAGAAGGATCTTCGGAA 481 TGATGAGCACACAAGGCGGGAGCTAGCCAAGATGAAGCAGGAGCCCGTAAAACCACAAGA 541 AGGCAGACATATGCCAAACAGGATTGGTGCTTTTGGGTACATGGAGTGTTCAGCAAAGAC 601 CAAAGATGGAGTGAGGAGGTTTTTGAAATGGCCACGAGACTGCTCTCCAATCCAGACG 661 TGGGAAGAAAAAATCTGGGTGCCTTGTCTTGTGAAACCCTGCTGCGAGCACAGCCCTCAT 721 GCGGTTACTTTTGAAGTGCTGTTTATTAATCTTAGTGTATGACTGGCCTTTTCCATT 781 TATCTATAATTTACCTAAGATTACAAATCAGAAGTCATCTTGCTAGAGTATTTAGAAGC 841 CAACCATGATTATTAATGATGTCCAACCCACCTGACCCTCTGGGCTCCTTCTGACACCGC 901 TCTAACAGCCCTCCTCTGCATCCCACCTGACACACAGGCGCTAATTCAAGGAATTTCTT 961 AACTTTTTGCTTCTTTCTAGAAAGAGAAACAGTTGGTAACTTTTGTGAATTAGGCTGTAA 1021 CTACTTTATAACTAACATGTCCTGACTGTCATCTGTCAGCTGCAAGGTACTCTGGTGAGT 1081 CACCACTTCAGAGCTTTACTCCTTAACAGATTTCATCGCATAGCTCTGGAGTGGGCATCC 1141 AGTTTTTTGAAAATGTACTCAGCCAGAAAGGCCCAAGTCCGTGAGCAGCTATGGCAAAGT 1201 TACAGTTCTGTGGTTTTCATGTTAGTTACCTTATAGTTGTACTGTGTAATTAGTGCCACTTAA 1261 TGTATGTTACCNAAAATAAAATATATCTACCCCGACTAGATGTAGTATTTTTGTATATAATT 1321 GGATTTCCTAATACTGTCATCCTCAAAGAAAGTGTATTGGTTTTTTAAAAAACGAAAGTGT 1381 ATTTGGAAATAAAGTCAGATGGAAAATTCAAAAAAAAAAAAAAAAAAA	SEQ ID NO:31
		1 M A A I R K K L V I V G D D G A C G K T C 1 ATGGCTGCCATCAGGAAGAAACTCGTGATTGTTGGTGATGGAGCCTGTGGCAAGACTTGC 21 L L I V F S K D Q F P E V Y V P T V F E 63 TTGCTCATCGTCTTTAGCAAGGACCAGTTCCCAGAGGTGTATGTACCCACGGTGTTTGAG 41 N Y V A D I E V D G K Q V E L A L W D T 121 AACTATGTGGCAGATATCGAAGTGGATGGGAAGCAGGTAGAGTTAGCTTTGTGGGACACA 61 A G Q E D Y D R L R P L S Y P D T D V I 181 GCTGGGCAGGAAGATTATGATCGCTTGAGGCCTCTCCTACCCAGACACCGATGTTATA 81 L M C F S I D S P D S L E N I P E K W T 241 CTGATGTGTTTCTCCATTGACAGCCCTGATAGTTTAGAAAACATCCCAGAAAAATGGACT 101 P E V K H F C P N V P I I L V G N K K D 301 CCTGAAGTCAAGCATTTCTGTCCCAACGTGCCCATCATCCTGGTTGGAAACAAGAAGGAT 121 L R N D E H T R R E L A K M K Q E P V K 361 CTTCGGAATGATGAGCACACAAGGCGGGAGCTAGCCAAGATGAAGCAGGAGCCGGTAAAA 141 P E E G R D M A N R I G A F G Y M E C S 421 CCAGAAGAAGGCAGAGATATGGCAAACAGGATTGGTGCTTTTGGGTACATGCAGTGTTCA 161 A K T K D G V R E V F E M A T R A A L Q 481 GCAAAGACCAAAGATGGAGTGAGGGAGGTTTTTTGAAATGGCCACGAGAGCTGCTCTCCAA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		181 S R R G K K K S G C L V L – 541 TCCAGACGTGGGAAGAAAAAATCTGGGTGCCTTGTCTTGTGA	
WBC027E07	No homology	1 ACTCATTTATATCTTGTAGTTTACTATTTTACCTCTAGAAATAGACTTAAAAGTAGTTTG 61 TGTGTGAATATTTAACTACACGAAAGTTAGCAAAATTAACATTTGGAAACCTTCTATTCC 121 ATATGTTAGCATTTATTCCAACATCTTTTTAGCCTTATTTAGTCTAATTTAAAATTTTCA 181 AGCAACCCTATCTTATCATCTTCACATGGTGTTTACAATTTTGCAACGTGGATTATTCTC 241 TGTATAATATGTGAAATTCATTGCTTGATACTTTTGACCCAAAATTATGTTTGTTACAGT 301 TGAACTTAAATAAAGATCTTTAAACAAAAAAAAAAAAAAAAAAACGCGAGACTAGTTCTCT 361 CGTGACACCCACTCTTCCACCTTCGATGCTGGGGCTGGCATTGCCCTCAACGACCACTTT 421 GTCAAGCTCATTTCCTGGTATGACAATGAATTTGGCTACAGCAATAGGGTGGTGGACCTT 481 ATGGCCCACATGGCCTCCAAGGAGTAAGAGCCCCCTGGACCACCAATCACCCAGCAAGAG 541 AAGGAGAAAGGCCCTCAGCTGCTGGGAATGCTTGTCCCAACTTGACCCCCTAACATATTG 601 AGAGTCTCCTGACCTCCACAGTTTCCATCTCAGACCCCCCTGAAGAAGGGGAGGGGCTTG 661 GGCAGCCCTACCTTGTCATGTACCATCAATAAAGTACACTGTACCCAAAAAAAAAAAAAA 721 AAAAAAAAA	SEQ ID NO:32
WBC027D07	No homology	1 TGCCAAATGCTTTTTCTGCATCTATTGATATGATCATGATTTTTCTTCTTTAGCCTGTTG 61 ATATGATGGATTACATTAACTGATTTTTGAATGTTGAACCAAGAATGTGTACCTGGAATA 121 AAGCCCACTTTGTAGTTGTGTATAATTCTTTTTATATATTGTTGGATTTAATTTGCTAAT 181 ATTTTATTGAGGAATTTTGCATCTATGTTCATGAGAGACAATGGTCTGTAGTTTTCTTTT 241 CTGGTAATGTCTTTGTCTGGTTTTGGTATGAGGGTAATGCTTGCTTCATAGGATGAGTTA 301 GGAAGTATTCCTTCTGATTCTAGCTTCCAGAAGAGATTGTAGGAGAATTGCTGTAATTTC 361 TTCCTTAAATGTTTTGTAGAATTCACCAGTGAACCCATTTGGGTCTGGTGCTTTCTATTT 421 TGGAAGGTGGTTAATTATTGTTTCAATCTCTTTAATAGACATAGGCTTATTGAGATTATG 481 TCTTCTTGTATGAGTTTTGGCAGATGCTGTCTTTCAAGGAATTGATCTATTTCATTTAGG 541 TTATTGAATTTGTAGTCATAGAGTTGTTTATAGTATTCCTTTATTATCCTTTTAATGTCC 601 ATGGAATCAGAGTGATATCCCCTATTTCATTTCTGATATTAGTAATTTGTGTCTTCCCTC 661 TTTGTTTCTTAGTGAGACTGCCTGGAAGCTTATCCATTTATTGATAAACTACTTCTTTTC 721 GCAGAACCAGCTTTTGGTTTTGTTGATTTTCTCTATTGATTTCCTGTTTTCAATTTCATT 781 GATTTCTGCTCTAATTTTTATTATTTCCTTTACTTCTGCTTACTTTGGATTTAATTTACT 841 CTTCTTTTTCTAGTTTCCTAAGGTGGAAGATTAGATTATTGATTTTAGATCTTTCTTCTT 901 TT	SEQ ID NO:33
		1 GTTTAATTACACTGTGATCTGCGAGCAGACGACATATGCCTTCTATTCTTTTAAATTGCT 61 TGTGTTTTATGGCCCAGAATATGGTCTGTCTTGTTCAATGTTCCATGTGAGCTTGAGGAG 121 AATGTGTATTCTGTTGTTGTTGGGTAAAATAGCCTATAGATGTCAATTATATTTACTTTA 181 TAATTATATCCAATTATATTATGTCTTCTTGAAGAGTAAGCCTCTTTATCATTCTCTAAT 241 GCCCTTCTTTATCCCTGATAATTTTCCTCACTTGGTTGTTTGCTCTCTCTGAAATTAATA 301 TAGCTGCTCCAGCTTTCTTTTGCCTAGTGTTAGCATGGTATATTTTTCTCCATCCCTTTA 361 CTTTTAATCTGTATGTGTCCTTATATTTATATTTAAAGTGGGTTTCCTCTAGATAGCATA 421 TAGTTGGCTCTTGTTTTTTGATTCACTCTGATTAACTCTGTCTTTTAGCTGGTATGTTTA	SEQ ID NO:34

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		481 GACCATTGATGTTTAAAGTGATTATTGATATAGGTGGATTAATATCTACTGTATTATACT 541 GTTTTCTACTGGTTGCCCTTATTCTTTGTTCCTATTTTTGTCTTTCACTCTTTTCCTGCT 601 TTTTGTGGTTTTAATGAAAAAGATGCTTGGTCTGTATTATAAGTTATATAACACGAAAGA 661 AGGCAAGCAGTGTTCAAGCTACTCTTGATAAGTTTTTTACAAGGAAATAAAACACTTTAT 721 TTCTCAAAAAAAAAAAAAAAAAAA	
WBC026E02	Migration-inducing gene 10 protein	1 tctccccagc tgtatttcca aaatgtcgct ttctaacaag ctgacgctgg acaagctgga 61 cgttaaaggg aagcgggtcg ttatgagagt cgacttcaat gttcctatga agaacaacca 121 gataacaaac aaccagagga ttaaggctgc tgtcccaagc atcaaattct gcttggacaa 181 tggagccaag tcggtagtcc ttatgagcca cctaggccgg cctgatggtg tgcccatgcc 241 tgacaagtac tccttagagc cagttgctgt agaactcaaa tctctgctgg gcaaggatgt 301 tctgttcttg aaggactgtg taggcccaga agtggagaaa gcctgtgcca acccagctgc 361 tgggtctgtc atcctgctgg agaacctccg ctttcatgtg gaggaagaag ggaagggaaa 421 agatgcttct gggaacaagg ttaaagccga gccagccaaa atagaagctt tccgagcttc 481 actttccaag ctaggggatg tctatgtcaa tgatgctttt ggcactgctc acagagccca 541 cagctccatg gtaggagtca atctgccaca gaaggctggt gggtttttga tgaagaagga 601 gctgaactac tttgcaaagg ccttggagag cccagagcga cccttcctgg ccatcctggg 661 cggagctaaa gttgcagaca agatccagct catcaataat atgctggaca aagtcaatga 721 gatgattatt ggtggtggaa tggcttttac cttccttaag gtgctcaaca acatggagat 781 tggcacttct ctgtttgatg aagagggagc caagattgtc aaagacctaa tgtccaaagc 841 tgagaagaat ggtgtgaaga ttaccttgcc tgttgacttt gtcactgctg acaagtttga 901 tgagaatgcc aagactggcc aagccactgt ggcttctggc atacctgctg gctggatggg 961 cttggactgt ggtcctgaaa gcagcaagaa gtatgctgag gctgtcactc gggctaagca 1021 gattgtgtgg aatggtcctg tgggggtatt tgaatgggaa gcttttgccc ggggaaccaa 1081 agctctcatg gatgaggtgg tgaaagccac ttctaggggc tgcatcacca tcataggtgg 1141 tggagacact gccacttgct gtgccaaatg gaacacggag gataaagtca gccatgtgag 1201 cactgggggt ggtgccagtt tggagctcct ggaaggtaaa gtccttcctg gggtggatgc 1261 tctcagcaat atttagtact ttcctgcctt ttagttcctg tgcacagccc ctaagtcaac 1321 t	SEQ ID NO:35
		1 M S L S N K L T L D K L D V K G K R V V 1 ATGTCGCTTTCTAACAAGCTGACGCTGGACAAGCTGGACGTTAAAGGGAAGCGGGTCGTT 21 M R V D F N V P M K N N Q I T N N Q R I 61 ATGAGAGTCGACTTCAATGTTCCTATGAAGAACAACCAGATAACAAACAACCAGAGGATT 41 K A A V P S I K F C L D N G A K S V V L 121 AAGGCTGCTGTCCCAAGCATCAAATTCTGCTTGGACAATGGAGCCAAGTCGGTAGTCCTT 61 M S H L G R P D G V P M P D K Y S L E P 181 ATGAGCCACCTAGGCCGGCCTGATGGTGTGCCCATGCCTGACAAGTACTCCTTAGAGCCA 81 V A V E L K S L L G K D V L F L K D C V 241 GTTGCTGTAGAACTCAAATCTCTGCTGGGCAAGGATGTTCTGTTCTTGAAGGACTGTGTA	SEQ ID NO:36

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		101 G P E V E K A C A N P A A G S V I L L E 301 GGCCCAGAAGTGGAGAAAGCCTGTGCCAACCCAGCTGCTGGGTCTGTCATCCTGCTGGAG 121 N L R F H V E E E G K G K D A S G N K V 361 AACCTCCGCTTTCATGTGGAGGAAGAGGGAAAGGATGCTTCTGGGAACAAGGTT 141 K A E P A K I E A F R A S L S K L G D V 421 AAAGCCGAGCCAGCCAAAATAGAAGCTTTCCGAGCTTCACTTTCCAAGCTAGGGATGTC 161 Y V N D A F G T A H R A H S S M V G V N 481 TATGTCAATGATGCTTTTGGCACTGCTCACAGAGCCCACAGCTCCATGGTAGGAGTCAAT 181 L P Q K A G G F L M K K E L N Y F A K A 541 CTGCCACAGAAGGCTGGTGGGTTTTTGATGAAGAAGAGCTGAACTACTTTGCAAAGGCC 201 L E S P E R P F L A I L G G A K V A D K 601 TTGGAGAGCCCAGAGCGACCCTTCCTGGCCATCCTGGGCGGAGCTAAAGTTGCAGACAAG 221 I Q L I N N M L D K V N E M I I G G G M 661 ATCCAGCTCATCAATAATATGCTGGACAAAGTCAATGAGATGATTATTGGTGGTGGAATG 241 A F T F L K V L N N M E I G T S L F D E 721 GCTTTTACCTTCCTTAAGGTGCTCAACAACATGGAGATTGGCACTTCTCTGTTTGATGAA 261 E G A K I V K D L M S K A E K N G V K I 781 GAGGGAGCCAAGATTGTCAAAGACCTAATGTCCAAAGCTGAGAAGAATGGTGTGAAGATT 281 T L P V D F V T A D K F D E N A K T G Q 841 ACCTTGCCTGTTGACTTTGTCACTGCTGACAAGTTTGATGAGAATGCCAAGACTGGCCAA 301 A T V A S G I P A G W M G L D C G P E S 901 GCCACTGTGGCTTCTGGCATACCTGCTGGCTGGATGGGCTTGGACTGTGGTCCTGAAAGC 321 S K K Y A E A V T R A K Q I V W N G P V 961 AGCAAGAAGTATGCTGAGGCTGTCACTCCGGCTAAGCAGATTGTGTGGAATGGTCCTGTG 341 G V F E W E A F A R G T K A L M D E V V 1021 GGGGTATTTGAATGGGAAGCTTTGCCCGGGGAACCAAAGCTCTCATGGATGAGGTGGTG 361 K A T S R G C I T I I G G G D T A T C C 1081 AAAGCCACTTCTAGGGCTGCATCACCATCATAGGTGGTGGAGACACTGCCACTTGCTGT 381 A K W N T E D K V S H V S T G G G A S L 1141 GCCAAATGGAACACGGAGGATAAAGTCAGCCATGTGAGCACTGGGGGTGGTGCCAGTTTG 401 E L L E G K V L P G V D A L S N I – 1201 CAGCTCCTGGAAGGTAAAGTCCTTCCTGGGGTGGATGCTCTCAGCAATATTTAG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
WBC024F08	No homology	1 GGATAGTGCAGCATCCTAGAGCTTTGGTGTCACACAGACCCAGGTTCGAGTCTTCACTTT 61 GCCACCTCTTGCCTGCCGAGGGGCTGTGAGCTGAATTTCCTACCTCATAGGGTTGTAATG 121 AGCAGTGGATGCTGAAGCAGACACCTCTTGGTCAAGGTGACTGCTCATCCCAGATTCTCC 181 CTTTTTCTGAGAATTTGTTCCCCTCAGTCCTCATATAGGAGCTGAATGGATGAGAGGCGA 241 GCATCTGGCTGTACTTGGGCCAGTCTGGTTCTCTCTCTCAGGAATAAGCAGCGAGACTCA 301 GGGATGCTGTTTCCAGCTCTGCAAGTCACTTACCTGAAGATATACAAACTCTGGAGCTGT 361 GAGCGTGTGTCTACATGTGTGTCTCTATGTACCCAAGCCTTGGGGGTGGTGGCGGCAGGG 421 GGTGGCCACCTGCATGAGTGTATTAGAGAAAATGGCTCGACTCAGAGAGAAGATGCAGAT 481 GTGCAGAGCAAATCAGAGACCAGAGGGAGACCCCAGGAGCCTGGAGAGGCCAGGGGGAGG 541 CGCTTCCCGGAGCCTGCCGGCGCTCCTCCTCTGGGCCAAACCCTTCTCGAGCCTCAAAGT 601 CCGCCCTCCTTCCTTTGAGTCCTGTGAGATGCCCTTGTTAGGATGCATTCTCTTGTTTTG 661 CTTGAGCTGATTTGAAGTATTATCTATTACTTGCAACCAAAAGAGCTCTGAATAAGATAA 721 AATCTTGTTGCTAAAGCACAGTGTCTCTCGAATTTCGGTCATCCCTGTACCCTCCTCACA 781 ATTTTTGCATATCTATGTACCATCTGTATGTTTTACTAATAAATATTGTTCTTTAAATCT 841 TTAAAAAAAAAAAAAAAAAA	SEQ ID NO:37
WBC024C12	No homology	1 GGGACCTCTACTTGAGTCTCAGGCTCTTGCTGGTGGTATTTACTTTCTCCTTTGGGCTCA 61 TCAAGTGCTGGTACTATAAAGAATGATGGAGATTGGCAGGGAAAAACTAGCATTAGTAAG 121 GTCCCAGGGAGGTAATGAGATGAAAAATGAACTTAAGGAGGGAAAAAACCAAAACGCAAG 181 TGGAAGAAGAAGGTTTCCAGGTATACTGTGAAGGGTGAGCTTCAACAAAGTAACAGAAGA 241 TGTTGAGAGCAGGTAGGAGAACACCCATGAGCATCATGGAAAAGTCCTCTCAGGTAATTT 301 ATGTATATTTTTGCTTTCGTTTCTTTGTGGGAGCATCTTTCTTTGTGGAAAAAGAAAGCG 361 AACAATGACAAAGCTGGAGATTTTCTTTGGGTTTATTAAAAATCAGTACAATTTCAACAA 421 AGCAGAGGAAAGCAAGGAGAGCAAAAGTCAACCTTCCTGCTCCCTCTTATTAGTAGGAAG 481 TCTAACACAAGCTTGTCAGAGTTAGTTTAAAAGGTGAGGAACAACATGTGTAATTTGTGT 541 GTGTGTAATTTTCTGAGCTGAACTGAAGCTTAGCAGCTTTAGTTTACCTAGGTTTGACGT 601 TCTTTAAAGAAATCCCTTGGAGAATTTGTTGGAAGCTAAGGACCTTCCCAAAATAATGCG 661 TGTGTTCACACGTGTGCACTTTTTGGATACCACTTCACTTGGTTCTTGGACCCTTCCTAA 721 AACTCATTGGTCTCTGTTCTTTGCTCTCTGTTCACCTCTATTTTCTACAGTTAATAAATG 781 GACATCTAATATCTGCCTAAAAATGTCTAAGAACAGAGACTCTGCCTTTTGTTCTGTCCA 841 ACAATGGAATAGGCAAAGGGTTATAAGAAGTCCTTCGTTCGGTTGATGTTGGCTGTTTTA 901 A	SEQ ID NO:38
		1 CCATGGATTAGTTTTGTCTGTCCTTTGATTTCGTATAAATGGAATCATACAGTATGTACT 61 CTTTTGGGTCTGGTTCATCCATGTTGTAGCATATATCAGTAGTTCATTCCTTTTTATCGC 121 TGAGTAGTGTTCTTTTGGTGAAATACGCCACAATTTGTCCACTCATCTTTAGTGGACATT 181 TGGGTAGTTTTCAGTTTTTACAATAAGGCTGCTATAAACATTCTTGTACAGGTCTTTTTG 241 TAAACATATGCTTTCATTTCTCTTGTGTAAATACCTAAGAGTAGAATCATTAGGTTACAG 301 AGTAAATGTGGGCTTAATTTTATAGGAAATTTCTTCTGCATTTATTTGTGCTAACCTCTG 361 AAATTCTTGATTCCAGTTGCAGTATTCACTGTTGTCTGTTCTTCTAGGTTTTGCATTTAT 421 AAATTTGATAATGTTTTCTCATATCCCTGTTATATAAAAATATTAAACAAGATGGAGGAG 481 AGGATGCAACTTTTCATTAGGATGTTAGATACCAACCTCCAAGATGCCAGAGATCAAAAC 541 TCCTTGGGTGTGATCACGCAGCAGTGTGTGAACCTACTTAACAATCCTCGTCCAGGCCAC	SEQ ID NO:39

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		601 ATATCTCCGTCTTTTTAATAAATACCAAACTGGAATGAATTTTAAAAAAAAAAAAAAAAA 661 A	
WBC024C11	No homology	1 CAGATGATGATCCCTGGGAGTAAAGACCACACCCTCCCCCAGGCTTTCATATGATTCCTG 61 AAACAGGGTTTTATCTTCTCTCTCTCTTACTTTCGTGATATTTTAACAATTTTAATAACT 121 GTCATTCATTTAAGAATGTCTAAAGTTAGTTATGATTAGTCTCCTCCCAAGATATACAAG 181 ATGACGCATATAATTTATAGGTATTCACTTTGGTTCTTTTCCAAATCTGCCTGGTCCTTA 241 CTGAAAGAGTTTTTCTTTTTCTTATTTTCAATTCCTTCTTTTATCTGTTTAATCACTTAC 301 ACATATTTTATAGTTTATTGATTTGTTTAGTGCTAGCTGTTGCTGCAAAAACGCAATCAG 361 TCTCTGTGCCATATATTCCTTGCAAACAGAAATCAGATCAACAGGTATTTGGGGCTGAGT 421 GGTCTTCCTTGTGCCTATTTGAGTATACATCTTGGATCCTCCTCCTCCAAACCCATACTG 481 TTCTCTCCATTCTGCAAGGTTGAGAATGGAGGATTGTATTTTGGAAGTTTCTATCAAGTA 541 GGCCTGAAAGTGACACATTCCATAGGCCAGAACTTGGTCATATGGCCATAGCCAACCATA 601 AGGGAAACTTGGAGATGTAATGACTCCATCTCTGAATCCGAGAGGAAGATGAAATACATT 661 GAGAGAACAGCTAGCCAGTCTACACCACATAGTCTCCGTCCAATAATTCTATTCTGCTTT 721 TCTTGACAGATTAGTGATGCGATTTGTTTCTGTCTGCTGCTGACATCATGATAGCTTGCT 781 TCCTCTTGTATTTTGTTATTTTAGATTCAAAGTTTCCATTTGGTGCGACTTTATCTCAAA 841 AATCCTGTGTCGTCTGAGTTCCCAGACCTCATAAGTAAAGCAATACAAATATGAGCACAA 901 AAATCCATGTGAATGG	SEQ ID NO:40
		1 GGATCTAGTATCCTATTCCTTCCTAGTGTGGAGACTTCCCTCCTCGTAAATGACACCCTT 61 TGTAAGTTCTTTTATGAATGTCTATAAGTGGTAGACACCTCCTGCCTCGTGGTTTCTCTA 121 GAAAATGTCTATTTCATGCCTACGCTTAATGGTAGTTTACCTGGGCTTGGAATTCTAGAA 181 TGATAGTTAATTTTTCTGAGCACCATGAATATATAATATTATCTTTCGACATTTTATTGA 241 TGTTAACTTTAACGTCAAGCTTACTGTTTTTTGTAGTTATCCTGTCTTTTTTCCCCAGGC 301 TGCTTGTAAGATCTGACTCTGAAATTTCCTTTAGAATATTTCTAGGTATAGATTTATTGT 361 TACTTATCCTTTTGGGGGGTAATTATACTTCTGGGATCTAACGATTTAAGATAAGTCTGG 421 AATATTTTCAATCATTTTCACATCATATATTGCCTCTTTCCTTTCCTCAAAGACATTCCA 481 TTAGATATGTTAGACCATACAGTTTTATCCCACAAGTTCATTAAACCTTACATATTTGTT 541 TTTCACTCTAATCTGCATTCCCTTTAGTCCTTTCTTCTGGTTAACTAATTCTGTCTTCAG 601 TTGTATCTAAACTGTTATTTTACCCGTGTAAGGTGTTTTAAATTTTAATAAAACTTTTGT 661 TTATAAAATTCTACTTTTTATACCTAAAAAAAAAAAAAAAAAA	SEQ ID NO:41
WBC024B05	Adducin 3 (gamma) (ADD3), transcript variant 2	1 GAGAGAAGCTGCTGCTGCTAATGCTGCTGCTGCTGCTGCCGCCGCCGCCGCTGCTGCTGC 61 TGCTGTTGGTCTGAGGCTGCAGTAGGTTTCTGTGCAGCATTGCAGAATCCACACCTAGAG 121 AACAGAAGACACAGACACGTACGTCTACTACCCTTGTTAGAAGGAAGCTTTGGATCTTCG 181 GTGGATAACAAGAGTAATCCACAGACTTAAAACATGAGCTCAGATGCCAGCCAAGGCGTG 241 ATTACCACTCCTCCTCCTCCCAGCATGCCTCACAAAGAGAGATATTTTGACCGCATCAAT 301 GAAAATGACCCAGAATACATTAGGGAGAGGAACATGTCTCCTGATCTACGACAAGACTTC 361 AACATGATGGAGCAGAGGAAACGAGTTACTCAGATCCTGCAAAGTCCTGCCTTTCGGGAA 421 GACTTGGAATGCCTTATTCAAGAACAGATGAAGAAAGGCCACAACCCAACTGGATTACTA 481 GCATTACAGCAGATTGCAGATTACATCATGGCCAATTCTTTCTCGGGTTTTTCTTCACCT 541 CCTCTCAGTCTTGGCATGGTCACACCTATCAATGACCTTCCTGGTGCAGATACATCCTCA	SEQ ID NO:42

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		601 TATGTGAAGGAGAAAAACTTACTCGCTGTAAACTTGCCAGCCTGTACAGACTTGTAGAC	
		661 TTGTTTGGATGGGCACACCTGGCAAATACCTATATCTCAGTAACAATAAGTAAGGAGCAA	
		721 GACCACATTATAATAATTCCCAGAGGCCTATCTTTTCTGAAGCTACAGCCTCCAATTTG	
		781 GTGAAAGTCAATATAATAGGAGAAGTGGTTGACCAGGGAAGTACCAATTTGAAAATTGAC	
		841 CATACAGGATTCAGTCCCCATGCTGCAATCTATTCAACACGTCCTGATGTTAAGTGTGTG	
		901 ATACACATCCATACCCTTGCAACAGCAGCTGTATCCTCCATGAAATGTGGGATCCTTCCA	
		961 ATTTCTCAAGAGTCTCTTCTTCTTGGGAGATGTTGCCTATTATGACTACCAAGGGTCACTT	
		1021 GAAGAACAGGAGGAGAGAATTCAACTGCAGAAGGTTCTGGGACCAAGTTGTAAGGTGCTG	
		1081 GTACTCAGGAATCATGGTGTGGTTGCACTTGGAGAAACATTAGAGGAGGCTTTTCATTAT	
		1141 ATTTTTAATGTCCCAACTAGCCCTGTGAGATTCAGGTGCAGGCCCTAGCAGGTGCAGGTGGA	
		1201 GTAGACAATCTCCCATGTACTGGACTTTCAGAAGTATAAAGCTTTCACTTACATGTAGCA	
		1261 GCGTCTGGTGGAGGAGGTGTGAATATGGGTTCCCATCAAAAATGGAAGGTTGGCGAAATT	
		1321 GAGTTTGAAGGGCTTATGAGGACTCTGGACACACTTGGGGTATAGAACAGGCTATGCTTAC	
		1381 AGGCATCCTCTCATTCGAGAGAAGCCTAGGCACAAGAGTGATGTGCAAATCCCAGCAACT	
		1441 GTGACTGCTTTTTCCTTTGAAGACGATACAGTGCCACTCTCTCCTCTCAAATACATGGCA	
		1501 CAGAGGCAACAGCGTGAAAAAACAGATGGCTGAACTCACCAAATACTTACATGAAAGTG	
		1561 AATGTGCCTGAGGAGTCTCGGAACGCAGAAACCACTCCCCGAACCAAAATCACGTGGATG	
		1621 AAAGCAGAAGACTCATCTAAAGTTAGTGGTGGAACACCTATCAAAATTGAAGATCCAAAT	
		1681 CAGTTTGTTCCTTTAAACACAAACCCGAATGAGGTACTAGAAAGAGAAATAAGATTCGG	
		1741 GAACAAAATCGATATGACTTGAAAACAGCAGGACCACAATCTCAGTTGCTTGCTGGAATT	
		1801 GTTGTGGATAAGCCACCTTCTACTATGCAATTTGAAGATGATGATCATGGCCCACCAGCT	
		1861 CCTCCTAACCCATTTAGTCATCTCACAGAAGGAGAACTTGAAGAGTATAAGAGGACAATC	
		1921 GAACGTAAACAACACAAGGCCTAGAAGAAAACCATGAGCTGTTTTCCAAGAGCTTCATCTCC	
		1981 ATGGAAGTGCCTGTCATGGTAGTAAATGGCAAGGATGATATGCATGATGTTTGAAGATGAG	
		2041 CTTGCTAAGCGAGTGAGTAGGTTAACGCACACAAGTACAACCATAGAAAACATCGAGATTACT	
		2101 ATTAAGTCTCCAGAGAAAATCGAAGAAGTCCTGTCACCTGAAGGCTCCCCTTCAAAATCG	
		2161 CCATCCAAGAAAAAGAAGAAATTCCGCACTCCTCTTTTCTGAAAAAGAACAAAAAAAAG	
		2221 GAGAAAGTTGAGGCCTAAATAAAGTCTTTTTATAATTATTATATAACAATGTGACATTG	
		2281 CACATCTAAATACCACATTTAAGTTCATCATTAATATGCAATGGTAGATCAGATTGGGGG	
		2341 ATGTAGCAAACTGGACTTTAAGAACTGGAAAAGAGGTTTTACAAAAGAAAAACTTTCAGAT	
		2401 TCATCTCTCATTTTATATGTCCAGAAATGGCTTTCGAATTTTAAGCAATTACTAGTTTTAA	
		2461 TTAGCTCTGCCCTCATGAAGTATTATTATAATTCACCATAAACAGCTATCTGTCTGAATT	
		2521 ACTTCAGGCCTTCTCCATAATATCTGTTAGAAAGAAATTGCCAGTGAGCAAGTGAGAATT	
		2581 TTTATTTCTCAATACCTGCTTCACTTGATAATCATATTATAATTTTTTTATCATGATTATT	
		2641 GACTATATTTTTGGAGTCCCATTGTTTCAGTGGGCATTAACAGAATGCTTTAAAAACTTC	
		2701 TAAGACAAGAATCTATAGCATTAGTATACACTGGCACATAATTTTTTAAAAGTTTTAAG	
		2761 AAAAGATTCATTTGGAATTTATTCACAGTATAAAATTTCCTCACCTGAAGTAACTTTGT	
		2821 TTGCCAAAAAAGTTGTTTTAATAAACTATATAATTTTTGAAACTTCCTTTTTTATTAGTTT	
		2881 AGAAAGCCCCTTATTTTTCAACAAAGGGGATTTTCTGTACACATAACATGGGTTATTTAGTT	
		2941 TAACTCTGGCAAAAAAAAAAAAAAAAATTTTGTATGTTGATGTTTGTATACCGTTCAGTA	
		3001 TAAAAGTGTCCTAAGCATATTAGCCAATCTTTTCACAGTAGAGCATACTTAAGGCTGCTT	
		3061 GGTACTGAGTATACTTAAATATAACTCCAGAATCCAGGGACTTGGTGTTAAAACAGGATT	
		3121 AGAGCATGTAAAGGTACATCTAGATTCATATTTGAATCTTAAACTGTATTTTCTCTTAG	
		3181 TATTGCTAATGAGTAAAGAAAAGTCTCATAAGGTAGCCAAATGAAAAAGAATGCAAAGGGA	
		3241 AAGTGAAAAATTAAGGGCACAAAAGATGGGATGTGCAAAAGAAGAATTCTAGTTTGATGGT	
		3301 GACTCATATTCACGATAGGATACAAAGTGTGATTTGTTGGAAACATGTCCCAAATTTCTA	
		3361 AAATTCTGCTTCTCTGCCAAAAGCAATGTCTTCTTGGTTGATATTTGAGTTTTAAAAGG	
		3421 GTCAAATCTTTCTAATTTTTTGTATCTTTAGAGGGCAGCACTAGAAGAAATCAGCAGGTC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		3481 TAATCCCACCAGTAAGAAACTACCACTTCTTGATTTTTACAGATTTAAAAAATCTTTT 3541 CACTGACCTTTCTTTTTAATGTAAATACAAATTTAAACCTAGGCTTAATATAGGCGTTTC 3601 CCCTTTCACCCAAGTGATGTCACAGTTCGATGCAAAATCAATGATCCAGAATGATCGTGG 3661 GTAAAAATAACTCAAAGTGTTTCTTAAGGTGAGTTGGCATGCAAAAAATTACATTGATT 3721 ACAGTGTGTTTTGGAGCTGGCTCTGTTGTGTGCATATGATAATGCAGAGTTGAGCCAGA 3781 GCCTGGAAATGTCATTCTAGATCTCACTAACTACTGGAATCAGTGTTTTAATCTCTTGGT 3841 GGAAACTTTCAGTTGCTTAACTCTCTATTGGAAGATTTTTTTAATGTTCTACATCATTTA 3901 TGTTGTATTACAATGTATGTAGAAATAGTAACCTGTGAACTATGCTTTTCCATAACTTTT 3961 TAAAAATATATATATCTAAATGAATGCAATGTGCATAAAATATTTTTTAAACATAACAGTG 4021 AACTATTGCACCTTTTGCTAATGCCTCTATTTACTTGCTTTGGCATAAAGAATGAGCCAA 4081 TGAACCTCTGTGTCCTGTGGAAAAATGTATAAATGTTATCTGATATTGCTCTCTTAGATGTA 4141 ATGCTAATTAATGTTAAATCACAAATAAACAGTATTTTAAATATAAAAAAAAAA	SEQ ID NO:43
		1 M S S D A S Q G V I T T P P P S M P H 1 ATGAGCTCAGATGCCAGCCAAGGCGTGATTACCACTCCTCCTCCCAGCATGCCTCAC	
		21 K E R Y F D R I N E N D P E Y I R E R N 61 AAAGAGAGATATTTTGACCGCATCAATGAAAATGACCCAGAATACATTAGGGAGAGGAAC	
		41 M S P D L R Q D F N M M E Q R K R V T Q 121 ATGTCTCCTGATCTACCAACAAGACTTCAACATGATGGAGCAGAGGAAACGAGTTACTCAG	
		61 I L Q S P A F R E D L E C L I Q E Q M K 181 ATCCTGCAAAGTCCTGCCTTTCGGGAAGACTTGCAATGCCTTATTCAAGAACAGATGAAG	
		81 K G H N P T G L L A L Q Q I A D Y I M A 241 AAAGGCCACAACCCAACTGGATTACTAGCATTACAGCAGATTGCAGATTACATCATGGCC	
		101 N S F S G F S S P P L S L G M V T P I N 301 AATTCTTTCTCGGGTTTTTCTTCACCTCCTCTCAGTCTTGGCATGGTCACACCTATCAAT	
		121 D L P G A D T S S Y V K G E K L T R C K 361 GACCTTCCTGGTGCAGATACATCCTCATATGTGAAGGGAGAAAAACTTACTCGCTGTAAA	
		141 L A S L Y R L V D L F G W A H L A N T Y 421 CTTGCCAGCCTGTACAGACTTGTAGACTTGTTGGATGGGCACACCTGGCAAATACCTAT	
		161 I S V R I S K E Q D H I I I I P R G L S 481 ATCTCAGTAAGAATAAGTAAGGAGCAAGACCACATTATAATAATTCCCAGAGGCCTATCT	
		181 F S E A T A S N L V K V N I I G E V V D 541 TTTTCTGAAGCTACAGCCTCCAATTTGGTGAAAGTCAATATAATAGGAGAAGTGGTTGAC	
		201 Q G S T N L K I D H T G F S P H A A I Y 601 CAGGGAAGTACCAATTTGAAAATTGACCATACAGGATTCAGTCCCCATGCTGCAATCTAT	
		221 S T R P D V K C V I H H T L A T A A V 661 TCAACACGTCCTGATGTTAAGTGTGTGATACACATCCATACCCTTGCAACAGGCAGCTGTA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFTER:
		241 S S M K C G I L P I S Q E S L L L G D V 721 TCCTCCATGAAATGTGGGATCCTTCCAATTTCTCAAGAGTCTCTTCTTCTGGGAGATGTT	
		261 A Y Y D Y Q G S L E E Q E E R I Q L Q K 781 GCCTATTATGACTACCAAGGGTCACTTGAAGAACAGGAGGAGAGAATTCAACTGCAGAAG	
		281 V L G P S C K V L V L R N H G V V A L G 841 GTTCTGGGACCAAGTTGTAAGGTGCTGGTACTCAGGAATCATGGTGTGGTTGCACTTGGA	
		301 E T L E E A F H Y I F N V Q L A C E I Q 901 GAAACATTAGAGGAGGCTTTTCATTATATTTTTAATGTGCAACTAGCCTGTGAGATTCAG	
		321 V Q A L A G A G G V D N L H V L D F Q K 961 GTGCAGGCCCTAGCAGGTGCAGGTGGACTAGACAATCTCCATGTACTGGACTTTCAGAAG	
		341 Y K A F T Y T V A A S G G G G V N M G S 1021 TATAAAGCTTTCACTTACACTGTAGCACGCGTCTGGTGGAGGAGGTGTGAATATGGGTTCC	
		361 H Q K W K V G G E I E E F E G L M R R T L D N 1081 CATCAAAAATGGAAGGTTGGCGAAATTCAGTTTGAAGGCTTATGAGGACTCTGGACAAC	
		381 L G Y R T G Y A Y R H P L I R E E K P R R H 1141 TTGGGGTATAGACAGGCTATGCTTACAGGCATCCTCTCATTCGAGAGAAGCCTAGGCAC	
		401 K S D V E I P A T V T A F S F E E D D T V 1201 AAGAGTGATGTGGAAATCCCAGCCAACTGTGACTGCTTTTTCCTTTGAAGACGATACAGTG	
		421 P L S P L K Y M A Q R Q Q R E K T R W L 1261 CCACTCTCCTCCTCTCAAATACATGGCACAGAGGCAACAGCGTGAAAAAACAAGATGGCTG	
		441 N S P N N T Y M K V N V P E E S R N G E T 1321 AACTCACCAAATACTTACATGAAAGTGAATGTGCCTGAGGAGTCTCGGAACGGAGAAACC	
		461 S P R T T K I T W M K A E D S S K V S G G 1381 AGTCCCCGAACCAAAATCACGTGGATGAAAGCAGAAGACTCATCTAAAGTTAGTGGTGGA	
		481 T P I K I E D P N Q F V P L N T N P N E 1441 ACACCTATCAAAATTGAAGATCCAATCAGTTTGTTCCTTTAACACAAACCCGAATGAG	
		501 V L E K R N K I R E Q N R Y D L K T A G 1501 GTACTAGAAAAGAGAAATAAGATTCGGGACAAAATCGATATGACTTGAAAACAGCAGGA	
		521 P Q S Q L L A G I V V D K P P S T M Q F 1561 CCACAATCTCAGTTGCTTGCTGGAATTGTTGTGGATAAGCCACCTTCTACTATGCAATTT	
		541 E D D D H G P P A P P N P F S H L T E G 1621 GAAGATGATGATCATGGCCCACCAGCTCCTCCTAACCCATTTAGTCATCTCACAGAAGGA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		561 E L E E E Y K R R T I E R K Q Q G L E E N H 1681 GAACTTGAAGAGTATAAGAGGACAATCGAACGTAAACACAACAAGGCCTAGAAGAAACCAT	
		581 E L F S K S F I S M E V P V M V V N G K 1741 GAGCTGTTTTCCAAGAGCTTCATCTCCATGGAAGTGCCTGTCATGGTAGTAAATGGCAAG	
		601 D D M H D V E D E L A K R V S R L S T S 1801 GATGATATGCATGATGTTGAAGATGAGCTTGCTAAGCGAGTGAGTAGGTTAAGCACAAGT	
		621 T T I E N I E E I T I K S P E K I E E V L 1861 ACAACCATAGAAACATCGAGATTACTATTAAGTCTCCAGAGAAAATCGAAGAAGTCCTG	
		641 S P E G S P S K S P S K K K K K F R R T P 1921 TCACCTGAAGGCTCCCCTTCAAAATCGCCATCCAGAAAAAGAGAAGTTCCGCACTCCT	
		661 S F L K K N K K K E K V E A - 1981 TCTTTTCTGAAAAAGAACAAAAAAAAGGAGAAAGTTGAGGCCTAA	
WBC022F08	Phosphogluconate dehydrogenase	1 CGCGTCGCCGCTCTTCGGTTCTGCTCTGTCCGCCGCCATGGCCCAAGCTGACATCGCGCT 61 GATCGGATTGGCCGTCATGGGCCAGAACTTAATTCTGAACATGAATGACCACGGCTTTGT 121 GGTCTGTGCTTTTAATAGGACTGTCTCCAAAGTTGATGATTTCTTGGCCAATGAGGCAAA 181 GGGAACCAAAGTGGTGGGTGCCCAGTCCCTGAAAGAGATGGTCTCCAAGCTGAAGAAGCC 241 CCGGCGGATCATCCTCCTGGTGAAGGCTGGGCAAGCTGTGGATGATTTCATCGAGAAATT 301 GGTACCATTGTTGGATACTGGTGACATCATCACATTGACGGAGGAAATTCTGAATATAGGGA 361 CACCACAAGACGGTGCCGAGACCTCAAGGCCAAGGGAATTTTATTTGTGGGCAGCGGACT 421 CAGTGGTGGAGAGGAAGGGCCCGGTATGGCCCATCGCTCATGCCAGGAGGGAACAAAGA 481 AGCGTGGCCCCACATCAAGACCATCTTCCAAGGCATTGCTGCTCAAAAGTGGGAACTGGAGA 541 ACCCTGCTGTGACTGGGTGGGAGATGAGGGAGCAGGACACTTTCTGAAGATGCTGCACAA 601 TGGCATAGAGTACGGCGATATGCAGCTGATCTGTGAAGCTTACCATCTGATGAAAGACGT 661 TCTGGGCATGGAGCATAACGAGATGGCAAAGGCATTTGAGGAGTGGGATAACAGAGCT 721 AGACTCATTCCTGATTGAAATCACAGCCAATATTCTCAAGTTTCAAGATACCGATGGCAA 781 GTACCTGCTGCCAAAGATCAGGGACAGTGCGGGGCAGAAGGGCACTGGGAAGTGGACTGC 841 CATCTCGGCCCTGGAGTACGGTGTTCCCGTCACCCTCATCGCGAGAAGCGGTCTTTGCTCG 901 ATGCTTATCGTCTCTGAAGGATGAGAGGATTCAAGCTAGCGGGAAGCTGAAGGGTCCTCG 961 AAAGATCCAGTTTGAAGGTGATAAGAAATCTTTCCTGGAGGACATTCGAAAGGCCCTCTA 1021 TGCTTCCAAGATCATCTCTTATGCTCAGGGCTTTATGCTGCTAAGACAGGCAGCCACTGA 1081 ATTTGGCTGGACCCTCAACTACGCGCGGCATTGCCCTGATGTGGAGGGGCGGCTGCATCAT 1141 CAGAAGTGTTCCTAGGAAAAATAAAAGATGCATTTGATCGAAACCCAGAACTTGAGAA 1201 TCTGCTGCTGGATGACTTCTTCAGGTCGGCTGTTGAAAGCTGCCAGGACTCCTGGCGGCG 1261 GGCAGTCAGTACTGGTGTCCAGATGGGCATTCCCATGCCCTGCTTCACCACTGCTCTTTC 1321 CTTCTATGATGGATACAGACATGAAATGCTACCAGCCAACCTAATCCAGGCTCAGCGGGA 1381 TTACTTTGGGGCTCACACGTATGAACTCTTAGCCAAACCCGGACAGTTTATCCACACTAA 1441 TTGGACAGGCCATGGCGGCAGTGTGTCATCCTCTTCGTACAATGCCTAATCAGACTCCTT 1501 GTGTTACCCACCACCATGATTCCATAGACCAGGACATTCCATTTGCCACACAGCACTGCTTAC	SEQ ID NO:44

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1561 ATGGCCCTTGCCCTATTTCTGCTCACATCTCTTAAAGTGTTGTAAGACTCCTGAAA 1621 AAGTCAACCTGAGTTTATTGTAAGGTAGTTCTGTGAGAACCGTCATGCCCTCTGCCCTT 1681 GTCTCTTGGGACTGACCAGGAAGTGATCATGTTCGTGAGAGTGGGAACCATCTCCTTGCG 1741 GCAGTGGCTTCCGCGTGCCCCGTGTCGTGGTGCGGTTCCCATCACGCAGACAGGAAGGGT 1801 GTTTGCGCACTCTGATCAACTGGAACCTTTGTATCATGCAGGTGAATTCCCTTTTCCTC 1861 TACTTAATAAAAGCTACATCACACTGAAAAAAAAAAAAAAAAAA 1 M A Q A D I A L I G L A V M G Q N L I L 1 ATGGCCCAAGCTGACATCGCGCTGATCGGATTGGCCGTCATGGGCCAGAACTTAATTCTG 21 N M N D H G F V V C A F N R T V S K V D 61 AACATGAATGACACCACGGCTTTGTGGTCTGCTTTTAATAGGACTGTCTCCAAAGTTGAT 41 D F L A N E A K G T K V V G A Q S L K E 121 GATTTCTTGGCCAATGAGGCAAAGGGAACCAAAGTGGTGGGTGCCCAGTCCCTGAAAGAG 61 M V S K L K K P R R I I L L V K A G Q A 181 ATGGTCTCCAAGCTGAAGAAGCCCCGGCGGATCATCCTCCTGGTGAAGGCTGGGCAAGCT 81 V D D F I E K L V P L L D T G D I I I D 241 GTGGATGATTTCATCGAGAAATTGGTACCATTGTTGGATACTGGTGACATCATCATTGAC 101 G G N S E Y R D T T R R C R D L K A K G 301 GGAGGAAATTCTGAATATAGGGACACCACAAGACGGTGCCGAGACCTCAAGGCCAAGGGA 121 I L F V G S G G V S G G E E G A R Y G P.S 361 ATTTTATTTGTGGGGAGCCGAGTCAGTGGTGGAGAGCAAGGGGCCCGGTATGGCCCATCG 141 L M P G G N K E A W P H I K T I F Q G I 421 CTCATGCCAGGAGGGAACAAAGAAGCGTGGCCCCACATCAAGACCATCTTCCAAGGCATT 161 A A K V G T G E P C C D W V G D E G A G 481 GCTGCAAAAGTGGGAACTGGAGAACCCTGCTGTGACTGGGTGGGAGATGAGGGAGCAGGA 181 H F V K M V H N G I E Y G D M Q L I C E 541 CACTTTGTGAAGATGGTGCACAATGGCATAGAGTACGGCGATATGCAGCTGATCTGTGAA 201 A Y H L M K D V L G M E H N E M A K A F 601 GCTTACCATCTGATGAAAGACGTTCTGGGCATGGACCATAACGAGATGGCAAAGGCATTT 221 E E W N K T E L D S F L I E I T A N I L 661 GAGGAGTGGAATAAGACAGAGCTAGACTCATTCCTGATTGAAATCACAGCCAATATTCTC 241 K F Q D T D G K Y L L P K I R D S A G Q 721 AAGTTTCAAGATACCGATGGCAAGTACCTGCTGCCAAAGATCAGGGACAGTGCGGGGCAG 261 K G T G K W T A I S A L E Y G V P V T L 781 AAGGGCACTGGGAAGTGGACTGCCATCTCGGCCCTGGAGTACGGTGTTCCCGTCACCCTC	SEQ ID NO:45

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		281 I G E A V F A R C L S S L K D E R I Q A 841 ATCGGAGAAGCGGTCTTTGCTCGATGCTTATCGTCTCTGAAGGATGAGGATTCAAGCT	
		301 S G K L K G P R K I Q F E G D K K S F L 901 AGCGGGAAGCTGAAGGGTCCTCGAAAGATCCAGTTTGAAGGTGATAAGAAATCTTTCCTG	
		321 E D I R K A L Y A S K I I S Y A Q G F M 961 GAGGACATTCGAAAGGCCCTCTATGCTTCCAAGATCATCTCTTATGCTCAGGGCTTTATG	
		341 L L R Q A A T E F G W T L N Y G G I A L 1021 CTGCTAAGACAGGCAGCCACTGAATTTGGCTGGACCCTCAACTACGGCGGCATTGCCCTG	
		361 M W R G G C I I R S V F L G K I K D A F 1081 ATGTGGAGGGGCGGCTGCATCATCAGAAGTGTTCCTAGGAAAATAAAAGATGCATTT	
		381 D R N P E L E N L L L D D F F R S A V E 1141 GATCGAAACCCAGAACTTGAGAATCTGCTGCTGGATGACTTCTTCAGGTCGGCTGTTGAA	
		401 S C Q D S W R R A V S T G V Q M G I P M 1201 AGCTGCCAGGACTCCTGGCGGCGGGCAGTCAGTACTGGTGTCCAGATGGGCATTCCCATG	
		421 P C F T T A L S F Y D G Y R H E M L P A 1261 CCCTGCTTCACCACTGCTCTTCCTTCTATGATGGATACAGACATGAAATGCTACCAGCC	
		441 N L I Q A Q R D Y F G A H T Y E L L A K 1321 AACCTAATCCAGGCTCAGCGGGATTACTTTGGGGCTCACACGTATGAACTCTTAGCCAAA	
		461 P G Q F I H T N W T G H G G S V S S S S 1381 CCCGGACAGTTTATCCACACTAATTGGACAGGCCATGGCGGCAGTGTGTCATCCTCTTCG	
		481 Y N A - 1441 TACAATGCCTAA	
WBC022B06	Immunoglobulin superfamily, member 6 variant	1 ATACACAGAAATGGGACTGCGAGCAGAAGCAACATCGCTCGCCATCTGCAAACCAATCT 61 CATTCTATTTTGTGTCGGTGCTGTGGGCGCCTGTACTCTCTCTGTCACACAACCGTGGTA 121 CCTAGAAGTGGACTACACTCATGAGGCCGTCACCATAAAGTGTACCTTCTCGCAACCGG 181 ATGCCCTTCTGAGCAACCAACATGCCTGTGGTTTCGCTACGGTGCTCACCAGCCTGAGAA 241 CCTGTGCTTGGACGGGTGCAAAAGTGAGGCAGACAAGTTCACAGTGAGGAGGCCCTCAA 301 AGAAAACCAAGTTTCCCTCACTGTAAACAGAGTGACTTCAAATGACAGTGCAATTTACAT 361 CTGTGGAATAGCATTCCCCAGTGTGCCGGAAGCGAGCTAAACAGACAGGAGGAGGGAC 421 CACACTGGTGGTAAGAGAAATTAAGCTGCTCACGCAAGGAACTGCGGAGCTTCCTGACAGC 481 TCTTGTATCACTGCTCTCTGTCTATGTGACCGGTGTGTGCGTGGCCTTCATACTCCTCTC 541 CAAATCAAAATCCAACCCTCTAAGAAACAAAGAAATAAAAGAAGACTCACAAAAGAAGAA 601 GAGTGCTCGGCGTATTTTTCAGGAAATTGCTCAAGAACTATACCATAGAGACATGTGGA 661 AACAAATCAGCAATCTGAGAAAGATAACACTTATGAAAACAGAAGACTACTTTCCAA	SEQ ID NO:46

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		721 CTATGAAAGCCCATAGAAACGTTTTAATTTTCAATGAAGTCACTGAAAATCCAACTCCAG 781 GAGCTATGGCAGTGTTAATGAACATATATCATCAGGTCTTAAAAAAAAATAAAGGTAAAC 841 TGAAAAGACAACTGGCTACAAAGAAGGATGCCAGAATGTAAGGAAACTATAACTAATAGT 901 CATTACCAAAATACTAAAACCCAACAAAATGCAACTGAAAAATACCTTCCAAATTGCCA 961 AGAAAAAAAATTCTATTTTAAACTTGTATCCTGAGTCTGTTTCATTCAACATGAGATGTG 1021 TGATGACTGCCATCCTGAAGATCTGAAGCCAAACCATGTGCCTCAGTCTTGAGTGGAAGA 1081 ATCACCTTTATGGTTTGTGGAAATCATGGCACAATTAAAATAAGTTGGGAGGGACAACGT 1141 GACAAAATTTGAGTTAGACATTCATTTTGAAAAGCACCTTAGTAAAGTTATTTCCTCT 1201 GATGTTGTAATGGGGCAGTGGGTAACGCACATTTGCCTGCCAGGGTATGCAAAGTAACT 1261 TACATCATGCTATCAGCAAAATGAGAATATATAGTGGCTAGAGTAGACCATAAAAGCC 1321 AAAATACAGAAAATCCAAAGCTGAAGGTTAAACAGAGGTAACTTCAGAACAAATAAGCCA 1381 CAACGGACTCTAGATGTCAGTGTTGTCGCCAAATAACAGCACCACGGGAAGATGTGGGCAAC 1441 ACATCTACTTTACAAGCACGTTTGTAATACTGATTTTTTTTCTTTTCTTTTTTTTTTT 1501 TTTGAGACAGAGTCTCGTTCTGTTGCCCAGGGTGGAGTGCAGTGGTGCAATCTCGGCTCA 1561 CTGCAACCTCCACCTCCCGGGTTCATGCCATTCTTCTGCCTCAGTTTCCCAGTAGCTGG 1621 GATTGCAGGTGCGCACCACCACGCCCGGCTAATTTTTTTTTTTTTTT	SEQ ID NO:47
		1 M G T A S R S N I A R H L Q T N L I L F 1 ATGGGGACTGCGAGCAGAAGCAACATCGCTCGCCATCTGCAAACCAATCTCATTCTATTT	
		21 C V G G A V G A C T L S V T Q P W Y L E V 61 TGTGTCGGTGGCTGTGGGCGCCTGTACTCTCTGTCACACAACCGTGGTACCTAGAAGTG	
		41 D Y T H E A V T I K C T F S A T G C P S 121 GACTACACTCATGAGGCCGTCACCATAAAGTGTACCTTCTCCGCAACCGGATGCCCTTCT	
		61 E Q P T C L W F R Y G A H Q P E N L C L 181 GAGCAACCAACATGCCTGTGGTTTCGCTACGGTGCTCACCAGCCTGAGAACCTGTGCTTG	
		81 D G C K S E A D K F T V R E A L K E N Q 241 GACGGGTGCAAAAGTGAGGCAGACAAGTTCACAGTGAGGGAGGCCCTCAAAGAAAACCAA	
		101 V S L T V N R V T S N D S A I Y I C G I 301 GTTTCCCTCACTGTAAACAGAGTGACTTCAAATGACAGTGCAATTTACATCTGTGGAATA	
		121 A F P S V P E A R A K Q T G G G T T L V 361 GCATTCCCCAGTGTGCCGGAAGCGAGAGCTAAACAGACAGGAGGAGGGACCACACTGGTG	
		141 V R E I K L L S K E L R S F L T A L V S 421 GTAAGAGAAATTAAGCTGCTCAGCAAGGAACTGCGGAGCTTCCTGACAGCTCTTGTATCA	
		161 L L S V Y V T G V C V A F I L L S K S K 481 CTGCTCTCTGTCTATGTGACCGGTGTGCGTGGCCTTCATACTCCTCTCCAAATCAAAA	
		181 S N P L R N K E I K E D S Q K K K S A R 541 TCCAACCCTCTAAGAACAAAGAAATAAAGAAGACTCACAAAAGAAGAAGAGTGCTCGG	
		201 R I F Q E I A Q E L Y H K R H V E T N Q	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		601 CGTATTTTTCAGGAAATTGCTCAAGAACTATACCATAAGAGACATGTGGAAACAAATCAG 221 Q S E K D N N N T Y Y E N N R R V L S N Y E R 661 CAATCTGAGAAAGATAACAACACTTATGAAAACAGAAGAGTACTTTCCAACTATGAAAGG 241 P - 721 CCATAG	
WBC022B05	Toll-like receptor 8 (TLR8)	1 CTCCTGCATAGAGGGTACCATTCTGCGCTGCTCAAGTTACGGAATGAAAAATTAGAACA 61 ACAGAAACGTGGTTCTCTTGACACTTCAGTGTTAGGGAACATCAGCAAGACCCATCCCAG 121 GAGACCTTGAAGGAAGCCTTTGAAAGGCAGAATGAAGGAGTCATCTTTGCAAAATAGCTC 181 CTGCAGCCTGGGAAAGGAGACTAAAAAGGAAAACATGATCCTTCAGCCTTTGCTTCTGAC 241 CTGCCTTTCCTGATAATCTCTGATTCCTGTGAGTTCTTCACTGAAACAAATTATTCTAG 301 AAGCTATCCTTGTGATGAGAAAAGGGAAAATGTTTCTGTCATTGCAGAGTGCAACGATCG 361 CCGACTGGAAGAAGTTCCCCAAACAGTGGGCAAGTACGTGACAGAACTAGACCTATCTGA 421 TAATTTCATCATCCACATAACAAATGAATCATTTCAAGGGCTGCAAAATCTTACTATAAAAT 481 AAATCTAAACCACAACCCCAATGTACAGCACCAGAACGGAAATCCCGGTATACAACAAA 541 TGGCATGAATATTACAGATGGGGCATTCCTCAACCTACAAAACCTAAGAGAGGTTACTGCT 601 TGAAGACAACCAGTTAGACAAAAATACCCACTGGTTTGCCAGGGTCTTTAAGAGAACTTAG 661 TCTAATTCAAAACAATATATACAACATAACTAAAGAGGGCATTTCAAGACTTATGAATTT 721 GGAATATCTCTATTTGGGCTGGAACTGCTATTTTGGCAACATTTGCAATAAAACTTTTGA 781 CATAGAAGACGGAACATTTGAAAGGCTTACAAACTTGAAGGTGCTATCATTATCTTTTAA 841 CAACTTTCTCATGTGCCACCCAAACTGCCAAACTCCTTGAGAGAGCTTTATCTTAGCAA 901 CACCAAGATCAAATACATCACTCAAGAAGACTTCAAGGAATTGAGAAATTTGACAGTACT 961 GGATCTAAGCGGGAACTGTCCAAGGTGCTTCAATGCACCATTTCCATGCGTGCCTTGTGA 1021 TGGTGGTGCTTCAATTAATATAGATCGTTTTGCTTTTCAAAACTTGACCCAACTTCGATA 1081 CCTAAACCTCTCTAGCACTTCCCTCAGGAAGATTAATGCTGCCTGGTTTAAAAATATGCC 1141 TCATCTGAAGGTGCTGGATCTTGAATTCAACTATTTAGTGGGAGAAATAGCCTCTGGGGC 1201 ATTTTTAACGATGCTGCCCCGCTTAGAAATACTTGACTTGTCTTTTAACTATATAAAGGG 1261 GAGTTATCCACAGCATATTAATATTTCCAGAAACTTCTCTAAACCTTTGTCTCTACGGGC 1321 ATTGCATTTAAGAGGTTATGTGTTCCAGGAACTCAGAGAAGATGATTTCCAGCCCCTGAT 1381 GCAGCTTCCAAACTTATCGACTATCAACTTGGGTATTATTTTATTAAGCAAATCGATTT 1441 CAAACTTTTCCAAAATTTCTCCAATCTGGAAATTATTTTACTTGTCAGAAAACAGAATATC 1501 ACCGTTGGTAAAAGATACCCGGCAGAGTTATGCAAATAGTTCCTCTTTTCAACGTCATAT 1561 CCGGAAACGACGCTCAACAGATTTTCAGTTTGACCCACATTCGAACTTTTATCATTTCAC 1621 CCGTCCTTTAATAAAGCCACAATGTCGCTTATGGAAAAGCCTTAGATTTAAGCCTCAA 1681 CAGTATTTTCTTCATTGGGCCAAACCAATTTGAAAATCTTCCTGACATTGCCTGTTTAAA 1741 TCTGTCTGCAAATAGCAATGCTCAAGTGTTAAGTGGAACTGAATTTTCAGCCATTCCTCA 1801 TGTCAAATATTTGGATTTGACAAACAATAGACTAGACTTGATAATGCTAGTGCTCTTAC 1861 TGAATTGTCCGACTTGGAAGTTCTAGATCTCAGCTATAATTCACACTATTTCAGAATAGC 1921 AGGCGTAACACATCATCTAGAATTTATTCAAAATTTCACAAATCTAAAAGTTTTAAACTT 1981 GAGCCACAACACATTTATACTTTAACAGATAAGTATAACCTGGAAAGCAACGTCCCTGGT 2041 AGAATTAGTTTTCAGTGGCAATCGCCTTGACATTTTGTGGAATGATGATGACAACAGGTA 2101 TATCTCCATTTTCAAAGGTCTCAAGAATCTGACACGTCTGGATTTATCCCTTAATAGGCT 2161 GAAGCACATCCCCAAATGAAGCATTCCTTAATTTGCCAGCGAGTCTCACTGAACTACATAT 2221 AAATGATAATATGTTAAAGTTTTTAACTGGACATTACTCCAGCAGTTTCCTCGCTCTCGA	SEQ ID NO:48

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2281 GTTGCTTGACTTACGTGGAAACAAACTACTCTTTTTAACTGATAGCCTATCTGACTTTAC 2341 ATCTTCCCTTCGGACACTGCTGCTGAGTCATAACAGGATTTCCCACCTACCCTCTGGCTT 2401 TCTTTCTGAAGTCAGTAGTCTGAAGCACCTCGATTTAAGTTCCAATCTGCTAAAAACAAT 2461 CAACAAATCCGCACTTGAAACTAAGACCACCACCAAATTATCTATGTTGGAACTACACGG 2521 AAACCCCTTTGCAATGCACCTGTGACATTGGAGATTTCCGAAGATGGATGGATGAACATCT 2581 GAATGTCAAAATTCCCAGACTGGTAGATGTCATTTGTGCCAGTCCTGGGGATCAAAGAGG 2641 GAAGAGTATTGTGAGTCTGGAGCTAACAACTTGTGTTTCAGATGTCACTGCAGTGATATT 2701 ATTTTTCTTCACGTTCTTTATCACCACCATGGTTATGTTGGCTGCCCTAGCTCACCATTG 2761 GTTTTACTGGGATGTTTGTTTATCTATCACATGTGTTTAGCTAAGATAAAAGGCTACAG 2821 GTCTCTTTCCACATCCCAAACTTTCTACGATGCTTACGTTTCTTATGACACCAAAGACGC 2881 CTCTGTTACGGACTGGGTGATAAATGAGCTGCGCTTCCACCTAGAAGAGAGTGAAGAAAA 2941 AAACGTGCTCCTCTGTTTAGAGGAGAGGCATTGGGACCCGGGATTAGCCATCATCGATAA 3001 CCTCATGCAGAGCATAAACCAAAGCAAGAAGACAATATTTGTTTTAACCAAAAAATATGC 3061 AAAGAACTGGAACTTTAAAACAGCATTCTACTTGGCCTTGCAGAGGCTAATGGATGAGAA 3121 TATGGATGTGATTGTATTTATTCTGCTGGAGCCAGTGTTACAGCATTCCCAGTATTTGCG 3181 GCTGCGGCAAAGGATCTGCAAGAGCTCCATCCTCCAGTGGCCTGACAACCCAAGGCAGA 3241 AGGCTTGTTTTGGCAAAGTCTGAAAAATGTGGTCTTAACTGAAAATAATTCACGGTATAA 3301 CATTTGTATGTTGATTCCATTAAGCATACTACTAACTGATGTTAAGTCATGATTTCGCGCCAT 3361 AATAAAGA	
		1 M K E S S L Q N S S C S L G K E T K K E 1 ATGAAGGAGTCATCTTTGCAAAATAGCTCCTGCAGCCTGGGAAAGGAGACTAAAAAGGAA	SEQ ID NO:49
		21 N M I L Q P L L L T C L F L I I S D S C 61 AACATGATCCTTCAGCCTTTGCTTCTGACCTGCCTTTTCCTGATAATCTCTGATTCCTGT	
		41 E F F T E T N Y S R S Y P C D E K R E N 121 GAGTTCTTCACTGAAACAAATTATTCTAGAAGCTATCCTTGTGATGAGAAAAGGGAAAAT	
		61 V S V I A E C N D R R L E E V P Q T V G 181 GTTTCTGTCATTGCAGAGTGCAACGATCGCCGACTGGAAGAAGTTCCCCAAACAGTGGGC	
		81 K Y V T E L D L S D N F I I H I T N E S 241 AAGTACCTGACAGAACTAGACCTATCTGATAATTTCATCATCCACATAACAAATGAATCA	
		101 F Q G L Q N L T K I N L N H N P N V Q H 301 TTTCAAGGGCTGCAAAATCTTACTAAAATAAATCTAAACCACACAACCCCAATGTACAGCAC	
		121 Q N G N P G I Q S N G M N I T D G A F L 361 CAGAACGGAAATCCCGGTATACAATCAATGGCATGAATATTACAGATGGGCATTCCTC	
		141 N L Q N L R E L L L E D N Q L D K I P T 421 AACCTACAAAACCTAAGAGAGTTACTGCTTGAAGACAACCAGTTAGACAAAATACCCACT	
		161 G L P G S L R E L S L I Q N N I Y N I T 481 GGTTTGCCAGGGTCTTTAAGAGAACTTAGTCTAATTCAAAACAATATATACAACATAACT	
		181 K E G I S R L M N L E Y L Y L G W N C Y	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		541 AAAGAGGGCATTTCAAGACTTATGAATTTGGAATATCTCTATTTGGGCTGGGAACTGCTAT	
		201 F G N I C N K T F D I E D G T F E R L T	
		601 TTTGGCAACATTTGCAATAAAACTTTGACATAGAAGACGGAACATTTGAAAGGCTTACA	
		221 N L K V L S L S F N N L S H V P P K L P	
		661 AACTTGAAGGTGCTATCATTATCTTTTAACAACCTTTCTCATGTGCCACCCAAACTGCCA	
		241 N S L R E L Y L S N T K I K Y I T Q E D	
		721 AACTCCTTGAGAGAGCTTTATCTTAGCAACACCAAGATCAAATACATCACTCACTCAAGAAGAC	
		261 F K E L R N L T V L D L S G N C P R C F	
		781 TTCAAGGAATTGAGAAATTTGACAGTACTGGATCTAAGCGGGAACTGTCCAAGGTGCTTC	
		281 N A P F P C V P C D G G A S I N I D R F	
		841 AATGCACCATTTCCATGCGTGCCTTGTGATGGTGGTGCTTCAATTAATATAGATCGTTTT	
		301 A F Q N L T Q L R Y L N L S S T S L R K	
		901 GCTTTCAAACTTGACCCAACTTCGATACCTAAACCTCTCTAGCACTTCCCTCAGGAAG	
		321 I N A A W F K N M P H L K V L D L E F N	
		961 ATTAATGCTGCCTGGTTTAAAATATGCCTCATCTGAAGGTGCTGGATCTTGAATTCAAC	
		341 Y L V G E I A S G A F L T M L P R L E I	
		1021 TATTTAGTGGGAGAAATAGCCTCTGGGCATTTTTAACGATGCTGCCCCGCTTAGAAATA	
		361 L D L S F N Y I K G S Y P Q H I N I S R	
		1081 CTTGACTTGTCTTTAACTATATAAAGGGAGTTATCCACACGCATATTAATATTTCCAGA	
		381 N F S K P L S L R A L H L R G Y V F Q E	
		1141 AACTTCTCTAAACCTTTGTCTCTACGGCATTGCATTTAAGAGGTTATGTGTTCCAGGAA	
		401 L R E D D F Q P L M Q L P N L S T I N L	
		1201 CTCAGAGAAGATGATTTCCAGCCCCTGATGCAGCTTCCAAACTTATCGACTATCAACTTG	
		421 G I N F I K Q I D F K L F Q N F S N L E	
		1261 GGTATTAATTTTATTAAGCAAATCGATTTCAAACTTTTCCAAAATTTCTCCAATCTGGAA	
		441 I I Y L S E N R I S P L V K D T R Q S Y	
		1321 ATTATTTACTTGTCAGAAAACAGAATATCACCGTTGGTAAAAGATACCCGGCAGAGTTAT	
		461 A N S S F Q R H I R K R R S T D F E F	
		1381 GCAAATAGTTCCTCTTTTCAACGTCATATCCGGAAACGACGCTCAACAGATTTTGAGTTT	
		481 D P H S N F Y H F T R P L I K P Q C A A	
		1441 GACCCACATTCGAACTTTATCATTTCACCCGTCCTTTAATAAAGCCACAATGTGCTGCT	
		501 Y G K A L D L S L N S I F F I G P N Q F	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1501 TATGGAAAAGCCTTAGATTTAAGCCTCAACAGTATTTTCTTCATTGGGCCAAACCAATTT	
		521 E N L P D I A C L N L S A N S N A Q V L	
		1561 GAAAATCTTCCTGACATTGCCTGTTTAAATCTGTCTGCAAATAGCAATGCTCAAGTGTTA	
		541 S G T E F S A I P H V K Y L D L T N N R	
		1621 AGTGGAACTGAATTTTCAGCCATTCCTCATGTCAAATATTTGGATTTGACAAACAATAGA	
		561 L D F D N A S A L T E L S D L E V L D L	
		1681 CTAGACTTTGATAATGCTAGTGCTCTTACTGAATTGTCCGACTTGGAAGTTCTAGATCTC	
		581 S Y N S H Y F R I A G V T H H L E F I Q	
		1741 AGCTATAATTCACACTATTTCAGAATAGCAGGCGTAACACATCATCTAGAATTTATTCAA	
		601 N F T N L K V L N L S H N N I Y T L T D	
		1801 AATTTCACAAATCTAAAAGTTTTAACTTGAGCCACAACACATTTATACTTTAACAGAT	
		621 K Y N L E S K S L V E L V F S G N R L D	
		1861 AAGTATAACCTGGAAAGCAAGTCCCTGGTAGAATTAGTTTTCAGTGGCAATCGCCTTGAC	
		641 I L W N D D D N R Y I S I F K G L K N L	
		1921 ATTTTGTGGAATGATGATGACAACAGGTATATCTCCATTTTCAAAGGTCTCAAGAATCTG	
		661 T R L D L S L N R L K H I P N E A F L N	
		1981 ACACGTCTGGATTTATCCCTTAATAGGCTGAAGCACATCCCAAATGAAGCATTCCTTAAT	
		681 L P A S L T E L H I N D N M L K F F N W	
		2041 TTGCCAGCGAGTCTCACTGAACTACATATAAATGATAATATGTTAAAGTTTTTTAACTGG	
		701 T L L Q Q F P R L E L L D L R G N K L L	
		2101 ACATTACTCCAGCAGTTTCCTCGTCTCGAGTTGCTTGACTTACGTGGAAACAAACTACTC	
		721 F L T D S L S D F T S S L R T L L L S H	
		2161 TTTTTAACTGATAGCCTATCTGACTTTACATCTTCCCTTCGGACACTGCTGCTGAGTCAT	
		741 N R I S H L P S G F L S E V S S L K H L	
		2221 AACAGGATTTCCCACCTACCCTCTGGCTTTCTTCTGAAGTCAGTAGTCTGAAGCACCTC	
		761 D L S S N L L K T I N K S A L E T K T T	
		2281 GATTTAAGTTCCAATCTGCTAAAAACAATCAACAAATCCGCACTTGAAACTAAGACCACC	
		781 T K L S M L E L H G N P F E C T C D I G	
		2341 ACCAAATTATCTATGTTGGAACTACACGGAAACCCTTTGAATGCACCTGTGACATTGGA	
		801 D F R R W M D E H L N V K I P R L V D V	
		2401 GATTTCCGAAGATGGATGGATGAACATCTGAATGTCAAAATTCCCAGACTGGTAGATGTC	
		821 I C A S P G D Q R G K S I V S L E L T T	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFTER:
		2461 ATTTGTGCCAGTCCTGGGGATCAAAGAGGGAAGAGTATTGTGAGTCTGGAGCTAACAACT	
		841 C V S D V T A V I L F F F T F F I T T M	
		2521 TGTGTTTCAGATGTCACTGCAGTGATATTATTTTTCTTCACGTTCTTTATCACCACCATG	
		861 V M L A A L A H H W F Y W D V W F I Y H	
		2581 GTTATGTTGGCTGCCCTAGCTCACCATTGGTTTTACTGGGATGTTTGGTTTATCTATCAC	
		881 M C L A K I K G Y R S L S T S Q T F Y D	
		2641 ATGTGTTTAGCTAAGATAAAAGGCTACAGGTCTCTTTCCACATCCCAAACTTTCTACGAT	
		901 A Y V S Y D T K D A S V T D W V I N E L	
		2701 GCTTACGTTTCTTATGACACCAAAGACGCCCTCTGTTACGGACTGGGTGATAAATGAGCTG	
		921 R F H L E E S E E K N V L L C L E E R D	
		2761 CGCTTCCACCTAGAAGAGAGTGAAGAAAAAAACGTGCTCCTCTGTTTAGAGGAGAGGGAT	
		941 W D P G L A I I D N L M Q S I N Q S K K	
		2821 TGGGACCCGGGATTAGCCATCATCGATAACCTCATGCAGAGCATAAACCAAGCAAGAAG	
		961 T I F V L T K K Y A K N W N F K T A F Y	
		2881 ACAATATTTGTTTTAACCAAAAAATATGCAAAGAACTGGAACTTTAAAACAGCATTCTAC	
		981 L A L Q R L M D E N M D V I V F I L L E	
		2941 TTGGCCTTGCAGAGGCTAATGGATGAGAATATGGATGTGATTGTATTTATTCTGCTGGAG	
		1001 P V L Q H S Q Y L R L R Q R I C K S S I	
		3001 CCAGTGTTACAGCATTCCCAGTATTTGCGGCTGCGGCAAAGGATCTGCAAGAGCTCCATC	
		1021 L Q W P D N P K A E G L F W Q S L K N V	
		3061 CTCCAGTGGCCTGACAACCCCAAGGCAGAAGGCTTGTTTTGGCAAAGTCTGAAAAATGTG	
		1041 V L T E N N S R Y N I C M L I P L S I L	
		3121 GTCTTAACTGAAAATAATTCACGGTATAACATTTGTATGTTGATTCCATTAAGCATACTA	
		1061 T D V K S -	
		3181 ACTGATGTTAAGTCATGA	
WBC021D01	No homology	1 GATTCACTCCTTTTTGGGTAATCTTTGGTGACTTTGCACCTGGTGACTATCAAAAAGCCT	SEQ ID NO:50
		61 GTTATTATGTTAAGATAACTTTAACCTCATGACAATGTTACTATATCAAAAAAAAATGAT	
		121 ATTTTGATTAAAAAAAATCTTGCATTTCCCCCCTTTGAATTATATATTACTGTAAAACCT	
		181 TTAGTTCTTGAAATTTGGTTAGACTCCAAATAACTTAAACTGTCTTCTTAATAACCATCA	
		241 GGTCACTTTATTTGGCTAAATGGTGAATAACTTTTACATCTTCAGCATTTCTTTAAAGGAA	
		301 AAGTTAATTCTACTTGTGTGTGCATATGTGTATATGTATTGTTGTTGTATGTA	
		361 TATATGTATAGATGGATAAAATATAGTCTTTAGACAACTTTCTTTTAGAGATCTTTACTG	
		421 CAGTATATTGTTCTCAACTCAGGTGCCAAAGGAGCTCTCTTCTTACGACATGTAAATATA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		481 CATTTAAATTCTTTAAGAAGTAGCTTGTTGGTTCAATAAACTAGCCATTGCAGAAGCTAA 541 ATTGGGCTCTTGTATATCTAAAACTGATGAGTTTTTCCTAAAATGTTGATTGTCCATGTA 601 TTTGCCTTCAGCATTAAGCTAATGCAGGTACAGCTTAATAAGACATTGCAAAAAGAGGAA 661 ATGATTACTTTTTACAAAAGACCATACTATATTTTTAAATTTCTAG	SEQ ID NO:51
		1 GCAGTGAAATTGTAATGGCACTTGAAAGAAGTAAGCAGCACCCGTTCTCCGGTCTGTAGC 61 GATTTGAGGCGCCTGTGCCAGATTATAATCAACACATCGCTTCCTTTATCAAGAAAGTCT 121 GGTTATAAAAAAAAAGTCAGCTGATGAGTGACACACTTAGCTTTCTTTCTGGCACAAGCTC 181 ACTCTTTCATGTTGGATGGATCACAAATCGTTCATAGACCATATTTTGAATAGCCTTGTT 241 CTAAGCAACATTTATAAATGTTGATATTTTTATAACTGTTTACATTTCTTCTGTTTATTTT 301 TGGATATTCAGTGTGATATCTGACTTAGAAACTTGTCCTTATTCATTGTTGTATAGACAA 361 TTGTACTTTAATTTTAAATTGTGTTAAAATTAAGTTATCTGACTTCCAATTTGGGGAATT 421 ATTATCAATTTATATAATTTTATAAAAGTTTAAAGAACTTTAAACTGTAATTGTAAATTTCA 481 CACAAGTTACAACTGCCCTCCATCTTAACTTTTATTAAATAATCATGTTGCTTAAGTCAT 541 ATTGACCGACGTTATTATGAATACTCCAGGAAAAAAAAAAAACGCTTATTACATCAACTTA 601 ATGATCCTTTGGTTAAAAATTAAAAAGCACTTTTTTTTATGTTAAAAAAAAAAAAAAAA 661 AAAAAAAA	SEQ ID NO:52
WBC021B08	Hypothetical protein FLJ20481	1 CAGGCGTCTAAGTAACTTCAGCGCCTGCGCAGAGGCTCCCCAGCGTCGCCCTAGGCTGGG 61 ACTCTAGTAGGTCTTCCGCTCAGTTTTGGCTGCCACGCCCCGCGTAGATCGCTTCGGCCGG 121 GTTCTACGCCCGGCTCAACTATGAGCCGGTGCGCCCAGGCGGCGGAAGTGGCGGCCACAG 181 TGCCAGGTGCCGGCGTCGGGAACGTGGGCTGCGCCGCCCATGGTGCCCCGTCAGGCGT 241 CCTTCTTCCCGCCGCCGGTGCCCGAACCCCTTCGTGCAGCAGACGCAGATCGGCTCCGCGA 301 GGCGGGTCCAGATTGTCCTTCTTGGGATTATCTTCGCTTCCAATTCGTGTCTTATTGGTTG 361 CATTAATTTTATTACTGGCCATGGCCATTTGCTGCGATTTCAACAGCATGCTGTCCTGAAA 421 AGCTGACCCACCCAGTAACTGGTTGGAGAGGAGAAAATTACCCAACCGGTTTTGCAAGTTCC 481 TGGGTCGTGCCTTGTTCTTTCAATGGGATTTATAGTTACTGTGCAAAGGAAAGCGTCGCAA 541 ATGCTGTGGAAGCCCCCAATTTTTGTGGTTGCCCCTCACTCAACGTTCTTTGATGGGATTG 601 CCTGTGTCATAGCTGGCTTACCGTCTATGGTGTCTCGAAATGAGAATGCACAGGCCCCTC 661 TGGTTGGCAGACTGTTACGAGCTCTTCAACCAGTGCTGGTGTCCCGTGTTGATCCAGATT 721 CTCGAAAGAACACAATAAATGAAATAATAAGGCGTGCCACTTCAGGAGGGGAATGGCCCC 781 AGATGCTAGTTTTCCCAGAAGGTACTTGTACTAATCGTTCCTGTTTGATTACTTTTAAAC 841 CAGGGGCCTTCATTCCAGGAGTTCCCGTTCAGCCAATCCTCCTCCAGATACCCAAACAAGC 901 TGGATACTGTGACTTGGACGTGGCAAGGATATACATTCATTCAGCTTTGTATGCTTACTT 961 TCTGTCAGCCCTTCACAAGGGTGGAAGTTCAGTTTATGCCAGTTCAAGTACCAAATGAAG 1021 AAGAAAGAAATGATCCGGTCCTTTTTGCCGATAGAGTCCGGAATTTAATGGCTCAAGCTC 1081 TGGGGATTCCAGTAACAGACCACACCTATGAAGACTGCAGATTGATGATTTCAGCAGGAC 1141 AGCTAACATTGCCTATGGAAGCTGGCTGGTGGAATTTACTAAAATTAGCCGAAAATTGA 1201 AATTAGATTGGGATGCTGTTCGTAAGCATTTGGATGATGAATATGCATCTATTGCGAGTTCCT 1261 CAAAAGGAGGAAGAATTGGAATTGAAGAATTCGCCAAGTATTTAAAGTTGCCTGTTTCAG 1321 ATGTCTTGAGACAACTTTTTGCACTCTTTGACAGGAACCATGATGGCAGCATTGACTTCC 1381 GAGAGTATGTGATTGGCCTGGCTGTCTTGTGCAACCCTTCCAACACAGAGGAGATCATCC 1441 AGGTGGCATTTAAGCTGTTTGACGTTGATGAGGATGGCTACATAACGGAGGAAGAGTTCT 1501 CCACCATTCTACAGGCTTCCCTTGGAGTGCCTGACCTTGATGTTTCTGGTCTCTTCAAGG 1561 AAATAGCTCAGGGCGATTCTGTGTCGTACGAGGAATTTAAAAGTTTGCCCTGAAGCATC 1621 CAGAATATGCTAAGATATTTACAACATACTTAGACCTCCAGACGAGCCATGTGTTTCAC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1681 TGCCAAAAGAAGCTCAGGCAACTCCCTCATTCACAAGTAATAAAGTCAGTCCTGAAAATC 1741 GTGAAGAGAGCGCCTCAGACAAGAAGGATGACTGAAAGCAGTATTTCCAATAAGGAAAAC 1801 ACAGTAGCTTTTGCTTGAAATTGTAAGGCACTTATTGATAAATACTTTTAATGTGTTGGT 1861 AATGATGTTTAAAATTGAAAGATTTTTAAAATAAAAATGATAGATTTTCTTACTAAAAAA 1921 AAAAAAAAAAAAAAAA 1 M S R C A Q A A A E V A A T V P G A G V G 1 ATGAGCCGGTGCGCCCAGGCGGCGGAAGTGGCGGCCACAGTGCCAGGTGCCGGCGTCGGG 21 N V G L R P P M V P R Q A S F F P P P V 61 AACGTGGGGCTGCGGCCGCCATGGTGCCCCGTCAGGCGTCCTTCTTCCCGCCGCCGGTG 41 P N P F V Q Q T Q I G S A R R V Q I V L 121 CCGAACCCCTTCGTGCAGCAGACGCAGATCGGCTCCGCGAGGCGGGTCCAGATTGTCCTT 61 L G I I L L P I R V L L V A L I L L L A 181 CTTGGGATTATCTTGCTTCCAATTCGTGTCTTATTGGTTGCATTAATTTTATTACTGGCA 81 W P F A A I S T A C C P E K L T H P V T 241 TGGCCATTTGCTGCGATTTCAACAGCATGCTGTCCTGAAAAGCTGACCCACCCAGTAACT 101 G W R R K I T Q P V L K F L G R A L F F 301 GGTTGGAGGAGGAAAATTACCCAACCGGTTTTGAAGTTCCTGGGTCGTGCCTTGTTCTTT 121 S M G F I V T V K G K V A N A V E A P I 361 TCAATGGGATTTATAGTTACTGTGAAAGGAAAGGTCGCAAATGCTGTGGAAGCCCCAATT 141 F V V A P H S T F F D G I A C V I A G L 421 TTTGTGGTTGCCCCTCACTCAACGTTCTTGATGGGATTGCCTGTGTCATAGCTGGCTTA 161 P S M V S R N E N A Q A P L V G R L L R 481 CCGTCTATGGTGTCTCGAAATGAGAATGCACAGGCCCCTCTGGTTGGCAGACTGTTACGA 181 A L Q P V L V S R V D P D S R K N T I N 541 GCTCTTCAACCAGTGCTGGTGTCCCGTGTTGATCCAGATTCTCGAAAGAACACAATAAAT 201 E I I R R A T S G G E W P Q M L V F P E 601 GAAATAATAAGGCGTGCCACTTCAGGAGGGGAATGGCCCCAGATGCTAGTTTTCCCAGAA 221 G T C T N R S C L I T F K P G A F I P G 661 GGTACTTGTACTAATCGTTCCTGTTTGATTACTTTTAAACCAGGGGCCTTCATTCCAGGA 241 V P V Q P I L L R Y P N K L D T V T W T 721 GTTCCCGTTCAGCCAATCCTCCTCAGATACCCAAACAAGCTGGATACTGTGACTTGGACG 261 W Q G Y T F I Q L C M L T F C Q P F T R 781 TGGCAAGGATATACATTCATTCAGCTTTGTATGCTTACTTTCTGTCAGCCCTTCACAAGG	SEQ ID NO:53

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		281 V E V E F M P V Q V P N E E E R N D P V 841 GTGGAAGTTGAGTTTATGCCAGTTCAAGTACCAAATGAAGAAAGAAATGATCCGGTC	
		301 L F A D R V R N L M A Q A L G I P V T D 901 CTTTTTGCCGATAGAGTCCGGAATTTAATGGCTCAAGCTCTGGGGATTCCAGTAACAGAC	
		321 H T Y E D C R L M I S A G Q L T L P M E 961 CACACCTATGAAGACTGCAGATTGATGATTTCAGCAGGACAGCTAACATTGCCTATGGAA	
		341 A G L V E F T K I S R K L K L D W D G V 1021 GCTGGGCTGGTGGAATTTACTAAAATTAGCCGAAAATTGAAATTAGATTGGGATGGTGTT	
		361 R K H L D E Y A S I A S S S K G G R I G 1081 CGTAAGCATTTGGATGAATATGCATCTATTGCGAGTTCCTCAAAAGGAGGAAGAATTGGA	
		381 I E E F A K Y L K L P V S D V L R Q L F 1141 ATTGAAGAATTCGCCAAGTATTTAAAGTTGCCTGTTTCAGATGTCTTGAGACAACTTTT	
		401 A L F D R N H D G S I D F R E Y V I G L 1201 GCACTCTTTGACAGGAACCATGATGGCAGCATTGACTTCCGAGAGTATGTGATTGGCCTG	
		421 A V L C N P S N T E E I I Q V A F K L F 1261 GCTGTCTTGTGCAACCCTTCCAACACAGAGGAGATCATCCAGGTGGCATTTAAGCTGTTT	
		441 D V D E D G Y I T E E E F S T I L Q A S 1321 GACGTTGATGAGGATGGCTACATAACGGAGGAAGAGTTCTCCACCATTCTACAGGCTTCC	
		461 L G V P D L D V S G L F K E I A Q G D S 1381 CTTGGAGTGCCTGACCTTGATGTTCTCGTCTCTTCAAGGAAATAGCTCAGGGCGATTCT	
		481 V S Y E E F K S F A L K H P E Y A K I F 1441 GTGTCGTACGAGGAATTTAAAAGTTTGCCCTGAAGCATCCAGAATATGCTAAGATATTT	
		501 T T Y L D L Q T S H V F S L P K E A Q A 1501 ACAACATACTTAGACCTCCAGACGAGCCATGTGTTTTCACTGCCAAAAGAAGCTCAGGCA	
		521 T P S F T S N K V S P E N R E E S A S D 1561 ACTCCCTCATTCACAAGTAATAAAGTCAGTCCTGAAAATCGTGAAGAGAGCGCCTCAGAC	
		541 K K D D - 1621 AAGAAGGATGACTGA	
WBC020B04	No homology	1 GATTGTGTGGACCCTGGGGGAGCAGCTAGAGGAGATAGGGCCCTGGCCATGTCATCTACT 61 GAGATAATGAAGAAGATTCGTTTCCTGTTGAAGCTGTAACAACCTACCCCAGACACTTCA 121 GTTTAAAACAACACCAATTCATTTTCTTTTCGTTCTAGAGAGCAGGAGTCTAAAAAGTGT 181 CTGCAGCCCTGCGTTCCTCTTTTAGGCTGTGGTCTGTGTTCCTGCCTTTCCAGTTTCTG	SEQ ID NO:54

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		241 GGCTCCGCCTGCATTCCTTGCCTTCTGGATCCCTCCTCCATCTCCAAACCCACCAGTGTA 301 GCATCTTCTCCTCCTCTCTGACCTCTGCTTCCTTCCCGCCTTCTTCTCTCTCTTGTCCCCA 361 CCCTCCTGCTTCCCCTCTTATAAGGACCCTTGTGGTGACATTCGGCCCAAGAAGATAATCC 421 AGGATAATCTCTCAGTTTCCAGATTCTCATCTTCCTCGCCTCACAATGTCCCTTTGCTGT 481 GGCAGGTCCCACTCACAGTTCTGGGATTTAGACGAGCACACAACTTGAGGGGGACCATTCAG 541 CCGACCTCCCGGAGCTCAGTATATCTGACCATAGCGCAGGGCTGTGCTTGCACTTGTGCA 601 CTAACTCCTGGGGGAGACGTGGGGATTGAATATTTAATATTCTTTAGAATTTGAGACAGG 661 ACATGATCTAAATAGAGAGAGAGATCCTTAACGAATCCTGGTTCTGTATGTCTGAATG 721 TGTAAGTTCCGGAGTTATTGCACTTGAGGGGAAAAAAATTGGTCTAGGAATAAAAATGCT 781 GATTTTTTCAATAACGTCCTTTACTT 1 TTGGGGTTTATTTTTGTTTTTTCTGAAAAGGAACACCTTTAAGAGCATGGCACTAAACA 61 ACAGACTCACAGAATGGTCAGATCAGACTCCTGTTACAGCTGAGTTGATGAAATCATTCT 121 GGAACTCTTAGCTCCAACCTACTGAAGTAAATCACAAATATCCTCAGAGTTTAACAAGAA 181 GGATACTCCGTTCTGTAGACACAGGTAGAGTCTAAGGTCCACCACTTGTTCTTTGTTCTC 241 CTCTCTGCCCCGTGATGACACTCTCTAAGAGCTCTCTAACACTGGCTGCTGTCACCTCAC 301 CAAATTTCCCTTCTTTCTGGCTAATTCCTACACTTTTTCTCAGTGTTAGCACATGCATAAC 361 TTTTTCTTGGATGTTTTATCTGAACGCCTGCTCAGACTCTTCCTGCCGTCACTGTCATGT 421 TCTAAATGACAGCTTTTTCTAACGGACAAATAGTAAATATATTGGGCTTTGTCAGTCTTC 481 TGATCTTCTTCACGACCACTCAATTCTGCTGTTGTCGCACAAGCTACTGTAGGTGACAC 541 AGAGCCACACGAACCTGGCTGGGTTCCATAAAATTTGTTTACAACACTAAAAAAAAAA	SEQ ID NO:55
WBC019B05	Homo sapiens mRNA; cDNA DKFZp686M2414	1 agctacaaca tattttccca ctttaaataa tatttaacat atgacaaacc ccagacaagg 61 cttttaatat gtataaagaa ctgcagtgtt aggtggttta tttgcaaact gttttcagtg 121 ttgtccattt ttatggcacc tttaacaata ttcttgtttc caaagtacaa aaaaaatagg 181 ttaaataatc tagccataac tgaatgtcaa gcaataaaac aaatgacttt tgtgcataga 241 cttaaaaaat acaaatttta gacatctgca tgtaaatgca atctcttgtt tactgctttc 301 ttcaacttga gcaatcgatt cctttatttac tattaactta agaactttgta acggcctgta 361 aacatttttct ctcttactct tctttcaaat ttacctgtcc ctgcttttga gtcataatat 421 ttaatgttgt tctgcacatc tctatacagt taacttttg gctttcattc tgtatagata 481 agaaaatgtt atattataaa cagcctactc agtgcaaata tttatctgtt tatcaaatcc 541 acaatatgct gtataatacc ggtttactta tataatctat tttagacata gctgtttaga 601 actagagtgt gctatttttg tgttttctig atgtgtggtg ctagacaagt tacttttgtg 661 aacaacaaaa attatccctt ttattcctag acaataccac ctttgggtct tgttaatttc 721 actgagtata actatatatt tgtatatata tacatatata tatatatcta cctatgccca 781 actggcagct gtatcagagt gctggatttg ggacatgctt ttctctttaa atacatatata 841 tcattatata aattattcta gagtgtattt aattaggata aaattacttc cttagtatgg 901 atatttgaca tctataggggt gaattgtttt ataaaatatgg ctatatggaa acttattagc 961 atttacttta tgtttgctac ttggctttac agcatatctc ctaagctgaa aaataatttg 1021 ccaggccttc aagatcctaa agaaacttgt ttaatggagt aatatacttt ttttcttat 1081 taaggaattg tattactggc acctaacaca gttgtattct tagctcctat tatagataat 1141 gggcatttac ataaaatatc ctagatggct tgatggcaga ataaaccttt cccctcctac 1201 ctgagtcatg agaaggatgg agacgtcctc tgccataaca tgggccataa agcaaattcg 1261 acatgggatg ttctgtttca gtatgacctc aaccagttcc atgaactgag tgaaggacct 1321 tcattttcaa agttatttaa taagtagctt aattaagcct ttctacccat tctcccaaga 1381 tctattggca ttattgaaaa gcaaagttta tcaaatatct aactaaggat gtagttaacc	SEQ ID NO:56

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1441 ttattaaata ttgattagaa ttgttctgta atattactga atttgtaaga tctttagcaa 1501 agatttttga gcaatttata aatgtagagc aaatgtttct gtttactgca ctttttgtaa 1561 ctgaaggtga taaattctca agccatgatt attggcttcc atgcactgca gtatttatcc 1621 acaattctag acatttccca ttttttgtga agagttgctg ttaccttaat tataaatgca 1681 attgtgtggt taatgagagc taatgccagt agttaacctt ttaaagtgga ttggctacag 1741 ttgagggaga aatctctttt aatataaatc acatcattcc ttaactgcct ctcttggaaa 1801 gagattgaaa cctttttta aagcacgatt tagcatccta agcttcctga gggtagagat 1861 tgtatctttt tgcgtctgca caatggctag cacatgtcag catttgacaa ttgttaaatg 1921 ataacaagtg tgccccaatt aagacgtttt tcctgggttg tttgttaaa tttacaaagt 1981 aagccaagcc ttacggttaa cattctcctc tacaaccaag tattaaagcc acatttaaaa 2041 agaccacatg aaatgctgat tctaattgtg tgtaggtctt gaggattaag cacacaaatt 2101 tcacaaactt ctgtttgagt aaacaaactc agccttctgt aaatatacat gcaagtttgg 2161 aaacagtaat actgtaccta taaatatatg ctgtctgttt tgtgtacagt atgtaaaaac 2221 tccttttctg ccacactaaa aatgcaagcc atttatggga atcctaaaac tagtattgaa 2281 ctaaaacttt gctaatgatc tttattagag gatcgtccaa cttttcactt accttgggtt 2341 ttcttttcaa ttcactctta cactagtctg cttatttcca gctgtttatt ttattgagtc 2401 ctgaatttaa aaaaaaaata ttttgattca ttttgtaaat acaagctgta caaaaaagag 2461 agatttaatg ttgtctttta aatactccaa tttcattct aatatgaatg ttgttatatt 2521 gtacttagaa actgtacctt taatattaca ttacctttat taaaagtgca ttgaacacat 2581 caattttaga tgtgctttat gtactgttat cctataataa aacttcagct tctaatggaa 2641 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaggaaaaaa 2701 aaaaaaaaaa aa	
WBC018D05	Predicted: Mitogen-activated protein kinase kinase kinase 1 (MAP3K1)	1 ATGGGCAGCCAGGCCCTGCAGGAGTGGGGACAGAGGAACCCGGCCGGTGGCCCGACCCT 61 GCAGGGAAGAAGGACGTGCGGCGACAAGCATCGGATTCGGGGAGGGCCGGGACCTGGCCG 121 AGGACAGCCAAGGAAAAACTAAAGATCGACGGGCACACCCGCCTCCCTTCCTCGCCCCAA 181 CGGTTTCTCAGAGGCTGTGGGGACTTGCACCACAGAAACCCAAGTTGGAACTAATTCTTTCT 241 TTCGGAAGGTGCAACTCCCCTCCCGCGAGCTCCGCGGTGCCGGGCCGAGATTGCCGAGAG 301 GAAGCGGCGCAGCGCTCGCCGCCCAAGGCTCCTCCTGTCGCCGGTGCGGCCGGACTACCTG 361 GCGGCGGCGGCGGGGCCGAGCGAATGTAGCCCGCGAGAGAAAATGGCGGCCGGCGGGGG 421 AATCGCGCCTCGTCGTCGGGATTCCCGGGCGCCAGGGCTACGAGCCCTGAGGCAGGCGGC 481 GGCGGAGAGCCCCTCAAGGCGAGCACGCGCCCCGCGCTGCCCGGGACTGCTGCGGGAG 541 GCGGGCAGCGGGGGCCGAGCGGGCGGACTGGCGCGGCGCAGCTGCGCAAAGTGCGG 601 AGTGTGGAGCTGGACCAGCTGCCTGAGCAGCCGCTCTTCCTTGCCGCCTCACCGCCGGCC 661 TCCTCGACTTCCCCGTCGCCGGAGCCCGCGGAGCCAGCGGGAGTGGGACCCGGCTTCCAG 721 CCTGTGGCGGTGCCGCCGCCCCACGAGCCGCGAGCCGCGGCGCCCACCTTACCGAG 781 TCGGTGGCGGCGCCGGACAGCGGCGCCTCGAGTCCCGCAGCGGCCGAGCCCGGGGAGAAG 841 CGGGCGCCCGCCGCCGAGCCGTCTCCTGCAGCGGCCCCCGCCGGTCGTGAGATGGAGAAT 901 AAAGAAACTCTCAAAGGGTTGCACAAGATGGATGATCGTCCTCCAGAGGAACGAATGATCAGG 961 GAGAAACTGAAGGCAACCTGTATGCCAGCCTGGAAGCACGAATGGTTGGAAAGGAGAAAT 1021 AGGCGAGGGCCTGTGGTGGTAAAACCAATCCCAGTTAAAGGAGATGGATCTGAAATGAAT 1081 CACTTAGCAGCTGAGTCTCCAGGAGAGGTCCAGGCAAGTGCCGCTTCACCAGCTTCCAAA 1141 GGCCGACGCAGTCCTTCTCCTGGCAACTCCCCATCAGGTCGCACAGTGAAATCAGAATCT 1201 CCAGGAGTAAGGAGAAAAAGAGTTTCCCCAGTGCCTTTCAGAGTGGCAGAATCACACCA 1261 CCCCGAAGAGCCCCTTCACCAGATGGCTTCTCACCATATAGCCCTGAGGAAACAAACCGC 1321 CGTGTTAACAAAGTGATGCGGGCCAGACTGTACTTACTGCAGCAGATAGGGCCTAACTCT	SEQ ID NO:57

Gene Name	GenBank HomoLogy	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1381 TTCCTGATTGGAGGAGACAGCCCAGACAATAAATACCGGGTGTTTATTGGGCCTCAGAAC	
		1441 TGCAGCTGTGCACGTGGAACATTCTGTATTCATCTGCTATTTGTGATGCTCCGGGTGTTT	
		1501 CAACTAGAACCTTCAGACCCAATGTTATGGAGAAAAACTTTAAGAATTTGAGGTTCAG	
		1561 AGTTTGTTCCAGAAATATCACAGTAGGCGTAGCTCAAGGATCAAAGCTCCATCTCGTAAC	
		1621 ACCATCCAGAAGTTTGTTTCACGCATGTCAAATTCTCATACATTGTCATCATCTAGTACT	
		1681 TCTACGTCTAGTTCAGAAAACAGCATAAAGGATGAAGAGGAGGAACAGATGTGTCCTATTTGC	
		1741 TTGTTGGGCATGCTTGATGAAGAAAGTCTTACAGTGTGTGAAGACGGCTGCAGGAACAAG	
		1801 CTGCACCACCACTGCATGTCAATTTGGGCAGAAGAGTGTGTAGAAGAAATAGAGAACCTTTA	
		1861 ATATGTCCCCTTTGTAGATCTAAGTGAGATCTCATGATTTCTACAGCCACGAGTTGTCA	
		1921 AGTCCTGTGGATTCCCCTTCTTCCCTCAGAGCTGCACAGCAGCAAACCGTACAGCAGCAG	
		1981 CCTTTGGCTGGATCACGAAGGAATCAAGAGAGCAATTTTAACCTTACTCATTATGGAACT	
		2041 CAGCAAATCCCTCCTGCTTACAAAGATTTAGCTGAGCCATGGATTCAGGTGTTTGGAATG	
		2101 GAACTCGTTGGCTGCTTATTTTCTAGAAACTGGAATGTGAGAGAGATGGCCCTCAGGCGT	
		2161 CTTTCCCATGATGTCAGTGGGGCCCTGCTGTTGGCAAATGGGAGAGCACTCGGAAATTCT	
		2221 GGGGGCAGCAGTGGAAGCAGCCCGAGTGGGGGAGCCACCAGTGGGTCTTCCCAGACCAGT	
		2281 ATCTCAGGAGATGTGGTGGAGGCATGCTGCAGCGTTCTGTCAATGGTCTGTGCTGACCCT	
		2341 GTCTACAAAGTGTACGTTGCTGCTTTAAAAACATTGAGAGCCATGCTGGTATATACTCCT	
		2401 TGCCACAGTTTAGCGGAAGAATCAAACTTCAGAGACTTCTCCAGCCAGTTGTAGACACC	
		2461 ATCCTAGTCAAATGTGCAGATGCCAATAGCCGCACAAGTCAGCTGTCCATATCAACACTG	
		2521 TTGGAACTGTGCAAAGGCCAAGCAGGAGAGTTGGCAGTTGGCAGAGAAATACTAAAAGCT	
		2581 GGATCCATTGGTATTGGTGGTGTTGATTATGTCTTAAATTGTATTCTTGGAAACCAAACT	
		2641 GAATCAAACAATTGGCAAGAACTCTTGGCCGCCTTTGTCTATAGATAGACTGTTGTTG	
		2701 GAATTTCCTGCTGAATTTTATCCTCATATTGTCAGTACTGATGTTTCACAAGCTGAGCCT	
		2761 GTTGAAATCAGGTATAAGAAGCTGCTGTCCCTCTTAACCTTTGCTTTGCAGTCGCATTGAT	
		2821 AATTCCCACTCAATGGTTGGCAAACTTTCCAGAAGGATCTACTTCGAGTTCTGCAAGAATG	
		2881 GTTACTACAGTACCCCATGTGTTTTCAAAACTGTTAGAAATGCTGAGTGTTTCCAGTTCC	
		2941 ACTCACTTCACCAGGATGCGTCGCCGTTTGATGGCTATTGCAGATGAGGTGGAAATTGCC	
		3001 GAAGCCATCCAGTTGGGCGTAGAAGACACTTTGGATGGTCAACAGGACAGCTTCTTGCAG	
		3061 GCATCTGTTCCCAACAACTATCTGGAAACCACAGAGAACAGTTCCCCTGAGTGCACAGTC	
		3121 CATTTAGAGAAAACTGGAAAAGGATTATGTGCTACAAATTGAGTGCCAGTTCAGAGGGAC	
		3181 ATTTCTGAGAGACTGGCCAGCATTTCAGTAGGACCTTCTAGTTCAACAACAACAACAACA	
		3241 ACAACACAGAGCAACCAAAGCCAATGGTTCAAACAAAAGGCAGACCCCACAGTCAGTGT	
		3301 TTGAACTCCTCTCCTTTATCTCATCATTCCCAATTAATGTTTCCAGCCTTGTCAACCCCT	
		3361 TCTTCTTCTACCCCATCTGTACCAGCTGGCACTGCAACAGATGTCTCTAAGCATAGACTT	
		3421 CAGGGATTCATTCCCTGCAGAATACCTTCTGCATCTCCTCAAACACAGCGCAAGTTTTCT	
		3481 CTACAATTCCACAGAAACTGTCCTGAAAACAAAGACTCAGATAAACTTTCCCCAGTCTTT	
		3541 ACTCAGTCAAGACCCTTGCCCTCCAGTAACATACACAGGCCAAAGCCATCTAGACCTACC	
		3601 CCAGGTAATACAAGTAAACAGGGAGATCCCCTCAAAAAATAGCATGACACTTGATCTGAAC	
		3661 AGTAGTTCCAAATGTGATGACAGCTTTGGCTGTAGCAGCAATAGTAGTAATGCTGTTATA	
		3721 CCCAGTGACGAGACAGTGTTCACCCCAGTAGAGGAGAAATGCAGATTAGATGTCAATACA	
		3781 GAGCTCAACTCCAGTATTGAGGACCTTCTTGAAGCATCTATGCCTTCAAGTGATACAACA	
		3841 GTAACTTTTAAGTCAGAAGTTGCTGTCCTGTCTCCTGAAAAGGCTGGAAAATGATGATACC	
		3901 TACAAAGATGATGTGAATCATAATCAAAAGTGCAAAGAGAAGATGGAAGCTGAAGAAGAA	
		3961 GAAGCTTTAGCAATTGCCATGGCAATGTCAGCGTCTCAGGATGCCCTCCCCATAGTTCCT	
		4021 CAGCTGCAGGTTGAAAATGGAGAAGATATCATCATTATTCAACAGGATACACCAGAGACT	
		4081 CTACCAGGACATACCAAAGCAAAACAACCGTATAGAGAAGACACTGAATGGCTGAAAGGT	
		4141 CAACAGATAGGCCTTGGAGCATTTTCTTCTTGTTATCAGGCTCAAGATGTGGGAACTGGA	
		4201 ACTTTAATGCGCTGTTAAACAGGTGACTTATGTCACAAACACATCTTCTGAGCAAGAAGAA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		4261 GTAGTAGAAGCACTAAGAGAAGAGATAAGAATGATGAGCCATCTGAATCATCCAAACATC	
		4321 ATTAGCATGTTGGGAGCCACGTCTGAGAAGAGCAATTACAATCTCTTCATTGAATGGATG	
		4381 GCAGGGCGATCGGTGGCTCATTTGCTGAGTAAATATGGAGCCTTCAAAGAATCAGTAGTT	
		4441 ATTAACTACACTCGAACAGTTACTCCGTGGCCTTTCGTATCTCCATGAAAACCAAATCATT	
		4501 CACAGAGATGTCAAAGGTGCCAATTTGCTAATTGACAGCACTGGTCAGACTAAGAATT	
		4561 GCAGATTTTGGAGCTGCAGCCAGGTTGGCATCAAAAGGAACTGGTGCAGGAGAGTTTCAG	
		4621 GGACAATTACTGGGGACAATTGCATTTATGGCACCTGAGGTACTAAGAGGTCAACAGTAT	
		4681 GGAAGGAGCTGTGATGTATGGAGTGTTGGCTGTGCTATTATAGAAATGGCTTGTGCAAAA	
		4741 CCACCATGGAATGCAGAAAAAACACTCCAATCATCTTGCTTTGCATATTTAAGATTGCTAGT	
		4801 GCAACTACTGCTCCATCGATCCCTTCACATTTGTCTCCTGGTTTACGAGATGTGGCTCTT	
		4861 CGTTGTTTAGAACTTCAACCTCAGGACAGACCTCCATCAAGAGAGCTACTGAAGCATCCA	
		4921 GTCTTTCGTACTACATGGTAGCCAATTATGCAGATCAACTACAGTAGAAACAGGATGCTC	
		4981 AACAAGAGAAAAAAAACTTGTGGGGAACCACATTGATATTCTACTGGCCATGATGCCACT	
		5041 GAACAGCTATGAACGAGGCCAGTGGGGAACCCTTACCTAAGTATGTGATTGACACAAATCAT	
		5101 GATCTGTACCTAAGCTCAGTATGCAAAAGCCCAAACTAGTGCAGAAACTGTAAACTGTGC	
		5161 CTTTCAAAGAACTGGCCCTAGGTGAACAGGAAACAATGAAGTTTGCATGACTAAATTGC	
		5221 AGAAGCATAATTTTATTTTTTGGAGCACTTTTTCAGCAATATTAGCGGCTGAGGGCTC	
		5281 AGCATCTATTTTAATATTTCAATTATTCTTCCATTTCATATAGTGATCACAAGCAGGGGG	
		5341 TTCTGCAATTCCGTTCAAATTTTTTGTCACTGGCTATATAAAATCAGTATCTGCCTCTTTTA	
		5401 GGTCAGAGTATGCTATGAGTAGCAATACATACATATATTTTTAAAAGTTGATACTTCTTT	
		5461 ATGACCCACAGTTGACCTTTATTTTCTTTAAATACCAGGGCAGTTGTGGCTCATTGTGCAT	
		5521 TTTACTGTTGGCCCATTCATTTCGTTTTTGGAAATTATGGTTTTGTATTTTCATGTTTAT	
		5581 TTACATTCATTTTTGTTTATTCAGGGAAAGCTGATCTTTTTTTTCAAACCAGAAAAAAAAA	
		5641 ATGAACTAGATATGAAGTAGAGTTCATTAAATATCTTCGCTATTGTCAGAGTTTTTAAAAT	
		5701 ATAGACTTAATTTTGTTTTTTTAAATTGGAATACAATAAAGTACTACCTACATTTGAGTC	
		5761 AGTCACCACTCTTATTGTGCAGGTTAAGTACAAGTTAACTAAAAATAAACTGTCCTCTCT	
		5821 GGTGCAACTCACAACCAAGATCAAGATTACCTTAAAATTTATTTGAATTTTTTACGATGTT	
		5881 TTGGTTGTCAAACTGTAGGAAACTTCACAACATTTAAGTCTTACTCTGTATGTAACAATC	
		5941 CATCATTCACCTTCACTACTGGTAGTAACATAGAGCTGCCATTTCCTTTACCATGCAT	
		6001 CATCTCTTTACAGTAGGCCTGGCAGATCATTTTTTAAAAAGATTTATTCAACTACCAATCA	
		6061 GTAATGTTTTTAAACAGTACATTTGCTTTGAACTTGGAAAATGTGTTCAGAAAGAAAAAT	
		6121 GGAATTGAATTTCATTTATATACACTAATTCCTTGGATTTTGCACAGTTACCTAAGGTTTT	
		6181 AGTCTGGAGTTAAATTCAGATGCATGGAATCCTGAAGGAAAATGGTAGCTTTTTAATCTT	
		6241 TTTGTTGTGTGTGAGTCTTTTAAATCAAGTACTGATTAACTATTAAGTACAACTTTGAG	
		6301 ATTTTAGTTTTAACTCTTCAGAAGCCAGTGTGAAATAGAATTGGTTATTCTCAAAGACTC	
		6361 AGGATAAACTAAATAACCTATATATAGAGTACATTTAAAATGTACAACACAAATTGGAAA	
		6421 TAAAATAAGTTACAAGATAAGTTTACAGGGATATATTGCTTACAATTTTTTAAAAGGCAGT	
		6481 TTGTTTTTATGTGAATATGTTTCTTAGTGAAATTTTACATTCCTTTGTTTTGCAAGATT	
		6541 GGCGATATTTGAAGAGTTAAAAATAGTACAGAAATGTGAACTTTGGTATCTCTAAATGTG	
		6601 TTGTACTTGACTTTCTTTTTATTTGTTTTTTTTTTTTTGACTACTTAGAATTTTCA	
		6661 CAATTCTAATAAGATTGTTTCCAAGTCTCTCATGTGCAAGCTTTAAAGGATGCACTCTTG	
		6721 CCATTTTATGTACTGGAAGATCATTGGTCAGATGAATACTGTGTCTGACAAAAATGTAAA	
		6781 CTGTATAAACTGAGGAACCTCAGCTAATCAGTATTACTTTGTAGATCACCATGCCCACCA	
		6841 CATTTCAAACTCAAACTATCTGTAGATTTCAAAATCCATTGTGTTTGAGTTTCTTTGCAG	
		6901 TTCCCTCAGCTTGCTGGTAATTGTGGTGTTTTGTTTTTTTGTTTTTGTTTCAATGCAAATG	
		6961 TGATGTAATATTCTTATTTCTTTGGATCAAAGCTGGACTGGAAATTGTATCGTGTAATT	
		7021 ATTTTTGTGTTCTTAATGTTATTTGGTACTCAAGTTGTAAATAACGTCTACTACTGTTTA	
		7081 TTCCAGTTTCTACTACCTCAGGTGTCCTATAGATTTTTCTTCTACCAAAGTTCACTTTCA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		7141 CAATGAAATTATATTTGCTGTGTGACTATGATTCCTAAGATTTCCAGGGCTTAAGGGCTA 7201 ACTTCTATTAGCACCTTACTGTGTAAGCAAATGTTACAAAAAAAAAAAAAAAAAATCTCT 7261 GGGTTAAGAAAATTTGGCTTAAATGTATCCTTTGTTATTTTAAATATATTGAGATATTTT 7321 AATTAAAATTTTTACCCCATTGAACCGATTTTATAGTATTTGTACCTATTTTGGTGTTTT 7381 TGTCTTTATAGTAAATAAAAGTTTTTGAAC	
		1 M G S Q A L Q E W G Q R E P G R W P D P 1 ATGGGCAGCCAGGCCCTGCAGGAGTGGGGACAGAGGGAACCCGGCCGGTGGCCCGACCCT	SEQ ID NO:58
		21 A G K K D V R R E A S D S G R A G T W P 61 GCAGGGAAGAAGGACGTGCGGCGAGAAGCATCGGATTCGGGGAGGGCCGGGACCTGGCCG	
		41 R T A K E K L K I D G D T R L P S S P Q 121 AGGACAGCCAAGGAAAAACTAAAGATCGACGGGGACACCCGCCTCCCTTCCTCGCCCCAA	
		61 R F L R G C G D L H Q K P K L E L I L S 181 CGGTTTCTCAGAGGCTGTGGGGACTTGCACCAGAAACCCAAGTTGGAACTAATTCTTTCT	
		81 F G R C N S P P A S S A V P G R D C R E 241 TTCGGAAGGTGCAACTCCCCCTCCCGCGAGCTCCGCGGTGCCGGGCCGAGATTGCCGAGAG	
		101 E A A Q R C R Q G S S C R R C G R D Y L 301 GAAGCGGCGCAGCGCTGCCGCCAAGGCTCCTCCTGTCGCCGGTGCGGCCGGGACTACCTG	
		121 A A R R G P S E C S P R R E K M A A A A G 361 GCGGCCGCGGCGCGGCCGAGCGAATGTAGCCCGCGAGAGAAAATGGCGGCGGCGGCGGGG	
		141 N R A S S S G F P G A R R A T S P E A G G 421 AATCGCGCCTCGTCGTCGGGATTCCGGGCGCCAGGGCTACGAGCCCTGAGGCAGGCGGC	
		161 G G G A L K A S S A P A A A A G L L R E 481 GGCGGAGGAGCCCTCAAGGCGAGCAGCGCCGCCCGCTGCCGCGGGACTGCTGCGGGAG	
		181 A G S G G R E R A D W R R R Q L R K V R 541 GCGGGCAGCGGGGGCCGCGAGCGGGCGGACTGGCGGCGGCGGCAGCTGCGCAAAGTGCGG	
		201 S V E L D Q L P E Q P L F L A A S P P A 601 AGTGTGGAGCTGGACCAGCTGCCTGAGCAGCCGCTCTTCCTTGCCGCCTCACCGCCGGCC	
		221 S S T S P S P E P A D A A G S G T G F Q 661 TCCTCGACTTCCCCGTCGCCGGAGCCCGCGGACGCAGCGGGGAGTGGGACCGGCTTCCAG	
		241 P V A V P P P H G A A S R G G A H L T E 721 CCTGTGGCCGGTGCCGCCCGCCCCACGGAGCCGCGAGCCGCGGCGGCGCCCACCTTACCGAG	
		261 S V A A P D S G A S S P A A A E P G E K 781 TCGGTGGCGGCGCCGGACAGCGGCGCCTCGAGTCCCGCAGCGGCCGAGCCCGGGGAGAAG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		281 R A P A A E P S P A A A P A G R E M E N 841 CGGGCGCCCGCCGCCGAGCCGTCTCCTGCAGCGGCCCCCGCCGGTCGTGAGATGGAGAAT	
		301 K E T L K G L H K M D D R P E E E R M I R 901 AAAGAAACTCTCAAAGGGTTGCACAAGATGGATGATCGTCCAGAGGAACGAATGATCAGG	
		321 E K L K A T C M P A W K H E W L E R R N 961 GAGAAACTGAAGGCAACCTGTATGCCACCCTGGAAGCACGAATGGTTGGAAAGGAGAAAT	
		341 R R G P V V V K P I P V K G D G S E M N 1021 AGGCGAGGGCCTGTGGTGTAAACCAATCCCAGTTAAAGGAGATGGATCTGAAATGAAT	
		361 H L A A E S P G E V Q A S A A S P A S K 1081 CACTTAGCAGCTGAGTCTCCAGGAGAGGTCCAGGCAAGTGCGGCTTCACCAGCTTCCAAA	
		381 G R R S P S P G N S P S G R T V K S E S 1141 GGCCGACGCAGTCCTTCTCCTGGCAACTCCCCATCAGGTCGCACAGTGAAATCAGAATCT	
		401 P G V R R K R V S P V P F Q S G R I T P 1201 CCAGGAGTAAGGAGAAAAAGAGTTTCCCCAGTGCCTTTTCAGAGTGGCAGAATCACACCA	
		421 P R R A P S P D G F S P Y S P E E T N R 1261 CCCCGAAGAGCCCCTTCACCAGATGGCTTCTCACCATATAGCCCTCAGGAAACAAACCGC	
		441 R V N K V M R A R L Y L L Q Q I G P N S 1321 CGTGTTAACAAAGTGATGCGGGCCAGACTGTACTTACTGCAGCAGATAGGGCCTAACTCT	
		461 F L I G G D S P D N K Y R V F I G P Q N 1381 TTCCTGATTGGAGGAGACAGCCCAGACAATAAATACCGGGTGTTTATTGGGCCTCAGAAC	
		481 C S C A R G T F C I H L L F V M L R V F 1441 TGCAGCTGTGCACGTGCAACATTCTGTATTCATCTGCTATTTGTGATGCTCCGGTGTTT	
		501 Q L E P S D P M L W R K T L K N F E V E 1501 CAACTAGAACCTTCAGACCCAATGTTATGGAGAAAACTTTAAAGAATTTTGAGGTTGAG	
		521 S L F Q K Y H S R R S S R I K A P S R N 1561 AGTTTGTTCCAGAAATATCACAGTAGGCGTAGCTCAAGGATCAAAGCTCCATCTCGTAAC	
		541 T I Q K F V S R M S N S H T L S S S S T 1621 ACCATCCAGAAGTTTGTTTCACGCATGTCAAATTCTCATACATTGTCATCATCTAGTACT	
		561 S T S S S E N S I K D E E E Q M C P I C 1681 TCTACGTCTAGTTCAGAAAACAGCATAAAGGATGAAGAGGAACAGATGTGTCCTATTTGC	
		581 L L G M L D E E S L T V C E D G C R N K 1741 TTGTTGGGCATGCTTGATGAAGAAAGTCTTACAGTGTGTGAAGACGGCTGCAGGAACAAG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		601 L H H H C M S I W A E E C R R N R E P L 1801 CTGCACCACCACTGCATGTCAATTTGGGCAGAAGAGTGTAGAAGAAATAGAGAACCTTTA	
		621 I C P L C R S K W R S H D F Y S H E L S 1861 ATATGTCCCCTTTGTAGATCTAAGTGGAGATCTCATGATTTCTACAGCCACGAGTTGTCA	
		641 S P V D S P S S L R A A Q Q Q T V Q Q Q 1921 AGTCCTGTGGATTCCCCTTCTTCCCTCAGAGCTGCACAGCAGCAAACCGTACAGCAGCAG	
		661 P L A G S R R N Q E S N F N L T H Y G T 1981 CCTTTGGCTGGATCACGAAGGAATCAAGAGCAATTTTAACCTTACTCATTATGGAACT	
		681 Q Q I P P A Y K D L A E P W I Q V F G M 2041 CAGCAAATCCCTCCTGCTTACAAAGATTTAGCTGAGCCATGGATTCAGGTGTTTGGAATG	
		701 E L V G C L F S R N W N V R E M A L R R 2101 GAACTCGTTGGCTGCTTATTTCTAGAAACTGGAATGTGAGAGATGGCCCTCAGGCGT	
		721 L S H D V S G A L L L A N G E S T G N S 2161 CTTTCCCATGATGTCAGTGGGGCCCTGCTGTTGGCAAATGGGGAGCACTGGAAATTCT	
		741 G G S S G S S P S G G A T S G S S Q T S 2221 GGGGGCAGTGGAAGCAGCCCGATGGGGGAGCCACCAGTGGGTCTTCCCAGACCAGT	
		761 I S G D V V E A C C S V L S M V C A D P 2281 ATCTCAGGAGATGTGGTGGAGGCATGCTGCAGCGTTCTGTCAATGGTCTGTGCTGACCCT	
		781 V Y K V Y V A A L K T L R A M L V Y T P 2341 GTCTACAAAGTGTACGTTGCTGCTTTAAAAACATTGAGAGCCATGCTGGTATATACTCCT	
		801 C H S L A E R I K L Q R L L Q P V V D T 2401 TGCCACAGTTTAGCGGAAAGAATCAAACTTCAGAGACTTCTCCAGCCAGTTGTAGACACC	
		821 I L V K C A D A N S R T S Q L S I S T L 2461 ATCCTAGTCAAATGTGCAGATGCCAATAGCCGCACAAGTCAGCTGTCCATATCAACACTG	
		841 L E L C K G Q A G E L A V G R E I L K A 2521 TTGGAACTGTGCAAAGGCCAAGCAGGAGAGTTGGCAGTGGCAGAGAAATACTAAAAGCT	
		861 G S I G I G G V D Y V L N C I L G N Q T 2581 GGATCCATTGGTATTGGTGGTGTTGCATTATGTCTTAAATTGTATTCTTGGAAACCAAACT	
		881 E S N N W Q E L L G R L C L I D R L L L 2641 GAATCAAACAATTGGCAAGAACTTCTTGGCCGCCTTTGTCTTATAGATAGACTGTTGTTG	
		901 E F P A E F Y P H I V S T D V S Q A E P 2701 GAATTTCCTGCTGAATTTTATCCTCATATTGTCAGTACTGATGTTTCACAAGCTGAGCCT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		921 V E I R Y K K L L S L L T F A L Q S I D 2761 GTTGAAATCAGGTATAAGAAGCTGCTGTCCCTCTTAACCTTTGCTTTGCAGTCCATTGAT	
		941 N S H S M V G K L S S R R I Y L S S A R M 2821 AATTCCCACTCAATGGTTGGCAAACTTCCAGAAGGATCTACTTGAGTTCTGCAAGAATG	
		961 V T T V P H V F S K L L E M L S V S S S 2881 GTTACTACACTACCCCATTGTGTTTCAAAACTGTTAGAAATGCTGAGTGTTTCCAGTTCC	
		981 T H F T R M R R R L M A I A D E V E I A 2941 ACTCACTTCACCAGGATGCGTCGCCGTTTGATGGCTATTGCAGATGAGGTGGAAATTGCC	
		1001 E A I Q L G V E D T L D G Q Q D S F L Q 3001 GAAGCCATCCAGTTGGGCGTAGAAGACACTTTGGATGGTCAACAGGACAGCTTCTTGCAG	
		1021 A S V P N N Y L E T T E N S S P E C T V 3061 GCATCTGTTCCCAACAACTATCTGGAAACCACAGAGAACAGTTCCCCTGAGTGCACAGTC	
		1041 H L E K T G K G L C A T K L S A S S E D 3121 CATTTAGAGAAACTGGAAAAGGATTATGTGCTACAAAATTGAGTGCCAGTTCAGAGGAC	
		1061 I S E R L A S I S V G P S S S T T T T T 3181 ATTTCTGAGAGACTGGCCAGCATTTCAGTAGGACCTTCTAGTTCAACAACAACAACA	
		1081 T T T E Q P K P M V Q T K G R P H S Q C 3241 ACAACAACAGAGCAACCAAAGCCAATGGTTCAAACAAAAGGCAGACCCCACAGTCAGTGT	
		1101 L N S S P L S H H S Q L M F P A L S T P 3301 TTGAACTCCTCTCCTTTATCTCATCATTCCCAATTAATGTTTCCAGCCTTGTCAACCCCT	
		1121 S S S T P S V P A G T A T D V S K H R L 3361 TCTTCTTCTACCCCATCTGTACCAGCTGGCACTGCAACAGATGTCTCTAAGCATAGACTT	
		1141 Q G F I P C R I P S A S P Q T Q R K F S 3421 CAGGGATTCATTCCCTGCAGAATACCTTCTGCATCTCCTCAAACACAGCGCAAGTTTTCT	
		1161 L Q F H R N C P E N K D S D K L S P V F 3481 CTACAATTCCACAGAAACTGTCCTGAAAACAAAGACTCAGATAAACTTTCCCCAGTCTTT	
		1181 T Q S R P L P S S N I H R P K P S R P T 3541 ACTCAGTCAAGACCCTTGCCCTCCAGTAACATACACAGGCCAAGCCATCTAGACCTACC	
		1201 P G N T S K Q G D P S K N S M T L D L N 3601 CCAGGTAATACAAGTAAACAGGGAGATCCCTCAAAAAATAGCATGACACTTGATCTGAAC	
		1221 S S S K C D D S F G C S S N S S N A V I 3661 AGTAGTTCCAAATGTGATGACAGCTTTGGCTGTAGCAGCAATAGTAGTAATGCTGTTATA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1241 P S D E T V F T P V E E K C R L D V N T 3721 CCCAGTGACGAGACAGTGTTCACCCCAGTAGAGGAGAAATGCAGATTAGATGTCAATACA	
		1261 E L N S S I E D L L E A S M P S S D T T 3781 GAGCTCAACTCCAGTATTGAGGACCTTCTTGAAGCATCTATGCCTTCAAGTGATACAACA	
		1281 V T F K S E V A V L S P E K A E N D D T 3841 GTAACTTTTAAGTCAGAAGTTGCTGTCCTGTCTCCTGAAAAGGCTGAAAATGATGATACC	
		1301 Y K D D V N H N Q K C K E K M E A E E E 3901 TACAAAGATGATGTGAATCATAATCAAAAGTGCAAAGAGATGCAAGCTGAAGAAGAA	
		1321 E A L A I A M A M S A S Q D A L P I V P 3961 GAAGCTTTAGCAATTGCCATGGCCAATGTCAGCGTCTCAGGATGCCCTCCCCATAGTTCCT	
		1341 Q L Q V E N G E D I I I I Q Q D T P E T 4021 CAGCTGCAGGTTGAAAATGGAGAAGATATCATCATTATTCAACAGGATACACCAGAGACT	
		1361 L P G H T K A K Q P Y R E D T E W L K G 4081 CTACCAGGACATACCAAAGCAAAACAACCGTATAGAGAAGACACTGAATGGCTGAAAGGT	
		1381 Q Q I G L G A F S S C Y Q Q A Q D V G T G 4141 CAACAGATAGGCCTTGGAGCATTTTCTTCTTGTTATCAGGCTCAAGATGTGGGAACTGGA	
		1401 T L M A V K Q V T Y V R N T S S E Q E E 4201 ACTTTAATGGCTGTTAAACAGGTGACTTATGTCAGAAACACATCTTCTGAGCAAGAAGAA	
		1421 V V E A L R E E I R M M S H L N H P N I 4261 GTAGTAGAAGCACTAAGAGAAGATAAGAATGATGAGCCATCTGAATCATCCAAACATC	
		1441 I R M L G A T C E K S N Y N L F I E W M 4321 ATTAGGATGTTGGGAGCCACGTGTGAGAAGAGCAATTACAATCTCTTCATTGAATGGATG	
		1461 A G G S V A H L L S K Y G A F K E S V V 4381 GCAGGGGGATCGGTGGCTCATTTGCTGAGTAAATATGGAGCCTTCAAAGAATCAGTAGTT	
		1481 I N Y T E Q L L R G L S Y L H E N Q I I 4441 ATTAACTACACTGAACAGTTACTCCGTGGCCTTTCGTATCTCCATGAAACCAAATCATT	
		1501 H R D V K G A N L L I D S T G Q R L R I 4501 CACAGAGATGTCAAAGGTGCCAATTTGCTAATTGACAGCACTGGTCAGACTAAGAATT	
		1521 A D F G A A A R L A S K G T G A G E F Q 4561 GCAGATTTTGGAGCTGCAGCCAGGTTGGCATCAAAAGGAACTGGTGCAGGAGAGTTTCAG	
		1541 G Q L L G T I A F M A P E V L R G Q Q Y 4621 GGACAATTACTGGGGACAATTGCATTTATGGCACCTGAGGTACTAAGAGGTCAACAGTAT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1561 G R S C D V W S V G C A I I E M A C A K 4681 GGAAGGAGCTGTGATGTATGGAGTGTTGGCTGTGCTATTATAGAAATGGCTTGTGCAAAA 1581 P P W N A E K H S N H L A L I F K I A S 4741 CCACCATGGAATGCAGAAAAACACTCCAATCATCTTGCTTTGATATTTAAGATTGCTAGT 1601 A T T A P S I P S H L S P G L R D V A L 4801 GCAACTACTGCTCCATCGATCCCTTCACATTTGTCTCCTGGTTTACGAGATGTGGCTCTT 1621 R C L E L Q P Q D R P P S R E L L K H P 4861 CGTTGTTTAGAACTTCAACCTCAGGACAGACCTCCATCAAGAGACCTACTGAAGCATCCA 1641 V F R T T W - 4921 GTCTTTCGTACTACATGGTAG	
WBC018B01_V1.3_s_at	Homo sapiens gene for JKTBP2, JKTBP1 (alternative splicing).	1 tctagacgtg tcctatagct caaaaaatca gcgctatgga ccacagcgcc taacagagta 61 aaataataca ctgtgcagtt tggccactaa cagcaagagt gggaaggggc gaagaggaac 121 cttgattgcc cgacaccagg gccacctgaa aagtcatctt gacacttcag tctttccatt 181 ttgagatcgg aagctttaag gaccattaaa tcgctgccgc tgccacacca ggcccgacgg 241 agcagaaagg ctgcgctcac ctgcggaagc gaccggtgcc acacctgccg ggtggcgagg 301 cccgcaccgt cacaccccgc cccggcttac ctgcccttcg gtgatttta gcgtcaactt 361 ccatcccttc ccacccatct ggatccaacc aagcgcaagg gcggggagg gagaagctag 421 tgtcgcgagg aaaagcatcc ccgcaaccca ccgcaggctt tctctcctc ctcccattc 481 cacacaagag gcaaagccac accgcctctc ctaaccctcg tctccaatgc aaggcctgaa 541 atacttagaa aaaataatаа ctgtttttaa ggaaaagtaa catccccgct ccctccgcc 601 cctcaccttc acgaaagcaa tcgggttgt ggtacttcg atatctaaca ggatcacggt 661 gacttcggcg gggaccgaaa gcacgaccat ttccctaccg gatgctacgg gactcggcct 721 gctgttgggg aggcggagg gcggcgccgg ctgcggctgc ggccccggt accgtcttgg 781 gcttccggcg gcccgcgcg atctcggagc cagcgaccaa gtgcagcccg ccgcgcgtgg 841 ggagaggaca cttctgcaca cctggaactg gaaaagcggg ccgcccagga gccctgaact 901 cgtgagcagg acgggcagg agcccgagac cacgtgggca ggaaaagggg cggccttga 961 cgggttcggc ggggcgggga gggtgaaggc gccagcgccg atggccgcc gtcaggcctc 1021 gaactggatc cgtcaaaatg ggcctcgcgt gggcgggaac aaagaagcga acgcgggagc 1081 agggtgcgcg agagcgcgcc ctccgcagac agttgagcg agcgggagag gcccgggca 1141 cgtgcagaaa ggagcccgc gagtggcgcg ccggggatgt gagtgcccct tgccctctac 1201 tgaatccagc cccctccccg cccaccgcct ccgcctttgc atagatacag tcatctggcc 1261 agccccgcgc cctcctcccg gcgtcagccc gccagaggcc gcgcgggccc cgggcttcgg 1321 ccgatcagcc cgggaggccc cgccgcgccc cctggcccg cgcgcccgtg gtcacagtgg 1381 aagaggcgcc cgcgctgcgc tgcccggagg agccgtcgcg cgcccgcttc ctgttcggct 1441 ggttcctgcc agctcgagga caaaacacgc gtgcgcgcgg cgggcgagcg cgctcgccgc 1501 ctcagtcgcc agcgccgggc gcagtccgcc tttttccgga gcagactggc cgcggtgcta 1561 gtcggtagca gcggccgccg cagcggctcc gcactggcga accgagggca gaaaaggccg 1621 gggttgacgg cttttttgta ggagtgggct ggaccggacg ccagagacaa aggctcccaa 1681 ggcaagaggg actgtggccc tgcgtcggct ctgctcggaa ctgctgaccc caggaattta 1741 cgccccttcg ttttctcttt ctgattcttc tcttctccca agcccgcgtc ccctcacgcg 1801 tggcctctct ccttgccggg agggccgcga tggaggtccc gcccaggctt tcccatgtgc	SEQ ID NO:59

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1861 cgccgccatt gttcccctcc gctccgcta ctttagcctc ccgcagcctc tcccattggc	
		1921 ggccgcggcc gccgcggcag ctagccccgc tcctcccttc gctcgctccc agctcgccc	
		1981 ggcaggggcc gcgccggccc cagcgccacg tcaccgccca gcagccctcc cgattggcgg	
		2041 gcgggcggc tataaaggga gggcgcaggc ggcgcccgga tctcttccgc cgccatttta	
		2101 aatccagctc catacaacgc tccgccgccg ctgctgccgc gacccggact gcgcgccagc	
		2161 acccccctgc cgacgctccc gtcactatgg aggatatgaa cgagtacagc aatatagagg	
		2221 aattcgcaga gggatccaag atcaacgcga gcaagaatca gcaggatgac gggtacgcac	
		2281 gcttcttccc ccgctccccc tccccagcg cgccgcacgn ccttcgttcc tcgtgagccg	
		2341 cgcgctgccc ccattctttc tcagagtcga ttccccgcgt gcntnctggg ccccnactag	
		2401 antgnaggna agagnanagt aagagatcga gggngtgact ggagagaccc ggnaagagtn	
		2461 gggnaaggnc gnaggggttn nngnagnagg ncgncgncgt ctgtgtcccg agcgcgcagg	
		2521 cgncgcgtgg gacccnnngg gnangngccg gcctcnccag cgctgcacgc tgcagctgcc	
		2581 gccgcctctt catntntcct ctnttaccac tctgcgcggt ttncctggga agagttttag	
		2641 aggactgagt tgggcacaa gcaggcgact ggtacccaga ttcacaaaac gtgttatgat	
		2701 tgatgagttc tctgggtgga acgttggctt gacagctgag aacgaagatg gacctaagta	
		2761 agataagatg tgagggattc atctaggaag ttgtgccttc tacctaaagg aatctgggca	
		2821 gaaccttac tgtatttat tggtctcttt tgagctttgc tttatgtagt gcggacagtg	
		2881 agctgtccgc tggtttgagt aacttcgttg ggatattggg attttgtgt gacatagatt	
		2941 aaatgtaaac atgaattaaa ttgcctacac ttagtgggta aatgtccctg tttttatttc	
		3001 acgatttaat tccagaactg aaggatcatt tgagttattg ttaattttt ttaaaaacac	
		3061 ttttatttct agtaaaatgt ttattggagg cttgagctgg gatacaagca aaaaagatct	
		3121 gacagagtac ttgtctcgat ttgtgggaagt tgtagactgc acaattaaaa cagatccagt	
		3181 cactgggaga tcaagaggat ttggatttgt gctttcaaaa gatgctgcta gtgttgataa	
		3241 ggtaggnact atgttttgca ttgtgctgct tcttgtngtg tttgcaaan ttttctgnnn	
		3301 gntatatngt ncttgtcaan attaaataaa tctntctttg taggttttgg aactgaaaga	
		3361 acacaaactg gatggcaaat tgatagatcc caaaaggcc aaagctttaa aagggaaaga	
		3421 acctcccaaa aaggttttg tgggtggatt gagcccggat actttgaag aacaaattaa	
		3481 agaatatttt ggagcctttg gagaggtgtg tgattatgtt tacacatgtt aagcttgatg	
		3541 tgtttataaa atgttcaatc cttgtccgat ttatgcaggg cagattcatg ttcctgtaa	
		3601 gagtagaatt aaatgactgc tcaagtcgct tccagtgact gtaccttgat ttcattgctg	
		3661 ctctgatgga aacccaacta tctaatttag ctaaaacatg ggcacttaaa tgtggtcagt	
		3721 gtttggactt gttaactagt ggcatctttg ggtacaaaat aatattaatt tctctcagtg	
		3781 cttcaaatat acaacaaatc actgtaggct gatgttgatc ataaagcagt gatgtctgta	
		3841 tagaagtcac ccgataagaa taacatgttt aagttgaagc ctgaaaaggc ctttggcatt	
		3901 ctgacactgt aacgttttac aattatggga tgacgttgag tgtgcatctc gatttcagat	
		3961 tgaaaatatt gaacttccca tggatacaaa aacaaatgaa agaagaggat tttgttttat	
		4021 cacatatact gatgaagagc cagtaaaaaa attgttagaa agcagatacc atcaaattgg	
		4081 ttctgggaag gtaaagccat ttaagcactt taaatgaaaa tttaaataat tgaaataatt	
		4141 tcttgatgtg gagaaaaata aaatgatntn antntagaac nncggtaana antatncttn	
		4201 catgntttt gtttatagtg tgaaatcaaa gttgcacaac ccaaagaggt atataggcag	
		4261 caacagcaac aacaaaaagg tggaagaggt gctgcagctg gtggacgagg tggtacgagg	
		4321 ggtcgtggcc gaggtgagac tnaanncntg anatatgact ccgtgntnta tntaangctg	
		4381 tatactgctg aatatgagta gtcctgtacn anagcnaaaa ctntnaacn nnaaaacna	
		4441 tnnccagcng nagggggac tgtncagctt agtgnagnnt gtgtgtggtg ntnttntgtt	
		4501 gtgagctcac tggtntcaaa anactgntna anagtgtgnc cactntgaca attagtgtca	
		4561 tcactgatag naaaagtgta ccattacatg ataccacgtg gtgtgatagg ttctcttggg	
		4621 cagnagtcct tgtnttaaac agaacagtgt accgtcttc gnctttaatg gaaaattgaa	
		4681 tgatttttcca ttaagtttag gaagtttgat actggcacaa ttggacttte tgcctcctnt	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		4741 tttataacag ctggaaaaat agtttntcaa gcagatagca atatatatgt ccattctgcc 4801 ctttaagatt tgcagagtga gagacaagaa cgcatcattt tatgttagaa ttgggggtca 4861 gaagttgttt cctaacaatc attgtgcatt gtttcaggtc agggccaaaa ctggaaccaa 4921 ggatttaata actatttatga tcaaggatat ggaaattaca atagtgccta tggtggtgat 4981 caaactatta gtggctatgg cggatatgat tatactgggt ataactatgg gaactatgga 5041 tatggacagg gatatgcaga ctacagtggt aagaatattt aacttaattt tataaagcag 5101 tggtattaaa attcattgtt aacatacaat cctgttctga aattgtgtgt atgggctttc 5161 cattaaagtg ttcggagtta agtgttntgag gcatgttaca atcataggat gattatacta 5221 acatagactg gtggttataa atgaactagg atgtatgatt tatgagtagc atctaatggg 5281 tgctaaaata tcttaatact ttttatttag catgcaaagc atttgtagat ttaatagttt 5341 gtgtttgtaa agaagtttt gtagaaaact atcttaatga gaattcttgtg ttttcaaaat 5401 aggccaacag agcacttatg gcaaggcatc tcgagggggt ggcaatcacc aaaacaatta 5461 ccagccatac taaaggagaa cattggagaa aacaggtgtg tataagagta caggaaaaca 5521 gtagaaatgt ctaatttaat ttaaagatca atagacaaat gaaacgtaaa aacaaaatac 5581 tatgtagcct gttttacta aattgttgat tttttaattg ctttatgagc ctgttttgcc 5641 taaagtgtct atagatcttt aactttaaag tcttatctca ctttctttag tattgcagaa 5701 aaacttaaga gttttctgt ttgctttgt gtaccaggtg gtctagagga ataattaaac 5761 atttagaac tattaacagg taaagtactg aaatgggtac aacttaagga aaacaagaat 5821 gttgtcttct aactctgaca ttataccttg tttgtacccg ccagcgggaa cttcattgca 5881 ggccgtgtgt caccctgacc acgtctatct ctgggggtcg cacgttgcgg gcagagcgca 5941 aggcatacac cagaaaacgc tgtcctgtgg tatggtctct tccaacttca tgtaccagcg 6001 taaagattaa agtggaaaac ttcagacttt ggcttcattt ttaatctttt tggagattaa 6061 gtgtctaaac ttaacttaaa tggttttta caggagttaa agtacataaa tgccttttta 6121 cagcttaatc attttggtct tctgtttagt gttgtatttc aattgtggag cctcatttta 6181 agtgttcatt ctttaagat ttaatgcttg ctttttcttt ttatagctaa tagtgaaatc 6241 tacaaaccaa aacaagaact tttaaatctg ggntataaat taaaggtcat atgcacagat 6301 caatttatgt tcttgtaata aacttattag aaattgggtg ttgtgatag catttacttt 6361 gggttacta gagatgcttc tagtagacct taatctagca tagttgaacc tctgaatatg 6421 ggaaggttga gtttattgac tacccaaact gtatttttncc aatanatatg catatgatct 6481 ttaattattg aagaaaatna agtgaggnct taaaacaatn catgaaagtg gncctttaaa 6541 agcttgtcag agttgcacaa atctaactgg tatttgttt ttgttttag gaggagatgt 6601 taaagtaacc catcttgcag gacgacattg aagattggtc ttctgttgat ctaagatgat 6661 tattttgtaa aagacttcct agtgtacaag acaccattgt gtccaactgt atatagctgc 6721 caattagttt tctttgtttt tacttttgtcc tttgctatct gtgttatgac tcaatgtgga 6781 tttgtttata cacatttttat ttgtatcatt tcatgttaaa cctcaaataa atgcttcctt 6841 atgtgattgc ttttctgcgt caggtactac atagctctgt aaaaaatgta atttaaaata 6901 agcaataatt aaggcacagt tgatttttgta gagtattggt ccatacagag aaactgtggt 6961 cctttataaa tagccagcca gcgtcaccct cttctccaat ttgtaggtgt atttatgct 7021 cttaaggctt catcttctcc ctgtaactga gatttctacc acacctttga acaatgttct 7081 ttccttctg gttatctgaa gactgtcctg aaagaagaca taagtgttgt gattagtaga 7141 agctttctag tagaccatat ttcttntgga ntgtaannaa attgnttagt agcnccttt 7201 tactttgtnc ctgtcnntgg aaagccnatt tttgaattgc tgattnctt ggctttaann 7261 agtggtcncc tagaaaaagc ttgtanncat ancncatgag tantctgata aaagttcaga 7321 tacaaaggag cactgtaaac tgtagagcta tgttaagagc attgnagtag tacaacccaa 7381 gatttgtaga agtatgagtt ggcgaaatta aatagtgcaa atagatttag ttgtgttttc 7441 tcagagccgc cacaagattg aacaaaatgt ttctgtttg ggcatcctga ggaagttgta 7501 ttagctgtta atgctctgtg agtttagaaa aagtcttgat agtaaaatct agttttgac 7561 acagtgcatg aactaagtag ttaaatattt acatattcag aaaggaatag tggaaaaggt	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		7621 atcttggtta tgacaaagtc attacaaatg tgactaagtc attacaaatg tgactgagtc 7681 attacagtgg accctctggg tgcattgaaa agaatccgtt ttatatccag gtttcagagg 7741 acctggaata ataataagct ttggattttg cattcagtgt agttggattt tgggaccttg 7801 gcctcagtgt tatttactgg gattggcata cgtgttcaca ggcagagtag ttgatctcac 7861 acaacgggtg atctcacaaa actggtaagt ttcttatgct catgagccct ccctttttt 7921 ttttaatttg gtgcctgcaa ctttcttaac aatgattcta cttcctgggc tatcacatta 7981 taatgctctt ggcctctttt ttgctgctgt tttgctattc ttaaacttag gccaagtacc 8041 aatgttggct gttagaaggg attctgttca ttcaacatgc aactttaggg aatggaagta 8101 agttcatttt taagttgtgt tgtcagtagg tgcggtgtct agggtagtga atcctgtaag 8161 ttcaaattta tgattaggtg acgagttgac attgagattg tccttttccc tgatcaaaaa 8221 atgaataaag ccttttaaa caaaatccaa acttttaatc aagtcttgat atgtatgact 8281 gagaaaaaat acactacatc taga **MEVPPRLSHVPPPLFPSAPATLASRSLSHWRPRPPRQLAPLLPS** **LAPSSARQCARRAQRHVTAQQPSRLAGGAAIKGGRRRRPDLFRRHFKSSSIQRSAAAA** **AATRTARQHPPADSSVT**MEDMNEYSNIEEFAEGSKINASKNQQDDGKMFIGGLSWDTS KKDLTEYLSRFGEVVDCTIKTDPVTGRSRGFGFVLFKDAASVDKVLELKEHKLDGKLI DPKRAKALKGKEPPKKVFVGGLSPDTSEEQIKEYFGAFGEIENIELPMDTKTNERRGF CFITYTDEEPVKKLLESRYHQIGSGKCEIKVAQPKEVYRQQQQQQKGGRGAAAGGRGG TRGRGRGQGQNWNQGFNNYYDQGYGNYNSAYGGDQNYSGYGGYDYTGYNYGNYGYGQG YADYSGQQSTYGKASRGGGNHQNNYQPY MEDMNEYSNIEEFAEGSKINASKNQQDDGKMFIGGLSWDTSKKD LTEYLSRFGEVVDCTIKTDPVTGRSRGFGFVLFKDAASVDKVLELKEHKLDGKLIDPK RAKALKGKEPPKKVFVGGLSPDTSEEQIKEYFGAFGEIENIELPMDTKTNERRGFCFI TYTDEEPVKKLLESRYHQIGSGKCEIKVAQPKEVYRQQQQQQKGGRGAAAGGRGGTRG RGRGQGQNWNQGFNNYYDQGYGNYNSAYGGDQNYSGYGGYDYTGYNYGNYGYGQGYAD YSGQQSTYGKASRGGGNHQNNYQPY	SEQ ID NO:60 SEQ ID NO:61
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Gene Name	GenBank HomoLogy	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1 GAGGCATTTAAATTCATGTATGATACTCTTATAATCATAACTGCTGCTAATGCTTGATT 61 ATATACTCAGGGACAATGTATAACGTAAGATTACAAATTTGTTCTCACCAACTCCCTTTT 121 GGATTTCATTAAGAAACAAAAACTCCTGGTCAGAGATAATGTATAAATCAGAGATGTAAA 181 TGGCTAGTTGTCTATAGCATTAAATGAAGGGAAAACTGATAATTAGGCAGTTAATTTGGT 241 CAATTAAACAACCATGTCTGCATCTAGGGGAGCCTGGCTTATTTGATTGATTCCTACTA 301 GTCTTTGACTCTCCCCTTCATTCTGGTTTCCATGTGAATTTGCTTTAGAAAAGCCAAGTAT 361 GGGCTGTTTCACGTGTTCAGACTTGTCTTTTCATAGCATTCATGGCGGGGCTGCAAGGCT 421 TGGAAGTGACCAGGAAGACAGTGAGAACGCGTGGTTGGACAACTGAAATGATGCAGATCA 481 GATGGCGTTTCTCCCAGCTCAGTGGATTTTCTTTGGGTTATTCTTAAAAATATCCATCA 541 CTACACTGGAAGTCCCTGTTCTGACTATGTACTGTCCACCTGCATTACANACATTCTGCA 601 GAGCTGCTAAGTATATACATATCCGATGTGTTACATCTTGTATTTAATTAAATGCTAT 661 GAAACTGAAAAAAAAAAAAAAA	SEQ ID NO:63
WBC014H06	Homo sapiens mRNA; cDNA DKFZp564C012	1 ggggggattt cggcggcgga aacatggcgg tcgcggccgg gccggtaacg gagaaagttt 61 acgccgacac tggcctgtat tagcgcgtat ggcctcgggc cctcgttccc caaggcgtgc 121 cgcctccctg ttctcagtcg caggctgaag ccttgtctgc tctcctcctt tttggtttgg 181 tttggaact gactccgagg gttgggagag cgcgttggtg gcgacggccg agtcagatca 241 ctataaacaa aatttccaca agagaaaatg ttgaaatagg agttgcggat acattggata 301 tactggatga aatacaagcg gttaattttt gtaacgtgag ggaaaagccc acattgctgg 361 ttacatgtgt aaatcactgc gttattgctt tagtcattgt ctctatttag caatgacaag 421 actggaagaa gtaaatagag aagtgaacat gcattcttca gtgcggtatc ttggctattt 481 agccagaatc aatttatgg ttgctatatg cttaggtcta tacgtaagat gggaaaaaac 541 agcaaattcc ttaattttat tcttggtctt tttgttcttg gaatcgccag 601 catactctat tactatttt caatggaagc agcaagttta agtctctcca atctttggtt 661 tggattcttg cttggcctcc tatgttttct tgataattca tcctttaaaa atgatgtaaa 721 agaagaatca accaaatatt tgcttctaac atccatagtg ttaaggatat tgtgctctct 781 ggtggagaga atttctggct atgtccgtca tcggcccact ttactaacca cagttgaatt 841 tctggagctt gttggatttg ccattgccag cacaactatg ttggtggaga agtctctgag 901 tgtcatttttg cttgttgtag ctctggctat gctgattatt gatctgagaa tgaaatcttt 961 cttagctatt ccaaacttag ttatttttgc agttttgtta ttttttttcct cattggaaac 1021 tcccaaaaat ccgattgctt ttgcgtgttt tttattttgc ctgataactg atcctttcct 1081 tgacatttat tttagtggac tttcagtaac tgaaagatgg aaacccttt tgtaccgtgg 1141 aagaatttgc agaagacttt cagtcgtttt tgctggaatg attgagctta catttttat 1201 tctttccgca ttcaaactta gagacactca cctctggtat tttgtaatac ctggcttttc 1261 catttttgga attttcagga tgatttgtca tattatttct cttttaactc tttggggatt 1321 ccataccaaa ttaaatgact gccataaagt atattttact cacaggacag attacaatag 1381 cttgatagta atcatggcat ccaaagggat gcgccatttt tgcttgattt cagagcagtt 1441 ggtgttcttt agtcttcttg caacagcgat tttgggagca gtttcctggc agccaacaaa 1501 tggaattttc ttgagcatgt tcctaatcgt ttggccattg gaatccatgg ctcatgggct 1561 cttccatgaa ttgggtaact gtttaggagg aacatctgtt ggatatgcta ttgtgattcc 1621 caccaacttc tgcagtcctg atggtcagcc aacactgctt ccccagaac atgtacagga 1681 gttaaatttg aggtctactg gcatgctcaa tgctatccaa agatttttg catatcatat 1741 gattgagacc tatggatgtg actattccac aagtggactg tcatttgata ctctgcattc 1801 caaactaaaa gctttcctcg aacttcggac agtggatgga cccagacatg atacgtatat 1861 tttgtattac agtgggcaca cccatggtac aggagagtgg gctctagcag gtggagatac 1921 actacgcctt gacacactta tagaatggtg gagagaaaag aatggttcct tttgttcccg	SEQ ID NO:64

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1981 gcttattatc gtattagaca gcgaaaattc aacccttgg gtgaaagaag tgaggaaaat 2041 taatgaccag tatattgcag tgcaaggagc agagttgata aaaacagtag atattgaaga 2101 agctgacccg ccacagctag gtgactttac aaaagactgg gtagaatata actgcaactc 2161 ctgtaataac atctgctgga ctgaaaaggg acgcacagtg aaagcagtat atggtgtgtc 2221 aaaacggtgg agtgactaca ctctgcattt gccaacggga agcgatgtgg ccaagcactg 2281 gatgttacac tttcctcgta ttacatatcc cctagtgcat ttggcaaatt ggttatgcgg 2341 tctgaacctt ttttggatct gcaaaacttg tttaggtgc ttgaaaagat taaaaatgag 2401 ttggtttctt cctactgtgc tggacacagg acaaggcttc aaacttgtca aatcttaatt 2461 tggaccccaa agcgggatat taataagcac tcatactacc aattatcact aacttgccat 2521 ttttgtatg ctgtatttt atttgtggaa aatacctgc tacttctgta gctgctctca 2581 ctttgtcttt tcttaagtaa ttatggtata tataaggcgt tgggaaaaaa cattttataa 2641 tgaaagtatg tagggagtca aatgcttact gtaaatgcat aagagacgtt aaaaataaca 2701 ctgcatttc aggaatgttt gcttatggtc ctgattagaa agaaacagtt gtctatgctc 2761 tgcaatggtc aatgatgaat tactaatgcc ttatttcta ggcatataat aatagtttag 2821 agaatgtaga ccagataaat ttgtttactg tttaagaaa actaccagtt tacttacaga 2881 agattctttt ttccaaacag taggtttcat ccaagaccat ttgaagaact gcaaactctt 2941 tctcttagaa aagaaagagg gcagcctaaa ataaacgcaa aatttgctta tactccatca 3001 cattcagatg tcttggttgt gacttattac cagtgtggca gagaacccaa gttacatttt 3061 agatcaaaat attctttatg taggtattgt taaaaggcta gagcctacaa gttgctcttc 3121 catgcgttgg tcagggggcc ctgaaaacac tggtaatatt aagagtcttt ctcaggtaa 3181 cttaatgttt tcttaatgaa cagtgtttcc agctacaaat tcttccaata aattgtcttc 3241 cttttgaaa agtactctca tagaagaaat ttagcaattt ctcgttgact gactcagtct 3301 attttaagta ttcagaaaag attttgatcc ccattgagtt aatgctctgc cttgaaaatt 3361 attttctga tccttgttag tgataacatt ttttttctac tgaaggtcag aggataggaa 3421 acaagtattt ctcttctggt atacatgtaa tgtattctgt aaaaaagtat tcatattggc 3481 aattttagtt aggcataata ttgtggttgt aatttttaaa acttagtgtt ttgtctgatt 3541 aaagcaggca ctgatcaggg tatcctcctaa gaggtaattc acttcttatt ccttttccaat 3601 aattattaca ttctaaattt tcatctatga gaaataacaa acaagaaggg aatagaatta 3661 aattgggtta taatctaatc ttcattgttt aaatggtttg ccttctcacc attgaagcca 3721 ttttttata gcctcagaaa gaggaaataa tgcctccacc attttctacc tggtgacttg 3781 aaaattgaac tttaagtta ggaagaagtt agagtcaggg aacttgtata ccactatcta 3841 tgcagcattg ttatagtctg attatttctg tgttttgaat atgatttcc taatgctcta 3901 aataaaattt tgttaaaaat caaaaaaaaa aaaaaaaaat cgac 1 M C K S L R Y C F S H C L Y L A M T R L 1 ATGTGTAAATCACTGCGTTATTGCTTTAGTCATTGTCTCTATTTAGCAATGACAAGACTG 21 E E V N R E V N N M H S S V R Y L G Y L A 61 GAAGAAGTAAATAGAGAAGTAACATGCATTCTTCAGTGCGGTATCTTGGCTATTTAGCC 41 R I N L L V A I C L G L Y V R W E K T A 121 AGAATCAATTTATTGGTTGCTATATGCTTAGGTCTATACGTAAGATGGGAAAAAACAGCA 61 N S L I L V I F I L G L F V L G I A S I 181 AATTCCTTAATTTTGGTAATTTTTATTCTTGGTCTTTTTGTTCTTGGAATCGCCAGCATA 81 L Y Y Y F S M E A A S L S L S N L W F G 241 CTCTATTACTATTTTTCAATGGAAGCAGCAAGTTTAAGTCTCTCCAATCTTTGGTTTGGA	SEQ ID NO:65

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		101 F L L G L L C F L D N S S F K N D V K E 301 TTCTTGCTTGGCCTCCTATGTTTCTTGATAATTCATCCTTAAAAATGATGTAAAGAA	
		121 E S T K Y L L L T S I V L R I L C S L V 361 GAATCAACCAAATATTTGCTTCTAACATCCATAGTGTTAAGGATATTGTGCTCTCTGGTG	
		141 E R I S G Y V R H R P T L L T T V E F L 421 GAGAGAATTTCTGGCTATGTCCGTCATCGGCCCACTTTACTAACCACAGTTGAATTTCTG	
		161 E L V G F A I A S T T M L V E K S L S V 481 GAGCTTGTTGGATTTGCCATTGCCAGCACAACTATGTTGGTGGAGAAGTCTCTGAGTGTC	
		181 I L L V V A L A M L I I D L R M K S F L 541 ATTTTGCTTGTTGTAGCTCTGGCTATGCTGATTATTGATCTGAGAATGAAATCTTTCTTA	
		201 A I P N L V I F A V L L F S S L E T P 601 GCTATTCCAAACTTAGTTATTTTTGCAGTTTTGTTATTTTTTTCCTCATTGGAAACTCCC	
		221 K N P I A F A C F F I C L I I T D P F L D 661 AAAAATCCGATTGCTTTTGCGTGTTTTTTATTTGCCTGATAACTGATCCTTTCCTTGAC	
		241 I Y F S G L S V T E R W K P F L Y R G R 721 ATTTATTTTAGTGGACTTTCAGTAACTGAAAGATGGAAACCCTTTTGTACCGTGGAAGA	
		261 I C R R L S V V F A G M I E L T F F I L 781 ATTTGCAGAAGACTTTCAGTCGTTTTGCTGGAATGATTGAGCTTACATTTTTATTCTT	
		281 S A F K L R D T H L W Y F V I P G F S I 841 TCCGCATTCAAACTTAGAGACACTCACCTCTGGTATTTTGTAATACCTGGCTTTTCCATT	
		301 F G I F R M I C H I I F L L T L W G F H 901 TTTGGAATTTTCAGGATGATTTGTCATATTATTTTTCTTTTAACTCTTTGGGATTCCAT	
		321 T K L N D C H K V Y F T H R T D Y N S L 961 ACCAAATTAAATGACTGCCATAAAGTATATTTTACTCACAGGACAGATTACAATAGCCTT	
		341 D R I M A S K G M R H F C L L S E Q L V 1021 GATAGAATCATGGCATCCAAAGGGATGCGCCATTTTTGCTTGATTTCAGAGCAGTTGGTG	
		361 F E S L L A T A I L G A V S W Q P T N G 1081 TTCTTTAGTCTTCTTGCAACAGCGATTTTGGGAGCAGTTTCCTGGCAGCCAACAAATGGA	
		381 I F L S M F L I V L P L E S M A H G L F 1141 ATTTTCTTGAGCATGTTCCTAATCGTTTGCCATTGGAATCCATGGCTCATGGGCTCTTC	
		401 H E L G N C L G G T S V G Y A I V I P T 1201 CATGAATTGGGTAACTGTTTAGGAGGAACATCTGTTGGATATGCTATTGTGATTCCCACC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		421 N F C S P D D G Q P T L L P P E H V Q E L 1261 AACTTCTGCAGTCCTGATGGTCAGCCAACACTGCTTCCCCCAGAACATGTACAGGAGTTA	
		441 N L R S T G M L N A I Q R F F A Y H M I 1321 AATTTGAGGTCTACTGGCATGCTCAATGCTATCCAAAGATTTTTTGCATATCATATGATT	
		461 E T Y G C D Y S T S G L S F D T L H S K 1381 GAGACCTATGGATGTGACTATTCCACACAAGTCGACTGTCATTTGATACTCTGCATTCCAAA	
		481 L K A F L E L R T V D G P R H D T Y I L 1441 CTAAAAGCTTTCCTCGAACTTCGGACAGTGCATGGACCCAGACATGATACGTATATTTTG	
		501 Y Y S G H T H G T G E W A L A G G D T L 1501 TATTACAGTGGGCACACCCATGGTACAGGAGAGTGGGCTCTAGCAGGTGGAGATACACTA	
		521 R L D T L I E W W R E K N G S F C S R L 1561 CGCCTTGACACACTTATAGAATGGTGGAGAAAAGAATGGTTCCTTTGTTCCCGGCTT	
		541 I I V L D S E N S T P W V K E V R K I N 1621 ATTATCGTATTAGACAGCGAAAATTCAACCCCTTGGGTGAAAGAAGTGAGGAAAATTAAT	
		561 D Q Y I A V Q G A E L I K T V D I E E A 1681 GACCAGTATATTGCAGTGCAAGGAGCAGAGTTGATAAAAACAGTAGATATTGAAGAAGCT	
		581 D P P Q L G D F T K D W V E Y N C N S C 1741 GACCCGCCACAGCTAGGTGACTTTACAAAAGACTGGGTAGAATATAACTGCAACTCCTGT	
		601 N N I C W T E K G R T V K A V Y G V S K 1801 AATAACATCTGCTGGACTGAAAAGGGACGCACAGTGAAAGCAGTATATGGTGTGTCAAAA	
		621 R W S D Y T L H L P T G S D V A K H W M 1861 CGGTGGAGTGACTACACTCTGCATTTGCCAACGGGAAGCGATGTGGCCAAGCACTGGATG	
		641 L H F P R I T Y P L V H L A N W L C G L 1921 TTACACTTCCTCGTATTACATATCCCTAGTGCATTTGGCAAATTGGTTATGCGGTCTG	
		661 N L F W I C K T C F R C L K R L K M S W 1981 AACCTTTTTTGGATCTGCAAAACTTGTTTTAGGTGCTTGAAAAGATTAAAAATGAGTTGG	
		681 F L P T V L D T G Q G F K L V K S - 2041 TTTCTTCCTACTGTGCTGGACACAGGACAAGGCTTCAAACTTGTCAAATCTTAA	
WBC014G08_V1.3_at	RTN4-C (RTN4)		
		1 GGAGACTGCAGGCTTCGGTTGAGGAAACGGGTATTTCATGTCTCGGGGTAGATTTTCACA 61 GTTGCAGCTTTCTTCGGCTGGTATGCATAATTGATAATTGCATCTGTAGGGCAGATTGTGAC 121 AAGACATGGACGGTCAGAAGAAAAATTGGAAGGACAAGGTTGTTGACCTCCTCTACTGGA	SEQ ID NO:66

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		181 GAGACATTAGAAGACTGGAGTGGTGTTTGGTGCCAGCTTGTTCCTGCTGCTCTCGCTGA 241 CACTATTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTA 301 TCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACC 361 CATTCAGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACA 421 GCAATTCTGCTCTTGGTCATGTTAACTGCACAATAAAGAACTCAGACGCCTCTTCTTAG 481 TTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTG 541 GTGCCTTGTTCAATGGTCTCGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTC 601 CTGTTATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGACTTGCAAATAAGA 661 ATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTG 721 AATGAGAAACGCCTGAAAGACTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATT 781 TGATTCCATTGGGGAGGGTCAGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTTTCACA 841 GATCTTTATTTTCAGCAATGCAGTGTCTGAGGAGAAATCACCTGTCTTGACTGCCATGTG 901 TTCATCACCTTAAGTATTGTAAGCTGCTATGTATGGATTTGAACCGTAATCATTTGTTTT 961 TCCTATATGAGGCACTGGTGAATAAAAAAAGATCTGAGAAAGCTGTATATTACATTTTGT 1021 TACAGGTAGTCTTGCTGTATTTTGGGAATTGCAGAGAAAGTGGAGCTGAAAAAAATAACC 1081 CTTTTCACAGTTTGTGCACTGTGTATGGTCTGTGTAGATTGGATGCAGATTTTCTGAAAT 1141 GAAATGTTTAGACGAGATCATACCACTAAAGCAGAAGTGAGAAAAACTTGCCTTTCTGGTA 1201 TGTTCTAGGTGTATTGTGAATTTTACTGTTATATTAATTGCCAATATAAGTAAATATAGA 1261 TTATATATATTCTATATATAGTGTTTCACAAAGCTTAGAGACCTTTACCTTCCAGCTGC 1321 CCCACAGTGCTTGATCTTTCAGAGAGTCTTTGGTTGTACGTGTGTAGTTCCAAAGCACAT 1381 AAGCTAGAAAAAGAAAATATATTTCTAGGTGCACTACCATCTGTTTTCAACGTGAACCGA 1441 CGCCATGCACATAGAACTCTTCACGTCGACTGCATCGCACACAGACTTGCTATAGTTAATTT 1501 TGTCACAAACTCTGACTCTGTGGACTGAATCTAATGCTTCCAAAAACGTTGTTTGCAAAT 1561 ATCAAACATTGTTATGCAAGAAATCATAAAATGAAGATTTATACAATTGTGGTTTAAGCT 1621 GTACTGAACTAAATCTGTGGAATGCATTGTGAACTGTTAAAGCAAAGTATCAATAAAGCT 1681 TATAGACTTAAAAAAAAAAAAAAAAA	SEQ ID NO:67
		1 M D G Q K K N W K D K V V D L L Y W R D 1 ATGGACGGTCAGAAGAAAAATTGGAAGGACAAGGTTGTTGACCTCCTCTACTGGAGAGAC 21 I K K T G V V F G A S L F L L L S L T V 61 ATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCTTGTTCCTGCTGCTCTCGCTGACAGTA 41 F S I V S V T A Y Y I A L A L L S V T I S 121 TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC 61 F R I Y K G V I Q A I Q K S D E G H P F 181 TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC 81 R A Y L E S E V A I S E E L V Q K Y S N 241 AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT 101 S A L G H V N C T I K E L R R L F L V D 301 TCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT 121 D L V D S L K F A V L M W V F T Y V G A 361 GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		141 L F N G L T L L I L A L I S L F S V P V 421 TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTT 161 I Y E R H Q A Q I D H Y L G L A N K N V 481 ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT 181 K D A M A K I Q A K I P G L K R K A E - 541 AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	
WBC013H03_V1.3_at	RAB6 interacting protein 1 (RAB6IP1)	1 CGCTCTCGGCTAGCTGCAGCGGCGGCGCCGCGGAGGGAAGGCATCCAGGATGCGGTGCG 61 GGCCGGCCCCGGTGCCCCCCCCGCCCCGTCACGGCAGCCGCGGCGGCCGAGGGGACCGGGCC 121 AGGGCCGGGGCGGCGGCCCGAGCCGCGTAGCGGCGGCGGCGGGAGGGGCGGCCTGAGG 181 GCGGACGGGCGGGGCGCCCGGGTTGCGGGGGCTCGGTGCCGCTCCGCACTGCCCGGCCGGT 241 CTCGGCCCCGGCGCCGCCATGAGTGGCGGCGGCGGAGGGGGCTCGGCGCCCAGTCGCTTC 301 GCCGACTACTTGTCATCTGCGGACTGGACACGGAGACCGGGCTGGAGCCGGACGAGCTG 361 TCGGCATTATGCCAGTACATACAGGCTTCTAAAGCCAGGGATGGTGCCCAGCCCTTTCATT 421 TCAAGTACGACTGAAGGAGAAAATTTTGAGCAGACACCATTGAGAAGAACATTCAAATCT 481 AAGGTCCTTGCACGATATCCTGAGAACGTAGAATGGAAATCCCTTTGACCAAGATGCAGTA 541 GGAATGCTATGTATGCCGAAAGGGCTGGCATTCAAGACCCAGGCTGATCCCAGGGAGCCC 601 CAATTCCATGCCTTTATTATTATCACAAGGGAGGATGGCTCTCTCGGACATTTGGGTTTGCCCTC 661 ACATTTTATGAAGAGGTGACTAGCAAGCAGATCTGCAGTGCAATGCAGACCCTCTACCAC 721 ATGCACAATGCTGAGTATGATGTCCTACATGCTCCCCCTGCTGATGACAGAGACCAGAGC 781 AGCATGGAGGATGGTGAAGACACTCCTGTGACCAAACTGCAGCGCTTCAACTCCTATGAC 841 ATTAGCCGGACACTCTCTACGTCTCTAAGTGCATCTGCCTCATCACACCCATGTCTTTC 901 ATGAAGGCATGTCGGACGCGTGCTGGAGCAACTCCACCAGGCAGTCACTTCACCTCAGCCC 961 CCTCCACTGCCCCTTGAGAGCTACATATACAACGTACTCTACGAGGTGCCGCTCCCACCT 1021 CCTGGCCGGTCCTTGAAGTTTTCTGGGTCTATGGGCCAATAATCTGCCAGACACCAAGT 1081 ACCAATGAGCTTCCCCTATTTGACTTTCCTGTCAAAGAGGTTTTTGAACTGCTCGGGGTG 1141 GAGAATGTGTTTCAGCTTTTTACTTGTGCCCTTCTGGAGTTTCAAATCCTGCTCTACTCA 1201 CAGCATTACCAGAGACTGATGACTGTGGCGGAGACGATTACAGCTCTCATGTTTCCTTTC 1261 CAGTGGCAGCATGTCTATGTCCCTATTCTCCCAGCTTCTCTCCTGCATTTCTTAGATGCT 1321 CCTGTTCCATACCTGATGGGTTTGCATTCCAATGGCCTGGATGACCGGTCAAAGCTGGAG 1381 CTGCCTCAAGAGGCTAACCTCTGCTTTGTGGACATTGACAACCACTTCATTGAGTTGCCA 1441 GAGGACTTGCCACAGTTCCCCAACAAATTGGAGTTTGTCCAGGAAGTCTCTGAGATTCTC 1501 ATGGCATTTGGAATTCCCCCTGAAGGGAATCTTCATTGCAGTGAGAGTGCCTCCAAGCTG 1561 AAGAGGCTGCGGGCCTCTGAGCTTGTCTCGGACAAGAGGAATGGGAACATTGCTGGCTCC 1621 CCTTTGCATTCCTACGAGCTTCTTAAGGAGAATGAAACTATTGCCCGGCTGCAAGCCTTG 1681 GTCAAGAGAACTGGGGTGAGCCTGGAAAAGTTGGAAGTGCGTGAAGACCCCAGCAGCAAT 1741 AAGGATCTCAAAGTTCAGTGTGATGAAGAACTCAGGATTTACCAGCTAAACATTCAG 1801 ATCCGGGAAGTTTTTGCAAATCGTTTCACTCACTCAGATGTTTGCAGATTATGAGGTGTTTGTC 1861 ATCCAACCCAGCCAGGATAAGGAATCCTGGTTTACCAACAGGGAGCAAATGCAAAACTTT 1921 GATAAAGCATCTTTTCTGTCAGATCAGCCTGAGCCCTACCTGCCCTTCCTCTCAAGATTC 1981 CTGGAGACCCAGATGTTTGCATCTTTCATTGACAACAAAATAATGTGTCATGATGATGAT 2041 GATAAAGACCCTGTACTCCGGGTATTTGATTCCCGAGTTGACAAGATCAGGCTGTTGAAT 2101 GTTCGGACACCTACTCTCCGTACATCCATGTACCAGAAGTGTACCACTGTGGATGAAGCA 2161 GAGAAAGCAATTGAGCTGCGTCTGGCAAAAATTGACCATACTGCAATTCACCCACATTTA 2221 CTTGACATGAAGATTGGACAAGGGAAATATGAGCCGGGCTTCTTCCCTAAGCTGCAGTCT	SEQ ID NO:68

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2281 GATGTACTTTCCACTGGGCCAGCCAGCAACAAGTGGACGAAAAGGAATGCCCCTGCCCAG	
		2341 TGGAGGCGGAAAGATCGGCAGAAGCAGCACACAGAACACCTGCGTTTAGATAATGACCAG	
		2401 AGGGAGAAGTACATCCAGGAAGCCAGGACTATGGGCAGCACTATCCGCCAGCCCAAACTG	
		2461 TCCAACCTCTCTCCATCAGTGATTGCCCAGACCAATTGGAAGTTTGTAGAGGGCCTGCTG	
		2521 AACGAATGCCGCAATAAGACCAAGAGGATGCTGGTGGAAAAGATGGGCCGAGAAGCTGTG	
		2581 GACCTAGGGCATGGGGAGGTGAACATCACAGGGGTGGAAGAGAACACCCTGATTGCCAGC	
		2641 CTTTGTGATCTCCTGGAAAGGATCTGGAGTCATGGACTACAAGTGAAACAGGGCAAATCA	
		2701 GCCTTATGGTCCCACCTGTTACATTATCAGGACAACCGGCAGAGAAACTCACATCAGGA	
		2761 AGCCTCAGTACCTCAGGAATACTTCTTGATTCAGAACGTAGGAAGTCTGATGCCAGCTCA	
		2821 CTCATGCCTCCCCTGAGGATCTCCCTGATTCAGGATATGAGGCACATCCAGAACATCGGG	
		2881 GAAATCAAGACTGATGTGGGAAAGGCCAGAGCATGGGTGCGACTGTCCATGGAAAAAAAG	
		2941 TTACTTTCCAGACACCTGAAGCAGCTCCTCTCAGACCATGAGCTCACCAAAAAGTTATAT	
		3001 AAGCGCTATGCCTTCCTGCGCTGTGATGACGAGAAGGAGCAGTTCCTCTATCACCTCCTG	
		3061 TCTTTCAATGCCGTCGATTACTTTTGCTTCACCAATGTCTTCACAACTATCCTGATCCCG	
		3121 TACCACATTCTGATCGTACCAAGCAAGAACTGGGGGCGCTCCATGTTCACTGCCAACCCA	
		3181 TGGATCTGTATATCAGGAGAATTGGGTGACACAGATCATGCAGATTCCCAGGAATGTG	
		3241 CTAGAGATGACCTTCGAGTGCCAGAACTTGGGGAAGCTTACTATGTCCAGATTGGCCAT	
		3301 GATAACTCTGGGCTGTATGCCAAATGGCTGGTGGAGTATGTGATGGTCAGGAATGAGATC	
		3361 ACAGGACATACCTACAAGTTCCCGTGTGGCCGCTGGTTAGGGAAGGCATGGATGATGGA	
		3421 AGCCTGGAGCGGATCCTAGTTGGGGAGCTGCTCACATCCCAGCCTGAGGTGGATGAGAGG	
		3481 CCATGCCGGACCCCGCCGCTGCAGCAGTCCCCCAGTGTCATCCGGAGGCTTGTTACCATC	
		3541 TCTCCCAACAACAAGCCCAAGCTGAACACCGGGCAGATCCAGGAGTCCATCGGGAGGCA	
		3601 GTCAACGGCATCGTGAAGCACTTTCATAAGCCTGAGAAAGAGCGAGGCAGTCTGACGCTG	
		3661 TTGCTTGTGGAGAGTGCGGCCTCGTCTCGGCCCTGGAACAGGCTTTCCAGCATGGATTT	
		3721 AAATCGCCCCGGCTCTTCAAAAATGTCTTCATTTGGGATTTCCTGGAAAAAGCACAAACC	
		3781 TATTATGAGACTTTGGAGCAGAATGAAGTTGTCCCTGAGGAAAACTGGCATATGAGGGCC	
		3841 CGGAACTTCTGCCGATTTCTCACTGCGATCAACAATACTCCGCGCAGCATCGGCAAGGAC	
		3901 GGCAAGTTTCAGATGCTGGTGTGCCTGGGAGCCAGAGATCACCTCCTACATCACTGGATT	
		3961 GCCCTGCTGGCCGACTGCCCCATCACCGCGCACATGTATGAGGATGTGGCACTGATCAAA	
		4021 GACCACACACTGGTCAACTCCTTGATCCGCGTGCTGCAGACATTCCAGGAGTTCAACATC	
		4081 ACGCTGGAGACGTCCCTTGTCAAGGCATCGACATCTGACTTCCAGCACCAGCGAGCAGC	
		4141 GGGACCGAGAGAGACTCACCCTGCAGCTCTGACCCTTCTTCCCAAAGGGACTTCAGCGAG	
		4201 TTGTGCAGGAGACGGAGAGGAAATGTACACTCACTGTAAAAAGAAAACTAGAGGATTTTT	
		4261 GGAATAAATAATCTATTTTAGAGTTTATTTGCTGATTTGCTTTTTACACACTTTCATGTG	
		4321 AAAGAATGATAGAGAGAGGGAGACGAGGTTGGTGCCGCTTATTTGAAGCTGGCGCCCTC	
		4381 CCTCGCCGCGGCCGCGAGCTGGGAGCCTACGGCCTCCCTGGACTGAGCCCTGTGGCACTGC	
		4441 GTGCGGGACAGTTATGTTTCCTTGCCCCGTCGCATTAATGAGGCCCTTCCACATCATTTT	
		4501 TAAACTAATGTTTTTCTATATTAACATTATTATGCATATTTGGCTTTCATAGGCCACACA	
		4561 CAGGTGTGCTGCGCGGGAAGCCCCCATGCTCCAATCAAAGGGATTTTTAGTAGTGCCTCTA	
		4621 AGCAAGCACCGATGAGTCAGTCCCACGTATTTCTTTTTTGTCAGTATTGTTTGGGAAGG	
		4681 AGACATGCCGGGATGTGTCATCGTGCCAAATACCACATTTCCTGTTGGCACATTTCACA	
		4741 GAAGTAAACATAAGCATGTTTTTAACAGGTTTTTCTTTTCTTTTTTCTTTTTAAAATGTT	
		4801 TTATTTATTTAACCCGCCATTGTGTGTTTTTAAGTATTTTCTTTTTTTTAAGGAAAGGAAA	
		4861 AGCTTGTCACAGTCTAACTGGCTATGTTATTACTGTTAAATTTATGTTGTTTTTGCAACTT	
		4921 AGAAACCAGCTACAGTATGGCCCACTTAATAAACACCTGAAACGAGAAAAAAAAAAAAA	
		4981 AAAAAAAAAA	
		1 M S G G G G G G S A P S R F A D Y F V	SEQ ID NO:69

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1 ATGAGTGGCGGCGGCGGCGGAGGGGGCTCGGCGCCCAGTCGCTTCGCCGACTACTTTGTC	
		21 I C G G L D T E E T G G L E E P D D E L S S A L C Q	
		61 ATCTGCGGACTGGACACGGAGACCGGGCTGGAGCCGGACGAGCTGTCGGCATTATGCCAG	
		41 Y I Q A S K A R D G A S P F I S S T T E	
		121 TACATACAGGCTTCTAAAGCCAGGGATGGTGCCAGCCCTTTCATTTCAAGTACGACTGAA	
		61 G E N F E Q T P L R R R T F F K S K V L A R	
		181 GGAGAAAATTTTGAGCAGACACCATTGAGAAGAACATTCAAATCTAAGGTCCTTGCACGA	
		81 Y P E N V E W N P F D Q D A V G M L C M	
		241 TATCCTGAGAACGTAGAATGGAATCCCTTTGACCAAGATGCAGTAGGAATGCTATGTATG	
		101 P K G L A F K T Q A D P R E P Q F H A F	
		301 CCGAAAGGGCTGGCATTCAAGACCCAGCCTGATCCCAGGGAGCCCCAATTCCATGCCTTT	
		121 I I T R E D G S R T F G F A L T F Y E E	
		361 ATTATCACAAGGGAGGATGGCTCTCGGACATTTGGGTTTGCCCTCACATTTTATGAAGAG	
		141 V T S K Q I C S A M Q T L Y H M H N A E	
		421 GTGACTAGCAAGCAGATCTGCAGTGCAATGCAGACCCTCTACCACATGCACAATGCTGAG	
		161 Y D V L H A P P A D D R D Q S S M E D G	
		481 TATGATGTCCTACATGCTCCCCCTGCTGATGACAGAGACCAGAGCAGCATGGAGGATGGT	
		181 E D T P V T K L Q R F N S Y D I S R D T	
		541 GAAGACACTCCTGTGACCAAACTGCAGCGCTTCAACTCCTATGACATTAGCCGGGACACT	
		201 L Y V S K C I C L I T P M S F M K A C R	
		601 CTCTACGTCTCTAAGTGCATCTGCCTCATCACACCCATGTCTTTCATGAAGGCATGTCGG	
		221 S V L E Q L H Q A V T S P Q P P P L P L	
		661 AGCGTGCTGGAGCAACTCCACCAGGCAGTCACTTCACCTCAGCCCCCTCCACTGCCCCTT	
		241 E S Y I Y N V L Y E V P L P P P G R S L	
		721 GAGAGCTACATATACAACGTACTCTACGAGGTGCCGCTCCCACCTCCTGGCCGGTCCTTG	
		261 K F S G V Y G P I I C Q R P S T N E L P	
		781 AAGTTTTCTGGGGTCTATGGGCCAATAATCTGCCAGAGACCAAGTACCAATGAGCTTCCC	
		281 L F D F P V K E V F E L L G V E N V F Q	
		841 CTATTTGACTTTCCTGTCAAAGAGGTTTTTGAACTGCTCGGGGTGGAGAATGTGTTTCAG	
		301 L F T C A L L E F Q I L L Y S Q H Y Q R	
		901 CTTTTTACTTGTGCCCTTCTGGAGTTTCAAATCCTGCTCTACTCACAGCATTACCAGAGA	
		321 L M T V A E T I T A L M F P F Q W Q H V	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		961 CTGATGACTGTGGCGGAGACGATTACACCTCTCATGTTTCCTTTCCAGTGGCAGCATGTC	
		341 Y V P I L P A S L L H F L D A P V P Y L 1021 TATGTCCCTATTCTCCCAGCTTCTCTCCTGCATTTCTTAGATGCTCCTGTTCCATACCTG	
		361 M G L H S N G L D D R S K L E L P Q E A 1081 ATGGGTTTGCATTCCAATGGCCTGGATGACCGGTCAAAGCTGGAGCTGCCTCAAGAGGCT	
		381 N L C F V D I D N H F I E L P E D L P Q 1141 AACCTCTGCTTTGTGGACATTGACAACCACTTCATTGAGTTGCCAGAGGACTTGCCACAG	
		401 F P N K L E F V Q E V S E I L M A F G I 1201 TTCCCCAACAAATTGGAGTTTGTCCAGGAAGTCTCTGAGATTCTCATGGCATTTGGAATT	
		421 P P E G N L H C S E S A S K L K R L R A 1261 CCCCCTGAAGGGAATCTTCATTGCAGTGAGAGTGCCTCCAAGCTGAAGAGGCTGCGGGCC	
		441 S E L V S D K R N G N I A G S P L H S Y 1321 TCTGAGCTTGTCTCGGACAAGAGGAATGGGAACATTGCTGGCTCCCCTTTGCATTCCTAC	
		461 E L L K E N E T I A R L Q A L V K R T G 1381 GAGCTTCTTAAGGAGAATGAAACTATTGCCCGGCTGCAAGCCTTGGTCAAGAGAACTGGG	
		481 V S L E K L E V R E D P S S N K D L K V 1441 GTGAGCCTGGAAAAGTTGGAAGTGCGTGAAGACCCCAGCAGCAATAAGGATCTCAAAGTT	
		501 Q C D E E E L R I Y Q L N I Q I R E V F 1501 CAGTGTGATGAAGAAGAACTCAGGATTTACCAGCTAAACATTCAGATCCGGGAAGTTTTT	
		521 A N R F T Q M F A D Y E V F V I Q P S Q 1561 GCAAATCGTTTCACTCAGATGTTTGCAGATTATGAGGTGTTTGTCATCCAACCCAGCCAG	
		541 D K E S W F T N R E Q M Q N F D K A S F 1621 GATAAGGAATCCTGGTTTACCAACAGGGAGCAAATGCAAAACTTTGATAAAGCATCTTTT	
		561 L S D Q P E P Y L P F L S R F L E T Q M 1681 CTGTCAGATCAGCCTGAGCCCTACCTGCCCTTCCTCTCAAGATTCCTGGAGACCCAGATG	
		581 F A S F I D N K I M C H D D D D K D P V 1741 TTTGCATCTTTCATTGACAACAAAATAATGTGTCATGATGATGATGATAAAGACCCTGTA	
		601 L R V F D S R V D K I R L L N V R T P T 1801 CTCCGGGTATTTGATTCCCGAGTTGACAAGATCAGGCTGTTGAATGTTCGGACACCTACT	
		621 L R T S M Y Q K C T T V D E A E K A I E 1861 CTCCGTACATCCATGTACCAGAAGTGTACCACTGTGGATGAAGCAGAGAAAGCAATTGAG	
		641 L R L A K I D H T A I H P H L L D M K I	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1921 CTGCGTCTGGCAAAAATTGACCATACTGCAATTCACCCACATTTACTTGACATGAAGATT	
		661 G Q Q G K Y E P G F F P K L Q S D V L S T	
		1981 GGACAAGGGAAATATGAGCCGGGCTTCTTCCCTAAGCTGCAGTCTGATGTACTTTCCACT	
		681 G P A S N K W T K R N N A P A Q W R R K D	
		2041 GGGCCAGCCAACAAGTGGACGAAAAGGAATGCCCCTGCCCAGTGGAGGCGGAAAGAT	
		701 R Q K Q H T E H L R L D N D Q R E K Y I	
		2101 CGGCAGAAGCAGCACACAGAACACCTGCGTTTAGATAATGACCAGAGGGAGAAGTACATC	
		721 Q E A R T M G S T I R Q P K L S N L S P	
		2161 CAGGAAGCCAGGACTATGGGCAGCACTATCCGCCAGCCCAAACTGTCCAACCTCTCTCCA	
		741 S V I A Q T N W K F V E G L L K E C R N	
		2221 TCAGTGATTGCCCAGACCAATTGGAAGTTTGTAGAGGGCCTGCTGAAGGAATGCCGCAAT	
		761 K T K R M L V E K M G R E A V E L G H G	
		2281 AAGACCAAGAGGATGCTGGTGGAAAAGATGGCCGAGAAGCTGTGGAGCTAGGGCATGGG	
		781 E V N I T G V E E N T L I A S L C D L L	
		2341 GAGGTGAACATCACAGGGGTGGAAGAGAACACCCTGATTGCCAGCCTTTGTGATCTCCTG	
		801 E R I W S H G L Q V K Q G K S A L W S H	
		2401 GAAAGGATCTGGAGTCATGGACTACAAGTGAAACAGGGGAAATCAGCCTTATGGTCCCAC	
		821 L L H Y Q D N R Q R K L T S G S L S T S	
		2461 CTGTTACATTATCAGGACAACCGGCAGAGAAAACTCACATCAGGAAGCCTCAGTACCTCA	
		841 G I L L D S E R R K S D A S S L M P P L	
		2521 GGAATACTTCTTGATTCAGAACGTAGGAAGTCTGATGCCAGCTCACTCATGCCTCCCCTG	
		861 R I S L I Q D M R H I Q N I G E I K T D	
		2581 AGGATCTCCCTGATTCAGGATATGAGGCACATCCAGAACATCGGGGAAATCAAGACTGAT	
		881 V G K A R A W V R L S M E K K L L S R H	
		2641 GTGGGAAAGGCCAGAGCATGGGTGCGACTGTCCATGGAAAAAAAGTTACTTTCCAGACAC	
		901 L K Q L L S D H E L T K K L Y K R Y A F	
		2701 CTGAAGCAGCTCCTCTCAGACCATGAGCTCACCAAAAAGTTATATAAGCGCTATGCCTTC	
		921 L R C D D E K E Q F L Y H L L S F N A V	
		2761 CTGCGCTGTGATGACGAGAAGGAGCAGTTCCTCTATCACCTCCTGTCTTTCAATGCCGTC	
		941 D Y F C F T N V F T T I L I P Y H I L I	
		2821 GATTACTTTTGCTTCACCAATGTCTTCACAACTATCCTCGATCCCCGTACCACATTCTGATC	
		961 V P S K K L G G S M F T A N P W I C I S	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2881 GTACCAAGCAAGAAGCTGGGGGGGCTCCATGTTCACTGCCAACCCATGGATCTGTATATCA	
		981 G E L G E T Q I M Q I P R N V L E M T F	
		2941 GGAGAATTGGGTGAGACACAGATCATGCAGATTCCCAGGAATGTGCTAGAGATGACCTTC	
		1001 E C Q N L G K L T T V Q I G H D N S G L	
		3001 GAGTGCCAGAACTTGGGGAAGCTTACTACTGTCCAGATTGGCCATGATAACTCTGGGCTG	
		1021 Y A K W L V E Y V M V R N E I T G H T Y	
		3061 TATGCCAAATGGCTGGTGGAGTATGTGATGGTCAGGAATGAGATCACAGGACATACCTAC	
		1041 K F P C G R W L G K G M D D G S L E R I	
		3121 AAGTTCCCGTGTGGCCGGTGGTTAGGGAAGGGCATGGATGATGGAAGCCTGGAGCGGATC	
		1061 L V G E L L T S Q P E V D E R P C R T P	
		3181 CTAGTTGGGGAGCTGCTCACATCCCAGCCTGAGGTGGATGAGAGGCCATGCCGGACCCCG	
		1081 P L Q Q S P S V I R R L V T I S P N N K	
		3241 CCGCTGCAGCAGTCCCCCAGTGTCATCCGCAGGCTTGTTACCATCTCTCCCAACAACAAG	
		1101 P K L N T G Q I Q E S I G E A V N G I V	
		3301 CCCAAGCTGAACACCGGGCAGATCCAGGAGTCCATCGGGGAGGCAGTCAACGGCATCGTG	
		1121 K H F H K P E K E R G S L T L L L C G E	
		3361 AAGCACTTTCATAAGCCTGAGAAAGAGCGAGGCAGTCTGACCGTGTTGCTTTGTGGAGAG	
		1141 C G L V S A L E Q A F Q H G F K S P R L	
		3421 TGCGGCCTCGTCTCGGCCCTGGAACAGGCTTTCCAGCATGGATTTAAATCGCCCCGGCTC	
		1161 F K N V F I W D F L E K A Q T Y Y E T L	
		3481 TTCAAAAATGTCTTCATTTGGGATTTCCTGGAAAAAGCACAAACCTATTATGAGACTTTG	
		1181 E Q N E V V P E E N W H M R A R N F C R	
		3541 GAGCAGAATGAAGTTGTCCCTGAGGAAAACTGGCATATGAGGGCCCGGAACTTCTGCCGA	
		1201 F V T A I N N T P R S I G K D G K F Q M	
		3601 TTTGTCACTGCGATCAACAATACTCCGCGCAGCATCGGCAAGGACGGCAAGTTTCAGATG	
		1221 L V C L G A R D H L L H H W I A L L A D	
		3661 CTGGTGTGCCTGGGAGCCAGAGATCACCTCCTACATCACTGGATTGCCCTGCTGGCCGAC	
		1241 C P I T A H M Y E D V A L I K D H T L V	
		3721 TGCCCCATCACCGCGCACATGTATGAGGATGTGGCACTGATCAAAGACCACACACACTGGTC	
		1261 N S L I R V L Q T L Q E F N I T L E T S	
		3781 AACTCCTTGATCCCGCTGCAGACATTGCAGGAGTTCAACATCACGCTGGAGACGTCC	
		1281 L V K G I D I -	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		3841 CTTGTCAAGGGCATCGACATCTGA	
WBC013E10	Homo sapiens cDNA FLJ45679 fis, clone ERLTF2001835	1 aaaaacccca gcaggttagc ttctcattaa atagcttctc ctgagggcag accttgttaa 61 gaagaacaaa atgctctggc gtatttcaaa atggctcctt ttccccaccc actaccagag 121 gcatggataa tcaccctgag gacctgtgag agatccagga gcttaaaaaa aattggggag 181 cggggaagag ggaatggcta ggtccctctg acttgtccac actgatcctt caggtttacc 241 tatcctggta cttgttccat tggaggcttc agcggctagt ttctgctctg tggttaccaa 301 tgacacagga gctgagcttc caaaaattta ttgaacaatc tgacttacta ggagaactta 361 aatatgactt caatgaaaaa gatgaattca gacatactga gacacaaagg ccttttgtct 421 ttaactatta tgaaaatgtc cttgagaaaa atagcaagcg ctaccaggcc cttggccatt 481 tgcttgaaca atacatttat gagcttttgg agaaagtgtg caaattagaa aaagtatata 541 tcccacctga ggctgataaa gaagaaccaa gaagcttctt tttcatgagc gagaaagcat 601 taacaaatca ccattctgct cttcttatcc ttcttcaaga ccatggggtc tttcgagctg 661 gtcagtggag tcaacaggca ataatacatc atggtctcca acatggaagt cagataccat 721 gtattcaaat ggcattgcag gcacactatg atgtaattgt gctaaacccc aatgataatt 781 ttgtggaacc aaaggtggaa aaagagtgga aaggcctttt aacacaaaat attgagtcat 841 cttctctaaa aatggttcaa ggtgggagct ttttctctct ccagcatcct cccaaatgca 901 ttccaaaaag atgcagcaac acccccgaag aacacacggc ttacatatgg gattacttca 961 tttcaaagac tgaaggcaag gatattgcct tcattgtaca tggttatgga ggcttggttt 1021 ttatggactt gcttgttcgt agaaggtggg aagtgatgag caaagtatat gctgttgcac 1081 ttatcgactc tgaacatcac gtaggacacc agctgggaag tgatgtacaa ttattagcat 1141 ggataaagca ccactgccgt gaatgggtga caagtcctaa gcctttggat aaacctgcag 1201 ctactgtttt caaaaaggaa tttcctatgg tttctgctgg cacagaaaag tacatcttag 1261 ccccttcctc tagccttcag tcaattttta agtactttaa aaaagcttta aaagccagaa 1321 caaccattaa tttctctcga atgccaatag tgactagaag ctccacaaaa agaaagcaaa 1381 gtgcttaaac tacttttgtc atctaagatt tttttgtcct tctgcaactt tgctaataca 1441 gattctggaa gaaaaaaaaa cactttcaac tcacacacaa tatgatgttc tggcttgagg 1501 tttgatttgt tacttttttat tatttggttt ttatgaggca gggtctgact ttgctgccca 1561 gggtggtatg gaaatctggc ctcaagcgaa cctcccacct cagcctccca aagtgctgag 1621 attataggca ttagccactg cacatggcca tggccaggtt tgttgctttt ttttttttg 1681 gaggaggagg aggaggagtc tctgtcaccc aggttggagt gcagtggcac catctcagct 1741 cactgcaacc tccacctcct ggtttcaagc agttctcctg cctcagcctc ccaagtagct 1801 gggactacag gcacatgcca ccacgcccag ctaatttttg tatttttact agagacgggc 1861 tgttcgccag gctggtctag gactcttgac ctcaggtgat ccacccacct tggcctccca 1921 aagtgctggg cttacaggca taagccactg cacctggcca ttttgttgtt tttttgaaaa 1981 gtgaacatat tctctctttt gtagcctgtt gatgaactgg gaattcagtg tcatcgttaa 2041 tattttacag tgttagttaa gtgtgaagat ctttctttta aaaagctgtg gtttgatata 2101 atgacaacaa aatggcaatt gataaaaatt agatattgaa tcaatctttg atttctataa 2161 taataccata gtaaaattac aagtgaacat aaaaattaaa catcataagc aaactgcatt 2221 ctttgtgtgt ttatgttttt tgttaagatt tgttgtactc cctgttcacc aggtctgaag 2281 aaaaataaat tttaaat	SEQ ID NO:70
WBC013C03_V1.3_at	Ras GTPase-activating-like	1 GGTATTAAAACTGATCTTTTGACATTTTTGACAATGTTCTTATAAATTACTTTCTTTTTT	SEQ ID NO:71

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
	protein (IQGAP1)	61 ATCATATATGGATGGATGAAGCACAGAGTAAGATAGAGTGCCACAGCAAAGGGGATCTGC 121 CCCTCCTATCTGTCCAATACCCCACAGGTTTGGTGATAATCTTGGGCAATGTTCCAGTC 181 AAACCTGCCTCCCACTTCTCACTAAAGTTAGTGAACATGTGACCCACATTCCCCAAATAA 241 GAGCCTCTTATAAACTCCATTCTTGGCTTTTTCATTCATAGAGATAGCTATTTTATGAGA 301 CATAGATAAAGCATTTTTTATGTGATGCCACCATGCCTTTTTTCTTAATTATTAACTTCT 361 CAAAACATAAACACATTGGAGGCACTTAATAAAGGGAGCTGTACGTACCGCCGTCCGCGC 421 CTCCAAGGTTTCACGGCTTCCTCAGCAGACTCGGGCTCGTCCGCCATGTCCGCCGCAG 481 ACGAGGTTGACGGGCTGGGCGTGGCCCGGCCGCACTATGGCTCTGTCCTGGATAATGAAA 541 GACTTACTGCAGAGGAGATGGATGAAAGGAGACGCTCAGAACGTGGCTTATGAGTACCTTT 601 GTCATTTGCAACAAGCGAAGAGGTGGATGGAAGCATGCCTAGGGGAAGATCTGCCTCCCA 661 CCACAGAACTGGAGGAGGGGCTTAGGAATGGGGTCTACCTTGCCAAACTGGGGAACTTCT 721 TCTCTCCCAAAGTAGTGTCCCTGAAAAAAATCTATGATCGAGAACAGACCAGATACAAGG 781 CGACTGGCCTCCACTTTAGACACACTGATAATGTGATTCAGTGGTTGAATGCCATGGATG 841 AGATTGGATTGCCTAAGATTTTTTACCCAGAAACTACAGATATCTATGATCGAAAGAACA 901 TGCCAAGATGTATCTACTGTATCCATGCACTCAGTTTGTACCTGTTCAAGCTAGGCCTGG 961 CCCCTCAGATTCAAGACCTATATTGGAAAGGTTGACTTCACAGAAGAAGAAATCAACAACA 1021 TGAAGACTGAGTTGGAGAGAATGTATGGCATCCAGATGCCTGCCTTTAGCAAGATTGGGGGCA 1081 TCTTGGCTAATGAACTGTCAGTGGATGAAGCCGCATTACATGCTGCTGTTATTGCTATTA 1141 ATGAAGCTATTGACCGTAGAATTCCAGCCGACACATTTGCAGCTTTGAAAAATCCGAATG 1201 CCATGCTTGTAAATCTTGAAGACGCCCTTGGCATCCACTTACCAGGATATACTTTACCAGG 1261 CTAAGCAGGACAAAATGACAAATGCTAAAAACAGGACAGAAAACTCAGAGAGAGAAAGAG 1321 ATGTTTATGAGAGGAGCTGCTCACGCAAGCTGAAATTCAAGGCAATATAAACAAAGTCAATA 1381 CATTTTCTGCATTAGCAAATATCGACCTGGCTTTAGAACAAGGAGATGCACTGGCCTTGT 1441 TCAGGGCCTCTGCAGTCACCAGCCCTGGGCCTTCGAGGACTGCAGCAACAGATAGCGACT 1501 GGTACTTGAAGCCAGCTCCTGAGTGATAAACAGCAGAAGAGACAGAGTGGTCAGACTGACC 1561 CCCTGCAGAAGGAGGAGCTGCAGTCTGGAGTGGATGCTGCAAACACGTGCTGCCCAGCAAT 1621 ATCAGAGAAGATTGGCAGCAGTAGCACTGATTAATGCTGCAATCCAGAAGGGTGTTGCTG 1681 AGAAGACTGTTTTGGAACTGATGAATCCCGAAGCCCAGCTGCCCCAGGTGTATCCATTTG 1741 CCGCCGATCTCTATCAGAAGGAGCTGGCTACCCTGCAGCGACAAAGTCCTGAACATAATC 1801 TCACCCACCCAGAGCTCTCTGTCGCAGTGGAGATGTTGTCATCGGTGGCCCTGATCAACA 1861 GGGCATTGGAATCAGGAGATGTGAATACAGTGTGGAAGCAATTGAGCAGTTCACTTACTG 1921 GTCTTACCAATATTGAGGAAGAAAACTGTCAGAGGTATCTCGATGAGTTGATGAAACTGA 1981 AGGCTCAGGCACATGCAGAGAATATGAATTCATTACATGGAATGATATCCAAGCTTGCG 2041 TGGACCATGTGAACCTGGTGGTGCAAGAGGAACATGAGAGGATTTTAGCCATTGGTTTAA 2101 TTAATGAAGCCCTGGATGAAGGTGATGCCCAAAAGACTCTGCAGGCCCTACAGATTCCTG 2161 CAGCTAAACTTCAGGGAGTCCTTGCAGAAGTGGCCCAGCATTACCAAGACACGCTGATTA 2221 GAGCGAAGAGAGAAAGCCCAGGAAATCCAGGATGAGTCAGCTGTGTTATGGTTGGATG 2281 AAATTCAAGGTGGAATCTGGCAGTCCAACAAAGACACCCAAGAAGCACAGAAGTTTGCCT 2341 TAGGAATCTTTGCCATTAATGAGGCAGTAGAAAGTGGTGATGTTGGCAAAACACTGAGTG 2401 CCCTTCGCTCCCCTGATGTTGGCTTGTATGGAGTCATCCCTGAGTGTGGTGAAACTTACC 2461 ACAGTGATCTTGCTGAAGCCAAGAAGAAAAAACTGGCAGTAGGAGATAATAACAGCAAGT 2521 GGGTGAAGCACTGGGTAAAAGGTGGATATTATTATTACCACAATCTGGAGACCCAGGAAG 2581 GAGGATGGGATGAACCTCCAAATTTGTGCAAAATTCTATGCAGCTTTCTCGGAGGAGA 2641 TCCAGAGTTCTATCTCTGGGGTGACTGCCGCATATAACCGAGAACAGCTGTGCCTGGCCA 2701 ATGAAGGCCTGATCACCAGGCTGCAGGCTCGCTGCCGTGGATACTTAGTTCGACAGGAAT 2761 TCCGATCCAGGATGAATTTCCTGAAGAAACAAATCCCTGCCATCACCTGCATTCAGTCAC 2821 AGTGGAGAGGATACAAGCAGAAGAAGGCATATCAAGATCGGTTAGCTTACCTGCGCTCCC 2881 ACAAAGATGAAGTTGTAAAGATTCAGTCCCTGGCAAGGATGCACCAAGCTCGAAAGCGCT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2941 ATCGAGATCGCCTGCAGTACTTCCGGGACCATATAAATGACATTATCAAAATCCAGGCTT	
		3001 TTATTCGGGCAAACAAAGCTCGGGATGACTACAAGACTCTCATCAATGCTGAGGATCCTC	
		3061 CTATGGTTGTGGTCCCGAAAATTTGTCCACCTGCTGGACCAAAGTGACCAGGATTTTCAGG	
		3121 AGGAGCTTGACCTTATGAAGATGCGGAAGAGGTTATCACCCTCATTCGTTCTAACCAGC	
		3181 AGCTGGAGAATGACCTCAATCTCATGGATATCAAAATTGGACTGCTAGTGAAAAATAAGA	
		3241 TTACGTTGCAGGATGTGGTTTCCCACAGTAAAAACTTACCAAAAAAATAAGGAACAGT	
		3301 TGTCTGATATGATGATAAATAAACAGAAGGGAGGTCTCAAGGCTTTGAGCAAGGAGA	
		3361 AGAGAGAAGTTGGAAGCTTACCAGCACCTGTTTTATTATTGCAAACCAATCCCACCT	
		3421 ATCTGGCCAAGCTCATTTTTCAGATGCCCCAGAACAAGTCCACCAAGTTCATGGACTCTG	
		3481 TAATCTTCACACTCTACAACTACGCGTCCAACCAGCGAGAGGAGTACCTGCTCCTGCGGC	
		3541 TCTTTAAGACAGCACTCCCAAGAGGCAAATCAAGTCGAAGGTAGATCAGATTCAAGAGATTG	
		3601 TGACAGGAAATCCTACGGTTATTAAAATGGTTGTAAGTTTCAACCGTGGTGCCCGTGGCC	
		3661 AGAATGCCCTGAGACAGATCTTTGGCCCCAGTCGTGAAGGAAATTATGGATGACAAATCTC	
		3721 TCAACATCAAAACTGACCCTGTGGATATTTACAAATCTTGGGTTAATCAGATGGAGTCTC	
		3781 AGACAGGAGAGGCAAGCAAACTGCCCTATGATGTCACCCTCAGCAGGCGCTAGCTCATG	
		3841 AAGAAGTGAAGACAGCGCTAGACAGCTCCATCAGGAACATGCGGGCTGTGACAGACAAGT	
		3901 TTCTCTCAGCCATTGTCAGCTCTGTGGACAAAATCCCTTATGGGATGCGCTTCATTGCCA	
		3961 AAGTGCTCAAGGACTCGTTGCATGAGAAGTTCCCTGATGCTGGTGAGGATGAGCTGCTGA	
		4021 AGATTATTGGTAACTTGCTTTACTACCGATACATCAACCCCGCCATTGTTGCTCCTGATG	
		4081 CCTTTGACATCATTGACCTGTCGGCAGGAGGCCAGCTTACCACAGACCAACGCCGAAATC	
		4141 TTGGCTCCATTGCAAAGATGCTCCAGCATGCAGCTTCCAATAAGATGTTTCTGGGAGATA	
		4201 ATGCTCACTTAAGCATCATTAATGATATCTTTCCCAGTCCTACCAGAAATTCAGACGGT	
		4261 TTTTCCAGACTGCTTGTGATGTCCCAGAGCTTCAGATAAATTTAATGTGGACGAGTACT	
		4321 CTGACTTGTGTGACCCTCACAAAACCAGTCATCTACATTTCCATTGGTGAGATCATCAACA	
		4381 CCCACACTCTCCTGTTAGATCACCAGGACGCCATTGCTCCTGAGCACACAACGACCCAATCC	
		4441 ATGAGCTGCTGGACGACCTGGGCGAGGTGCCCACCATCGAGTCCCTGATAGGAGAAAGCT	
		4501 CTGGCAATTTAAATGACCCAAACAAGGAGGCGCTGGCTAAGACAGAAGTCTCTCTCACAT	
		4561 TGACCAACAAGTTCGACGTGCCTGGCGATGAGAATGCAGAAATGGACGCTCGGACCATCT	
		4621 TGCTGAACACAAAGCGTTTAATTGTGGATGTCATCCGGTTCCAGCCCGGAGAGACCTTGA	
		4681 CTGAAATCCTGGAGACACCAGCTACCAGTGAACAGGAAGCAGAACATCAGAGGCCATGC	
		4741 AGAGACGTGCTATTCGTCGACGCCAAACTCCTGACAAGATGAAAAAGTCAAAATTTGTAA	
		4801 AGGAAGACAACAACCTCACTCTTCAGGAGAAGAGGAGATCCAGTCGGGCTTGAAGA	
		4861 AGCTGACAGAGCTTGGGACCGTGGACCCAAAGAACAGATACCAGGAACTGATCAACGACA	
		4921 TTGCCAGGGATATTCGGAATCAGCGGAGGTACCGACAGAGGAGAAAGGCCCGAACTAGTGA	
		4981 AACTGCAACAGACATACGCTGCTCTGAACTCTAAGGCCACCTTTATGGGAGCAGGTGG	
		5041 ATTACTATAAAAGCTATATCAAAACCTGCTTGGATAACTTAGCCAGCAAGGGCAAAGTCT	
		5101 CCAAAAAGCCTAGGGAAATGAAGGAAAGACAAAAAGATTTCTCTGAAATATACAG	
		5161 CAGCAAGACTACATGAAAAAGGAGTTCTTCTGGAAATTGAGGACCTGCAAGTGAATCAGT	
		5221 TTAAAAATGTTATATTTGAAATCAGTCCAACAGAAGAAGTTGGAGACTTCGAAGTGAAAG	
		5281 CCAAATTCATGGGAGTTCAAATGGAGACTTTTATGTTACATTATCAGGACCTGCTGCAGC	
		5341 TACAGTATGAAGGAGTTGCAGTCATGAAATTATTTGATAGAGGCTAAAGTAAATGTCAACC	
		5401 TCCTGATCTTCCTTCTCAACAAAAAGTTCTACGGGAAGTAATTGATCGTTTGCTGCCAGC	
		5461 CCAGAAGGATGAAGGAAACAAGCACCTCACAGCTCCTTCTAGGTCCTTCTTTCCTCATT	
		5521 GGAAGCAAAGACCTAGCCAACACAGCACCTCAATCTGATACACTCCCGATGCCACATTT	
		5581 TTAACTCCTCTCGCTCTGATGGGACATTTGTTACCCTTTTTTCATAGTGAAATTGTGTTT	
		5641 CAGGCTTAGTCTGACCTTTCTGGTTTCTTCATTTCTTCCATTACTTAGGAAAGAGTGGA	
		5701 AACTCCACTAAAAATTTCTCTGTGTTGTTACAGTCTTAGAGGTTGCAGTACTATATTGTAA	
		5761 GCTTTGGTGTTTGTTTAATTAGCAATAGGGATGGTAGGATTCAAATGTGTCATTTAGA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		5821 AGTGGAAGCTATTAGCACCAATGACATAAATACATACAAGACACAGAACTAAAATGTCAT	
		5881 GTTATTAACAGTTATTAGGTTGTCATTTAAAAATAAAGTTCCTTTATATTTCTGTCCCAT	
		5941 CAGGAAAACTGAAGGATATGGGGAATCATTGGTTATCTTCCATTGTGTTTTTCTTTATGG	
		6001 ACAGGAGCTAATGGAAGTGACAGTCATGTTCAAAGGAAGCATTTCTAGAAAAAAGGAGAT	
		6061 AATGTTTTTAAATTTCATTATCAAACTTGGGCAATTCTGTTTGTGTAACTCCCCGACTAG	
		6121 TGGATGGGACAGTCCCATTGCTAAAATTCAGCTACTCAGATAAATTCAGAATGGGTCAAG	
		6181 GCACCTGCCTGTTTTTGTTGGTGCACAGAGATTGACTTGATTCAGAGAGACAATTCACTC	
		6241 CATCCCTATGGCAGAGGAACGGGTTAGCCCTAGTGGAGAAGGGAATTGTTTTCAAAACTG	
		6301 TTTTATATCTTAAGAGTGCCTTATTAAAGTGTAGATTTACTTCTTAAAATGTGGATGATA	
		6361 GGAATTTAAAGATTTATATAATGCTTCAAAAGCCTTTAGAATACTGTAAGAAAAGGGTTT	
		6421 TTTAAAAATTGGGCTTATCTGTATATCTGAACTCTTAGAACTTTCTTATAGCTGAAACAC	
		6481 TAGGATTTATCTGCAGGGTTGCAGAGAGAATCCTGCCTGAAATAGACTCAAACAAAAC	
		6541 CAAACAAAACCAGCCGACGCTGTTACACTTGATATTAAAATCTGTTTTCCCTCATTTCTT	
		6601 TCTCTTTTCTCTTGGTGCCCACATGGTGCCTTTATTTTTATGAGCTCCAGTTTTATGGGT	
		6661 TTAGTTTAAAAAAAAAATCAAGTCTAAACATTGCATTTAGAAAGCTTTGTTCTTGGATA	
		6721 AAAAGTCATACACTTTAAAAAAAAAAAAAAAAACTTTTTTCCAGGAAATATATTGAAATC	
		6781 ATGCTGCTGAGCCTCCACTTTCTCTGATGTGTTGGTTCAGTTTTCTTTATCATAAATTT	
		6841 TTAGCATTTAAAAATTCACTGATGTACATTAAGCCAATAAACTGCTTTAATGAATAACAA	
		6901 ACTATGTAGTGTGTCCCTATTATAAAATGCATTGGAGAAGTATTTTTTATGAGACTCTTTAC	
		6961 TCAGGTGCATGGTTACAGCCACAGGGAGGCATGGAGTGCCATGGAAGGATTCGCCACTAC	
		7021 CCAGACCTTGTTTTTTTGTTGTATTTTGGAGACAGGTTTTTTAAAGAAACATTTTCCTCA	
		7081 GATTAAAAGATGATGCTATTACAACTAGCATTGCCTCAAAAACTGGGACCAACCAAAGTG	
		7141 TGTCAACCCTGTTCCTTAAAAGAGGCTATGAATCCCAAAGGCCACATCCAAGACAGGCA	
		7201 ATAATGAGCAGAGTTTACAGCTCCTTTAATAAAATGTGTCAGTAATTTTAAGGTTTATAG	
		7261 TTCCCTCAACACAATTGCTAATGCAGAATAGTGTAAAATGCGCCTTCAAGAATGTTGATGA	
		7321 TGATGATATAGAATTGTGGCTTTAGTAGCACAGAGGATGCCCCAACAAACTCATGGCGTT	
		7381 GAAACCACACAGTTCTCATTACTGTTATTTATTAGCTGTAGCATTCTCTGTCTCCTCTCT	
		7441 CTCCTCCTTTGACCTTCTCCTCGACCAGCCATCATGACATTTACCATGAATTTACTTCCT	
		7501 CCCAAGAGTTTGGACTGCCCGTCAGATTGTTTCTGCACATAGTTGCCTTTGTATCTCTGT	
		7561 ATGAAATAAAAGGTCATTTGTTC	
		1 M S A A D E V D G L G V A R P H Y G S V	SEQ ID NO:72
		1 ATGTCCGGCCGACAGGAGGTTGACGGGCTGGCCGTGGCCCGGCCGCACTATGGCTCTGTC	
		21 L D N E R L T A E E M D E R R R Q N V A	
		61 CTGGATAATGAAAGACTTACTGCAGAGGAGATGGATGAAAGGAGACGTCAGAACGTGGCT	
		41 Y E Y L C H L E E A K R W M E A C L G E	
		121 TATGAGTACCTTTGTCATTTGGAAGAAGCGAAGAGGTGGATGGAAGCATGCCTAGGGGAA	
		61 D L P P T T E L E E G L R N G V Y L A K	
		181 GATCTGCCTCCCACCACAGAACTGGAGGAGGGGCTTAGGAATGGGGTCTACCTTGCCAAA	
		81 L G N F F S P K V V S L K K I Y D R E Q	
		241 CTGGGGAACTTCTTCTCTCCCAAAGTAGTGTCCCTGAAAAAAATCTATGATCGAGAACAG	
		101 T R Y K A T G L H F R H H T D N V I Q W L	
		301 ACCAGATACAAGGCGACTGGCCTCCACTTTAGACACACTGATAATGTGATTCAGTGGCTTG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		121 N A M D E I G L P K I F Y P E T T D I Y 361 AATGCCATGGATGAGATTGGATTGCCTAAGATTTTTTACCCAGAAACTACAGATATCTAT	
		141 D R K N M P R C I Y C I H A L S L Y L F 421 GATCGAAAGAACATGCCAAGATGTATCTACTGTATCCATGCACTCAGTTTGTACCTGTTC	
		161 K L G L A P Q I Q D L Y G K V D F T E E 481 AAGCTAGGCCTGGCCCCTCAGATTCAAGACCTATATGGAAAGGTTGACTTCACAGAAGAA	
		181 E I N N M K T E L E K Y G I Q M P A F S 541 GAAATCAACAACATGAAGACTGAGTTGGAGAAGTATGGCATCCAGATGCCTGCCTTTAGC	
		201 K I G G I L A N E L S V D E A A L H A A 601 AAGATTGGGGGCATCTTGGCTAATGAACTGTCAGTGGATGAAGCCGCATTACATGCTGCT	
		221 V I A I N E A I D R R I P A D T F A A L 661 GTTATTGCTATTAATGAAGCTATTGACCGTAGAATTCCAGCCGACACATTTGCAGCTTTG	
		241 K N P N A M L V N L E E P L A S T Y Q D 721 AAAAATCCGAATGCCATGCTTGTAAATCTTGAACAGCCCTTGGCATCCACTTACCAGGAT	
		261 I L Y Q A K Q D K M T N A K N R T E N S 781 ATACTTTACCAGGCTAAGCAGGACAAAATGACAAATGCTAAAAACAGGACAGAAAACTCA	
		281 E R E R D V Y E E L L T Q A E I Q G N I 841 GAGAGAGAAAGAGATGTTATGAGGAGCTGCTCACGCAAGCTGAAATTCAAGGCAATATA	
		301 N K V N T F S A L A N N I D L A L E Q G D 901 AACAAAGTCAATACATTTTCTGCATTAGCAAATATCGACCTGGCTTTAGAACAAGGAGAT	
		321 A L A L F R A L Q S P A L G L R G L Q Q 961 GCACTGGCCTTGTTCAGGGCTCTGCAGTCACCAGCCCTGGCGCTTCGAGGACTGCAGCAA	
		341 Q N S D W Y L K Q L L S D K Q Q K R Q S 1021 CAGAATAGCGACTGGTACTTGAAGCAGCTCCTGAGTGATAAACAGCAGAAGAGACAGACT	
		361 G Q T D P L Q K E E L Q S G V D A A N S 1081 GGTCAGACTGACCCCCTGCAGAAGGAGGAGCTGCAGTCTGGAGTGGATGCTGCAAACAGT	
		381 A A Q Q Y Q R R L A A V A L I N A A I Q 1141 GCTGCCCAGCAATATCAGAGAAGATTGGCAGCAGTAGCACTGATTAATGCTGCAATCCAG	
		401 K G V A E K T V L E L M N P E A Q L P Q 1201 AAGGGTGTTGCTGAGAAGACTGTTTTGGAACTGATGAATCCCGAAGCCCAGCTGCCCCAG	
		421 V Y P F A A D L Y Q K E L A T L Q R Q S 1261 GTGTATCCATTTGCCGCCGATCTCTATCAGAAGGAGCTGGCTACCCTGCAGCGACAAAGT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		441 P E H N L T H P E L S V A V E M L S S V 1321 CCTGAACATAATCTCACCCACCCAGAGCTCTCTGTCGCAGTGGAGATGTTGTCATCGGTG 461 A L I N R A L E S G D V N T V W K Q L S 1381 GCCCTGATCAACAGGGCATTGGAATCAGGAGATGTGAATACAGTGTGGAAGCAATTGAGC 481 S S V T G L T N I E E E N C Q R Y L D E 1441 AGTTCAGTTACTGGTCTTACCAATATTGAGGAAGAAAACTGTCAGAGGTATCTCGATGAG 501 L M K L K A Q A H A E N N E F I T W N D 1501 TTGATGAAACTGAAGGCTCAGGCACATGCAGAGAATAATGAATTCATTACATGGAATGAT 521 I Q A C V D H V N L V V Q E E H E R I L 1561 ATCCAAGCTTGCGTGGACCATGTGAACCTGGTGGTGCAAGAGGAACATGAGAGGATTTTA 541 A I G L I N E A L D E G D A Q K T L Q A 1621 GCCATTGGTTTAATTAATGAAGCCCTGGATGAAGGTGATGCCCAAAAGACTCTGCAGGCC 561 L Q I P A A K L E G V L A E V A Q H Y Q 1681 CTACAGATTCCTGCAGCTAAACTTGAGGGAGTCCTTGCAGAAGTGGCCCAGCATTACCAA 581 D T L I R A K R E K A Q E I Q D E S A V 1741 GACACGCTGATTAGAGCGAAGAGAGAGAAAGCCCAGGAAATCCAGGATGAGTCAGCTGTG 601 L W L D E I Q G G I W Q S N K D T Q E A 1801 TTATGGTTGGATGAAATTCAAGGTGGAATCTGGCAGTCCAACAAAGACACCCAAGAAGCA 621 Q K F A L G I F A I N E A V E S G D V G 1861 CAGAAGTTTGCCTTAGGAATCTTTGCCATTAATGAGGCAGTAGAAAGTGGTGATGTTGGC 641 K T L S A L R S P D V G L Y G V I P E C 1921 AAAACACTGAGTGCCCTTCGCTCCCCTGATGTTGGCTTGTATGGAGTCATCCCTGAGTGT 661 G E T Y H S D L A E A K K K K L A V G D 1981 GGTGAAACTTACCACAGTGATCTTGCTGAAGCCAAGAAGAAAAAACTGGCAGTAGGAGAT 681 N N S K W V K H W V K G G Y Y Y Y H N L 2041 AATAACAGCAAGTGGGTGAAGCACTGGGTAAAAGGTGGATATTATTATTACCACAATCTG 701 E T Q E G G W D E P P N F V Q N S M Q L 2101 GAGACCCAGGAAGGAGGATGGGATGAACCTCCAAATTTTGTGCAAAATTCTATGCAGCTT 721 S R E E I Q S S I S G V T A A Y N R E Q 2161 TCTCGGGAGGAGATCCAGAGTTCTATCTCTGGGGTGACTGCCGCATATAACCGAGAACAG 741 L W L A N E G L I T R L Q A R C R G Y L 2221 CTGTGGCTGGCCAATGAAGGCCTGATCACCAGGCTGCAGGCTCGCTGCCGTGGATACTTA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		761 V R Q E F R S R M N F L K K Q I P A I T 2281 GTTCGACAGGAATTCCGATCCAGGATGAATTTCCTGAAGAAACAAATCCCTGCCATCACC	
		781 C I Q S Q W R G Y K Q K K A Y Q D R L A 2341 TGCATTCAGTCACAGTGGAGAGGATACAAGCAGAAGGCATATCAAGATCGGTTAGCT	
		801 Y L R S H K D E V V K I Q S L A R M H Q 2401 TACCTGCGCTCCCACAAAGATGAAGTTGTAAAGATTCAGTCCCTGCCAAGGATGCACCAA	
		821 A R K R Y R D R L Q Y F R D H I N D I I 2461 GCTCGAAAGCGCTATCGAGATCGCCTGCAGTACTTCCGGGACCATATAAATGACATTATC	
		841 K I Q A F I R A N K A R D D Y K T L I N 2521 AAAATCCAGGCTTTTATTCGGGCAAACAAAGCTCGGGATGACTACAAGACTCTCATCAAT	
		861 A E D P P M V V V R K F V H L L D Q S D 2581 GCTGAGGATCCTCCTATGGTTGTGGTCCGAAAATTTGTCCACCTGCTGGACCAAAGTGAC	
		881 Q D F Q E E L D L M K M R E E V I T L I 2641 CAGGATTTTCAGGAGGAGCTTGACCTTATGAAGATGCGGGAAGAGGTTATCACCCTCATT	
		901 R S N Q Q L E N D L N L M D I K I G L L 2701 CGTTCTAACCAGCAGCTGGAGAATGACCTCAATCTCATGGATATCAAAATTGGACTGCTA	
		921 V K N K I T L Q D V V S H S K K L T K K 2761 GTGAAAAATAAGATTACGTTGCAGGATGTGGTTTCCCACAGTAAAAAACTTACCAAAAAA	
		941 N K E Q L S D M M I N K Q K G G L K A 2821 AATAGGAACAGTTGTCTGATATGATGATAAATAAACAGAAGGGAGGTCTCAAGGCT	
		961 L S K E K R E K L E A Y Q H L F Y L L Q 2881 TTGAGCAAGGAGAAGAGAGAGGAAGCTTACCAGCACCTGTTTTATTTATTGCAA	
		981 T N P T Y L A K L I F Q M P Q N K S T K 2941 ACCAATCCCACCTATCTGGCCAAGCTCATTTTCAGATGCCCCAGAACAAGTCCACCAAG	
		1001 F M D S V I F T L Y N Y A S N Q R E E Y 3001 TTCATGGACTCTGTAATCTTCACACTCTACAACTACGCGTCCAACCAGCGAGAGGAGTAC	
		1021 L L L R L F K T A L Q E E I K S K V D Q 3061 CTGCTCCTGCGGCTCTTTAAGACAGCACTCCAAGAGGAAATCAAGTCGAAGGTAGATCAG	
		1041 I Q E I V T G N P T V I K M V V S F N R 3121 ATTCAAGAGATTGTGACAGGAAATCCTACGGTTATTAAAATGGTTGTAAGTTTCAACCGT	
		1061 G A R G Q N A L R Q I L A P V V K E I M 3181 GGTGCCCGTGGCCAGAATGCCCTGAGACAGATCTTGGCCCCAGTCGTGAAGGAAATTATG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1081 D D K S L N I K T D P V D I Y K S W V N 3241 GATGACAAATCTCTCAACATCAAAACTGACCCTGTGGATATTTACAAATCTTGGTTAAT	
		1101 Q M E S Q T G E A S K L P Y D V T P E Q 3301 CAGATGGAGTCTCAGACAGGAGAGGCAAGCAAACTGCCCTATGATGTGACCCCTGAGCAG	
		1121 A L A H E E V K T R L D S S I R N M R A 3361 GCGCTAGCTCATGAAGAAGTGAAGACACGGCTAGACAGCTCCATCAGGAACATGCGGGCT	
		1141 V T D K F L S A I V S S V D K I P Y G M 3421 GTGACAGACAAGTTTCTCTCAGCCATTGTCAGCTCTGTGGACAAAATCCCTTATGGGATG	
		1161 R F I A K V L K D S L H E K F P D A G E 3481 CGCTTCATTGCCAAAGTGCTGAAGGACTCGTTGCATGAGAAGTTCCCTGATGCTGGTGAG	
		1181 D E L L K I I G N L L Y Y R Y M N P A I 3541 GATGAGCTGCTGAAGATTATTGGTAACTTGCTTTACTACCGATACATGAACCCCGCCATT	
		1201 V A P D A F D I I D L S A G G Q L T T D 3601 GTTGCTCCTGATGCCTTTGACATCATTGACCTGTCGGCAGGAGCCAGCTTACCACAGAC	
		1221 Q R R N L G S I A K M L Q H A A S N K M 3661 CAACGCCGAAATCTTGGCTCCATTGCAAAGATGCTCCAGCATGCAGCTTCCAATAAGATG	
		1241 F L G D N A H L S I I N E Y L S Q S Y Q 3721 TTTCTGGGAGATAATGCTCACTTAAGCATCATTAATGAGTATCTTTCCCAGTCCTACCAG	
		1261 K F R R F F Q T A C D V P E L Q D K F N 3781 AAATTCAGACGGTTTTTCCAGACTGCTTGTGATGTCCCAGAGCTTCAGGATAAATTTAAT	
		1281 V D E Y S D L V T L T K P V I Y I S I G 3841 GTGGACGAGTACTCTGACTTGGTGACCCTCACAAAACCAGTCATCTACATTTCCATTGGT	
		1301 E I I N T H T L L L D H Q D A I A P E H 3901 GAGATCATCAACACCCACACTCTCCTCGTTAGATCACCAGGACGCCATTGCTCCTGAGCAC	
		1321 N D P I H E L L D D L G E V P T I E S L 3961 AACGACCCAATCCATGAGCTGCTGGACGACCTGGGCGAGGTGCCCACCATCGAGTCCCTG	
		1341 I G E S S G N L N D P N K E A L A K T E 4021 ATAGGAGAAAGCTCTGGCAATTTAAATGACCCAAACAAGGAGGCGCTGGCTAAGACAGAA	
		1361 V S L T L T N K E D V P G D E N A E M D 4081 GTCTCTCTCACATTGACCAACAAGTTCGACGTGCCTGGCGATGAGAATGCAGAAATGGAC	
		1381 A R T I L L N T K R L I V D V I R F Q P 4141 GCTCGGACCATCTTGCTGAACACAAAGCGTTTAATTGTGGATGTCATCCGGTTCCAGCCC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1401 G E T L T E I L E T P A T S E Q E A E H 4201 GGAGAGACCTTGACTGAAATCCTGGAGACACCAGCTACCAGTGAACAGGAAGCAGAACAT 1421 Q R A M Q R R A I R D A K T P D K M K K 4261 CAGAGGGCCATGCAGAGACGTGCTATTCGTGACGCCAAAACTCCTGACAAGATGAAAAAG 1441 S K F V K E D N N L T L Q E K K E K I Q 4321 TCAAAATTTGTAAAGGAAGACAACAACCTCACTCTTCAGGAGAAGAAGGAGAAGATCCAG 1461 S G L K K L T E L G T V D P K N R Y Q E 4381 TCGGGCTTGAAGAAGCTGACAGAGCTTGGGACCGTGGACCCAAAGAACAGATACCAGGAA 1481 L I N D I A R D I R N Q R R Y R Q R R K 4441 CTGATCAACGACATTGCCAGGGATATTCGGAATCAGCGGAGGTACCGACAGAGGAGAAAG 1501 A E L V K L Q Q T Y A A L N S K A T F Y 4501 GCCGAACTAGTGAAACTGCAACAGACATACGCTGCTCTGAACTCTAAGGCCACCTTTTAT 1521 G E Q V D Y Y K S Y I K T C L D N L A S 4561 GGGGAGCAGGTGGATTACTATAAAAGCTATATCAAAACCTGCTTGGATAACTTAGCCAGC 1541 K G K V S K K P R E M K G K K S K K I S 4621 AAGGGCAAAGTCTCCAAAAAGCCTAGGGAAATGAAAGGAAAGAAAAGCAAAAAGATTTCT 1561 L K Y T A A R L H E K G V L L E I E D L 4681 CTGAAATATACAGCAGCAAGACTACATGAAAAAGGAGTTCTTCTGGAAATTGAGGACCTG 1581 Q V N Q F K N V I F E I S P T E E V G D 4741 CAAGTGAATCAGTTTAAAAATGTTATATTTGAAATCAGTCCAACAGAAGAAGTTGGAGAC 1601 F E V K A K F M G V Q M E T F M L H Y Q 4801 TTCGAAGTGAAAGCCAAATTCATGGGAGTTCAAATGGAGACTTTTATGTTACATTATCAG 1621 D L L Q L Q Y E G V A V M K L F D R A K 4861 GACCTGCTGCAGCTACAGTATGAAGGAGTTGCAGTCATGAAATTATTTGATAGAGCTAAA 1641 V N V N L L I F L L N K K F Y G K - 4921 GTAAATGTCAACCTCCTGATCTTCCTTCTCAACAAAAAGTTCTACGGGAAGTAA	
WBC013A09	Sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase), transcript variant 2	1 GAGGAGGTTCCTGTAGGGCGGCACAACCAGGGAGGGCGTGGAAGCTCTGCATCCCTTCTC 61 CCATACCTTGCTCTACACATCTCTTCATCTGTATCCTCTGCAGCATCCTTGATGATAAAC 121 CAGTAAATATGAGTTTTGATCATCCTGAGAAAAATGGGCCTTGGCCTGCAGACCCAATAA 181 ACCTTCCCTCCCATGGATAATAGTGCTAATTCCTGAGGACCTGAAGGGCCTGCCGCCCCT 241 GGGGGATTAGCCAGAAGCAGGCTTGTTTTCCTGCTCAGAACAAAGTGACTTCCCTGAACA 301 CATCTTCATTATGATTCACACCAACCTGAAGAAAAAGTTCAGCTGCTGCGTCCTGGTCTT	SEQ ID NO:73

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		361 TCTTCTGTTTGCAGTCATCTGTGTGTGGAAGGAAAGAAGGAGTTACTATGATTC	
		421 CTTTAAATTGCAAACCAAGGAATTCCAGGTGTTAAAGAGTCTGGGGAAATTGGCCATGGG	
		481 GTCTGATTCCCAGTCTGTATCCTCAAGCAGCACCCAGGACCCCCACAGGGGCCGCCAGAC	
		541 CCTCGGCAGTCTCAGAGGCCTAGCCAAGGCCAAACCAGAGGCCTCCTTCCAGGTGTGGAA	
		601 CAAGGACAGCTCTTCCAAAAACCTTATCCCTAGGCTGCAAAAGATCTGGAAGAATTACCT	
		661 AAGCATGAACAAGTACAAAGTGTCCTACAAGGGGCCAGGACCATCAAGTTCAGTGC	
		721 AGAGGCCCTGCGCTGCCACCTCCGGGACCATGTGAATGTATCCATGGTAGAGGTCACAGA	
		781 TTTTCCCTTCAATACCTCTGAATGGGAGGGTTATCTGCCCAAGGAGAGCATTAGGACCAA	
		841 GGCTGGGCCTTGGGCCAGTGTGCTGTTGTCGTCAGCGGGATCTCTGAAGTCCTCCCA	
		901 ACTAGGCAGAGAAATCGATGATCATGACGCAGTCCTGAGGTTTAATGGGGCACCCACAGC	
		961 CAACTTCCAACAAGATGTGGGCACAAAAACTACCATTCGCCTGATGAACTCTCAGTTGGT	
		1021 TACCACAGAGAAGCGCTTCCTCAAAGACAGTTTGTACAATGAAGGAATCCTAATTGTATG	
		1081 GGACCCATCTGTATACCACTCGATATCCCCAAAGTGGTACCAGAATCCGGATTATAATTT	
		1141 CTTTAACAACTACAAGACTTATCGTAAGCTGCACCCCAATCAGCCCTTTACATCCTCAA	
		1201 GCCCCAGATGCCTTGGGAGCTATGGGACATTCTTCAAGAAATCTCCCCAGAAGAGATTCA	
		1261 GCCAAACCCCCATCCTCTGGGATGCTTGGTATCATCATCATGATGACGCTGTGTGACCA	
		1321 GGTGGATATTTATGAGTTCCTCCCATCCAAGCGCAAGACTGACGTGTGCTACTACTACCA	
		1381 GAAGTTCTTCGATAGTGCCTGCACGATGGGTGCCTACCACCCGCTGCTCTATGAGAAGAA	
		1441 TTTGGTGAAGCATCTCAACCAGGGCACAGATGAGGACATCTACCTGCTTGGAAAAGCCAC	
		1501 ACTGCCTGCTTCCGGACCATTCACTGCTAAGCACAGGCTCCTCACTCTTCTCCATCAGG	
		1561 CATTAAATGAATGGTCTCTTGGCCACCCCAGCCTGGGAAGAACATTTTCCTGAACAATTC	
		1621 CAGCCTGCTCCTTTTACTCTAGGGGCCTCTGTCAGCAAGACCATGGGGGCTTCAAGAGCC	
		1681 TGTGGTCAGGAAATCAGGTCCAGCCTTCCCTGTAGCCAGACAGTTTATGAGCCCAGAGCC	
		1741 TCCTGCCACACACATGCACACATATCTAGCATTCTTTCCAGACAGCATCCTCCCCGCCTT	
		1801 CCACCTTGGTAGATGCCAAGGTCTATCTCCCCATCAGGGCTGCCAAAGCTGGGCTTTGTT	
		1861 TTTCCCAGCAGAATGATGCCATTCTCACAAAACCAATGCTCTATATTGCTTGAAGTCTGCA	
		1921 TCTAAATATTGATTTCACGTTTTAAAGAAATTCTCTTAAATTACAATTGTGCCCAATGCA	
		1981 GGGTGGCTCTGGGGGCCAAGTAGGTGCTACAGGGGATTGGAAACATGCTCCCGCCTCCA	
		2041 GAGAAAAGTTGCTCCCGAGGTCCATGCCCCTGGAACGTGTTCCTATCACTCTGGCTGGTT	
		2101 GGGCTGGTCCTTAGACTGGGTGCTTATGATTAAAGGGTCTTGGTTAGCCCACTTTCCCTC	
		2161 TCCATGTGGAGATGGAAGGTAGAGAAGGATACACTGTCTATCCCTCAAGTTGCTACGGTTC	
		2221 AGTGAGAGAGGCAGACATCTGAACAGGCAGGTAGGATTCAGTGTGCTCAGTGCACTGGGG	
		2281 ATTTGGAGAGAGATGGCTTGCTCTCTCTGTGCACCCAGGAGGGCCACGCACTTAAAACT	
		2341 GTGTTTGTGGATCAGAGAAGGCTTTATAGCACAGGGGGCATTCAGATGAGTCTTAGAGGA	
		2401 AGAGAAGAAACATGGCAAGCAGATTACATCTGAGCCGTTTGAATTGTGTTTTTCTTTCTT	
		2461 CCCATGTTTATTTTCTAAGATCTACCTGAACTTAGAGACTCAAGATATTTTTTTAGGAAA	
		2521 CCTCCTACCCATGTCTGAGGTAGCAAGTGCCAGCCTCACGACACAGATACCAGGCAATCCAGA	
		2581 GCCACAAAACGTGATTCCTCCAGGCTCTGCCTGGCCTGACCCTGTCCTGTCAGCTGGGTT	
		2641 TACATACCAGTCCCATTCTTCCTTTCAATACCTACCCCCAAATCTTCTCCTAACCACCA	
		2701 TCTGTTTTTTTTTTTTTTAAAGCATTTTTTGCTTTAAAAGCATCCTGACCCCAATTTCTTTG	
		2761 AGCTCACGGGCCTTTGCTGAAGGTCTCTCAGGCTGTAGTGGTGTGGCTCTCTGGACTTA	
		2821 ACGTCACTCTCAGAGCTCAGAACCTTGGAGATCAGAACTGATTCTCACCAGCTGTGAGAG	
		2881 GTGTGGTAGCAGATTGCAATGCTCTGCACCTCTTCCTTGCAAGTGAGCAACTTCAGGCTC	
		2941 TCTGGCAGAGGCTGCCCCACTGTAGTTTGCAGACATGCTCTCCAGATGGTTTTACTAAG	
		3001 TCCCCTCTCCCTGATAGGGAATCCTGCTGGACCAGCGCAGCCCTGGTGTGGAGAGGGTAA	
		3061 AGGACTTGCACAGGATCACCAAGTCATGCTGTAGAGCCAGGATTCCTAGACCCAGGGCTC	
		3121 TGCACTCTCAAGGCTGGCCCCCATGTGCTCAAGGGCCTCCAATGTTTGCGCTCCCAGACCAG	
		3181 CCGTCTGCAAGCTGGACTTCTCATTTGCTGCCAAACCCTTGGCTTACATATGCAGTAGAA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		3241 AGAGCCCTGGAGTTAGAAGCCCTGGGTTTCAAGTTGATGTTCCTCTACTTACTAGCTGT 3301 GCCACTCTGGGCAAATGCTCTTCCTTGAGCCTGTTTCCACACCTGTAAAGTGGGGATGAT 3361 GATCCTATCTCACTGCTTTTGTGAGGATTACAGCAAAGCACCTGTCCTGGTTCTGCACCT 3421 GGCTCATGGCAGGTGCTCAGTACATGGTGGTGTCCTTCCTTCGTTCACTAAGGACCTGCT 3481 CTGAGCTCACACCTCGGCTGCATGCACCCTGCTGTGACGGAGGCTAGTGTGCAAGAGGTC 3541 CTGTCCTCAGGGAATTAACTGTCTTATTGGGACACAACACTACCCTGCCTGGGGCACCC 3601 AGGAAACCATCCGAGGCAGTGGACAACACAGAACACGCCCTCCTCCTCGCTGCCTGCAGC 3661 TCCAATCTGATTCTGCTTGGGAATGGGCTGAGCACGTGGGCTGCTTAACTGCTGTATAGG 3721 ACAAGCCCCTTACCCCTCTCTGGGCCCATGAATTCCTGGCTCTCTTTATGTTCTGATTTG 3781 ACACATTCATTGCAATCTTTGAATCATGAACATGAGTGCAGAGGAAGGTGGCATTCCATC 3841 AGCAGAAGAGATGTTGGTGTGGAGACCCTGAGACTACACTGGGTAGATGCTAGCTTTTA 3901 ATTATGATTAATATAAGGGATCAAATTAATTTAAATATGATTCTGAAGTCTACAGAACTT 3961 TTAGTTCTGTGCCTGTCTATGTGGACACTTTGGTAAAATGCAAATTATGATATGGACGTTA 4021 TCATTGGTCTGGTGAGCTGTTTAATATTTGTGACAGATAATTTAAAAATTATGACTTAAT 4081 GCTGCCTGTGTCTATGGGGTTCTGTCTCTTCTTTGATAGCCATCTATTCATCTGGATCATGG 4141 GACCCTCTCTAATCCTTCCAACAATCAAATAAGCTATCGATATTGTTTTGGAGTTGAGAT 4201 ATCAGTCTCGGAAACTTCTGAAAAATGCTAATAATTACCCAGGATTATGTCAAATTTA 4261 AAATAAATGTGTGTGTTTCTTTAAAAAAAAAAAAAAA	
		1 M I H T N L K K K F S C C V L V F L L F 1 ATGATTCACACCAACCTGAAGAAAAAGTTCAGCTGCTGGTCCTGGTCTTTCTTCTGTTT	SEQ ID NO:74
		21 A V I C V W K E K K K G S Y Y D S F K L 61 GCAGTCATCTGTGTGTGGAAGGAAAAGAAGAAAGGGAGTTACTATGATTCCTTTAAATTG	
		41 Q T K E F Q V L K S L G K L A M G S D S 121 CAAACCAAGGAATTCCAGGTGTTAAAGAGTCTGGGGAAATTGGCCATGGGGTCTGATTCC	
		61 Q S V S S S S T Q D P H R G R Q T L G S 181 CAGTCTGTATCCTCAAGCAGCACCCAGGACCCCCACAGGGGCGCCAGACCCTCGGCAGT	
		81 L R G L A K A K P E E A S F Q V W N K D S 241 CTCAGAGGCCTACCAAGGCCAAACCAGACGCCCTCCTTCCAGGTGTGGAACAAGGACAGC	
		101 S S K N L I P R L Q K I W K N Y L S M N 301 TCTTCCAAAAACCTTATCCCTAGGCTGCAAAAGATCTGGAAGAATTACCTAAGCATGAAC	
		121 K Y K V S Y K G P G P G I K F S A E A L 361 AAGTACAAAGTGTCCTACAAGGGGCCAGGACCAGGCATCAAGTTCAGTGCAGAGGCCCTG	
		141 R C H L R D H V N V S M V E V T D F P F 421 CGCTGCCACCTCCGGGACCATGTGAATGTATCCATGGTAGAGGTCACAGATTTTCCCTTC	
		161 N T S E W E G Y L P K E S I R T K A G P 481 AATACCTCTGAATGGGAGGGTTATCTGCCCAAGGAGACATTAGGACCAAGGCTGGGCCT	
		181 W G R C A V V S S A G S L K S S Q L G R 541 TGGGGCAGGTGTGCTGTTGTCGTCAGCGGGATCTCTGAAGTCCTCCCAACTAGGCAGA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		201 E I D D H D A V L R F N G A P T A N F Q 601 GAAATCGATGATCATGACGCAGTCCTGAGGTTTAATGGGGCACCCACAGCCAACTTCCAA 221 Q D V G T K T T I R L M N S Q L V T T E 661 CAAGATGTGGGCACAAAAACTACCATTCGCCTGATGAACTCTCAGTTGGTTACCACAGAG 241 K R F L K D S L Y N E G I L I V W D P S 721 AAGCGCTTCCTCAAAGACAGTTTGTACAATGAAGGAATCCTAATTGTATGGGACCCATCT 261 V Y H S D I P K W Y Q N P D Y N F F N N 781 GTATACCACTCAGATATCCCAAAGTGGTACCAGAATCCGGATTATAATTTCTTTAACAAC 281 Y K T Y R K L H P N Q P F Y I L K P Q M 841 TACAAGACTTATCGTAAGCTGCACCCCAATCAGCCCTTTTACATCCTCAAGCCCCAGATG 301 P W E L W D I L Q E I S P E E I Q P N P 901 CCTTGGGAGCTATGGGACATTCTTCAAGAAATCTCCCCAGAAGAGATTCAGCCAAACCCC 321 P S S G M L G I I I M M T L C D Q V D I 961 CCATCCTCTGGGATGCTTGGTATCATCATCATGATGACGCTGTGTGACCAGGTGGATATT 341 Y E F L P S K R K T D V C Y Y Y Q K F F 1021 TATGAGTTCCTCCCATCCAAGCGCAAGACTGACGTGTGCTACTACTACCAGAAGTTCTTC 361 D S A C T M G A Y H P L L Y E K N L V K 1081 GATAGTGCCTGCACGATGGGTGCCTACCACCCGCTGCTCTATGAGAAGAATTTGGTGAAG 381 H L N Q G T D E D I Y L L G K A T L P G 1141 CATCTCAACCAGGGCACAGATGAGGACATCTACCTGCTTGGAAAAGCCACACTGCCTGGC 401 F R T I H C - 1201 TTCCGGACCATTCACTGCTAA	
WBC012G02	Soc-2 suppressor of clear homolog (C. elegans)	1 ctattttacc agttggaatg aatgatcaga aatgggcata gtgcttttag atccaacatg 61 taacagatgg atgttactcc atgctgatta cttcttcaag ccagtacttt tttgattgtg 121 taggatcttt gtctcttcat ctttgaattc aattactgga aaataaaagg agttcatgta 181 gtttttgtcc aggcttgagt caccatgagt agtagtttag gaaaagaaaa agactctaaa 241 gaaaaagatc ccaaagtacc atcagccaag gaaagagaaa aggaggcaaa agcctctgga 301 ggttttggga aagagagcaa agaaaaagaa cctaagacca aagggaaaga tgccaaagat 361 ggaaagaagg actccagtgc tgcccaacca ggggtggcat tttcagttga caatacgatc 421 aaacggccaa acccagcacc tgggactaga aaaaaatcca gcaatgcaga ggtgattaaa 481 gagctcaaca aatgccggga agagaattca atgcgtttgg acttatccaa gagatctata 541 cacatattgc catcatcaat caaagagttg actcaattaa cagaacttta tttatacagt 601 aacaaattgc agtccctccc agcagaggtg ggatgtttag taaatctcat gacactggct 661 ctaagtgaaa attcacttac cagtttgcct gactctcttg ataacttgaa gaagctgcgg	SEQ ID NO:75

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		721 atgcttgatt tacggcataa taaactgaga gaaattcctt cagtggtgta taggctggat	
		781 tctctcacca ctctttacct tcgctttaat cgtataacta ctgtggaaaa ggacatcaaa	
		841 aacttgtcaa aactcagcat gcttagcatt cgagagaaca aaattaaaca actacctgct	
		901 gaaattggtg aattatgtaa cctcattacg ctggatgtag ctcacaatca acttgaacac	
		961 cttccaaagg agattggaaa ctgtacacag ataaccaacc ttgacttgca gcacaatgaa	
		1021 ctgctagacc tcccagatac tataggaaac ctgtccagtt taagtcgtct tggtctgaga	
		1081 tataacagac tgtcagcaat acccagatca ttagcaaaat gcagtgcact tgaagaatta	
		1141 aatttagaga acaataacat ttctacttta ccagagagtc ttttatcaag tcttgtgaaa	
		1201 ctgaatagtt tgaccttagc tagaaattgc ttccagttgt atccagtggg tggtccatct	
		1261 cagttttcta ccatctattc cctcaacatg gaacacaatc gaatcaacaa aattccattt	
		1321 ggaatttttct ccagagcaaa agtattaagt aagctgaata tgaaggacaa tcagttaaca	
		1381 tcacttccct tggatttgg aacttggacc agtatggtag aattgaattt agccactaat	
		1441 cagctcacaa agatccctga ggatgtgtct ggtctcgttt ctcttgaggt tcttatctta	
		1501 tcaaacaatc ttctaaagaa gcttccccat ggtcttggaa acctttaggaa gttaagagag	
		1561 ttggatctag aagagaacaa attggaatcc ttgccaaatg aaattgcata tcttaaggat	
		1621 ttacagaaat tagtcttgac aaacaaccag ttgaccactc ttcccagagg cattggtcac	
		1681 cttactaatc tcacacatct gggccttgga gagaacctac ttactcacct tcctgaagaa	
		1741 attggtacac tggagaacct agaagaactg tatttgaatg acaaccccaa cctgcatagc	
		1801 cttcccttg agctggcact ctgcagcaag ctttcaatca tgagtattga gaactgtcca	
		1861 ctcagtcacc ttccacctca gattgttgct gggggcctt ctttcatcat tcagttctta	
		1921 aagatgcagg gtccatatcg tgccatggtc tgatataaat ctgctggtcc cacacactgt	
		1981 tcaaaaatag actgccatta atgtttctta tctatatctg tatcttatta tgtagatatt	
		2041 ggtatatggc agatttataa aaattgcatt atgtgtttct gctaatagag gaatcatagc	
		2101 catttagaat ttttttttaa ttctgtacaa aaggcttata taagttttct ttgctgaatt	
		2161 tgatggatgt ttttctgttg tgtaatctga tatgccagtt tgcttaaaac atttgccaac	
		2221 acattatgaa gttattaaat ttaagggaca gaggtagtat agttagatat actttctctt	
		2281 aggaaaaata atgggcaaaa attttgttg caacttttca tatatatttt ccccttacca	
		2341 attgttttat cctttatagta ttgtaggccc tgaaagtaga atttttcttt aacttatttt	
		2401 gagatttgag atttaaattt tatgtattgt ttacagtcag agtaaatcac tggatttctt	
		2461 ttgtttgttt tgatttgctc tgttttattc agtcaaatct agagtttgaa tcctctgcta	
		2521 aagaatttgc atccactggt gtaaacagtg aaaggtattt gcttgtttgaa aaaaaaaact	
		2581 ggcaaagtga aaagatacag tcaaaaatct agaatttctt taattttgct tctctgacga	
		2641 gttgtgaagc aaaatacctg aagtgagtct ttgggtaggg gaagggtatt gagacctttt	
		2701 ctagtatgaa tatttttaa gtttgggga agagaaactt gcagtgaaaa ggagttttt	
		2761 cattcctgaa agttgcagat ccacaaaact aacaggataa ttgggcaaat aaattacata	
		2821 taaacacaca caatctatat atgtctatat agatatgtat ttattatatc	
		2881 ataaactaca gtaggtaact ttaaggattt cttcctatcc ttgtacaatg acatgaatgt	
		2941 ctttctttga aaactgcaat gtatgtatgt ttcaaggtta tttaacagtg tactatggtt	
		3001 ttatatcttg acttgccttg tacatctttc aattctggaa tatctgtgtc taagcacaat	
		3061 atcttcacac tgtgctgtat tgctgctgaa ctaaatgcac tttcccccac atatgggcca	
		3121 ctggcttcaa acaattcagt tcagtatcat tacttttaat ctcatctttc ctttcttggt	
		3181 agttgttaat acagttatgg aaaagaggca cattgcatag aagccattgg ggagttcagt	
		3241 ggaagttctg taagatgtgc atgtactatt tgatgcgttt tctttgcttc actgctttta	
		3301 atacttagca gtattgttgg tctaagtcaa ttgtattatt gaggagtctc agagcaaggt	
		3361 gcgttctaga tgtcatccta aaaaacactt catatataat taatcactat tttgtataat	
		3421 tacatattgc tgcttgtgtg ttttttttt ttttccattt agttgggcgt tgtgttttac	
		3481 acaaaaccat ttttgaatta aggctatgat attaagatag aaatttggac tgttgttctg	
		3541 cttttcctgg cactcaaatt catgactagt ttgaggtca aacctatgtt cgtaatgaga	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		3601 gattttataa ggatcaacta agaaatggaa ggcaggtgaa gatataaaac cctagaatgc 3661 ttaaatgtgc tgtaaaacta ttgtagatgt cactggattt taccaagtaa tatcctttct 3721 ttttttttc cccccatctg ctgtggcttt tcagttaaaa ttttgtttat aaaaggaatt 3781 tgtttattac agctctacct aaaaaaaaaa aaaaaaaaaa aaa 1 M S S S L G K E K D S K E K D P K V P S 1 ATGAGTAGTAGTTTAGGAAAAGAAAAAGACTCTAAAGAAAAAGATCCCAAAGTACCATCA 21 A K E E R E K E A K A S G G F G K E S K E 61 GCCAAGGAAAGAGAAAAAGGAGGCAAAAGCCTCTGGAGGTTTTGGGAAAGAGAGCAAAGAA 41 K E P K T K G K D A K D G K K D S S A A 121 AAAGAACCTAAGACCAAAGGGAAAGATGCCAAAGATGGAAAGAAGGACTCCAGTGCTGCC 61 Q P G V A F S V D N T I K R P N P A P G 181 CAACCAGGGGTGGCATTTTCAGTTGACAATACCATCAAACGGCCAAACCCAGCACCTGGG 81 T R K K S S N A E V I K E L N K C R E E 241 ACTAGAAAAAAATCCAGCAATGCAGAGGTGATTAAAGAGCTCAACAAATGCCGGGAAGAG 101 N S M R L D L S K R S I H I L P S S I K 301 AATTCAATGCGTTTGACTTATCCAAGAGATCTATACACATATTGCCATCATCAATCAAA 121 E L T Q L T E L Y L Y S N K L Q S L P A 361 GAGTTGACTCAATTAACAGAACTTTATTTATACAGTAACAAATTGCAGTCCCTCCCAGCA 141 E V G C L V N L M T L A L S E N S L T S 421 GAGGTGGGATGTTTAGTAAATCTCATGACACTGGCTCTAAGTGAAAATTCACTTACCAGT 161 L P D S L D N L K K L R M L D L R H N K 481 TTGCCTGACTCTCTTGATAACTTGAAGAAGCTGCGGATGCTTGATTTACGGCATAATAAA 181 L R E I P S V V Y R L D S L T T L Y L R 541 CTGAGAGAAATTCCTTCAGTGGTGTATAGGCTGGATTCTCTCACCACTCTTTACCTTCGC 201 F N R I T T V E K D I K N L S K L S M L 601 TTTAATCGTATAACTACTGTGGAAAAGGACATCAAAAACTTGTCAAAACTCAGCATGCTT 221 S I R E N K I K Q L P A E I G E L C N L 661 AGCATTCGAGAGAACAAATTAAACAACTACCTGCTGAAATTGGTGAATTATGTAACCTC 241 I T L D V A H N Q L E H L P K E I G N C 721 ATTACGCTGGATGTAGCTCACAATCAACTTGAACACCTTCCAAAGGAGATTGGAAACTGT 261 T Q I T N L D L Q H N E L L D L P D T I 781 ACACAGATACCAACCTTGACTTGCAGCACAATGAACTGCTAGACCTCCCAGATACTATA 281 G N L S S L S R L G L R Y N R L S A I P	SEQ ID NO:76

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		841 GGAAACCTGTCCAGTTTAAGTCGTCTTGGTCTGAGATATAACAGACTGTCAGCAATACCC	
		301 R S L A K C S A L E E L N L E N N N I S	
		901 AGATCATTAGCAAAATGCAGTGCACTTGAAGAATTAAATTTAGACAACAATAACATTTCT	
		321 T L P E S L L S S L V K L N S L T L A R	
		961 ACTTTACCAGAGAGTCTTTTATCAAGTCTTGTGAAACTGAATAGTTTGACCTTAGCTAGA	
		341 N C F Q L Y P V G G P S Q F S T I Y S L	
		1021 AATTGCTTCCAGTTGTATCCAGTGGGTGGTCCATCTCAGTTTTCTACCATCTATTCCCTC	
		361 N M E H N R I N K I P F G I F S R A K V	
		1081 AACATGGAACACAATCGAATCAACAAAATTCCATTTGGAATTTTCTCCAGAGCAAAAGTA	
		381 L S K L N M K D N Q L T S L P L D F G T	
		1141 TTAAGTAAGCTGAATATGAAGGACAATCAGTTAACATCACTTCCCTTGGATTTTGGAACT	
		401 W T S M V E L N L A T N Q L T K I P E D	
		1201 TGGACCAGTATGGTAGAATTGAATTTAGCCACTAATCAGCTCACAAAGATCCCTGAGGAT	
		421 V S G L V S L E V L I L S N N L L K K L	
		1261 GTGTCTGGTCTCGTTTCTCTTGAGGTTCTTATCTTATCAAACAATCTTCTAAAGAAGCTT	
		441 P H G L G N L R K L R E L D L E E N K L	
		1321 CCCCATGGTCTTGGAAACCTTAGGAAGTTAAGAGAGTTGGATCTAGAAGAGAACAAATTG	
		461 E S L P N E I A Y L K D L Q K L V L T N	
		1381 GAATCCTTGCCCAAATCGAAATTGCATATCTTAAGGATTTACAGAAATTAGTCTTGACAAAC	
		481 N Q L T T L P R G I G H L T N L T H L G	
		1441 AACCAGTTGACCACTCTTCCCAGAGGCATTGGTCACCTTACTAATCTCACACATCTGGGC	
		501 L G E N L L T H L P E E I G T L E N L E	
		1501 CTTGGAGAGAACCTACTTACTCACCTTCCTGAAGAAATTGGTACACTGGAGAACCTAGAA	
		521 E L Y L N D N P N L H S L P F E L A L C	
		1561 GAACTGTATTTGAATCACAACCCCAACCTGCATAGCCTTCCCTTTGAGCTGGCACTCTGC	
		541 S K L S I M S I E N C P L S H L P P Q I	
		1621 AGCAAGCTTTCAATCATGAGTATTGAGAACTGTCCACTCAGTCACCTTCCACCTCAGATT	
		561 V A G G P S F I I Q F L K M Q G P Y R A	
		1681 GTTGCTGGGGGGCCTTCTTTCATCATTCAGTTCTTAAAGATGCAGGGTCCATATCGTGCC	
		581 M V -	
		1741 ATGGTCTGA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
WBC012F07	Complement component 5 receptor 1 (C5a ligand)	1 atgaactcct tcaattatac cacccctgat tatgggcact atgatgacaa ggataccctg 61 gacctcaaca cccctgtgga taaaacttct aacacgctgc gtgttccaga catcctggcc 121 ttggtcatct ttgcagtcgt cttcctggtg ggagtgctgg gcaatgccct ggtggtctgg 181 gtgacggcat tcgaggccaa gcggaccatc aatgccatct ggttcctcaa cttggcggta 241 gccgacttcc tctcctgcct ggcgctgccc atcttgttca cgtccattgt acagcatcac 301 cactggccct ttggcggggc cgcctgcagc atcctgccct ccctcatcct gctcaacatg 361 tacgccagca tcctgctcct ggccaccatc agcgccgacc gctttctgct ggtgtttaaa 421 cccatctggt gccagaactt ccgaggggcc ggcttggcct ggatcgcctg tgccgtggct 481 tggggtttag ccctgctgct gaccataccc tccttcctgt accgggtggt ccgggaggag 541 tactttccac caaaggtgtt gtgtggcgtg gactacagcc acgacaaacg gcgggagcga 601 gccgtggcca tcgtccggct ggtcctgggc ttcctgtggc ctctactcac gctcacgatt 661 tgttacactt tcatcctgct ccggacgtgg agccgcaggg ccacgcggtc caccaagaca 721 ctcaaggtgg tggtggcagt ggtggccagt ttctttatct tctggttgcc ctaccaggtg 781 acggggataa tgatgtcctt cctggagcca tcgtcaccca ccttcctgct gctgaataag 841 ctggactccc tgtgtgtctc ctttgcctac atcaactgct gcatcaaccc catcatctac 901 gtggtggccg gccagggctt ccagggccga ctgcggaaat ccctccccag cctcctccgg 961 aacgtgttga ctgaagagtc cgtggttagg gagagcaagt cattcacgcg ctccacagtg 1021 gacactatgg cccagaagac ccaggcagtg tag	SEQ ID NO:77
		1 M N S F N Y T T P D Y G H Y D D K D T L 1 ATGAACTCCTTCAATTATACCACCCCTGATTATGGGCACTATGATGACAAGGATACCCTG 21 D L N T P V D K T S N T L R V P D I L A 61 GACCTCAACACCCCTGTGGATAAAACTTCTAACACGCTGCGTGTTCCAGACATCCTGGCC 41 L V I F A V V F L V G V L G N A L V V W 121 TTGGTCATCTTTGCAGTCGTCTTCCTGGTGGGAGTGCTGGGCAATGCCCTGGTGGTCTGG 61 V T A F E A K R T I N A I W F L N L A V 181 GTGACGGCATTCGAGGCCAAGCGGACCATCAATGCCATCTGGTTCCTCAACTTGGCGGTA 81 A D F L S C L A L P I L F T S I V Q H H 241 GCCGACTTCCTCTCCTGCCTGGCGCTGCCCATCTTGTTCACGTCCATTGTACAGCATCAC 101 H W P F G G A A C S I L P S L I L L N M 301 CACTGGCCCTTTGGCGGGGCCGCCTGCAGCATCCTGCCCTCCCTCATCCTGCTCAACATG 121 Y A S I L L L A T I S A D R F L L V F K 361 TACGCCAGCATCCTGCTCCTGGCCACCATCAGCGCCGACCGCTTTCTGCTGGTGTTTAAA 141 P I W C Q N F R G A G L A W I A C A V A 421 CCCATCTGGTGCCAGAACTTCCGAGGGGCCGGCTTGGCCTGGATCGCCTGTGCCGTGGCT 161 W G L A L L L T I P S F L Y R V V R E E 481 TGGGGTTTAGCCCTGCTGCTGACCATACCCTCCTTCCTGTACCGGGTGGTCCGGGAGGAG 181 Y F P P K V L C G V D Y S H D K R R E R	SEQ ID NO:78

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		541 TACTTTCCACCAAAGGTGTTGTGTGGCGTGGACTACAGCCACGACAAACGGCGGGAGCGA 201 A V A I V R L V L G F L W P L L T L T I 601 GCCGTGGCCATCGTCCGGCTGGTCCTGGGCTTCCTGTGGCCTCTACTCACGCTCACGATT 221 C Y T F I L L R T W S R R A T R S T K T 661 TGTTACACTTTCATCCTGCTCCGGACGTGGAGCCGCAGGGCCACGCGGTCCACCAAGACA 241 L K V V V A V V A S F F I F W L P Y Q V 721 CTCAAGGTGGTGGTGGCAGTGGTGGCCAGTTTCTTTATCTTCTGGTTGCCCTACCAGGTG 261 T G I M M S F L E P S S P T F L L L N K 781 ACGGGGATAATGATGTCCTTCCTGGAGCCATCGTCACCCACCTTCCTGCTGCTGAATAAG 281 L D S L C V S F A Y I N C C I N P I I Y 841 CTGGACTCCCTGTGTGTCTCCTTTGCCTACATCAACTGCTGCATCAACCCCATCATCTAC 301 V V A G Q G F Q G R L R K S L P S L L R 901 GTGGTGGCCGGCCAGGGCTTCCAGGGCCGACTGCGGAAATCCCTCCCCAGCCTCCTCCGG 321 N V L T E E S V V R E S K S F T R S T V 961 AACGTGTTGACTGAAGAGTCCGTGGTTAGGGAGAGCAAGTCATTCACGCGCTCCACAGTG 341 D T M A Q K T Q A V – 1021 GACACTATGGCCCAGAAGACCCAGGCAGTGTAG	
WBC012E07	Pinin, desmosome associated protein (PNN)	1 GGCTGTCAGTCCTTTCGCGCCTCGGCGGCGCGGCATAGCCCGGCTCGGCCTGTAAAGCAG 61 TCTCAAGCCTGCCGCAGGGAGAAGATGGCGGTCGCCGTGAGAACTTTGCAGGAACAGCTG 121 GAAAAGGCCAAAGAGAGTCTTAAGAACGTGGATGAGAACATTCGCAAGCTCACCGGGCGG 181 GATCCGAATGACGTGAGGCCCATCCAAGCCAGATTGCTGGCCCTTTCTGGTCCTGGTGGA 241 GGTAGAGGACGTGGTAGTTTATTACTGAGGCGTGGATTCTCAGATAGTGGAGGAGGACCC 301 CCAGCCAAACAGAGAGACCTTGAAGGGGCAGTCAGTAGGCTGGGCGGGGAGCGTCGGACC 361 AGAAGAGAATCACGCCAGGAAAGCGACCCGGAGGATGATGATGTTAAAAAGCCAGCATTG 421 CAGTCTTCAGTTGTAGCTACCTCCAAAGAGCGCACACGTAGAGACCTTATCCAGGATCAA 481 AATATGGATGAAAAGGGAAAGCAAAGGAACCGGCGAATATTTGGCTTGTTGATGGGTACC 541 CTTCAAAAATTTAAACAAGAATCCACTGTTGCTACTGAAAGGCAAAAGCGGCGCCAGGAA 601 ATTGAACAAAAACTTGAAGTTCAGGCAGAAGAAGAGAGAAAGCAGGTTGAAAATGAAAGG 661 AGAGAACTGTTTGAAGAGAGGCGTGCTAAACAGACAGAACTGCGGCTTTTGGAACAGAAA 721 GTTGAGCTTGCGCAGCTGCAAGAAGAATGGAATGAACATAATGCCAAAATAATTAAATAT 781 ATAAGAACTAAGACAAAGCCCCATTTGTTTTATATTCCTGGAAGAATGTGTCCAGCTACC 841 CAAAAACTAATAGAAGAGTCACAGAGAAAAATGAACGCTTTATTTGAAGGTAGACGCATC 901 GAATTTGCAGAACAAATAAATAAAATGGAGGCTAGGCCTAGAAGACAATCAATGAAGGAA 961 AAAGAGCATCAGGTGGTGCGTAATGAAGAACAGAAGGCGGAACAAGAAGAGGGTAAGGTG 1021 GCTCAGCGAGAGGAAGAGTTGGAGGAGACAGGTAATCAGCACAATGATGTAGAAATAGAG 1081 GAAGCAGGAGAGGAAGAGGAAAAGGAAATAGCGATTGTTCATAGTGATGCAGAGAAAGAA 1141 CAGGAGGAGGAAGAACAAAAACAGGAAATGGAGGTTAAGATGGAGGAGGAAACTGAGGTA	SEQ ID NO:79

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1201 ACGGAAAGTGAGAAGCAGCAGGATAGTCAGCCTGAAGAAGTTATGGATGTGCTAGAGATG 1261 GTTGAGAATGTCAAACATGTAATTGCTGACCAGGAGGTAATGGAAACTAATCGAGTTGAA 1321 AGTGTAGAACCTTCAGAAAATGAAGCTAGCAAAGAATTGGAACCAGAAATGGAATTTGAA 1381 ATTGAGCCAGATAAAGAATGTAAATCCCTTTCTCCTGGGAAAGAGAATGTCAGTGCTTTA 1441 GACATGGAAAAGGAGTCTGAGGAAAAAGAAGAAAAAGAATCTGAGCCCCAACCTGAGCCT 1501 GTGGCTCAACCTCAGCCTCAGTCTCAGCCCCAGCTTCAGCTTCAATCCCAGTCCCAACCA 1561 GTACTCCAGTCCCAGCCTCCCTCTCAGCCTGAGGATTTGTCATTAGCTGTTTTACAGCCA 1621 ACACCCCAAGTTACTCAGGAGCAAGGGCATTTACTACCTGAGAGGAAGGATTTTCCTGTA 1681 GAGTCTGTAAAACTCACTGAGGTACCAGTAGAGCCAGTCTTGACAGTACATCCAGAGAGC 1741 AAGAGCAAAACCAAAACTAGGAGCAGAAGTAGAGGTCGAGCTAGAAATAAAACAAGCAAG 1801 AGTAGAAGTCGAAGCAGTAGCAGTAGCAGTTCTAGTAGCAGTTCAACCAGTAGCAGCAGT 1861 GGAAGTAGTTCCAGCAGTGGAAGTAGTAGCAGTCGCAGTAGTTCCAGTAGCAGCTCCAGT 1921 ACAAGTGGCAGCAGCAGCAGAGATAGTAGCAGTAGCACTAGTAGTAGTAGTGAGAGTAGA 1981 AGTCGGAGTAGGGGCCGGGGACATAACAGAGATAGAAAGCACAGAAGGAGCGTGGATCGG 2041 AAGCGAAGGGATACTTCAGGACTAGAAAGAAGTCACAAATCTTCAAAAGGTGGTAGTAGT 2101 AGAGATACGAAAGGATCAAAGGATAAGAATTCCCGGTCCGACAGGAAAAGGTCTATATCC 2161 GAGAGTAGTCGATCAGGCAAAAGATCGTCGAGAAGTGAAAGAGACCGAAAATCAGACAGG 2221 AAAGACAAAAGGCGTTAATGGAAGAAGCCAGGCTTTCTTAGCCTATTCTTTGCAGCAGAA 2281 GATTTCTTGATGAGTAAAAGGATTACCTTTCCTTGTAAGGAGGATGCTGCCTTAAGAATT 2341 GCATGTTGTAAAAAATCTTTTTGGAAAATACAGACTGTTTGTTTACCAGACATTCTTGTA 2401 CTTTTTGCATAATTTTGTAAGAGTTATTTATCAAAATTATGTGAGGTTCCAAAATATGTA 2461 AAATAATAATAATAAAAAAAGATTAACATCCCTTGTCATCTTTTTTAAATATCCTATACT 2521 CTGCAGTAAGAATGTATATTTTAATAGGTAAATCTTTAAGTCTGTTCCCTTCTAATTCTG 2581 TATCATACATTGCTTTTGTAGAAATAAATGTGCATTTCTTTCATTAGTTTTGAGATGTCC 2641 TCGTTGACGCTTGTATAATAAATATCCTCTTGATACCATTTTCAGCTTTTATCACTAGAT 2701 ACTGAACGTGATTAGAATGTCTTTGAAAGTTTCCTCACTTTTATTTGCCTTAGGCAGTTA 2761 TTTTGAGTTGTCAAAATCAGATCTTTGCAGCTTTGAGGGGGAACATAATAGTTCTCCGTG 2821 AAATCATTTACTGTTTTTTCTAATCTCCCTTGTTATTTTAATCTAAGCATTTTCCCCTCC 2881 TCATCTTTAAACCACGTATTTGGTAGATAACTTAAAATAGTATAATTTGGTTGGCATTTT 2941 CTTCATGATTATGGGAGCATCATTCTTTTGTCTCCATGGTTACTTGTGTGATACAGCATA 3001 TATATCTGTTAAAGAAAATAATCACTTCTTTCTAGGGGAGGGAGGTAGAAAAGTATATTC 3061 TAAATTTGGTTTTTGAGTTTGTGGTCTTGTCTTAACTTTTGTGTTGGCTCTAACTCTGAA 3121 ACATGCCAATAATGTGTTTTCAAGAATTTTTGTTTAAGTATTGTATGAAAGTTTACAAAA 3181 TGAAGGAAGTTAATCTACACTTGAATCTGTGAGCAAGATAACACGCAAGTGTACCAAGTG 3241 ATTATTAACTTTGTTTTATAAATTTGTATGAATTTGGAGTATCTGTTGCCCATTACTATA 3301 CATGTGCAAATAAATGTGGCTTAGACTTGTGTGACTGCTTAAAAAAAAAAAAAAAA 1 M A V A V R T L Q E Q L E K A K E S L K 1 ATGGCGGTCGCCGTGAGAACTTTGCAGGAACAGCTGGAAAAGGCCAAAGAGAGTCTTAAG 21 N V D E N I R K L T G R D P N D V R P I 61 AACGTGGATGAGAACATTCGCAAGCTCACCGGGCGGGATCCGAATGACGTGAGGCCCATC 41 Q A R L L A L S G P G G G R G R G S L L 121 CAAGCCAGATTGCTGGCCCTTTCTGGTCCTGGTGGAGGTAGAGGACGTGGTAGTTTATTA 61 L R R G F S D S G G G P P A K Q R D L E 181 CTGAGGCGTGGATTCTCAGATAGTGGAGGAGGACCCCCAGCCAAACAGAGAGACCTTGAA	SEQ ID NO:80

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		81 G A V S R L G G E R R T R R E S R Q E S 241 GGGGCAGTCAGTAGGCTGGGCGGGGAGCGTCGGACCAGAAGAGAATCACGCCAGGAAAGC	
		101 D P E D D D V K K P A L Q S S V V A T S 301 GACCCGGAGGATGATGATGTTAAAAAGCCAGCATTGCAGTCTTCAGTTGTAGCTACCTCC	
		121 K E R R T R R D L I Q D Q N M D E K G K Q 361 AAAGAGCGCACACGTAGAGACCTTATCCAGGATCAAAATATGGATGAAAAGGGAAAGCAA	
		141 R N R R I F G L L M G T L Q K F K Q E S 421 AGGAACCGGCCAATATTTGGCTTGTTGATGGGTACCCTTCAAAAATTTAAACAAGAATCC	
		161 T V A T E R Q K R R Q E I E Q K L E V Q 481 ACTGTTGCTACTGAAAGGCAAAAGCGGCGCCAGGAAATTGAACAAAAACTTGAAGTTCAG	
		181 A E E E R K Q V E N E R R E E L F E E E R R 541 GCAGAAGAAGAGAGAAAGCAGGTTGAAAATGAAAGGAGAGAACTGTTTGAAGAGAGGCGT	
		201 A K Q T E L R L L L E Q K V E L A Q L Q E 601 GCTAAACAGACAGAACTGCGGCTTTTGGAACAGAAAGTTGAGCTTGCGCAGCTGCAAGAA	
		221 E W N E H N A K L I I K Y I R T T K T K P H 661 GAATGGAATGAACATAATGCCAAAATAATTAAATATATTAAGAACTAAGACAAAGCCCCAT	
		241 L F Y I P G R M C P A T Q K L I E E S Q 721 TTGTTTTATATTCCTGGAAGAATGTGTCCAGCTACCCAAAAACTAATAGAAGAGTCACAG	
		261 R K M N A L F E G R R R I E E F A E Q I N K 781 AGAAAAATGAACGCTTTATTTGAAGGTAGACGCATCGAATTGCCAGAACAAATAAATAAA	
		281 M E A R P P R R Q S M K K E K E H Q V V R N 841 ATGGAGGCTAGGCCTAGAAGACAATCAATGAAGGAAAAAGAGCATCAGGTGGTGCGTAAT	
		301 E E Q K A A E Q E E G K V A Q R E E E E L E 901 GAAGAACAGAAGGCGGAACAAGAAGAGGGTAAGGTGGCTCACGGAGAGGAAGAGTTGGAG	
		321 E T G N Q H N D V E I E E A G E E E E K 961 GAGACAGGTAATCAGCACAATGATGTAGAAATAGAGGAAGCAGGAGAGGAAGAGGAAAAG	
		341 E I A A I V H S D A E K E Q E E E E Q K Q 1021 GAAATAGCGATTGTTCATAGTGATGCAGAAAAGAACAGGAGGAGGAAGAACACAAAACAG	
		361 E M E V K M E E E E T E V R E E S E K Q Q D 1081 GAAATGGAGGTTAAGATGGAGGAGGAAACTGAGGTAAGGGAAGTGAGAAGCAGCAGGAT	
		381 S Q P E E V M D V L E M V E N V K H V I 1141 AGTCAGCCTGAAGAAGTTATGGATGTGCTAGAGATGGTTGAGAATGTCAAACATGTAATT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		401 A D Q E V M E T N R V E S V E P S E N E 1201 GCTGACCAGGAGGTAATGGAAACTAATCGAGTTGAAAGTGTAGAACCTTCAGAAAATGAA 421 A S K E L E P E M E F E I E P D K E C K 1261 GCTAGCAAAGAATTGGAACCAGAAATGGAATTTGAAATTGAGCCAGATAAAGAATGTAAA 441 S L S P G K E N V S A L D M E K E S E E 1321 TCCCTTTCTCCTGGGAAAGAGAATGTCAGTGCTTTAGACATGGAAAAGGAGTCTGAGGAA 461 K E E K E S E P Q P E P V A Q P Q P Q S 1381 AAAGAAGAAAAAGAATCTGAGCCCCAACCTGAGCCTGTGGCTCAACCTCAGCCTCAGTCT 481 Q P Q L Q L Q S Q S Q P V L Q S Q P P S 1441 CAGCCCCAGCTTCAGCTTCAATCCCAGTCCCAACCAGTACTCCAGTCCCAGCCTCCCTCT 501 Q P E D L S L A V L Q P T P Q V T Q E Q 1501 CAGCCTGAGGATTTGTCATTAGCTGTTTTACAGCCAACACCCCAAGTTACTCAGGAGCAA 521 G H L L P E R K D F P V E S V K L T E V 1561 GGGCATTTACTACCTGAGAGGAAGGATTTTCCTGTAGAGTCTGTAAAACTCACTGAGGTA 541 P V E P V L T V H P E S K S K T K T R S 1621 CCAGTAGAGCCAGTCTTGACAGTACATCCAGAGAGCAAGAGCAAAACCAAAACTAGGAGC 561 R S R G R A R N K T S K S R S R S S S S 1681 AGAAGTAGAGGTCGAGCTAGAAATAAAACAAGCAAGAGTAGAAGTCGAAGCAGTAGCAGT 581 S S S S S S S T S S S S G S S S S S G S 1741 AGCAGTTCTAGTAGCAGTTCAACCAGTAGCAGCAGTGGAAGTAGTTCCAGCAGTGGAAGT 601 S S S R S S S S S S S S T S G S S S R D 1801 AGTAGCAGTCGCAGTAGTTCCAGTAGCAGCTCCAGTACAAGTGGCAGCAGCAGCAGAGAT 621 S S S S T S S S S E S R S R S R G R G H 1861 AGTAGCAGTAGCACTAGTAGTAGTAGTGAGAGTAGAAGTCGGAGTAGGGGCCGGGGACAT 641 N R D R K H R R S V D R K R R D T S G L 1921 AACAGAGATAGAAAGCACAGAAGGAGCGTGGATCGGAAGCGAAGGGATACTTCAGGACTA 661 E R S H K S S K G G S S R D T K G S K D 1981 GAAAGAAGTCACAAATCTTCAAAAGGTGGTAGTAGTAGAGATACGAAAGGATCAAAGGAT 681 K N S R S D R K R S I S E S S R S G K R 2041 AAGAATTCCCGGTCCGACAGGAAAAGGTCTATATCCGAGAGTAGTCGATCAGGCAAAAGA 701 S S R S E R D R K S D R K D K R R – 2101 TCGTCGAGAAGTGAAAGAGACCGAAAATCAGACAGGAAAGACAAAAGGCGTTAA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
WBC010F04	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	1 cggacgcgtg ggtcgaccca cgcgtccgtc ctctgctgcc gctcggtcac gcttgctctt 61 tcaccatgcc tggatcactt cctttgaatg cagaagcttg ctggccaaaa gatgtgggaa 121 ttgttgccct tgagatctat tttccttctc aatatgttga tcaagcagag ttggaaaaat 181 atgatggtgt agatgctgga aagtatacca ttggcttggg ccaggccaag atgggcttct 241 gcacagatag agaagatatt aactctcttt gcatgactgt ggttcagaat cttatggaga 301 gaaataacct ttcctatgat tgcattgggc ggctggaagt tggaacagag acaatcatcg 361 acaaatcaaa gtctgtgaag actaatttga tgcagctgtt tgaagagtct gggaatacag 421 atatagaagg aatcgacaca actaatgcat gctatggagg cacagctgct gtcttcaatg 481 ctgttaactg gattgagtcc agctcttggg atggacggta tgccctggta gttgcaggag 541 atattgctgt atatgccaca ggaaatgcta gacctacagg tggagttgga gcagtagctc 601 tgctaattgg gccaaatgct cctttaattt ttgaacgagg gcttcgtggg acacatatgc 661 aacatgccta tgatttttac aagcctgata tgctatctga atatcctata gtagatggaa 721 aactctccat acagtgctac ctcagtgcat tagaccgctg ctattctgtc tactgcaaaa 781 agatccatgc ccagtggcag aaagagggaa atgataaaga ttttaccttg aatgattttg 841 gcttcatgat ctttcactca ccatattgta aactggttca gaaatctcta gctcggatgt 901 tgctgaatga cttccttaat gaccagaata gagataaaaa tagtatctat agtggcctgg 961 aagcctttgg ggatgttaaa ttagaagaca cctactttga tagagatgtg gagaaggcat 1021 ttatgaaggc tagctctgaa ctcttcagtc agaaaacaaa ggcatcttta cttgtatcaa 1081 atcaaaatgg aaatatgtac acatcttcag tatatggttc ccttgcatct gttctagcac 1141 agtactcacc tcagcaatta gcagggaaga gaattggagt gttttcttat ggttctggtt 1201 tggctgccac tctgtactct cttaaagtca cacaagatgc tacaccgggg tctgctcttg 1261 ataaaataac agcaagttta tgtgatctta aatcaaggct tgattcaaga actggtgtgg 1321 caccagatgt cttcgctgaa aacatgaagc tcagagagga cacctatcat ttggtcaact 1381 atattcccca gggttcaata gattcactct ttgaaggaac gtggtactta gttagggtgg 1441 atgaaaagca cagaagaact tacgctcggc gtcccactcc aaatgatgac actttggatg 1501 aaggagtagg acttgtgcat tcaaacatag caactgagca tattccaagc cctgccaaga 1561 aagtaccaag actccctgcc acagcagcag aacctgaagc agctgtcatt agtaatgggg 1621 aacattaaga tactctgtga ggtgcaagac ttcagggtgg ggtgggcatg gggtgggggt 1681 atgggaacag ttggaggaat gggatatctg gggataattt taaaggatta catgttatgt 1741 aaatttttat gtgactgaca tggagcctgg atgactatcg tgtacttggg aaagtctctt 1801 tgctctattt gctgacatgc ttcctgttgt ggtctggcca atgccaaatg tactcgaatg 1861 atgttaaggg ctctgtaaaa cttcatacct ctttggccat ttgtatgcat gatgtttggt 1921 ttttaaacat ggtataatga attgtgtact tctgtcagaa gaaagcagag gtactaatct 1981 ccaattaaaa aatttttaa catgtaagaa ttttgtactt tgaacaacaa gattacagaa 2041 agtacctgtg gtttttggaa aacatttcta gcttggggaa tgtgacaaca ttccccagtg 2101 tggtaaaatt ggggtaaaat gtggtaaaat gtgatacgca caaacccttt gaaaatagca 2161 aaacaaacat gccctttttc taaaattgat aaatcctaaa gaggaagaaa agagctggga 2221 caataaaaca ctggctctgg aatctggaat gttaagtcca ggccagcagt gacaaaagtt 2281 attgtaatga cctctgaaca gagaaacact gccattgaag aggcttctgg tatagaaaac 2341 atggtacatt caggagctgt gaatatagct ctaggtgtgc tcctgaatca gttcatggta 2401 gattatgctg aacaacagtg agatgttatt ggaggtgtgg atgagggagt ttgttgttgc 2461 agtccttctt tgcaccttat tttaaagaat aaatgaaaca tttttctggt tacttttta 2521 aaaatttaaa atggaaggga agaatagggg cagggcatta ttaggctatt tctgatgctt 2581 cagtgttata aattcaacat agaggctgac aacctaaatt catggtgtaa cacagctctt 2641 ttccttttcc ttttttttt ttttttttgg tatctgttca atgaaaataa ggtatgaccc	SEQ ID NO:81

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2701 aagtttttac ctagtctgac tagaagtatt ccacttcaag gtctgaagta ggacttttac 2761 cttaaaaaac aacaacaaac aaaactatca cacaggatag ataagaagat tggttaaaca 2821 gttttgtgta gatcttttg gtgctgaact atgacatgag ccttatagat tgtaaaatag 2881 ggatagttgg aactaatgta cagaactaaa ttttttaaac tttatttgct gttaaattct 2941 gtgaagtttc agttatctaa aataaatata cacaaatatg aaatataatg tttcagattg 3001 caaggtaata tgtaatagta gtgtttgtaa gatactcttg tctaatatta actagtagta 3061 ttttgatttg tacagtcata atttgttaaa atgacttcat ttaacattca ctgatgtaga 3121 ttaataatgt aagttctgat ttaaagaatg gtggcaaaat ggtgcatgta atacttttgc 3181 aagtgttggg gagatcggta tgtttgaaa agagtaattt aactttggg tgccaggaaa 3241 tgggttttct caaagtccat tgccgccaat gggcaggcct gcaaatactg gcacagagca 3301 ttaatcatac accttattaa cggtgaggtg aatacttttg aaataaagtt ttagagaaat 3361 gtttcaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3421 a	
		1 M P G S L P L N A E A C W P K D V G I V 1 ATGCCTGGATCACTTCCTTTGAATGCAGAAGCTTGCTGGCCAAAAGATGTGGGAATTGTT	SEQ ID NO:82
		21 A L E I Y F P S Q Y V D Q A E L E K Y D 61 GCCCTTGAGATCTATTTTCCTTCTCAATATGTTGATCAAGCAGAGTTGGAAAAATATGAT	
		41 G V D A G K Y T I G L G Q A K M G F C T 121 GGTGTAGATGCTGGAAAGTATACCATTGGCTTGGGCCAGGCCAAGATGGGCTTCTGCACA	
		61 D R E D I N S L C M T V V Q N L M E R N 181 GATAGAGAAGATATTAACTCTCTTTGCATGACTGTGGTTCAGAATCTTATGGAGAGAAAT	
		81 N L S Y D C I G R L E V G T E T I I D K 241 AACCTTTCCTATGATTGCATTGGGCGGCTGGAAGTTGGAACAGAGACAATCATCGACAAA	
		101 S K S V K T N L M Q L F E E S G N T D I 301 TCAAAGTCTGTGAAGACTAATTTGATGCAGCTGTTTGAAGAGTCTGGGAATACAGATATA	
		121 E G I D T T N A C Y G G T A A V F N A V 361 GAAGGAATCGACACAACTAATGCATGCTATGGAGGCACAGCTGCTGTCTTCAATGCTGTT	
		141 N W I E S S S W D G R Y A L V V A G D I 421 AACTGGATTGAGTCCAGCTCTTGGGATGGACGGTATGCCCTGGTAGTTGCAGGAGATATT	
		161 A V Y A T G N A R P T G G V G A V A L L 481 GCTGTATATGCCACAGGAAATGCTAGACCTACAGGTGGAGTTGGAGCAGTAGCTCTGCTA	
		181 I G P N A P L I F E R G L R G T H M Q H 541 ATTGGGCCAAATGCTCCTTTAATTTTGAACGAGGCTTCGTGGGACACATATGCACAT	
		201 A Y D F Y K P D M L S E Y P I V D G K L 601 GCCTATGATTTTTACAAGCCTGATATGCTATCTGAATATCCTATAGTAGATGGAAAACTC	
		221 S I Q C Y L S A L D R C Y S V Y C K K I	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		661 TCCATACACTGCTACCTCAGTGCATTAGACCGCTGCTATTCTGTCTACTGCAAAAAGATC	
		241 H A Q W Q K E G N D K D F T L N D F G F	
		721 CATGCCCAGTGGCAGAAAGAGGGAAATGATAAAGATTTTACCTTGAATGATTTTGGCTTC	
		261 M I F H S P Y C K L V Q K S L A R M L L	
		781 ATGATCTTTCACTCACCATATTGTAAACTGGTTCAGAAATCTCTAGCTCGGATGTTGCTG	
		281 N D F L N D Q N R D K N S I Y S G L E A	
		841 AATGACTTCCTTAATGACCAGAATAGAGATAAAAATAGTATCTATAGTGGCCTGGAAGCC	
		301 F G D V K L E D T Y F D R D V E K A F M	
		901 TTTGGGGATGTTAAATTAGAAGACACCTACTTTGATAGAGATGTGGAGAAGGCATTTATG	
		321 K A S S E L F S Q K T K A S L L V S N Q	
		961 AAGGCTAGCTCTGAACTCTTCAGTCAGAAAACAAAGGCATCTTTACTTGTATCAAATCAA	
		341 N G N M Y T S S V Y G S L A S V L A Q Y	
		1021 AATGGAAATATGTACACATCTTCAGTATATGGTTCCCTTGCATCTGTTCTAGCACAGTAC	
		361 S P Q Q L A G K R I G V F S Y G S G L A	
		1081 TCACCTCAGCAATTAGCAGGGAAGAGAATTGGAGTGTTTTCTTATGGTTCTGGTTTGGCT	
		381 A T L Y S L K V T Q D A T P G S A L D K	
		1141 GCCACTCTGTACTCTCTTAAAGTCACACAAGATGCTACACCGGGGTCTGCTCTTGATAAA	
		401 I T A S L C D L K S R L D S R T G V A P	
		1201 ATAACAGCAAGTTTATGTGATCTTAAATCAAGGCTTGATTCAAGAACTGGTGTGGCACCA	
		421 D V F A E N M K L R E D T Y H L V N Y I	
		1261 GATGTCTTCGCTGAAAACATGAAGCTCAGAGAGGACACCTATCATTTGGTCAACTATATT	
		441 P Q G S I D S L F E G T W Y L V R V D E	
		1321 CCCCAGGGTTCAATAGATTCACTCTTTGAAGGAACGTGGTACTTAGTTAGGGTGGATGAA	
		461 K H R R T Y A R R P T P N D D T L D E G	
		1381 AAGCACAGAAGAACTTACGCTCGGCGTCCCACTCCAAATGATGACACACTTTGGATGAGGA	
		481 V G L V H S N I A T E H I P S P A K K V	
		1441 GTAGGACTTGTGCATTCAAACATAGCAACTGAGCATATTCCAAGCCCTGCCAAGAAAGTA	
		501 P R L P A T A A E P E A A V I S N G E H	
		1501 CCAAGACTCCCTGCCACAGCAGCAGAACCTGAAGCAGCTGTCATTAGTAATGGGGAACAT	
		521 -	
		1561 TAA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
WBC009E12	Down-regulator of transcription 1, TBP-binding (negative cofactor 2)	1 gagcggcttc ctgcaaacct tccctggcat ctggagggac caccgttgcc gcgtctttcgg 61 cttccacgat ctgcgttcgg gctacgcggc cacggcggca gccactgcga ctcccactgt 121 gcctggctct gtccatatta gttcccaggc ggccgtcgcc gttccagcag cggcagcggc 181 agcggcagcg gcggacatgt tgtgaggcgg cggcgcggat gtctgaagga tggtttggcc 241 gaggcggcgg caacggctgc tggcggcggc ggcagcggca gcgggcctcc gggctctata 301 gagccgagcc cgctgggtac ccgcccggta ccgcggcgag gccagtgccc ctggatcttg 361 cctctgctcc gacgccgttg gggaccagtt aggcgacagc gcccgcccct ctgaggagac 421 acgaaggtgg ttccccagcc gctcaaattt ccggaccacc gcgctttccc ctcctcagcc 481 tgggctgtgc tctcctctaga atcctcgggc ccccactttc ttcccaaact catcctaaat 541 ctctcacaca cgcgagtgtt cccagccctc aagccagctg ctcctccgtt catttctgc 601 accctcttcg caaagcaccc cccgggatca ctctccgagg gcgacttttt gagaaatctc 661 ggtggagtag tggaccagag ctgggagttt tttaaaagcc gggcgcgag aaacaggaag 721 gtactatggc ttcctcgtct ggcaacgatg atgatctcac tatccccaga gctgctatca 781 ataaaatgat caaagagact cttcctaatg tccgggtggc caacgatgct cgagagctgg 841 tggtgaactg ctgcactgaa ttcattcacc ttatatcttc tgaagccaat gagatttgta 901 acaaatcgga aagaagacc atctcaccag agcatgtcat acaagcacta gaaagtttgg 961 gatttggctc ttacatcagt gaagtaaaag aagtcttgca agagtgtaaa acagtagcat 1021 taaaaagaag aaaggccagt tctcgtttgg aaaaccttgg cattcctgaa gaagagttat 1081 tgagacagca acaagaatta tttgcaaaag ctagacagca acaagcagaa ttggcccaac 1141 aggaatggct tcaaatgcag caagctgccc aacaagccca gcttgctgct gcctcagcca 1201 gtgcatctaa tcaggcggga tcttctcagg atgaagaaga tgatgatgat atctgaaatt 1261 caccagctga gtttctattt cttctataaa tgttttccc tgcacaacaa aaacagtgaa 1321 agaaatgctt atctgtaatt ttgtatgcat cttggtggac ttgtcattgg tattctaggg 1381 atgtctgcta ttaagtttca tctattgtgt gctatacatg taaaaactgt ctctttgaac 1441 tattgaaaat ttaaggttca gtataatatc aattttgaat ttttaatggt gtttatgaaa 1501 ttttagatag cagcgagtcc ttcgtttgat caataaacag tgttacagat aacttcaagt 1561 ttataaaaat acagtgaaat ttctacaaag ctctaaatct gcatttgcat ttcctctgcc 1621 ctttaacta aactaaaact tgtgaatttt aaattattaa ggggggggtg ctgtgtgaat 1681 cagtagacat tggattgggt tggtgaaaga gttcagttct gtagtatctg aatttgtctt 1741 ttaaaatgag tacatatata ggcaataaat atatatgctc agatcaatat acttgtttag 1801 aaaaacttca agacattcaa aaactaggaa ggagtatgtt taatagtatt tgtataaatt 1861 tggtggttat gttttttat tttgtttctg tttgtgtag aggtaaaaac tatagtttta 1921 ttacagcata attcatttg agctccacta tgacatttca aagactgccc agtttggaag 1981 tctgtcatga tttttactct ttcactccaa ttcagtaatt gttgatagta ttacttacct 2041 agtccatcca tactcatatt attcaaatat ataggtggta ctttgaaac aattacattg 2101 gttctcttgg tttaactgag gtttatgaat attcaaacct ttgctgggggg aaagaaatga 2161 aagttaatga gcatgcttgc tatgagagag ggatttttaa tttaacttgt agttatagtt 2221 tacttattgt ttttagaatt actttacat tttcccaact agatggccta gagtccaaca 2281 ttacctttg agatgacatt attgtctcca taattgagtg atagctttaa aaaaaagatt 2341 agttttgctt aagaagttat gttacaactg atcagcccta tatgaattaa ctgatcagcc 2401 ctatatgaaa cataagttgt gttataactt atcagccgta tatggaacat aaatagtttc 2461 tacctgcttg ttagagaagc tttaatttgg ttctaataaa tacagtatgg tagtgtttat 2521 aggaatccag gatgttgaag aaatggcata atgtctatat tttggaaaca gaaaggaaaa 2581 gtcacttaag atagtattaa gtaattaaat tcctatgtca gttgccaaat cttttaaact 2641 tatgtattca ccaagcccaa aaatagattg tggctcccag gattccaatt ttaattggag 2701 agctaagtaa gtaaagtttt ataactgtta ggtttcttaa tgatcatatt ttgcagtttt 2761 agtaaaaggg aaatatgtt atacatttat taaatatact tcccccatga agtgaaaagg	SEQ ID NO:83

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2821 ttaattttgc tgaatgtttt aagttgaagt tacttcatgg atgtcatacc catgaagtgc 2881 atttggatga gatagaagaa attgtttttt aaaaagttta agtaccaaag gtagtctagt 2941 ctagaacgat aagttaatac gtgttggctt ttctaatttg tactgtaaca tccttatact 3001 ttctatttta agtatatctg tttcttaagt aaacaactta gatattttcc acacctttt 3061 ttttttctga tgcagagttc aggttaatat tttactgcat ctgataatgt attatacgtt 3121 tgaagcctag tgacttttca ttttgacatt cttgtgattt catatgctgt attcttcaag 3181 caataaaatt gtgatgtgtt ttataaaaaa aaaaaaaaaa aa 1 M A S S S G N D D D L T I P R A A I N K 1 ATGGCTTCCTCGTCTGGCAACGATGATGATCTCACTATCCCCAGAGCTGCTATCAATAAA 21 M I K E T L P N V R V A N D A R E L V V 61 ATGATCAAAGAGACTCTTCCTAATGTCCGGGTGGCCAACGATGCTCGAGAGCTGGTGGTG 41 N C C T E F I H L I S S E A N E I C N K 121 AACTGCTGCACTGAATTCATTCACCTTATATCTTCTGAAGCCAATGAGATTTGTAACAAA 61 S E K K T I S P E H V I Q A L E S L G F 181 TCGGAAAAGAAGACCATCTCACCAGAGCATGTCATACAAGCACTAGAAAGTTTGGGATTT 81 G S Y I S E V K E V L Q E C K T V A L K 241 GGCTCTTACATCAGTGAAGTAAAAGAAGTCTTGCAAGAGTGTAAAACAGTAGCATTAAAA 101 R R K A S S R L E N L G I P E E E L L R 301 AGAAGAAAGGCCAGTTCTCGTTTGGAAAACCTTGGCATTCCTGAAGAAGAGTTATTGAGA 121 Q Q Q E L F A K A R Q Q Q A E L A Q Q E 361 CAGCAACAAGAATTATTTGCAAAAGCTAGACAGCAACAAGCAGAATTGGCCCAACAGGAA 141 W L Q M Q Q A A Q Q A Q L A A A S A S A 421 TGGCTTCAAATGCAGCAAGCTGCCCAACAAGCCCAGCTTGCTGCTGCCTCAGCCAGTGCA 161 S N Q A G S S Q D E E D D D D I - 481 TCTAATCAGGCGGGATCTTCTCAGGATGAAGAAGATGATGATGATATCTGA	SEQ ID NO:84
WBC009B10_V1.3_at	Human mRNA for complement receptor type 1 (CR1, C3b/C4b receptor, CD35)	1 CGTGGTTTGTAGATGTGCTTGGGGAGAATGGGGGCCTCTTCTCCAAGAAGCCCGGAGCCT 61 GTCGGGCCGCCGGCGCCCGGTCTCCCCTTCTGCTGCGGAGGATCCCTGCTGGCGGTTGTG 121 GTGCTGCTTGCGCTGCCGGTGGCCTGGGGTCAATGCAATGCCCCAGAATGGCTTCCATTT 181 GCCAGGCCTACCAACCTAACTGATGAGTTTGAGTTTCCCATTGGGACATATCTGAACTAT 241 GAATGCCGCCCTGGTTATTCCGGAAGACCGTTTTCTATCATCTGCCTAAAAAACTCAGTC 301 TGGACTGGTGCTAAGGACAGGTGCAGACGTAAATCATGTCGTAATCCTCCAGATCCTGTG 361 AATGGCATGGTGCATGTGATCAAAGGCATCCAGTTCGGATCCCAAATTAAATATTCTTGT 421 ACTAAAGGATACCGACTCATTGGTTCCTCGTCTGCCACATGCATCATCTCAGGTGATACT 481 GTCATTTGGGATAATGAAACACCTATTTGTGACAGAATTCCTTGTGGGCTACCCCCCACC 541 ATCACCAATGGAGATTTCATTAGCACCAACAGAGAGAATTTTCACTATGGATCAGTGGTG 601 ACCTACCGCTGCAATCCTGGAAGCGGAGGGAGAAAGGTGTTTGAGCTTGTGGGTGAGCCC	SEQ ID NO:85

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		661 TCCATATACTGCACCAGCAATGACGATCAAGTGGGCATCTGGAGCGGCCCCGCCCCTCAG	
		721 TGCATTATACCTAACAAATGCACGCCTCCAAATGTGGAAAATGGAATATTGGTATCTGAC	
		781 AACAGAAGCTTATTTTCCTTAAATGAAGTTGTGGAGTTTAGGTGTCAGCCTGGCTTTGTC	
		841 ATGAAAGGACCCCGCCGTGTGAAGTGCCAGGCCCTGAACAAATGGGAGCCGGAGCTACCA	
		901 AGCTGCTCCAGGGTATGTCAGCCACCTCCAGATGTCCTGCATGCTGAGCGTACCCAAAGG	
		961 GACAAGGACAACTTTTCACCTGGGCAGGAAGTGTTCTACAGCTGTGAGCCCGGCTACGAC	
		1021 CTCAGAGGGCTGCGTCTATGCGCTGCACACCCAGGGAGACTGGCAGCCCTGCAGCCCCC	
		1081 ACATGTGAAGTGAAATCCTGTGATGACTTCATGGGCCAACTTCTTAATGGCCGTGTGCTA	
		1141 TTTCCAGTAAATCTCCAGCTTGGAGCAAAAGTGGATTTTTGTTTGATGAAGGATTTCAA	
		1201 TTAAAAGGCAGCCTCTGCTAGTTACTGTGTCTTGGCTGGAATGGAAAGCCTTTGGAATAGC	
		1261 AGTGTTCCAGTGTGTGAACAAATCTTTGTCCAAGTCCTCCAGTTATTCCTAATGGGAGA	
		1321 CACACAGGAAAACCTCTGGAAGTCTTTCCCTTTGGAAAAGCAGTAAATTACACATGCGAC	
		1381 CCCCACCCAGACAGAGGACGAGCTTCGACCTCATTGGAGAGAGCACCATCCGCTGCACA	
		1441 AGTGACCCTCAAGGGAATGGGGTTTGGAGCAGCCCTGCCCCTCGCTGTGGAATTCTGGGT	
		1501 CACTGTCAAGCCCCAGATCATTTCTGTTTGCCAAGTTGAAAACCCAAACCAATGCATCT	
		1561 GACTTTCCCATTGGGACATCTTTAAAGTACGAATGCCGTCCTGAGTACTACGGGAGGCCA	
		1621 TTCTCTATCACATGTCTAGATAACCTGGTCTGGTCAAGTCCCAAAGATGTCTGTAAACGT	
		1681 AAATCATGTAAAACTCCTCCAGATCCAGTGAATGGCATGGTGCATGTGATCACAGACATC	
		1741 CAGGTTGGATCCACGAATCAACTATTCTTGTACTACAGGGCACCGACTCATTGGTCACTCA	
		1801 TCTGCTGAATGTATCCTCTCGGGCAATGCTGCCCATTGGAGCACGAAGCCGCCAATTTGT	
		1861 CAACGAATTCCTTGTGGGCTACCCCCCACCATCGCCAATGGAGATTTCATTAGCACCAAC	
		1921 AGAGAGAATTTTCACTATGGATCAGTGGTGACCTACCGCTCCAATCCTGGAAGCGGAGGG	
		1981 AGAAAGGTGTTTGAGCTTGTGGGTGAGCCCTCCATATACTGCACCAGCAATGACGATCAA	
		2041 GTGGGCATCTGGAGCGGCCGGCCCTCAGTGCATTATACCTAACAAATGCACGCCTCCA	
		2101 AATGTGGAAAATGGAATATTGGTATCTGACACAACAGAAGCTTATTTTCCTTAAATGAAGTT	
		2161 GTGGAGTTTAGGTGTCAGCCTGGCTTTGTCATGAAAGGACCCCGCCGTGTGAAGTGCCAG	
		2221 GCCCTGAACAAATGGGAGCCGGAGCTACCAAGCTGCTCCAGGGTATGTCAGCCACCTCCA	
		2281 GATGTCCTGCATGCTGAGCGTACCCAAAGGGACAAGGACAACTTTTCACCCGGGCAGGAA	
		2341 GTGTTCTACAGCTGTGAGCCCGGCTATGACCTCAGAGGGGCTGCGTCTATGCGCTGCACA	
		2401 CCCCAGGGAGACTGGAGCCCTGCAGCCCCCACATGTGAAGTGAAATCCTGTGATGACTTC	
		2461 ATGGGCCAACTTCTTAATGGCCGTGTGCTATTTCCAGTAAATCTCCAGCTTGGAGCAAAA	
		2521 GTGGATTTTGTTGTGATGAAGGATTTCAATTAAAAGGCAGCCTCTGCTAGTTATTGTGTC	
		2581 TTGGCTGGAATGGAAAGCCTTTGGAATAGCAGTGTTCCAGTGTGTGAACAAATCTTTGT	
		2641 CCAAGTCCTCCAGTTATTCCTAATGGGAGACACAGGAAAACCTCTGGAAGTCTTTCCC	
		2701 TTTGGAAAAGCAGTAAATTACACATGCGACCCCCCACCCCAGACAGAGGGACGAGCTTCGAC	
		2761 CTCATTGGAGAGAGCACCATCCGCTGCACAAGTGACCCTCAAGGGAATGGGGTTTGGAGC	
		2821 AGCCCTGCCCCTCGCTGTGGAATTCTGGGTCACTGTCAAGCCCCAGATCATTTTCTGTTT	
		2881 GCCAAGTTGAAAACCCAAACCAATGCATCTGACTTTCCCCATTGGGACATCTTTAAAGTAC	
		2941 GAATGCCGTCCTGAGTACTACGGGAGGCCATTCTCTATCACATGTCTAGATAACCTGGTC	
		3001 TGGTCAAGTCCCAAAGATGTCTGTAAACGTAAATCATGTAAAACTCCTCCAGATCCAGTG	
		3061 AATGGCATGGTGCATCTGATCACAGACATCCAGGTTGGATCCAGAATCAACTATTCTTGT	
		3121 ACTACAGGGCACCGACTCATTGGTCACTCATCTGCTGAATGTATCCTCTCAGGCAATACT	
		3181 GCCCATTGGAGCACGAAGCCGCCAATTTGTCAACGAATTCCTTGTGGGCTACCCCCAACC	
		3241 ATCGCCAATGGAGATTTCATTAGCACCAACAGAGAGAATTTTCACTATGGATCAGTGGTG	
		3301 ACCTACCGCTGCAATCTTGGAAGCAGAGGGAGAAAGGTGTTTGAGCTTGTGGGTGAGCCC	
		3361 TCCATATACTGCACCAGCAATGACGATCAAGTGGGCATCTGGAGCGGCCCCGCCCCTCAG	
		3421 TGCATTATACCTAACAAATGCACGCCTCCCAAATGTGGAAAATGGAATATTGGTATCTGAC	
		3481 AACAGAAGCTTATTTTCCTTAAATGAAGTTGTGGAGTTTAGGTGTCAGCCTGGCTTTGTC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		3541 ATGAAGGACCCCGCCGTGTGAAGTGCCAGGCCTGAACAAATGGGAGCCAGAGTTACCA	
		3601 AGCTGCTCCAGGGTGTGTCAGCCGCCTCCAGAAATCCTGCATGGTGAGCATACCCCAAGC	
		3661 CATCAGGACAACTTTCACCTGGGCAGGAAGTGTTCTACAGCTGTGAGCCTGGCTATGAC	
		3721 CTCAGAGGGCTGCGTCTCTGCACTGCACACCCCAGGGAGACTGGAGCCCTGAAGCCCCG	
		3781 AGATGTGCAGTGAAATCCTGTGATGACTTCTTGGGTCAACTCCCTCATGGCCGTGTGCTA	
		3841 TTTCCACTTAATCTCCAGCTTGGGGCAAAGGTGTCCTTTGTCTGTGATGAAGGGTTTCGC	
		3901 TTAAAGGGCAGTTCCGTTAGTCATTGTGTCTTGGTTGGAATGAGAAGCCTTTGGAATAAC	
		3961 AGTGTTCCTGTGTGTAACATATCTTTTGTCCAAATCCTCCAGCTATCCTTAATGGGAGA	
		4021 CACACAGGAACTCCCTCTGGAGATATCCCTATGGAAAAGAAATATCTTACACATGTGAC	
		4081 CCCCACCCAGACACAGAGGGATGACCTTCAACCTCATTGGGGAGAGCACCATCCGCTGCACA	
		4141 AGTGACCCTCATGGGAATGGGGTTTGGAGCAGCCCTCGCCCCCTCGCTGTGAACTTTCTGTT	
		4201 CGTGCTGGTCACTGTAAAACCCCAGAGCAGTTTCCATTTGCCAGTCCTACGATCCCAATT	
		4261 AATGACTTTGAGTTTCCAGTCGGGACATCTTTGAATTATGAATGCCGTCCTGGGTATTTT	
		4321 GGGAAAATGTTCTCTATCTCCTGCCTAGAAAACTTGGTCTGGTCAAGTGTTGAAGACAAC	
		4381 TGTAGACGAAAATCATGTGGACCTCCACCAGAACCCTTCAATGGAATGGTGCATATAAAC	
		4441 ACAGATACACAGTTTGGATCAACAGTTAATTATTCTTGTAATGAAGGGTTTCGACTCATT	
		4501 GGTTCCCCATCTACTACTTGTCTCGTCTCAGGCAATAATGTCACATGGGATAAGAGGCA	
		4561 CCTATTTGTGAGATCATATCTTGTGAGCCACCTCCAACCATATCCAATGGAGACTTCTAC	
		4621 AGCAACAATAGAACATCTTTTCACAATGGAACGGTGGTAACTTACCAGTGCCACACTGGA	
		4681 CCAGATGGAGAACAGCTGTTTGAGCTTGTGGGAGAACGGTCAATATATTGCACCAGCAAA	
		4741 GATGATCAAGTTGGTGTTTGGAGCAGCCCTCCCCCCTCGGTGTATTTCTACTAATAAATGC	
		4801 ACAGCTCCAGAAGTTGAAAATGCAATTAGAGTACCAGGAAACAGGAGTTTCTTTCCCTC	
		4861 ACTGAGATCATCAGATTTAGATGTCAGCCCGGGTTTCTCATGGTAGGGTCCCACACTGTG	
		4921 CAGTGCCAGACCAATGGCAGATGGGGGCCCAAGCTGCCACACTGCTCCAGGGGTGTGTCAG	
		4981 CCGCCTCCAGAAATCCTGCATGGTGAGCATACCCTAAGCCATCAGGACAACTTTTCACCT	
		5041 GGGCAGGAAGTGTTCTACAGCTGTGAGCCCAGCTATCACCTCAGAGGGGCTGCGTCTCTG	
		5101 CACTGCACGCCCCAGGGAGACTGGAGCCCTGAAGCCCCTAGATGTACAGTGAAATCCTGT	
		5161 GATGACTTCCTGGACCAACCCTAATGGTCGGGTGCTCTTTCCACTAAATTTCCAGCTT	
		5221 GGGGCAGAAGTGTCCTTCATTTGTGATGAGGGGTTCCGATTAAAAGGCAGCTCCACTAGT	
		5281 CGTTGTGTCTTGGTTGGAATGAAAAGCCTTTGGAGCAGCAGTGTTCCTGTGTGTGCAGCAA	
		5341 ATCTTTGTCCAAATCCTCCGGCTATCCTTAACGGGCGCCACACAGGAACTTCTCTGGGA	
		5401 GACATTCCCTATGGAAAAGAAATTACTTACACATGTGACCCGCACCCAGTCAGAGGGATG	
		5461 ACCTTCAACCTCGTCGGGGAGAGCACCATCCGCTGCACAAGTGACAGTCAAGGGAATGGG	
		5521 TTCTGGAGCAGCCCTGCCCCTCGCTGTGAACCTTCTGGTTCTGCTGCATGCCCACATCCA	
		5581 CCCAAGATCCACAATGGGCATAAGATTGGAGGACGTGCATCTCCATATCTTCCTGGGATG	
		5641 ACTGTCACCTACACTTGTGACCCAGGCTACCTGTTGGTGGGAAACGCCTTCATTTTCTGT	
		5701 ACACACCTGGGAACCTGGAGCCAGTCTGATCATTATTGCAAAGAGGTAAAATGTAGCCTC	
		5761 CCACAGTTTATGAATGGAATCCAGAAGGAGATGAAAATTAAAAACATCTATACTATGGA	
		5821 GATAATGTAACTTTGGAGTGTGAAGATGGATATAGTCTGAAAGGCAGTCCCCAGAGCCAG	
		5881 TGCCAGGCAGATAACACATGGGACCCTCCTCTGGCCATATGTACATCTCGCCCAGGTGAT	
		5941 GCTCTCATAGTGGCACTTTATCTGGTACCATCTTCTTTATTTACTCATCATTTTCCTC	
		6001 TCTTGGATAATTCTAAAGCACAGAAAAGGCAATAATGCACATGAAAACCCTAAAGAAGTG	
		6061 GCTATCCATTTACATTCTCAAGGAGGCAGCAGCGTTCATCCCCGAACTCTGCAAACAAAT	
		6121 GAAGAAATAGCAGGGTCCTTCCTTGACAAAGTACTATACAGCTGAAGAACATCTCGAAT	
		6181 ACAATTTGGTGTGGGAAAGGAGCCAATTGATTTCAACAGAATCAGATCTGAGCTTCATAAA	
		6241 GTCTTTGAAGTGACTTCACAGACAGCCAGACATGTGCACTTGAAGATGCTGCCCCTTCCC	
		6301 TGGTACCTAGCAAAGCTCCTGCCTCTTTGTGTGCGTCACTGTGAAACCCCCACCCTCTG	
		6361 CCTCGTGCTAAACGCACACAGTATCTAGTCAGGGGAAAAGACTGCATTTAGGAGATAGAA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		6421 AATAGTTTGGATTACTTAAAGGAATAAGGTGTTGCCTGGAATTTCTGGTTTGTAAGGTGG 6481 TCACTGTTCTTTTTTAAAATATTTGTAATATGGAATGGGCTCAGTAAGAAGAGCTTGGAA 6541 AATGCAGAAAGTTATGAAAAATAAGTCACTTATAATTATGCTACCTACTGATAACCACTC 6601 CTAATATTTTGATTCATTTTCTGCCTATCTTCTTTCACATATGTGTTTTTTTACATACGT 6661 ACTTTTCCCCCCTTAGTTTGTTTCCTTTTATTTTATAGAGCAGAACCCTAGTCTTTTAAA 6721 CAGTTTAGAGTGAAATATATGCTATATCAGTTTTTACTTTCTCTAGGGAGAAAAATTAAT 6781 TTACTAGAAAGGCATGAAATGATCATGGGAAGAGTGGTTAAGACTACTGAAGAGAAATAT 6841 TTGGAAAATAAGATTTCGATATCTTCTTTTTTTTTGAGATGGAGTCTGGCTCTGTCTCCC 6901 AGGCTGGAGTGCAGTGGCGTAATCTCGGCTCACTGCAACGTCCGCCTCCCG	
		1 M G A S S P R S P E P V G P P A P G L P 1 ATGGGGGCCTCTTCTCCAAGAAGCCCGGAGCCTGTCGGGCCGCCGGCGCCCGGTCTCCCC	SEQ ID NO:86
		21 F C C G G S L L A V V V L L A L P V A W 61 TTCTGCTGCGGAGGATCCCTGCTGGCGGTTGTGGTGCTGCTTGCGCTGCCGGTGGCCTGG	
		41 G Q C N A P E W L P F A R P T N L T D E 121 GGTCAATGCAATGCCCCAGAATGGCTTCCATTTGCCAGGCCTACCAACCTAACTGATGAG	
		61 F E F P I G T Y L N Y E C R P G Y S G R 181 TTTGAGTTTCCCATTGGGACATATCTGAACTATGAATGCCGCCCTGGTTATTCCGGAAGA	
		81 P F S I I C L K N S V W T G A K D R C R 241 CCGTTTTCTATCATCTGCCTAAAAAACTCAGTCTGGACTGGTGCTAAGGACAGGTGCAGA	
		101 R K S C R N P P D P V N G M V H V I K G 301 CGTAAATCATGTCGTAATCCTCCAGATCCTGTGAATGGCATGGTGCATGTGATCAAAGGC	
		121 I Q F G S Q I K Y S C T K G Y R L I G S 361 ATCCAGTTCGGATCCCAAATTAAATATTCTTGTACTAAAGGATACCGACTCATTGGTTCC	
		141 S S A T C I I S G D T V I W D N E T P I 421 TCGTCTGCCACATGCATCATCTCAGGTGATACTGTCATTTGGGATAATGAAACACCTATT	
		161 C D R I P C G L P P T I T N G D F I S T 481 TGTGACAGAATTCCTTGTGGGCTACCCCCCACCATCACCAATGGAGATTTCATTAGCACC	
		181 N R E N F H Y G S V V T Y R C N P G S G 541 AACAGAGAGAATTTTCACTATGGATCAGTGGTGACCTACCGCTGCAATCCTGGAAGCGGA	
		201 G R K V F E L V G E P S I Y C T S N D D 601 GGGAGAAAGGTGTTTGAGCTTGTGGGTGAGCCCTCCATATACTGCACCAGCAATGACGAT	
		221 Q V G I W S G P A P Q C I I P N K C T P 661 CAAGTGGGCATCTGGAGCGGCCCCGCCCCTCAGTGCATTATACCTAACAAATGCACGCCT	
		241 P N V E N G I L V S D N R S L F S L N E 721 CCAAATGTGGAAAATGGAATATTGGTATCTGACAACAGAAGCTTATTTTCCTTAAATGAA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		261 V V E F R R C Q P G G F V M K G P R R V K C 781 GTTGTGGAGTTTAGGTGTCAGCCTGGCTTTGTCATGAAAGGACCCCGCCGTGTGAAGTGC	
		281 Q A L N K W E P E L P S C S R V C Q P P 841 CAGGCCCTGAACAAATGGGAGCCGGAGCTACCAAGCTGCTCCAGGGTATGTCAGCCACCT	
		301 P D V L H A E R T Q R D K D N F S P G Q 901 CCAGATGTCCTGCATGCTGAGCGTACCCAAAGGACACAAGGACAACTTTTCACCTGGGCAG	
		321 E V F Y S C E P G Y D L R G A A S M R C 961 GAAGTGTTCTACAGCTGTGAGCCCGGCTACGACCTCAGAGGGCTGCGTCTATGCGCTGC	
		341 T P Q G D W S P A A P T C E V K S C D D 1021 ACACCCCAGGGAGACTGGAGCCCTGCAGCCCCCACATGTGAAGTGAAATCCTGTGATGAC	
		361 F M G Q L L N G R V L F P V N L Q L G A 1081 TTCATGGGCCAACTTCTTAATGGCCGTGTGCTATTTCCAGTAAATCTCCAGCTTGGAGCA	
		381 K V D F V C D E G F Q L K G S S A S Y C 1141 AAAGTGGATTTTGTTGTGATGAAGGATTTCAATTAAAAGGCAGCTCTGCTAGTTACTGT	
		401 V L A G M E S L W N S S V P V C E Q I F 1201 GTCTTGGCTGGAATGGAAGCCTTTGGAATAGCAGTGTTCCAGTGTGTGAACAAATCTTT	
		421 C P S P P V I P N G R H T G K P L E V F 1261 TGTCCAAGTCCTCCACGTTATTCCTAATGGGAGACACAGGAAAACCTCTGGAAGTCTTT	
		441 P F G K A V N Y T C D P H P D R G T S F 1321 CCCTTTGGAAAAGCAGTAAATTACACATGCGACCCCCACCCAGACAGAGGGACGAGCTTC	
		461 D L I G E S T I R C T S D P Q G N G V W 1381 GACCTCATTGGAGAGCACCATCCGCTGCACAAGTGACCCTCAAGGGAATGGGGTTTGG	
		481 S S P A P R C G I L G H C Q A P D H F L 1441 AGCAGCCCTGCCCCTCGCTGTGGAATTCTGGGTCACTGTCAAGCCCCAGATCATTTCTG	
		501 F A K L K T Q T N A S D F P I G T S L K 1501 TTTGCCAAGTTGAAAACCCAAACCAATGCATCTGACTTTCCCATTGGGACATCTTTAAAG	
		521 Y E C R P E Y Y G R P F S I T C L D N L 1561 TACGAATGCCGTCCTGAGTACTACGGGAGGCCATTCTCTATCACATGTCTAGATAACCTG	
		541 V W S S P K D V C K R K S C K T P P D P 1621 GTCTGGTCAAGTCCCAAAGATGTCTGTAAACGTAAATCATGTAAAACTCCTCCAGATCCA	
		561 V N G M V H V I T D I Q V G S R I N Y S 1681 GTGAATGGCATGGTGCATGTGATCACAGACATCCAGGTTGGATCCAGAATCAACTATTCT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		581 C T T G H R L I G H S S A E C I L S G N 1741 TGTACTACAGGGCACCGACTCATTGGTCACTCATCTGCTGAATGTATCCTCTCGGGCAAT 601 A A H W S T K P P I C Q R I P C G L P P 1801 GCTGCCCATTGGAGCACGAAGCCGCCAATTTGTCAACGAATTCCTTGTGGGCTACCCCCC 621 T I A N G D F I S T N R E N F H Y G S V 1861 ACCATCGCCAATGGAGATTTCATTAGCACCAACAGAGAGAATTTTCACTATGGATCAGTG 641 V T Y R C N P G S G G R K V F E L V G E 1921 GTGACCTACCGCTGCAATCCTGGAAGCGGAGGGAGAAAGGTGTTTGAGCTTGTGGGTGAG 661 P S I Y C T S N D D Q V G I W S G P A P 1981 CCCTCCATATACTGCACCAGCAATGACGATCAAGTGGGCATCTGGAGCGGCCCGGCCCCT 681 Q C I I P N K C T P P N V E N G I L V S 2041 CAGTGCATTATACCTAACAAATGCACGCCTCCAAATGTGGAAAATGGAATATTGGTATCT 701 D N R S L F S L N E V V E F R C Q P G F 2101 GACAACAGAAGCTTATTTTCCTTAAATGAAGTTGTGGAGTTTAGGTGTCAGCCTGGCTTT 721 V M K G P R R V K C Q A L N K W E P E L 2161 GTCATGAAAGGACCCCGCCGTGTGAAGTGCCAGGCCCTGAACAAATGGGAGCCGGAGCTA 741 P S C S R V C Q P P P D V L H A E R T Q 2221 CCAAGCTGCTCCAGGGTATGTCAGCCACCTCCAGATGTCCTGCATGCTGAGCGTACCCAA 761 R D K D N F S P G Q E V F Y S C E P G Y 2281 AGGGACAAGGACAACTTTTCACCCGGGCAGGAAGTGTTCTACAGCTGTGAGCCCGGCTAT 781 D L R G A A S M R C T P Q G D W S P A A 2341 GACCTCAGAGGGGCTGCGTCTATGCGCTGCACACCCCAGGGAGACTGGAGCCCTGCAGCC 801 P T C E V K S C D D F M G Q L L N G R V 2401 CCCACATGTGAAGTGAAATCCTGTGATGACTTCATGGGCCAACTTCTTAATGGCCGTGTG 821 L F P V N L Q L G A K V D F V C D E G F 2461 CTATTTCCAGTAAATCTCCAGCTTGGAGCAAAAGTGGATTTTGTTTGTGATGAAGGATTT 841 Q L K G S S A S Y C V L A G M E S L W N 2521 CAATTAAAAGGCAGCTCTGCTAGTTATTGTGTCTTGGCTGGAATGGAAAGCCTTTGGAAT 861 S S V P V C E Q I F C P S P P V I P N G 2581 AGCAGTGTTCCAGTGTGTGAACAAATCTTTTGTCCAAGTCCTCCAGTTATTCCTAATGGG 881 R H T G K P L E V F P F G K A V N Y T C 2641 AGACACACAGGAAAACCTCTGGAAGTCTTTCCCTTTGGAAAAGCAGTAAATTACACATGC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		901 D P H P D R G T S F D L I G E S T I R C 2701 GACCCCCACCCAGACAGAGGGACGAGCTTCGACCTCATTGGAGAGAGCACCATCCGCTGC 921 T S D P Q G N G V W S S P A P R C G I L 2761 ACAAGTGACCCTCAAGGGAATGGGGTTTGGAGCAGCCCTGCCCCTCGCTGTGGAATTCTG 941 G H C Q A P D H F L F A K L K T Q T N A 2821 GGTCACTGTCAAGCCCCAGATCATTTTCTGTTTGCCAAGTTGAAAACCCAAACCAATGCA 961 S D F P I G T S L K Y E C R P E Y Y G R 2881 TCTGACTTTCCCATTGGGACATCTTTAAAGTACGAATGCCGTCCTGAGTACTACGGGAGG 981 P F S I T C L D N L V W S S P K D V C K 2941 CCATTCTCTATCACATGTCTAGATAACCTGGTCTGGTCAAGTCCCAAAGATGTCTGTAAA 1001 R K S C K T P P D P V N G M V H V I T D 3001 CGTAAATCATGTAAAACTCCTCCAGATCCAGTGAATGGCATGGTGCATGTGATCACAGAC 1021 I Q V G S R I N Y S C T T G H R L I G H 3061 ATCCAGGTTGGATCCAGAATCAACTATTCTTGTACTACAGGGCACCGACTCATTGGTCAC 1041 S S A E C I L S G N T A H W S T K P P I 3121 TCATCTGCTGAATGTATCCTCTCAGGCAATACTGCCCATTGGAGCACGAAGCCGCCAATT 1061 C Q R I P C G L P P T I A N G D F I S T 3181 TGTCAACGAATTCCTTGTGGGCTACCCCCAACCATCGCCAATGGAGATTTCATTAGCACC 1081 N R E N F H Y G S V V T Y R C N L G S R 3241 AACAGAGAGAATTTTCACTATGGATCAGTGGTGACCTACCGCTGCAATCTTGGAAGCAGA 1101 G R K V F E L V G E P S I Y C T S N D D 3301 GGGAGAAAGGTGTTTGAGCTTGTGGGTGAGCCCTCCATATACTGCACCAGCAATGACGAT 1121 Q V G I W S G P A P Q C I I P N K C T P 3361 CAAGTGGGCATCTGGAGCGGCCCCGCCCCTCAGTGCATTATACCTAACAAATGCACGCCT 1141 P N V E N G I L V S D N R S L F S L N E 3421 CCAAATGTGGAAAATGGAATATTGGTATCTGACAACAGAAGCTTATTTTCCTTAAATGAA 1161 V V E F R C Q P G F V M K G P R R V K C 3481 GTTGTGGAGTTTAGGTGTCAGCCTGGCTTTGTCATGAAAGGACCCCGCCGTGTGAAGTGC 1181 Q A L N K W E P E L P S C S R V C Q P P 3541 CAGGCCCTGAACAAATGGGAGCCAGAGTTACCAAGCTGCTCCAGGGTGTGTCAGCCGCCT 1201 P E I L H G E H T P S H Q D N F S P G Q 3601 CCAGAAATCCTGCATGGTCAGCATACCCCAAGCCATCAGGACAACTTTTCACCTGGGCAG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1221 E V F Y S C E P G Y D L R G A A S L H C 3661 GAAGTGTTCTACAGCTGTGAGCCTGGCTATGACCTCAGAGGGGCTGCGTCTCTGCACTGC 1241 T P Q G D W S P E A P R C A V K S C D D 3721 ACACCCCAGGGAGACTGGAGCCCTGAAGCCCCGAGATGTGCAGTGAAATCCTGTGATGAC 1261 F L G Q L P H G R V L F P L N L Q L G A 3781 TTCTTGGGTCAACTCCCTCATGGCCGTGTGCTATTTCCACTTAATCTCCAGCTTGGGGCA 1281 K V S F V C D E G F R L K G S S V S H C 3841 AAGGTGTCCTTTGTCTGTGATGAAGGGTTTCGCTTAAAGGGCAGTTCCGTTAGTCATTGT 1301 V L V G M R S L W N N S V P V C E H I F 3901 GTCTTGGTTGGAATGAGAAGCCTTTGGAATAACAGTGTTCCTGTGTGTGAACATATCTTT 1321 C P N P P A I L N G R H T G T P S G D I 3961 TGTCCAAATCCTCCAGCTATCCTTAATGGGAGACACACAGGAACTCCCTCTGGAGATATT 1341 P Y G K E I S Y T C D P H P D R G M T F 4021 CCCTATGGAAAAGAAATATCTTACACATGTGACCCCCACCCAGACAGAGGGATGACCTTC 1361 N L I G E S T I R C T S D P H G N G V W 4081 AACCTCATTGGGGAGAGCACCATCCGCTGCACAAGTGACCCTCATGGGAATGGGGTTTGG 1381 S S P A P R C E L S V R A G H C K T P E 4141 AGCAGCCCTGCCCCTCGCTGTGAACTTTCTGTTCGTGCTGGTCACTGTAAAACCCCAGAG 1401 Q F P F A S P T I P I N D F E F P V G T 4201 CAGTTTCCATTTGCCAGTCCTACGATCCCAATTAATGACTTTGAGTTTCCAGTCGGGACA 1421 S L N Y E C R P G Y F G K M F S I S C L 4261 TCTTTGAATTATGAATGCCGTCCTGGGTATTTTGGGAAAATGTTCTCTATCTCCTGCCTA 1441 E N L V W S S V E D N C R R K S C G P P 4321 GAAAACTTGGTCTGGTCAAGTGTTGAAGACAACTGTAGACGAAAATCATGTGGACCTCCA 1461 P E P F N G M V H I N T D T Q F G S T V 4381 CCAGAACCCTTCAATGGAATGGTGCATATAAACACAGATACACAGTTTGGATCAACAGTT 1481 N Y S C N E G F R L I G S P S T T C L V 4441 AATTATTCTTGTAATGAAGGGTTTCGACTCATTGGTTCCCCATCTACTACTTGTCTCGTC 1501 S G N N V T W D K K A P I C E I I S C E 4501 TCAGGCAATAATGTCACATGGGATAAGAAGGCACCTATTTGTGAGATCATATCTTGTGAG 1521 P P P T I S N G D F Y S N N R T S F H N 4561 CCACCTCCAACCATATCCAATGGAGACTTCTACAGCAACAATAGAACATCTTTTCACAAT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1541 G T V V T Y Q C H T G P D G E Q L F E L 4621 GGAACGGTGGTAACTTACCACTGCCACACTGGACCAGATGGAGACAGCTGTTTGAGCTT	
		1561 V G E R S I Y C T S K D D Q V G V W S S 4681 GTGGGAGAACGGTCAATATATTGCACCAGCAAAGATGATCAAGTTGGTGTTTGGAGCAGC	
		1581 P P P R C I S T N K C T A P E V E N A I 4741 CCTCCCCCTCGGTGTATTTCTACTAATAAATGCACAGCTCCAGAAGTTGAAAATGCAATT	
		1601 R V P G N R S F S L T E I I R F R C Q 4801 AGAGTACCAGGAAACAGGAGTTTCTTTCCTCACTGAGATCATCAGATTTAGATGTCAG	
		1621 P G F V M V G S H T V Q C Q T N G R W G 4861 CCCGGGTTTGTCATGGTAGGGTCCCACACTGTGCAGTCCAGACCAATGGCAGATGGGGG	
		1641 P K L P H C S R V C Q P P P E I L H G E 4921 CCCAAGCTGCCACACTGCTCCAGGGTGTGTCAGCCGCCTCCAGAAATCCTGCATGGTGAG	
		1661 H T L S H Q D N F S P G Q E V F Y S C E 4981 CATACCCTAAGCCATCAGGACAACTTTTCACCTGGGCAGGAAGTGTTCTACAGCTGTGAG	
		1681 P S Y D L R G A A S L H C T P Q G D W S 5041 CCCAGCTATGACCTCAGAGGGGCTGCGTCTCTGCACTGCACGCCCCAGGGAGACTGGAGC	
		1701 P E A P R C T V K S C D D F L D Q L P N 5101 CCTGAAGCCCCTAGATGTACAGTGAAATCCTGTGATGACTTCCTGGACCAACTCCCTAAT	
		1721 G R V L F P L N F Q L G A E V S F I C D 5161 GGTCGGGTGCTCTTTCCACTAAATTTCCAGCTTGGGGCAGAAGTGTCCTTCATTTGTGAT	
		1741 E G F R L K G S S T S R C V L V G M K S 5221 GAGGGGTTCCGATTAAAAGGCAGCTCCACTAGTCGTTGTGTCTTGGTTGGAATGAAAAGC	
		1761 L W S S S V P V C E Q I F C P N P P A I 5281 CTTTGGAGCAGCAGTGTTCCTGTGTGTGAGCAAATCTTTTGTCCAAATCCTCCGGCTATC	
		1781 L N G R H T G T S L G D I P Y G K E I T 5341 CTTAACGGGCGCCACACAGGAACTTCTCTGGGAGACATTCCCTATGGAAAGAAATTACT	
		1801 Y T C D P H P V R G M T F N L V G E S T 5401 TACACATGTGACCCGCACCCAGTCAGAGGGATGACCTTCAACCTCGTCGGGGAGAGCACC	
		1821 I R C T S D S Q G N G F W S S P A P R C 5461 ATCCGCTGCACAAGTGACAGTCAAGGGAATGGGTTCTGGAGCAGCCCTGCCCCTCGCTGT	
		1841 E P S G S A A C P H P P K I H N G H K I 5521 GAACCTTCTGGTTCTGCTGCATGCCCACATCCACCCAAGATCCACAATGGGCATAAGATT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1861 G G R A S P Y L P G M T V T Y T C D P G 5581 GGAGGACGTGCATCTCCATATCTTCCTGGGATGACTGTCACCTACACTTGTGACCCAGGC 1881 Y L L V G N A F I F C T H L G T W S Q S 5641 TACCTGTTGGTGGGAAACGCCTTCATTTTCTGTACACACCTGGGAACCTGGAGCCAGTCT 1901 D H Y C K E V K C S L P Q F M N G I Q K 5701 GATCATTATTGCAAAGAGGTAAAATGTAGCCTCCCACAGTTTATGAATGGAATCCAGAAG 1921 E M K I K N I Y H Y G D N V T L E C E D 5761 GAGATGAAAATTAAAAACATCTATCACTATGGAGATAATGTAACTTTGGAGTGTGAAGAT 1941 G Y S L K G S P Q S Q C Q A D N T W D P 5821 GGATATAGTCTGAAAGGCAGTCCCCAGAGCCAGTGCCAGGCAGATAACACATGGGACCCT 1961 P L A I C T S R P R D A L I V G T L S G 5881 CCTCTGGCCATATGTACATCTCGCCCACGTGATGCTCTCATAGTTGGCACTTTATCTGGT 1981 T I F F I L L I I F L S W I I L K H R K 5941 ACGATCTTCTTTATTTTACTCATCATTTTCCTCTCTTGGATAATTCTAAAGCACAGAAAA 2001 G N N A H E N P K E V A I H L H S Q G G 6001 GGCAATAATGCACATGAAAACCCTAAAGAAGTGGCTATCCATTTACATTCTCAAGGAGGC 2021 S S V H P R T L Q T N E E N S R V L P - 6061 AGCAGCGTTCATCCCCGAACTCTGCAAACAAATGAAGAAAATAGCAGGGTCCTTCCTTGA	
WBC008F12	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein	1 gagctgcggg ccgggtgcgg acggcggagg cggcgggact ggtccctgct cttcagtggg 61 tcatctgtgt gtcacagcct cagaagacca gcgagatggc tgccaacaag agtaagggcc 121 agagctcctt ggccctccac aaggtgatca tggttggcag cggaggcgtt ggcaagtcag 181 ccctgacgct tcagttcatg tatgacgagt ttgtagaaga ctatgaacct accaaagctg 241 acagttatag aaagaaagtg gttcttgatg gggaagaagt tcagatagat attctggaca 301 ccgctgggca agaggactac gcagccattc gagataacta ctttcggagt ggggaagggt 361 ttcttcttgt gttctcaatc acagaacatg aatcctttac agcaactgcc gaattcaggg 421 aacagattct ccgtgtgaag gctgaagaag ataaaattcc actgctcgtc gtgggaaaca 481 agtctgacct agaggagcgg aggcaggtgc ctgtggagga ggccaggagt aaagccgaag 541 agtggggcgt gcagtacgtg gagacgtcag cgaagacccg ggccaacgtg gacaaggtgt 601 tctttgacct aatgagagaa atcagaacaa agaagatgtc agaaaacaaa gacaagaatg 661 gcaagaaaag cagcaagaac aagaaaagtt ttaaagaaag atgttgctta ctatgagtgt 721 caaggtgacg gatgaagcca gctgctccta aggacacagg gctgggttgg taaagagaag 781 gctatggttg acttcttgct tgtgcttccc actctccccg acttcattca ctcaaacttc 841 tttaaatggg gaaaaatatt tgtgactcag tggctggcag aagaaataag cccatgcaag 901 tggaagggct gctttgtcag gaggttgtgg aatttctttc ttctcccctt cttcctccc 961 aaaagcttag ctatgtataa agtgccacag ataggaaaca gctgttaatt acaaagagaa 1021 agaattgtca tagcatctta ttttgttcct agttttataa cattaccatc cttcgttttg 1081 aactacagat gttgtagtgg gttttggagg agggagtgga gtaagatgcc ctcccacttt	SEQ ID NO:87

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1141 tatcagttta gtagtagtac tgagaaaaat cccttcagct ctaagaacac tgaaaaatcc 1201 accgattttt tgggtaagct tcttggcaat accctgtgga tctgaaacag ctaaaaaaat 1261 gaatttgaat tgcgccagat aggtcaatac caagcttctg attcctcctc acatatgaaa 1321 agtgaaagtt gtgagttgtt ttcctcttat ttaaacattg gcctattata atctgtgttg 1381 gttatttttc tcctgtaagc atcctgattt ttctgtagga acttttcttt ggcagaccaa 1441 gtgaagactc aggaatggtg tgcattataa atgacacaca ttgccacttg tgtagatatt 1501 tttaagttct ttggctaagt cctctcctaa ctgcctgtcc tctggttagg cccctccctc 1561 tccactagtg gtgaatgcat gtgtctgtct gatcagcatc actgcacacg gaggtctagt 1621 gagcctcttg ctaagtgtca cacacactct tcccaaagac gtgatgagtt aaagttgtat 1681 tctgaaatca tgaagccaga gcctgtgcca gaccttctgc tacctctcat agaattgctc 1741 tgtaattcta aatttaaaat tagaagtaga gagagataag ccatcgcccc tttgcctctg 1801 agaattggct gctgtttcta atataattat tttctaagat agccagatag ttagaaaaag 1861 attttcattg atgacatatc tttaaacttt cttgcatcag tattctaaat tgagcaaact 1921 gaaagatttt catcaggaaa ggagcactgt gggaagagcc cagtattcac attttttccc 1981 cattttcag aagcgacatt tcatatatag gtgccaaaag tgaatcgggg tgcggagagt 2041 gggaaccttt tgaatttatg attgtcacag agatggtaga aattatgatc tgactggaaa 2101 acaatcctgt atcccctccc aaagaatcat gggctttttt tttgaattaa aaagcagaca 2161 aatagaaaaa aaaaaaaaaa 1 M A A N K S K G Q S S L A L H K V I M V 1 ATGGCTGCCAACAAGAGTAAGGGCCAGAGCTCCTTGGCCCTCCACAAGGTGATCATGGTT 21 G S G G V G K S A L T L Q F M Y D E F V 61 GGCAGCGGAGGCGTTGGCAAGTCAGCCCTGACGCTTCAGTTCATGTATGACGAGTTTGTA 41 E D Y E P T K A D S Y R K K V V L D G E 121 GAAGACTATGAACCTACCAAAGCTGACAGTTATAGAAAGAAAGTGGTTCTTGATGGGGAA 61 E V Q I D I L D T A G Q E D Y A A I R D 181 GAAGTTCAGATAGATATTCTGGACACCGCTGGGCAAGAGGACTACGCAGCCATTCGAGAT 81 N Y F R S G E G F L L V F S I T E H E S 241 AACTACTTTCGGAGTGGGGAAGGGTTTCTTCTTGTGTTCTCAATCACAGAACATGAATCC 101 F T A T A E F R E Q I L R V K A E E D K 301 TTTACAGCAACTGCCGAATTCAGGGAACAGATTCTCCGTGTGAAGGCTGAAGAAGATAAA 121 I P L L V V G N K S D L E E R R Q V P V 361 ATTCCACTGCTCGTCGTGGGAAACAAGTCTGACCTAGAGGAGCGGAGGCAGGTGCCTGTG 141 E E A R S K A E E W G V Q Y V E T S A K 421 GAGGAGGCCAGGAGTAAAGCCGAAGAGTGGGGCGTGCAGTACGTGGAGACGTCAGCGAAG 161 T R A N V D K V F F D L M R E I R T K K 481 ACCCGGGCCAACGTGGACAAGGTGTTCTTTGACCTAATGAGAGAAATCAGAACAAAGAAG 181 M S E N K D K N G K K S S K N K K S F K 541 ATGTCAGAAAACAAAGACAAGAATGGCAAGAAAAGCAGCAAGAACAAGAAAAGTTTTAAA	SEQ ID NO:88

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		201 E R C C L L - 601 GAAAGATGTTGCTTACTATGA	
WBC008F06_V1.3_at	No Homology	1 CATCCCTAACTTTCTCTTGACCCTTAGTTGAAGTGTTTAGGTGGCTTCTGGTGATATCCT 61 TTCATAATTTTATGTCGCTTAAAAGGGTGATGGATGTGACACCTCATAGAAGTGAGCTCT 121 GAACTCTAGATAAAATTAAAAGAAATTTCATTTCTTTTAAAAGAAATTAAAAGAAAATTA 181 AAATTTCATTTTAGAGAATTAAAATATTTGTGCTCAACTGCTTGATCTTTTTTCTTTTTG 241 TGTAATTGTGTTTAGTTCTATGCAATTTTATCACGTGTAGATTTGTGTGACCACCACAGC 301 AAGGTGCGGAACAGTTCCATCACACAGATCCCTTGTGCTCCCCTTTTACAGCCACAGCCA 361 CAGCCACCTCCCTTCTTTACCACCAAGCCCCATCCTCTGGCAACCACTCATCTGTTCTCC 421 ATCTCTAATTTTGCCATTTCAAGAATGTCATATAAATGGAATCATATAGTATGTAACCTT 481 TGAGATTGACTTTTTTCACTCAGCATAATTCCCTTGAAATCCATTCAAGTTGTTGCATGT 541 ATCAAGAGTTTGTTCCTTTTTCTTGCTCAGTAGTATTTCGTGGTATGGATGTACCAGTTT 601 TTTTTAACCATTCACCTACTGAAGGACATTGGGGTTGTTTTCAGTTTTGGGCCATTAATA 661 ATAAAGCTATTGTTAACATTCATGAACAGGTTTTTATGTGAACATAAATTTTCATTTGTC 721 TGCAATAATTGCCCAAGAGGGCAATTGCTAGGTTCCATGGTAAGCACGTGTTCATTTTTG 781 TAAGAAACTGCTACTCTTTTTCCAGAGTGACTGTGCCATTTTATGTTCCCACTAGAAATG 841 TATGACCAATCCAGTTTCTCTGCATCCTCACCAGTATTTGCTATATTATTATTTTTTTAG 901 TCATTCTGATAGGTGAGTATAATGATACCTCATGGTTTTAATTTGCATTTTCCTAATGGG 961 CTAGTAATGTT	SEQ ID NO:89
		1 ATACTAACCGACAGAGGATGCATCCAAGTAGGGAAAAGAATAACCAAATTTGTGCGTTAA 61 GTTCTATCCTTAGATGTTTAAAGGTGAAATTCTAATCTGTACCATTTAGCCTAACAAGAT 121 ATGCTTTCATATTTCTGATTGGTGCCTTTCCACTTTTTAGCAGCAATGAAAGCCACTTAG 181 TTGGTTATAGTCTTCTGTTCTGACAACATGTCAAGAAGATAGGACAGGACAATATTTTAT 241 TTTGCTGATGTTTTCGTTCCCAAATGTGACTTTGTGAAACTGAAATTCTTTCATGTCCTT 301 TCCCTTTCACTCATGCCAAAACAACCAGCTCGGACATTTGTGTTTTTGGTTTAAAGTTCA 361 TTGATATTACACCTTGATTTATCTAAAAGTTAAAATTATTTGCCTTGATAAAAGGCTAGT 421 GCAAGAGCAAATCAGCTTTAAAAACGAGGATGTTATCTGCTTTCCTTCATTTTTGAGCCT 481 GTTATTCGACACCATCTGTGTAATATAGATGAGAATGATCCGGTTTAAGTAAGTTTTGTT 541 ATACCATTGTCATAAACCCCATCATAAGCCGTTTTTCTGTTTAATGGAAAGAGGCATGTG 601 GATTTATACGGATTCACTTGTAAGTGTTGGATTGGGAATTTTTTGTGTAAATTTTCTCAA 661 ATAAAGGCTAGCAGAAACCAAAAAAAAAAAAAAAA	SEQ ID NO:90
WBC007G12_V1.3_at	No Homology	1 CAGTTTTGAGTGGTCTTTGAATATGAGGGGGAAAGATTAGCGGTAATTTCACTACATCCC 61 TTTTTCCTGACTTTCATGAATTTGTCATACATCTTCTCTCTGATGCTTGACTTTATTTGC 121 TCCTTAGCAATAGTCTGCATTTAAAGAAAGGTGTGTTCAGTTCATCAGCTTGAAATTGAC 181 TATTTCATTTTTCCAGAATTTTTTAGGAGAAGAGTACCCGTTTTGTTTGTTTTATAAAAC 241 AGATGACAAGTCTCTTTAAAAGAAACAGAAGTACAGTACTTTTGAAATACAATGCTGTTA 301 GTTTGGATTTCTTTTTTTATATATAATATTCATACAATTATCTGATGTTTGCCTTCATTA 361 ATAAAGCTGTTAGTTTATTCACCAAAATGTCAAGAATGGATGTGCTTTTCTTTATTCCAT 421 ACATTTAAAAATATTTTAGCTGCTAAGATTTAGTTAACTTTCTAAGAAACGAATTCAAGT 481 TGCCTTCAGCAGGAATTGAAAGCTTTCGTTCCCTTTCTTTATATAGTCTTCCGAAAATTC	SEQ ID NO:91

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		541 TGTTCAAGTGTTTTCTAGTTAATTATGTAACAGAATGTTAGCATCTCTCCAAATCTTGAA 601 ACTTGAATTTTGAGAGTGCATTGAATTATGCTTTCAGTGTTAAAGTAAAGGTTTCAATTA 661 TCCTTCTAGTGAAGTCTATTGTGGAATACCATTTCCCATGGAACTGAGGCCATTTCCACA 721 ACTTTGCACAGAATTGCAGTCTTGTTCTCCCTGGATCATGACAAATAAGTCTCACACAG 781 TGCCGTAATACTTGTGGATTCTTTTGTAATCTTTGTAATCTTAATAAGGCATTATGAGA 841 AGATGACTCCATGTTTTTTTAATATTTCAAACACATTGGGATGTAACAATGAATGTCAAC 901 TGTAGGAATGGTTGTTTCGTTTTAAGGAATAACCATGTTGGGGAAAGATG	SEQ ID NO:92
		1 AGGTAAACACAATGGTGTAGTTAATTAAATTCTGGGTGAATGGGAGCGGGACTGATTACT 61 GTGTCTTGCTCTTCGCCCTTTGTTTTTTTCAGAACCCAATAACAGAATTGTGTATGTGTG 121 TACTGTATCTGCCTTTCCACCACATTTTTATGACACTGTATTCCACTGCCTGCTTTTTTG 181 ACCTTTGTTCCCTCGGATTTGTCCTATAACTTAGCATCTGTGGTTAACAGTGATCCTAGG 241 GCTGACCGCACATGACAAGTCACACAGAGAAGAGCGGAAGGGCAAGAATTCAAAGCATTTG 301 TTCATACAATGTGGCAGCCTCTTTTGCATAGTCATGTAGGATCCTGTTTGTAATGCTATC 361 ATAAATATTCTGTAGTTTTGTTCCCCTCCCACCCCAACTGGAGCTATGAAACTTTTTATT 421 GGATTCAGTCTTGTCTTTTGTCTAGAAAGAATTTTATCTTGTTGACGCATGAGCTGTTTA 481 AAAATTATTCTATTAAAATGTTGGTTAATAGTTGTGCAGTTTTTCTTTTCAGAAGAAAAGG 541 CAATTCAAAGGTTGCCTTTGTTTTCTGTCACCTTCCAACCCCTCAGCACTTCTAGTCAGA 601 TACAGATTCATCAGTCGTATGCAACATCCTTTGTAATTTAAAATAAAAAAAAAAAAAAAA 661 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	SEQ ID NO:93
WBC007G03	Transmembrane protein 23	1 CAAAAATGAGGTGAATTAATACTTGGGCGCTCAGGAACCCTGGACAGCTACATGAGGTGT 61 TTAAAAACTGCCCTGACCATCTTGCCAAACAAGTCTCTGCTCATGAGGCCCCCACAGGATG 121 AACGAGCCCGAGGCAGGACAGTGTCCTGCCCTGTCGGAACAGTGACTGCTGACCTGCCAAG 181 AGAGAGCTGGGGACTGCCTGCTGTCTGCCAGTACAATGAAGGAAGTGGTTTATTGGTCAC 241 CCAAGAAGGTGGCAGACTGGCTGCTGGAGAATGCTATGCCAGAATACTGTGAGCCTCTGG 301 AGCATTTCACAGGCCAGGACTTGATCAACCTAACCCAAGAGGATTTCAAAAAACCCCCCT 361 TGTGCCGACTCTCCTCTGACAACGGCCAGCGGCTCCTGGACATGATAGAAACCCTGAAAA 421 TGGAGCACCATTTGGAAGCACACAAGAACGGCCATGCCAATGGGCACCTCAACATTGGCG 481 TAGACATCCCCACCCCCGACGGCAGCTTCAGCATCAAGATTAAACCCAACGGGATGCCAA 541 ATGGGTATAGGAAAGAGATGATAAAGATCCCCATGCCAGAACTGGAGCGCTCTCAGTACC 601 CCATGGAGTGGGGCAAGACTTTTCTGGCCTTTCTTTATGCACTTTCCTGTTTCGTTCTCA 661 CCACAGTGATGATCTCGGTCGTCCACGAACGAGTACCTCCTTAAGGAGGTGCAGCCTCCAC 721 TACCGGACACATTTTTTGACCATTTTAACCGGGTGCAGTGGGCTTTTCTATTTGTGAAA 781 TTAATGGCATGATCCTTGTAGGACTCTGGTTAATTCAGTGGCTGCTCTTAAAATACAAGT 841 CTATTATTAGCAGAAGATTTTTTCTGCATAGTTGGCACGCCTGTACCTGTATCGGTGTATTA 901 CAATGTATGTAACTACACACTCCCAGTACCTGGTATGCATTTCAACTGTTCTCCGAAGCTTT 961 TCGGAGACTGGGAAGCCCAACTGCGAAGAATAATGAAGCTCATTGCTGGAGGTGGCTTGT 1021 CTATCACTGGCTCTCACAACATGTGTGGGGACTATCTGTACAGCGGCCACACGGTCATGC 1081 TAACACTTACCTACTTATTATCAAAGAGTATTCCCCTCGGCGACTCTGGTGGTATCACT 1141 GGATTTGCTGGCTTCTCAGCGTAGTTGGAATCTTCTGTATTCTCTTAGCGCATGACCACT 1201 ACACTGTGGACGTGGTGGTGGCATATTACATCACCACGAGACTCTTCTGGTGGTATCACA 1261 CTATGGCCAATCAGCAAGTGCTAAAGGAAGCTTCCCAGATGAACCTCCTGGCCAGGGTGT 1321 GGTGGTACAGGCCATTTCAGTACTTTGAAAAGAATGTCCAAGGAATCGTACCTCGATCTT 1381 ACCATTGGCCCTTCCCCTGGCCAGTAGTGCACCTTGGTAGGCAAGTTAAATACAGCCGGT 1441 TGGTGAATGACACATAACAGCTGTACAAAGTGGGGGAAAGAGGAACTGTCCCAAGTGCTA	SEQ ID NO:93

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1501 AGAACTCCATGAGAGAAGATGCCATAAAATAAACACCTCCCTAATCCTATTATCTTTCAG 1561 CGGTTACCTTGACTTAACCTATTGAGTTACCTGGTCAGCACTGTGATCTTTTTTTCTCTC 1621 CAAAGGACCTGCGTTGGACAACAATAAAGAAAATTTAACCTATCATGCACTGTATACATT 1681 TCCTGTTCATAAGTTTGGGATTTACATAACCCGCAGCCACCATGTTCCTTTGTATATGAT 1741 GCAACAGCGTAAATGTAAGCTTTTATATCATAAGTTCTGGTCTTTCCAGTCACATCTGGA 1801 AATAAGCGTATTATTTTCTTGGGAAAACATACTTTCTATATCTCTTGCCCCAAGATTGG 1861 GCTGTAAGCCATTTTCTAGCAAATGTCTCTATGAAGGTTTCTAAGTACCTGAATGGGGTT 1921 CGATTCTGAAATCTTTCTACTTGTTGCACCGATATTCAAATAAAAATGACAGACACAGAA 1981 AGGTTTGGTAACTTTGGGTTTTGTAAAATCAGCAGACAGTGTGTCAAAAAGTGCAAAA 2041 AAAAAGATTCTGTTATATAAAGTGATTTTCTAAGTATTTCCTAGCTTTATTTTTCAAAATGA 2101 TGTTATGAAAACCAAATTTGAAGATTTTTACATGTCAAAGAGAAGAGGGTTAAAATTTAA 2161 AAATGCTTCTTGGGAGACGAAATTTGTCTATGTTTCTAGTGCCTTTCTTGTCTTGATTGTA 2221 TGGTCAGTAGGCAATCTTAAATGTTTTTATTTAAAATAAAGTATTCCATGAAAATATAAC 2281 TGTATGTATACACTACTAAATTTTGCATTTATAGCTAAATTGAATCAGAAGACTGCTTAT 2341 GGTTTTAAAATTGCAATCACTTAAATAATGAGGTTGTTAATTAGAGTCAGAGCCTGTTCA 2401 CATATTGTGATCAGGTAGCAATGACATGTACCACTTAAATTATTTTATCGTCGATTTGGT 2461 AGTTCGATTTTTAACTACTCAATGAAACAGCCATGAATATCTTTCTTAAAGAGAGTTTT 2521 GAAAATGATCACTTAACTAAAACTTGAAAGCTATAAATTAGTTATCCATACTCTCATGAC 2581 AATTTTGTTGGTGAACAACAAAAAGAGATCTATTTCTTTAAAATATATTTGTGCAGAAAC 2641 TGCATGTAATTCTAAGTTTTTACTCCTAACATAAGTATGTTTGGGGAAGTATTCTATTCTA 2701 TACTTGCCAATGTGGAGAACAAAATAGTTTTTTAAGAATGAAGAAGTATATATATCCATT 2761 CTGTATTTTACGTGCAGCAGAATTATCTTCCGTAGGGTTTTTTTGTGTATTCACAAGGTG 2821 ATATTTGTATTGTACAACAATAATGGTGAAGGAAATAAAAAGGCTTTTAAAATTTTGTTT 2881 GTTTTAAATCTTTGTAAAGTTACTATTCCAGAGAGTATACTGATATCTTAACAGCTTACC 2941 TAGATCATAAATTAATCAAAATGCACTTTTTAATAAAAACTGATACTTAAAATAAATGGC 3001 TCTTATTTCTAAAAAAAAAAAAAAA 1 M K E V V Y Y W S P K K V A D W L L E N A SEQ ID NO:94 1 ATGAAGGAAGTGGTTTATTGGTCACCCAAGAAGGTGGCAGACTGGCTGCTGCAGAATGCT 21 M P E Y C E P L E H F T G Q D L I N L T 61 ATGCCAGAATACTGTGAGCCTCTGGAGCATTTCACAGGCCAGGACTTGATCAACCTAACC 41 Q E D F K K P P L C R V S S D N G Q R L 121 CAAGAGGATTTCAAAAAACCCCCCTTGTGCCGAGTCTCCTCTGACAACGGGCAGCGGCTC 61 L D M I E T L K M E H H L E A H K N G H 181 CTGGACATGATAGAAACCCTGAAAATGGAGCACCATTTGGAAGCACACAAGAACGGCCAT 81 A N G H L N I G V D I P T P D G S F S I 241 GCCAATGGCCACCTCAACATTGGCGTAGACATCCCCCACCCCCGACGGCAGCTTCAGCATC 101 K I K P N G M P N G Y R K E M I K I P M 301 AAGATTAAACCCAACGGGATGCCAAATGGGTATAGGAAAGAGATGATAAAGATCCCCATG 121 P E L E R S Q Y P M E W G K T F L A F L 361 CCAGAACTGGAGCGCTCTCAGTACCCCATGGAGTGGGGCAAGACTTTTCTGGCCTTTCTT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		141 Y A L S C F V L T T V M I S V V H E R V 421 TATGCACTTTCCTGTTTCGTTCTCACCACAGTGATGATCTCGGTCGTCCACGAACGAGTA 161 P P K E V Q P P L P D T F F D H F N R V 481 CCTCCTAAGGAGGTGCAGCCTCCACTACCGGACACATTTTTTGACCATTTTAACCGGGTG 181 Q W A F S I C E I N G M I L V G L W L I 541 CAGTGGGCCTTTTCTATTTGTGAAATTAATGGCATGATCCTTGTAGGACTCTGGTTAATT 201 Q W L L L K Y K S I I S R R F F C I V G 601 CAGTGGCTGCTCTTAAAATACAAGTCTATTATTAGCAGAAGATTTTTCTGCATAGTTGGC 221 T L Y L Y R C I T M Y V T T L P V P G M 661 ACGCTGTACCTGTATCGGTGTATTACAATGTATGTAACTACACTCCCAGTACCTGGTATG 241 H F N C S P K L F G D W E A Q L R R I M 721 CATTTCAACTGTTCTCCGAAGCTTTTCGGAGACTGGGAAGCCCAACTGCGAAGAATAATG 261 K L I A G G G L S I T G S H N M C G D Y 781 AAGCTCATTGCTGGAGGTGGCTTGTCTATCACTGGCTCTCACAACATGTGTGGGGACTAT 281 L Y S G H T V M L T L T Y L F I K E Y S 841 CTGTACAGCGGCCACACGGTCATGCTAACACTTACCTACTTATTTATCAAAGAGTATTCC 301 P R R L W W Y H W I C W L L S V V G I F 901 CCTCGGCGACTCTGGTGGTATCACTGGATTTGCTGGCTTCTCAGCGTAGTTGGAATCTTC 321 C I L L A H D H Y T V D V V V A Y Y I T 961 TGTATTCTCTTAGCGCATGACCACTACACTGTGGACGTGGTGGTGGCATATTACATCACC 341 T R L F W W Y H T M A N Q Q V L K E A S 1021 ACGAGACTCTTCTGGTGGTATCACACTATGGCCAATCAGCAAGTGCTAAAGGAAGCTTCC 361 Q M N L L A R V W W Y R P F Q Y F E K N 1081 CAGATGAACCTCCTGGCCAGGGTGTGGTGGTACAGGCCATTTCAGTACTTTGAAAAGAAT 381 V Q G I V P R S Y H W P F P W P V V H L 1141 GTCCAAGGAATCGTACCTCGATCTTACCATTGGCCCTTCCCCTGGCCAGTAGTGCACCTT 401 G R Q V K Y S R L V N D T - 1201 GGTAGGCAAGTTAAATACAGCCGGTTGGTGAATGACACATAA	
WBC007A09	No homology	1 AGGTTCCAAGAGGGGGAGCCCATCCACCTGAGGTGCCACAAGTTGCAAAGCAAGCGTCTG 61 TTCAGGATCACATTCTTCCAGAATGGAAAATCCCTGACGTTTTTCCATAACACTTCCACC 121 TTCTCCATCCTACGAGCAAACCGCAACCACAGTGGCGAGTACCGCTGCTCAGGAACTATA 181 GATCGGATGCAGCTCTCGTCACAGCCTGTGAAGATCACTGTCCAAGGTCCGGCAACTGTA	SEQ ID NO:95

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		241 TTCTTCTTTCTACATTGGTTTCAAATCGCTTTCTGCCTGGTGATGGGACTCCTGTTTGCA 301 GTGGATACAGGGCTGTATGTTTCTGTGCAGAGAGACCTTCCAAGATCAGTGGGAGATGGG 361 AAGAATTGCAACGTGAGATGGAGCCAGAGCCCTGAAAACAAATGAGGTCTGGCCAAGGA 421 GACTCCAACCACCCTTGTGACCTGTGATCTTCAGAGCTAAATGCCAACAGGCCACACCCT 481 GACTGAGCTCCTGAAGGTCAAGGCACAGTCCAGCCCACCTAGCTTGACAAGGACTCACAG 541 CAAATGTGTTTTTCATAGCCCCCTAAACAGAGGCTCCTCAAATCTAGAAAAACTCAGTAAAT 601 CCTGCCTCTCCTTTCAATCAATCCAGCAATCTGACGCCTTCTCAGGACTGTACTACCAGC 661 ACCTCGGTCCAAGCCAGCATCATGTCTCACTTGGTTACTGCAGTAGCTCCCTGACGGGT 721 CTCCCTACACTCACCCTGCCACCCTACAGTCGATTCTCACCACACCGGCCAAAGTGATCT 781 TTTT	SEQ ID NO:96
		1 TAAACAGAGGCTCCTCAAATCTAGAAAAACTCAGTAAATCCTGCCTCTCCTTTCAATCAA 61 TCCAGCAATCTGAGCGCTTCTCAGGACTGTACTACCAGCACCTCGGTCCAAGCCAGCATC 121 ATGTCTCACTTGGGTTACTGCAGTAGCTCCCTGACGGGTCTCCCTACACTCACCCTGCCA 181 CCCTACAGTCGATTCTCACCACACCGGCCAAAGTGATCTTTTTAAGATGTGTGTTGTCTC 241 TTTCCCTTCCTTGCTCAAAGCCATGCCAGAGCTCCCCCTTGCAATTAAGAGGAAAGCTAA 301 GACCTTTGGAACGTTCTACTAGGCGCTACATGATCTTGCTCCTCACTGCCTCTCTGACCT 361 CATCTCCTGCTCTTCCTTGCTTCCTTTAACACACGAATTCTACTTCTGCCTAGGGCTTAT 421 GCTATTTCCTGTTTCTGGAAGGTTCTTTCTTACAGATATCTACATCGTACTTCATTATGA 481 TCTTTCCTCAAGTGTCACCTTATCAGTGAGGTCTCCTTGATCCTTTAGTATAAGCCCAGT 541 CTCCCACCATCCCCTAATCCCCCTTGTTTAATTGTTTAATTGACAATTGTTTAATAAACAA 601 TCTCTTTCTGTAAAAAAAAAAAAAAAAAAA	SEQ ID NO:97
WBC006H06	Ubiquitin-conjugating enzyme E2B (RAD6 homolog) (UBE2B)	1 cgtccctctt tctccacccc gccgagccta aactagtgac ggggagggag acgggatagt 61 gtttctgttt cgtggtcttt gaatccacaa cctctagtct gaacacagag aacacaaatt 121 tgtctattac ttcaggaagc ccagggggaa ccgcgccccg ctgaagggct cgggaaggcc 181 gcgctcccgc gtcccgcccc ctcctccccc agcactcaca ctgtggtagc ggcggagggc 241 ggagggatcc ggaggcggcg gagggagacg tcattgcagg gttgtttgtc agtctcggcg 301 gcggcggcgg cggcggcggc ggcggcgatc cacagtgatt cggccgccgc gccgggggct 361 ggggggcctg cgcgggactt ttttttttc agactgaccg cgggcgagct gcggagcatg 421 tcgaccccgg cccggaggag gctcatgcgg gatttcaagc ggttacaaga ggacccacct 481 gtgggtgtca gtggcgcacc atctgaaaac aacatcatgc agtggaatgc agttatattt 541 ggaccagaag ggacaccttt tgaagatggt acttttaaac tagtaatata atttctgaa 601 gaatatccaa ataaaccacc aactgttagg ttttttatcca aaatgtttca tccaaatgtg 661 tatgctgatg gtagcatatg tttagatatc cttcagaatc gatggagtcc aacatatgat 721 gtatcttcta tcttaacatc aattcagtct ctgctggatg aaccgaatcc taacagtcca 781 gccaatagcc aggcagcaca gctttatcag gaaaacaaac gagaatatga gaaaagagtt 841 tcggccattg ttgaacaaag ctggaatgat tcataatata caactggtct gttaatcttt 901 ttcatcattg ttgtgtataa tttacctctc attagaaagg ctaacaaatt ttaagtgcca 961 caggttttaa ggatttctgca gaaaaaaaag aaaaaagtcc ttcagtttag aacctacaaa 1021 agcttgtgta tcttgattaa tgtactttct attgcatggt gtgaactaag ttattgctgc 1081 ataaatttgt aatatatcct gtttgtattt tttccaagt gtataatgtt ggtgtggagt 1141 tttcatgaca gaatatacac atttgtaaa tctgtacttt tttcaaatat tgaatgcctt 1201 attttgaat tctttagatt tttaaattgg agaaaagcac ttaaagtttt ttatatatga 1261 atattacatg taaagtgtt aaaatacata acttcagtgc aagagacttt gtcacttatt 1321 tccttatgtg tgtaggaggg gttaataagt ctctagctct ccatctattg atagtttcat	SEQ ID NO:97

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1381 ttacaatttc aaaagaacat tcttatattt tatcaaggaa gtcttcaaat ttgattctaa 1441 atagcgatta taatctccaa ctttattttg aatgtacctc tattagtttc aattgagtaa 1501 ttctagacat aactggtttg actctgtcca actctgtatt taggccattt gttacagttt 1561 cttcatgcat tacttactgt taaaactgta ccttttgcga tttcacagtt ggcacttctg 1621 ccatgagcag agaactgatg cgacttgttt tgctgcttgg tagcacttta aaaaattttt 1681 tgattaatga agaaagtaaa accataaaca tttgccaaaa attcatgccc cagtattagc 1741 aatgaattag ttgcattggt ttgagaaagg cacatattgg agggaaatct tggtgtaact 1801 taaatatttg aaaattacct ttaatgcaat gcatatctgt ttattctggg aaatgtttta 1861 atgccagggc ctgctgagtt gcttcttctt gtggagattt ttttttaat ctcctgagtt 1921 gtataaaagt tgtactgcat cttagtttac tggataaatt taaaacacag tattgtagaa 1981 agctaataca aaactatcct atgccttcaa atagtataga aaatggaaaa tatacaagta 2041 aattctgttg aaccacctgt gtagtctctc tagtagttaa aacagctatt ttagtaaccc 2101 caagagtttc ttctcatatc cataaaattg gattacagta tggcaatatc tacagcttct 2161 attcattatg caacgtttaa cattgattgg ataaatgctt ataggctggg ccaggtggct 2221 cccacctgta gtcccagcac tttgggaggc aaaggcggga ggatcacttg aggccaggac 2281 tttgagacca gccagggcaa cataataaga cttttctcta ctttaaattt tttaaaaaat 2341 tagttgggca tagtggcact tgcctgtagt ctcagctact taggaggctg aggtggcaga 2401 atagcttatg cctaggaggt tgaggctgca gtgagctgtg attatgccat tgcactccag 2461 cctgggtgac agagcaatac cctgtcttta aaaataaaag ctattacttg gcaaattctg 2521 aggtaagtgt atgatcttag ggaactttga tacaaatggg aattcactca ctggaatcgt 2581 ggctcccaaa aagatgcttt aattgtgtgg tgcttttata gtttagctcc a 1 M S T P A R R R L M R D F K R L Q E D P 1 ATGTCGACCCCGGCCCGGAGGAGGCTCATGCGGGATTTCAAGCGGTTACAAGAGGACCCA 21 P V G V S G A P S E N N I M Q W N A V I 61 CCTGTGGGTGTCAGTGGCGCACCATCTGAAAACAACATCATGCAGTGGAATGCAGTTATA 41 F G P E G T P F E D G T F K L V I E F S 121 TTTGGACCAGAAGGGACACCTTTTGAAGATGGTACTTTTAAACTAGTAATAGAATTTTCT 61 E E Y P N K P P T V R F L S K M F H P N 181 GAAGAATATCCAAATAAACCACCAACTGTTAGGTTTTTATCCAAAATGTTTCATCCAAAT 81 V Y A D G S I C L D I L Q N R W S P T Y 241 GTGTATGCTGATGGTAGCATATGTTTAGATATCCTTCAGAATCGATGGAGTCCAACATAT 101 D V S S I L T S I Q S L L D E P N P N S 301 GATGTATCTTCTATCTTAACATCAATTCAGTCTCTGCTGGATGAACCGAATCCTAACAGT 121 P A N S Q A A Q L Y Q E N K R E Y E K R 361 CCAGCCAATAGCCAGGCAGCACAGCTTTATCAGGAAAACAAACGAGAATATGAGAAAAGA 141 V S A I V E Q S W N D S - 421 GTTTCGGCCATTGTTGAACAAAGCTGGAATGATTCATAA	SEQ ID NO:98

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
WBC006E03_V1.3_at	Homo sapiens methionine adenosyltransferase II, beta (MAT2B)	1 CGGCCGCTGAGGCTGCGGCGGCGCGAAGGCGGCGGGC**ATG**GTGGGACGGGAGAAGGAGCT 61 CGCCATCCACTTTGTTCCCGGGAACTGCCGGCTCGAAGAGGAGGAAGTGAACATCCCCAG 121 CAGGCGGGTTCTGGTTACTGGTGCCACTGGGCTTCTTGGCAGAGCTGTGTACAGAGAATT 181 TAAGCAGAATAATTGGCATGCCTTTGGCTGTGGTTATAGAAGAGCGAGGCCAAAGTTTGA 241 GCAGGTCAATCTGTTGGACTCCGATGCGGTTCGTCACATTGTTCATGACGTTCAGCCCCA 301 CGTCATAGTGCATTGTGCAGCAGAGAGAAGGCCCGATGTGGTGGAAAATCAGCCGGATGC 361 TGCTTCTCGACTTAATGTGGATGCTTCTCGGAATTTAGCAAAGGAAGCAGCTGCAATCGG 421 AGCATTTCTAATCTACATTAGCTCAGATTATGTATTTGATGGAACAAATCCACCTTATAG 481 GGAGGAAGACATACCAAGTCCCCTAAACCTGTATGGCAAAACCAAATTAGAAGGAGAAAA 541 GGCCGTCCTGGAGAACAATTTAGGAGCTGCTGTTTTGAGAATTCCTGTTCTGTATGCAGA 601 AGTTGAGAAGCTTGAAGAAAGTGCCGTGACTATTATGTTTGATAAAGTGCAGTTCAGCAA 661 CAAGTCAGCGAACATGGACCACTGGCAGCAGAGGTTCCCCACCCATGTCAAAGATGTAGC 721 CACCGTGTGTCGTCAGTTAGCCGAGAAGAGAATGCTGGATCCGTCAATTAAGGGAACCTT 781 TCATTGGTCTGGCAACGAACAGATGACTAAGTATGAAATGGCATGTGCCATTGCCGATGC 841 CTTCAACCTCCCCAGCAGTCACTTAAGACCTATAACTGACAGCCCTGTCCTAGGAGCACA 901 ACGTCCGAGAAATGCTCAGCTTGACTGCTCCAAATTGGAGATCTTGGGCATTGGCCAACG 961 AACACCATTTCGAATTGGAATCAAAGAATCACTTTGGCCTTTCCTCATTGACAAGACATG 1021 GAGACAAACGGTCTTTCAT**TAG**TTTATTTGTGTTGGGTTCTTTTTTTTTTTTTAAATGAA 1081 AAGTATAGTATGTGGCACTTTTTAAAGAAAAGGAAATAGTTTTGTATGAGTGCTCTTTAA 1141 TTGTGACTCATGATCTTTCAGGTAAATGATGCTCTTGCGCTAGTGAAATGGTCTAAAGAA 1201 ACTAAGGGCNATAATGCCTTGTTTCGGAAGTAACAGTTTTTCTGTTTATCATTTTGTTTG 1261 TTCTGGCTTAACTCGCTGTTTGCGTATAGTAAATTATGATTCTGAAATATTTGAGAGCCA 1321 AGTTGAAACAGATCTGCTGTAGACTTTTCAGATGAAATTGTTCATTCTCGTAACCTCCAT 1381 ATTTTCAGGATTTTTGAAGCTGTTGACCTTTTCATGTTGATTATTTTAAATTGTGTTAAA 1441 TAGTATGAAAATCATTGGTGTTCATTATTTGCTTTGCCTGAGCTCAGATCAAAATGTTTG 1501 AAGAAAGATACTTTATTTTTGCAACTTAAGTGAGGTTTTTATGCTCGAGATCTTTCGATG 1561 TGTTATGTATATTGGAACTCCTGCAGCTTCGCGCCTCCTGCTTTTGTAGCAGTGTATGGT 1621 GAGCACTTGAGAGAGCGTGTGTACATGTATTTTTTTTTCTAGGCAAACATTGAATGCAAAC 1681 GTGTATTTTTTTAATATATATATAAAACTGTCCTTTTCACTCCATGTCACACTAAGTGAT 1741 ATTTCATATGTGTGGTTATACTAATAATTGGCCTTGTAAGTCTTTTGACCATTCATGAAT 1801 AATAATAATAAATACGTACTGCTGGCATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1 M V G R E K E L A I H F V P G N C R L E 1 ATGGTGGGACGGGAGAAGGAGCTCGCCATCCACTTTGTTCCCGGGAACTGCCGGCTCGAA 21 E E E V N I P S R R V L V T G A T G L L 61 GAGGAGGAAGTGAACATCCCCAGCAGGCGGGTTCTGGTTACTGGTGCCACTGGGCTTCTT 41 G R A V Y R E F K Q N N W H A F G C G Y 121 GGCAGAGCTGTGTACAGAGAATTTAAGCAGAATAATTGGCATGCCTTTGGCTGTGGTTAT 61 R R A R P K F E Q V N L L D S D A V R H 181 AGAAGAGCGAGGCCAAAGTTTGAGCAGGTCAATCTGTTGGACTCCGATGCGGTTCGTCAC 81 I V H D V Q P H V I V H C A A E R R P D 241 ATTGTTCATGACGTTCAGCCCCACGTCATAGTGCATTGTGCAGCAGAGAGAAGGCCCGAT	SEQ ID NO:99 SEQ ID NO:100

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		101 V V E N Q P D A A S R L N V D A S R N L 301 GTGGTGGAAAATCAGCCGGATGCTGCTTCTCGACTTAATGTGGATGCTTCTCGGAATTTA 121 A K E A A A I G A F L I Y I S S D Y V F 361 GCAAAGGAAGCAGCTGCAATCGGAGCATTTCTAATCTACATTAGCTCAGATTATGTATTT 141 D G T N P P Y R E E D I P S P L N L Y G 421 GATGGAACAAATCCACCTTATAGGGAGGAAGACATACCAAGTCCCCTAAACCTGTATGGC 161 K T K L E G E K A V L E N N L G A A V L 481 AAAACCAAATTAGAAGGAGAAAAGGCCGTCCTGGAGAACAATTTAGGAGCTGCTGTTTTG 181 R I P V L Y G E V E K L E E S A V T I M 541 AGAATTCCTGTTCTGTATGGAGAAGTTGAGAAGCTTGAAGAAAGTGCCGTGACTATTATG 201 F D K V Q F S N K S A N M D H W Q Q R F 601 TTTGATAAAGTGCAGTTCAGCAACAAGTCAGCGAACATGGACCACTGGCAGCAGAGGTTC 221 P T H V K D V A T V C R Q L A E K R M L 661 CCCACCCATGTCAAAGATGTAGCCACCGTGTGTCGTCAGTTAGCCGAGAAGAGAATGCTG 241 D P S I K G T F H W S G N E Q M T K Y E 721 GATCCGTCAATTAAGGGAACCTTTCATTGGTCTGGCAACGAACAGATGACTAAGTATGAA 261 M A C A I A D A F N L P S S H L R P I T 781 ATGGCATGTGCCATTGCCGATGCCTTCAACCTCCCCAGCAGTCACTTAAGACCTATAACT 281 D S P V L G A Q R P R N A Q L D C S K L 841 GACAGCCCTGTCCTAGGAGCACAACGTCCGAGAAATGCTCAGCTTGACTGCTCCAAATTG 301 E I L G I G Q R T P F R I G I K E S L W 901 GAGATCTTGGGCATTGGCCAACGAACACCATTTCGAATTGGAATCAAAGAATCACTTTGG 321 P F L I D K R W R Q T V F H - 961 CCTTTCCTCATTGACAAGAGATGGAGACAAACGGTCTTTCATTAG	
WBC005F10	Polymeric immunoglobulin receptor 3 precursor (PIGR3)	1 ggtgcgacca agccctggct ccagctctag cgggtatctg cccaccatgg ccctggtgct 61 gatcctccag ctgctgaccc tctggcctct gtgtcacaca gacatcactc cgtctgtccc 121 cccagcttca taccacccta agccatggct gggagctcag ccggctacag ttgtgacccc 181 tggggtcaac gtgaccttga gatgccgggc accccaaccc gcttggagat ttggacttt 241 caagcctgga gagatcgctc cccttctctt ccgggatgtg tcctccgagc tggcagaatt 301 ctttctggag gaggtgactc cagcccaagg gggaagttac cgctgctgct accgaaggcc 361 agactggggg ccgggtgtct ggtcccagcc cagcgatgtc ctggagctgc tggtgacaga 421 ggagctgccg cggccgtcgc tggtggcgct gcccgggccg gtggtgggtc ctggcgccaa 481 cgtgagcctg cgctgcgcgg gccgcctgcg gaacatgaac ttcgtgctgt accgcgaggg 541 cgtggcggcc ccgctgcagt accgccactc cgcgcagccc tgggccgact tcacgctgct	SEQ ID NO:101

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		601 gggcgcccgc gccccggcca cctacagctg ctactatcac acgccctccg cgccctacgt 661 gctgtcgcag cgcagcgagg tgctggtcat cagctgggaa gactctggct cctccgacta 721 cacccgggag aacctagtcc gcctgggggct ggccgggctg gtcctcatct ccctgggcgc 781 gctggtcact tttgactggc gcagtcagaa ccgcgctcct gctggtatcc gcccctgagc 841 cccaggagca ctgcagcccg agacttccaa cctgagtggc ggagaagctg ggaccctggg 901 ctggactgtc ctttcctgca gccccacagt cctgctggct gagctccgcg gaacggtcct 961 tagacccccgc tgtgccctgt gctgtagctt ctttccaggc ctttcccaag gagtagctga 1021 aaggaagacg cgattagtgg ttaagacttc caagccagaa gacagagggt tcgaatccca 1081 gcactgccgt ctactcactg tagtagtagc agctacagaa aggtagtagt gagacgtgaa 1141 gccagctgga cttcctgggt tgaatgggga cctggagaac ttttctgtct tacaagagga 1201 ttgtaaaatg gaccaatcag cactctgtaa gatggaccaa tcagcgctct gtaaaatgga 1261 ccaatcagca ggacacgggc gggacaata agggaataaa agctggcgag cgcggcaccc 1321 caccagagtc tgcttccacg ttgtgggagc tttgttctct tgctctacac aataaatctt 1381 gctgctgctt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa	SEQ ID NO:102
		1 M A L V L L L Q L L T L W P L C H T D I 1 ATGGCCCTGGTGCTGATCCTCCAGCTGCTGACCCTCTGGCCTCTGTGTCACACAGACATC 21 T P S V P P A S Y H P K P W L G A Q P A 61 ACTCCGTCTGTCCCCCCAGCTTCATACCACCCTAAGCCATGGCTGGGAGCTCAGCCGGCT 41 T V V T P G V N V T L R C R A P Q P A W 121 ACAGTTGTGACCCCTGGGGTCAACGTGACCTTGAGATGCCGGGCACCCCAACCGCTTGG 61 R F G L F K P G E I A P L L F R D V S S 181 AGATTTGGACTTTTCAAGCCTGGAGAGATCGCTCCCCTTCTTCCGGGATGTGTCCTCC 81 E L A E F F L E E V T P A Q G G S Y R C 241 GAGCTGGCAGAATTCTTTCTGGAGGTGACTCCAGCCCAAGGGGGAAGTTACCGCTGC 101 C Y R R P D W G P G V W S Q P S D V L E 301 TGCTACCGAAGGCCAGACTGGGGGCCGGGTGTCTGGTCCCAGCCCAGCGATGTCCTGGAG 121 L L V T E E L P R P S L V A L P G P V V 361 CTGCTGGTGACAGAGGAGCTGCCGCGGCCGTCGCTGGTGGCGCTGCCCGGGGCCGGTGGTG 141 G P G A N V S L R C A G R L R N M N F V 421 GGTCCTGGCGCCAACGTGAGCCTGCGCTGCGCGGGCCGCCTGCGGAACATGAACTTCGTG 161 L Y R E G V A A P L Q Y R H S A Q P W A 481 CTGTACCGCGAGGGCGTGGCGGCCCCGCTGCAGTACCGCCACTCCGCGCAGCCCTGGGCC 181 D F T L L G A R A P G T Y S C Y Y H T P 541 GACTTCACGCTGCTGGGCGCCCGCGCCCCCGGCACCTACAGCTGCTACTATCACACGCCC 201 S A P Y V L S Q R S E V L V I S W E D S 601 TCCGCGCCCTACGTGCTGTCGCAGCGCAGCGAGGTGCTGGTCATCAGCTGGGAAGACTCT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		221 G S S D Y T R G N L V R L G L A G L V L 661 GGCTCCTCCGACTACACCCGGGGGAACCTAGTCCGCCTGGGGCTGGCCGGGCTGGTCCTC 241 I S L G A L V T F D W R S Q N R A P A G 721 ATCTCCCTGGGCGCGCTGGTCACTTTTGACTGGCGCAGTCAGAACCGCGCTCCTGCTGGT 261 I R P - 781 ATCCGCCCCTGA	
WBC005D02_V1.3_at	Homo sapiens hypothetical protein FLJ22662, mRNA	1 CGCAGAGGAAGGTCGCGGCCGTGGAGCGATGACCCGCGGCGGTCCGGGCGGGCGCCCGGG 61 GCTGCCACAGCCGCCGCCGCTTCTGCTGCTGCTGCTGCTGCCGCTGTTGTTAGTCACCGC 121 GGAGCCGCCGAAACCTGCAGGAGTCTACTATGCAACTGCATACTGGATGCCTGCTGAAAA 181 GACAGTACAAGTCAAAAATGTAATGGACAAGAATGGGGACGCCTATGGCTTTTACAATAA 241 CTCTGTGAAAACCACAGGCTGGGGCATCCTGGAGATCAGAGCTGGCTATGGCTCTCAAAC 301 CCTGAGCAATGAGATCATCATGTTTGTGGCTGGCTTTTTGGAGGGTTACCTCACTGCCCC 361 ACACATGAATGACCACTACACAAACCTCTACCCACAGCTGATCACGAAACCTTCCATCAT 421 GGATAAAGTGCAGGATTTTATGGCGAAGCAAGATCAGTGGACCCGGAGTAAGATCAAAGA 481 TTACAAGGATGACCCGTTTTGGAGACATATGGGCTATGTTATGGCACAATTAGATGGGCT 541 GTATGTAGGAGCAATGAAGAGGGCTTCATTAGAAGGGATAAAGCCCATGACCATGTTCCA 601 GATTCAGTTCCTGAATGCTGTTGGAGATCTGTTGGATCTGATTCCCTCACTTTCTCCCAC 661 ACAAGTCTACAATTTGAAGTTTTTTAAGAGATGGGATATGGGACATTGCTCTGCTCTTAT 721 TAAGGTTCTTCCTGGATTTGAGAACATCTTTTTTGCTCATTCAAGCTGGTACACGTATGC 781 AGCCATGCTCAGGATATATAAACACTGGGACTTCAACATCAGAGATAAAGACACCATCAG 841 TAATCGCCTCTCTTTCAGCAGTTACCCAGGGTTTTTGGAGTCTCTGGATGACTTTTACAT 901 TCTTAGCAGTGGGTTGATATTGCTGCAGACCACAAACAGTGTGTATAATAAGACCCTGCT 961 GAAGCTTGTGGTACCCCAGTCTCTCCTAGCCTGGCAAAGAGTCCGTGTGGCCAATATGAT 1021 GGCAAATGGTGGCAGGGAGTGGGCAGAGATCTTTTCAAAATACAACTCTGGCACCTATAA 1081 CAATCAGTACATGATCTTGGACCTGAAGAAGGTAAACGTGAGGCACAGCCTTGACAAAGG 1141 CACTCTGTACATTGTGGAGCAAATTCCTACATATGTAGAATTTTCTGAACAAACTGATGT 1201 TCTACGGAAAGGATATTGGCCCTCCTACAACATTCCTTTCCATGAAAAAATCTACAACTG 1261 GAGTGGCTACCCAATGCTGGTTCAGAAGCTGGGTTTGGACTTCTCTTATGATCTGGCTCC 1321 ACGAGCCAAAATCTTCCGGCGCGACCAAGGGAAAGTGACTGATGTGGAGTCCATGAAATA 1381 TATCATGCGATACAACAATTATGAGAAGGATCCTTACAGTAGGGGCGATCCCTGCAACAC 1441 CATCTGCTGCCGTGAGGACCTGAACTCACAGAACCCGAGTCCTGGAGGCTGCTACGATAC 1501 GAAGGTGGCAGATATCTATCTAGCATCAAAGTACACAGCCTATGCCATTAGTGGTCCCAC 1561 CGTACAAGGTGGTCTCCCTGTTTTTCACTGGAACCGGTTCAACAAAACTCTCCATGAGGG 1621 CATGCCAGAGGCCTACAACTTTGATTTTATTACCATGAAACCAATCTTGAAACCTTACGT 1681 AAAATGAAGGAAGGAGATGAGGGAATGGAAGGCTGCAAATAAGATACCAAGGCACTATTT 1741 TAGTTACGTTTTTTCCCATCAGAATTATGCAATAAAATATATTAATTTGTCACTTTAAAA 1801 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1 M T R G G P G G R P G L P Q P P P L L L 1 ATGACCCGCGGCGGTCCGGGCGGGCGCCCGGGGCTGCCACAGCCGCCGCCGCTTCTGCTG 21 L L L L P L L L V T A E P P K P A G V Y	SEQ ID NO:103 SEQ ID NO:104

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		61 CTGCTGCTGCTGCCGCTGTTGTTAGTCACCGCGGAGCCGCCGAAACCTGCAGGAGTCTAC	
		41 Y A A T A Y Y W M P A E K T V Q V K N V M D	
		121 TATGCAACTGCATACTGGATGCCTGCTGAAAAGACAGTACAAGTCAAAAATGTAATGGAC	
		61 K N G D A Y G F Y N N S V K T T G W G I	
		181 AAGAATGGGGACGCCTATGGCTTTTACAATAACTCTGTGAAAACCACAGGCTGGGGCATC	
		81 L E I R A G Y G S Q T L S N E I I M F V	
		241 CTCGAGATCAGAGCTGGCTATGGCTCTCAAACCCTGAGCAATGAGATCATCATGTTTGTG	
		101 A G F L E G Y L T A P H M N D H Y T N L	
		301 GCTGGCTTTTTGGAGGGTTACCTCACTGCCCCACACATGAATGACCACTACACAAACCTC	
		121 Y P Q L I T K P S I M D K V Q D F M A K	
		361 TACCCACAGCTGATCACGAAACCTTCCATCATGGATAAAGTGCAGGATTTTATGGCGAAG	
		141 Q D Q W T R S K I K D Y K D D P F W R H	
		421 CAAGATCAGTGGACCCGGAGTAAGATCAAAGATTACAAGGATGACCCGTTTTGGAGACAT	
		161 M G Y V M A Q L D G L Y V G A M K R A S	
		481 ATGGGCTATGTTATGGCACAATTAGATGGGCTGTATGTAGGAGCAATGAAGAGGGCTTCA	
		181 L E G I K P M T M F Q I Q F L N A V G D	
		541 TTAGAAGGGATAAAGCCCATGACCATGTTCCAGATTCAGTTCCTGAATGCTGTTGGAGAT	
		201 L L D L I P S L S P T Q V Y N L K F F K	
		601 CTGTTGGATCTGATTCCCTCACTTTCTCCCACACAAGTCTACAATTTGAAGTTTTTTAAG	
		221 R W D M G H C S A L I K V L P G F E N I	
		661 AGATGGGATATGGGACATTGCTCTGCTCTTATTAAGGTTCTTCCTGGATTTGAGAACATC	
		241 F F A H S S W Y T Y A A M L R I Y K H W	
		721 TTTTTTGCTCATTCAAGCTGGTACACGTATGCAGCCATGCTCAGGATATATAAACACTGG	
		261 D F N I R D K D T I S N R L S F S S Y P	
		781 GACTTCAACATCAGAGATAAAGACACCATCAGTAATCGCCTCTCTTTCAGCAGTTACCCA	
		281 G F L E S L D D F Y I L S S G L I L L Q	
		841 GGGTTTTTGGAGTCTCTGGATGACTTTTACATTCTTAGCAGTGGGTTGATATTGCTGCAG	
		301 T T N S V Y N K T L L K L V V P Q S L L	
		901 ACCACAAACAGTGTGTATAATAAGACCCTGCTGAAGCTTGTGGTACCCCAGTCTCTCCTA	
		321 A W Q R V R V A N M M A N G G R E W A E	
		961 GCCTGGCAAAGAGTCCGTGTGGCCAATATGATGGCAAATGGTGGCAGGGAGTGGGCAGAG	
		341 I F S K Y N N S G T Y N N Q Y M I L D L K	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1021 ATCTTTTCAAAATACAACCTCTGGCACCTATAACAATCAGTACATGATCTTGGACCTGAAG	
		361 K V N V R H S L D K G T L Y I V E Q I P	
		1081 AAGGTAAACCTGAGGCACAGCCTTGACAAAGGCACTCTGTACATTGTGGAGCAAATTCCT	
		381 T Y V E F S E Q T D V L R K G Y W P S Y	
		1141 ACATATGTAGAATTTTCTGAACAAACTGATGTTCTACGGAAAGGATATTGGCCCTCCTAC	
		401 N I P F H E K I Y N W S G Y P M L V Q K	
		1201 AACATTCCTTTCCATGAAAAAATCTACAACTGGAGTGGCTACCCAATGCTGGTTCAGAAG	
		421 L G L D F S Y D L A P R A K I F R R D Q	
		1261 CTGGGTTTGGACTTCTCTTATGATCTGGCTCCACGAGCCAAAATCTTCCGGCGCGACCAA	
		441 G K V T D V E S M K Y I M R Y N N Y E K	
		1321 GGGAAAGTGACTGATGTGGAGTCCATGAAATATATCATGCGATACAACAATTATGAGAAG	
		461 D P Y S R G D P C N T I C C R E D L N S	
		1381 GATCCTTACAGTAGGGGCGATCCCTGCAACACCATCTGCTGCCGTGAGGACCTGAACTCA	
		481 Q N P S P G G C Y D T K V A D I Y L A S	
		1441 CAGAACCCGAGTCCTGGAGGCTGCTACGATACGAAGGTGGCAGATATCTATCTAGCATCA	
		501 K Y T A Y A I S G P T V Q G G L P V F H	
		1501 AAGTACACAGCCTATGCCATTAGTGGTCCCACCGTACAAGGTGGTCTCCCTGTTTTTCAC	
		521 W N R F N K T L H E G M P E A Y N F D F	
		1561 TGGAACCGGTTCAACAAAACTCTCCATGAGGGCATGCCAGAGGCCTACAACTTTGATTTT	
		541 I T M K P I L K P Y V K –	
		1621 ATTACCATGAAACCAATCTTGAAACCTTACGTAAAATGA	
WBC004E04	TRAF-interacting protein with a forkhead-associated domain	1 gagaggacgt gctctgccag ccagtgggaa ggcaggccgc gcgcgcggga gcgcgggagg 61 atcggcggct cgcggtcact ggtccctggc tcggttcccc gcaccccggg gctcacactt 121 acccgcgcgg aggagcagcg gccgggtgtc caccccatc ctgcgcccag tctcctcgat 181 tcccctcgct ctgagccggg agagccgaac agctgaagag agttcactga ctccccagcc 241 ccaggtgggc cttgtgcaca tcatgaccag ttttgaagat gctgacacag aagagacagt 301 aacttgtctc cagatgacgg tttaccatcc tggccagttg cagtgtggaa tatttcagtc 361 ataagtttt aacagagaga aactcccttc cagcgaagtg gtgaaatttg gccgaaattc 421 caacatctgt cattatactt ttcaggacaa acaggtttcc cgagttcagt tttctctgca 481 gctgtttaaa aaattcaaca gctcagttct ctcctttgaa ataaaaaata tgagtaaaaa 541 gaccaatctg atcgtggaca gcagagagct gggctaccta aataaaatgg acctgccata 601 caggtgcatg gtcagattcg gagagtatca gtttctgatg gagaaggaag atggcgagtc 661 attggaattt tttgagactc aatttatttt atctccaaga tcactctttgc aagaaacaa 721 ctggccacca cacaggccca taccggagta tggcacttac tcgctctgct cctcccaaag 781 cagttctccg acagaaatgg atgaaaatga gtcatgaaca cagaaagtct aagaggagaa	SEQ ID NO:105

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		841 atatgatgga tgaagagctc tgtagatgct gtatagacac taaataagag ttgattaggg 901 tagtatatta tagtcatctg ttatgctgtg aaatttggaa ttcaaaattt tgaagtctgt 961 aaattgtgtt agtcattaac ttagtcacct gttgtattct ggatctacac aaaattattt 1021 taagtgctct tattaatctg tgaggattaa tatacaaaaa gtatcctttg agatgaagtc 1081 gtgttctcaa aataaggtta tattattttc ttttctgct tgattttcat cttgtgtttt 1141 gctttgtttt tgtaaggaac catctcttgg tttggtcaca tcagttcaca acagccattt 1201 gttttcaagg tcaaggctcc aggcaggttg ttactggtgt ttgcagcctg tcagtacttg 1261 cagtactgga ataggttcta ggctagtgtc tgcgcgtcac tgtggtttta gcatgggagg 1321 acttatttga gaaatactac cttacttttc tatgatttct ttttacagag ttatagtgtg 1381 tttactccta agatgacagt tctctttgtc tatattcagc atctaagaca aatatttaaa 1441 cattttaaag aaccactgtg ttaagtttag gattatttac ttaccaaatt agaagtttga 1501 cttttatgtg ttatacacaa tcttaaaatt tcacgaattc acctttttaa tagtatccat 1561 gtacataata aaatcaaagt ttaattaaaa aaaaaaaaaa aaaa 1 M T S F E D A D T E E T V T C L Q M T V 1 ATGACCAGTTTTGAAGATGCTGACACAGAAGAGACAGTAACTTGTCTCCAGATGACGGTT 21 Y H P G Q L Q C G I F Q S I S F N R E K 61 TACCATCCTGGCCAGTTGCAGTGTGGAATATTTCAGTCAATAAGTTTTAACAGAGAGAAA 41 L P S S E V V K F G R N S N I C H Y T F 121 CTCCCTTCCAGCGAAGTGGTGAAATTTGGCCGAAATTCCAACATCTGTCATTATACTTTT 61 Q D K Q V S R V Q F S L Q L F K K F N S 181 CAGGACAAACAGGTTTCCCGAGTTCAGTTTTCTCTGCAGCTGTTTAAAAAATTCAACAGC 81 S V L S F E I K N M S K K T N L I V D S 241 TCAGTTCTCTCCTTTGAAATAAAAAATATGAGTAAAAAGACCAATCTGATCGTGGACAGC 101 R E L G Y L N K M D L P Y R C M V R F G 301 AGAGAGCTGGGCTACCTAAATAAAATGGACCTGCCATACAGGTGCATGGTCAGATTCGGA 121 E Y Q F L M E K E D G E S L E F F E T Q 361 GAGTATCAGTTTCTGATGGAGAAGGAAGATGGCGAGTCATTGGAATTTTTTGAGACTCAA 141 F I L S P R S L L Q E N N W P P H R P I 421 TTTATTTTATCTCCAAGATCACTCTTGCAAGAAAACAACTGGCCACCACACAGGCCCATA 161 P E Y G T Y S L C S S Q S S S P T E M D 481 CCGGAGTATGGCACTTATTCGCTCTGCTCCTCCCAAAGCAGTTCTCCGACAGAAATGGAT 181 E N E S - 541 GAAAATGAGTCATGA	SEQ ID NO:106
WBC004D07_V1.3_at	No Homology	1 GGACTGACTATTGGGCTCCCTGGGCAAGGGGAAGGGGAAGGGAGAGCCTTTTAGATTCAT 61 TCTTGATTTCCATACTTCTACGATGTTGCTCAGAGGACTGCTCCGCCTTCTGGGCTTGTT	SEQ ID NO:107

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		121 GTCAGGTGGAATGAATGCACCTCTGGAGACCATTGGGCTCTGCTTTGTCATCCCCCGTGCC 181 TTTAATGGCCCCATGAGTCTATCACTACATTTTTAACACCAGTCCTGAAATCTGGACCAT 241 GATTTCTTTTGAACCTCTCAAACGGTAAAATTCCTCAGAAACCAAAGCTTTATTAACCAA 301 CTTCCACACTCATTTCTTTGATACTTATTCCTTCCCGGCTGGTTCTACCTATGACCAG 361 AAGCCTGTTTTCCTACAGAAGACCCATGCTAGACCTCATTTGAACTAAGCACACATTTTG 421 TTTGTAGCTACAGGCCTGGATATCTTACTGTTGGTAAATTTCTTTACCTGACATCACTGT 481 ATATTATTGTTGTTTTAAAACCTGTGAAAGAAGGATTCAGAATGACCACTAATTTTCAGA 541 TCAAGGAAATATGACAGTGAAGCGCAGCAGACATTGCTAACACACGGAACCTACCTGTT 601 TGAAACTAAACTTTCAAGCAATCTCAAACTCTCTCCCATAAGGACAAAGCAGCTGTGTGC 661 TCACACATAAATAGTTTGCATGGCCCTACGCCCTTTCTCCCCTAGGGGATTGGAA 1 CAGATGTCTAGAAGTCTTCCAAAGATGAAAACACTGGAAGCATTATCCTAGTCAATCAGTC 61 TGGAGCCTGACTCCTGTTCCTTTGGAGTCATTATAAATTCTATAAATGAATTATCCCCCT 121 TCAGTCTTCAGAAACATACCTTCTCATGTGCATTTCAGTTTTGTTGAAAGGATGGAGTCC 181 ACAAAGATATCATTCTTGAGTCATGGATTTCTTTGCTTACAAAACGGTCTGTGATTTTGG 241 AACTGGAAATAAACGAAATGGTAATAATTTAGACTGTGGCACACTGATGCACTGAATAAA 301 GGAACAGATAGAGGAGCTGGTCTGTTGACAGCTGTAGTTCAGTATGCAATTACAGAGAAA 361 GATACACCTCATCTGAATGTACATATTCAAGGTGAAAGACTTCTTAGCGTTCCAGTTTGC 421 TGGCCAATTGCACCTGCTGTTGTTTCCATCCCACAGTCAACTGGTTGAAAGGA 481 GTTATTTCTCCCCATGACTTCAAACAAAATTTAACCCAGAATTGTAAATAGTGGCTGCAG 541 GAATTCTTTTCTAAAATGCTTTCCCCTTCTTCTTACTGCCTTTTATAGCAAGATAATTG 601 TCTATTTACACACTTTTTGTTGTGGTTTTGTATTGTAACACCATTTTTCTTTGAGACTAT 661 TGTATTTAAAGGAAGTTTCATATAGTGTCAAGCAAGTAATTAAATTATGTCTGAAAGCTG 721 GCCATATTC	SEQ ID NO:108
WBC004B05	Heterogeneous nuclear ribonucleoprotein F	1 ggggcggttc ccgtagcctt agctctcggc cctgggccct ttttcctcct cggctgcgcc 61 gcgtgtcctc ggagcgcggt ccctgtattg gtctcctgct cctagaggtt gagaacaaaa 121 acatgcacct ggagttccc cggagccctc tgcgtggttg agcttcggtg gaatttcggg 181 gctcttggct gccagccgcg cttgcctggt agcaacagaa accagtcctg ctcgcctccg 241 tggacatttc attaccatcc agaagtgtct cccactgaag gcatccgtgg ttgtttttaa 301 gccacaaaaa agccacaccc aagatcacct gacacccacc ctgtcaagtg tccatgatgc 361 tgggccctga gggaggtgaa ggcttgtgtg tcaagctccg tggcctgccc tggtcctgct 421 ctgttgagga cgtgcagaac ttcctctctg actgcacgat tcatgatggg gccgcaggtg 481 tccatttcat ctacactaga gagggcaggc agagtggtga ggcttttgtt gaacttggat 541 cagaagatga tgtaaaaatg gccctgaaaa aagacaggga aagcatggga caccggtaca 601 ttgaggtgtt caggtcccac agaaccgaga tggattgggt gttgaagcac agtggtccca 661 acagtgccga cagcgccaac gatggcttcg tgcggcttcg aggactccca tttggatgca 721 caaaggaaga aattgttcag ttcttctcag ggttggaaat tgtgccaaac gggatcacat 781 tgcctgtgga ccccgaaggc aagattacag gggaagcgtt cgtgcagttt gcctcgcagg 841 agttagctga gaaggctcta gggaaacaca aggagaggat agggcacagg tacattgagg 901 tgtttaagag cagccaggag gaagttaggt catactcaga tccccctctg aagttcatgt 961 ccgtgcagcg gccagggccc tatgaccggc ccgggactgc caggaggtac attggcatcg 1021 tgaagcaggc aggcctggaa aggatgaggc ctggtgccta cagcacaggc tacgggggct 1081 acgaggagta cagtggcctc agtgatggct acggcttcac caccgacctg ttcgggagag 1141 acctcagcta ctgtctctcc ggaatgtatg accacagata cggcgacagt gagttcacag 1201 tgcagagcac cacaggccac tgtgtccaca tgaggggcct gccgtacaaa gcgaccgaga	SEQ ID NO:109

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1261 acgacattta caacttcttc tctcctctca accctgtgag agtccatatt gagattggcc 1321 cagatggaag agtgacgggt gaagcagatg ttgagtttgc tactcatgaa gaagctgtgg 1381 cagctatgtc caaagacagg gccaatatgc agcacagata tatagaactc ttcttgaatt 1441 caacaacagg ggccagcaat ggggcgtata gcagccaggt gatgcaaggc atgggggtgt 1501 ctgctgccca ggccacttac agtggcctgg agagccagtc agtgagtggc tgttacgggg 1561 ccggctacag tgggcagaac agcatgggtg gctatgacta gttttgttag gaacatttga 1621 gttacttcaa tcatttcac aggcagccaa caagcaatta agagcagtta taatagagga 1681 agctgggga cccattttgc accatgagtt tgtgaaaaat ctggattaaa aaattacctc 1741 ttcagtgttt tctcatgcaa aatttcttc tagcatgtga taatgagtaa actaaaacta 1801 ttttcagctt ttctcaatta acattttggt agtatacttc agagtgatgt tatctaagtt 1861 taagtagttt aagtatgtta aatgtggatc ttttacacca catcacagtg aacacactgg 1921 ggagacgtcc ttttttggaa aactcaaagg tgctagctcc ctgattcaaa gaaatatttc 1981 tcatgtttgt tcattctagt ttatattttc atttaaaatc ctttaggtta agtttaagct 2041 ttttaaaagt tagttttgag aattgagaca caatactaat actgtaggaa ttggtgaggc 2101 cttgacttaa aactttcttt gtactgtgat ttccttttgg gtgtattttg ctaagtgaaa 2161 cttgttaaat tttttgttaa ctaaattttt ttcttaaaat aaagactttt tcacaatgac 2221 tggcacagat tactcagcaa aagatagcaa aacgggtggt tgaagataat tcattttaat 2281 cgtaatgtat tttagtgtga atttaaaaat ttcatacatc aaatctatga tctcccttat 2341 attcttatga tgaggctaaa taaaagtcta ataaaaacga aaaaaaaaaa aaaaaaaaaa 2401 aaaaaaa	
		1 M M L G P E G G E G F V V K L R G L P W 1 ATGATGCTGGGCCCTGAGGGAGGTGAAGGCTTTGTGGTCAAGCTCCGTGGCCTGCCCTGG	SEQ ID NO:110
		21 S C S V E D V Q N F L S D C T I H D G A 61 TCCTGCTCTGTTGAGGACGTGCAGAACTTCCTCTCTGACTGCACGATTCATGATGGGGCC	
		41 A G V H F I Y T R E G R Q S G E A F V E 121 GCAGGTGTCCATTTCATCTACACTAGAGAGGGCAGGCAGAGTGGTGAGGCTTTTGTTGAA	
		61 L G S E D D V K M A L K K D R E S M G H 181 CTTGGATCAGAAGATGATGTAAAAATGGCCCTGAAAAAAGACAGGGAAAGCATGGGACAC	
		81 R Y I E V F K S H R T E M D W V L K H S 241 CGGTACATTGAGGTGTTCAAGTCCCACAGAACCGAGATGGATTGGGTGTTGAAGCACAGT	
		101 G P N S A D S A N D G F V R L R G L P F 301 GGTCCCAACAGTGCCGACAGCGCCAACGATGGCTTCGTGCGGCTTCGAGGACTCCCATTT	
		121 G C T K E E I V Q F F S G L E I V P N G 361 GGATGCACAAAGGAAGAAATTGTTCAGTTCTTCTCAGGGTTGGAAATTGTGCCAAACGGG	
		141 I T L P V D P E G K I T G E A F V Q F A 421 ATCACATTGCCTGTGGACCCCGAAGGCAAGATTACAGGGGAAGCGTTCGTGCAGTTTGCC	
		161 S Q E L A E K A L G K H K E R I G H R Y 481 TCGCAGGAGTTAGCTGAGAAGGCTCTAGGGAAACACAAGGAGAGGATAGGGCACAGGTAC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		181 I E V F K S S Q E E V R S Y S D P P L K 541 ATTGAGGTGTTTAAGAGCAGCCAGGAGGAAGTTAGGTCATACTCAGATCCCCCTCTGAAG 201 F M S V Q R P G P Y D R P G T A R R Y I 601 TTCATGTCCGTGCAGCGGCCAGGGCCCTATGACCGGCCCGGGACTGCCAGGAGGTACATT 221 G I V K Q A G L E R M R P G A Y S T G Y 661 GGCATCGTGAAGCAGGCAGGCCTGGAAAGGATGAGGCCTGGTGCCTACAGCACAGGCTAC 241 G G Y E E Y S G L S D G Y G F T T D L F 721 GGGGGCTACGAGGAGTACAGTGGCCTCAGTGATGGCTACGGCTTCACCACCGACCTGTTC 261 G R D L S Y C L S G M Y D H R Y G D S E 781 GGGAGAGACCTCAGCTACTGTCTCTCCGGGATGTATGACCACAGATACGGCGACAGTGAG 281 F T V Q S T T G H C V H M R G L P Y K A 841 TTCACAGTGCAGAGCACCACAGGCCACTGTGTCCACATGAGGGGCCTGCCGTACAAAGCG 301 T E N D I Y N F F S P L N P V R V H I E 901 ACCGAGAACGACATTTACAACTTCTTCTCTCCTCTCAACCCTGTGAGAGTCCATATTGAG 321 I G P D G R V T G E A D V E F A T H E E 961 ATTGGCCCAGATGGAAGAGTGACGGGTGAAGCAGATGTTGAGTTTGCTACTCATGAAGAA 341 A V A A M S K D R A N M Q H R Y I E L F 1021 GCTGTGGCAGCTATGTCCAAAGACAGGGCCAATATGCAGCACAGATATATAGAACTCTTC 361 L N S T T G A S N G A Y S S Q V M Q G M 1081 TTGAATTCAACAACAGGGGCCAGCAATGGGGCGTATAGCAGCCAGGTGATGCAAGGCATG 381 G V S A A Q A T Y S G L E S Q S V S G C 1141 GGGGTGTCTGCTGCCCAGGCCACTTACAGTGGCCTGGAGAGCCAGTCAGTGAGTGGCTGT 401 Y G A G Y S G Q N S M G G Y D - 1201 TACGGGGCCGGCTACAGTGGGCAGAACAGCATGGGTGGCTATGACTAG	
WBC004C03	Dendritic cell protein variant, clone: CAE03638	1 gtcttgcgag tggagtgtcc gctgtgcccg ggcctgcacc atgagcgtcc cggccttcat 61 cgacatcagt gaagaagatc aggctgctga gcttcgtgct tatctgaaat ctaaaggagc 121 tgagatttca gaagagaact cggaaggtgg acttcatgtt gatttagctc aaattattga 181 agcctgtgat gtgtgtctga aggaggatga taaagatgtt gaaagtgtga tgaacagtgt 241 ggtatcccta ctcttgatcc tggaaccaga caagcaagaa gctttgattg aaagcctatg 301 tgaaaagctg gtcaaatttc gcgaaggtga acgcccgtct ctgagactgc agttgttaag 361 caacctttc cacgggatgg ataagaatac tcctgtaaga tacacagtgt attgcagcct 421 tattaaagtg gcagcatctt gtggggccat ccagtacatc ccaactgagc tggatcaagt 481 tagaaaatgg atttctgact ggaatctcac cactgaaaaa aagcacaccc ttttaagact 541 actttatgag gcacttgtgg attgtaagaa gagtgatgct gcttcaaaag tcatggtgga	SEQ ID NO:111

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		601 attgctcgga agttacacag aggacaatgc ttcccaggct cgagttgatg cccacaggtg 661 tattgtacga gcattgaaag atccaaatgc atttcttttt gaccaccttc ttactttaaa 721 accagtcaag tttttggaag gcgagcttat tcatgatctt ttaaccattt ttgtgagtgc 781 taaattggca tcatatgtca agttttatca gaataataaa gacttcattg attcacttgg 841 cctgttacat gaacagaata tggcaaaaat gagactactt acttttatgg gaatggcagt 901 agaaaataag gaaatttctt ttgacacagt gcagcaagaa cttcagattg gagctgatga 961 tgttgaagca tttgttattg acgccgtaag aactaaaatg gtctactgca aaattgatca 1021 gacccagaga aaagtagttg tcagtcatag cacacatcgg acatttggaa aacagcagtg 1081 gcaacaactg tatgacacac ttaatgcctg gaaacaaaat ctgaacaaag tgaaaaacag 1141 ccttttgagt ctttctgata cctgagtttt tatgcttata atttttgttc tttgaaaaaa 1201 aagccctaaa tcatagtaaa acattataaa ctaaaaaaaa aaaaaaaaaa aa	
		1 M S V P A F I D I S E E D Q A A E L R A 1 ATGAGCGTCCCGGCCTTCATCGACATCAGTGAAGAAGATCAGGCTGCTGAGCTTCGTGCT	SEQ ID NO:112
		21 Y L K S K G A E I S E E N S E G G L H V 61 TATCTGAAATCTAAAGGAGCTGAGATTTCAGAAGAGAACTCGGAAGGTGGACTTCATGTT	
		41 D L A Q I I E A C D V C L K E D D K D V 121 GATTTAGCTCAAATTATTGAAGCCTGTGATGTGTGTCTGAAGGAGGATGATAAAGATGTT	
		61 E S V M N S V V S L L L I L E P D K Q E 181 GAAAGTGTGATGAACAGTGTGGTATCCCTACTCTTGATCCTGGAACCAGACAAGCAAGAA	
		81 A L I E S L C E K L V K F R E G E R P S 241 GCTTTGATTGAAAGCCTATGTGAAAAGCTGGTCAAATTTCGCGAAGGTGAACGCCCGTCT	
		101 L R L Q L L S N L F H G M D K N T P V R 301 CTGAGACTGCAGTTGTTAAGCAACCTTTTCCACGGGATGGATAAGAATACTCCTGTAAGA	
		121 Y T V Y C S L I K V A A S C G A I Q Y I 361 TACACAGTGTATTGCAGCCTTATTAAAGTGGCAGCATCTTGTGGGGCCATCCAGTACATC	
		141 P T E L D Q V R K W I S D W N L T T E K 421 CCAACTGAGCTGGATCAAGTTAGAAAATGGATTTCTGACTGGAATCTCACCACTGAAAAA	
		161 K H T L L R L L Y E A L V D C K K S D A 481 AAGCACACCCTTTTAAGACTACTTTATGAGGCACTTGTGGATTGTAAGAAGAGTGATGCT	
		181 A S K V M V E L L G S Y T E D N A S Q A 541 GCTTCAAAAGTCATGGTGGAATTGCTCGGAAGTTACACAGAGGACAATGCTTCCCAGGCT	
		201 R V D A H R C I V R A L K D P N A F L F 601 CGAGTTGATGCCCACAGGTGTATTGTACGAGCATTGAAAGATCCAAATGCATTTCTTTTT	
		221 D H L L T L K P V K F L E G E L I H D L 661 GACCACCTTCTTACTTTAAAACCAGTCAAGTTTTTGGAAGGCGAGCTTATTCATGATCTT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		241 L T I F V S A K L A S Y V K F Y Q N N K 721 TTAACCATTTTTGTGAGTGCTAAATTGGCATCATATGTCAAGTTTTATCAGAATAATAAA 261 D F I D S L G L L H E Q N M A K M R L L 781 GACTTCATTGATTCACTTGGCCTGTTACATGAACAGAATATGGCAAAAATGAGACTACTT 281 T F M G M A V E N K E I S F D T V Q Q E 841 ACTTTTATGGGAATGGCAGTAGAAAATAAGGAAATTTCTTTTGACACAGTGCAGCAAGAA 301 L Q I G A D D V E A F V I D A V R T K M 901 CTTCAGATTGGAGCTGATGATGTTGAAGCATTTGTTATTGACGCCGTAAGAACTAAAATG 321 V Y C K I D Q T Q R K V V V S H S T H R 961 GTCTACTGCAAAATTGATCAGACCCAGAGAAAAGTAGTTGTCAGTCATAGCACACATCGG 341 T F G K Q Q W Q Q L Y D T L N A W K Q N 1021 ACATTTGGAAAACAGCAGTGGCAACAACTGTATGACACACTTAATGCCTGGAAACAAAAT 361 L N K V K N S L L S L S D T - 1081 CTGAACAAAGTGAAAAACAGCCTTTTGAGTCTTTCTGATACCTGA	
WBC003H01	CGI-54 protein	1 ctggcgtccc ctttccggcc ggtccccatg gaggcgctgg ggaagctgaa gcagttcgat 61 gcctacccca agactttgga ggacttccgg gtcaagacct gcgggggcgc caccgtgacc 121 attgtcagtg gccttctcat gctgctactg ttcctgtccg agctgcagta ttacctcacc 181 acggaggtgc atcctgagct ctacgtggac aagtcgcggg gagataaact gaagatcaac 241 atcgatgtac tttttccgca catgccttgt gcctatctga gtattgatgc catggatgtg 301 gccggagaac agcagctgga tgtggaacac aacctgttca agcaacgact agataaagat 361 ggcatccccg tgagctcaga ggctgagcgg catgagcttg ggaaagtcga ggtgacggtg 421 tttgaccctg actccctgga ccctgatcgc tgtgagagct gctatggtgc tgaggcagaa 481 gatatcaagt gctgtaacac ctgtgaagat gtgcgggagg catatcgccg tagaggctgg 541 gccttcaaga acccagatac tattgagcag tgccggcgag agggcttcag ccagaagatg 601 caggagcaga agaatgaagg ctgccaggtg tatggcttct tggaagtcaa taaggtggcc 661 ggaaacttcc actttgcccc tgggaagagc ttccagcagt cccatgtgca cgtccatgac 721 ttgcagagct ttggccttga caacatcaac atgacccact acatccagca cctgtcattt 781 ggggaggact atccaggcat tgtgaacccc ctggaccaca ccaatgtcac tgcgccccaa 841 gcctccatga tgttccagta ctttgtgaag gtggtgccca ctgtgtacat gaaggtggac 901 ggagaggtac tgaggacaaa tcagttctct gtgaccagac atgagaaggt tgccaatggg 961 ctgttgggcg accaaggcct tcccggagtc ttcgtcctct atgagctctc gcccatgatg 1021 gtgaagctga cggagaagca caggtccttc acccacttcc tgacaggtgt gtgcgccatc 1081 attgggggca tgttcacagt ggctggactc atcgattcgc tcatctacca ctcagcacga 1141 gccatccaga agaaaattga tctagggaag acaacgtagt caccctcggt gcttcctctg 1201 tctcctcttt ctccctggcc tgtggttgtc ccccagcctc tgccaccctc cacctcctcg 1261 gtcagcccca gccccaggtt gataaatcta ttgattgatt gtgatagtaa aaaaa 1 M E A L G K L K Q F D A Y P K T L E D F 1 ATGGAGGCGCTGGGGAAGCTGAAGCAGTTCGATGCCTACCCCAAGACTTTGGAGGACTTC	SEQ ID NO:113 SEQ ID NO:114

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		21 R V K T C G G A T V T I V S G L L M L L 61 CGGGTCAAGACCTGCGGGGGCGCCACCGTGACCATTGTCAGTGGCCTTCTCATGCTGCTA 41 L F L S E L Q Y Y L T T E V H P E L Y V 121 CTGTTCCTGTCCGAGCTGCAGTATTACCTCACCACGGAGGTGCATCCTGAGCTCTACGTG 61 D K S R G D K L K I N I D V L F P H M P 181 GACAAGTCGCGGGGAGATAAACTGAAGATCAACATCGATGTACTTTTTCCGCACATGCCT 81 C A Y L S I D A M D V A G E Q Q L D V E 241 TGTGCCTATCTGAGTATTGATGCCATGGATGTGGCCGGAGAACAGCAGCTGGATGTGGAA 101 H N L F K Q R L D K D G I P V S S E A E 301 CACAACCTGTTCAAGCAACGACTAGATAAAGATGGCATCCCCGTGAGCTCAGAGGCTGAG 121 R H E L G K V E V T V F D P D S L D P D 361 CGGCATGAGCTTGGGAAAGTCGAGGTGACGGTGTTTGACCCTGACTCCCTGGACCCTGAT 141 R C E S C Y G A E A E D I K C C N T C E 421 CGCTGTGAGAGCTGCTATGGTGCTGAGGCAGAAGATATCAAGTGCTGTAACACCTGTGAA 161 D V R E A Y R R R G W A F K N P D T I E 481 GATGTGCGGGAGGCATATCGCCGTAGAGGCTGGGCCTTCAAGAACCCAGATACTATTGAG 181 Q C R R E G F S Q K M Q E Q K N E G C Q 541 CAGTGCCGGCGAGAGGGCTTCAGCCAGAAGATGCAGGAGCAGAAGAATGAAGGCTGCCAG 201 V Y G F L E V N K V A G N F H F A P G K 601 GTGTATGGCTTCTTGGAAGTCAATAAGGTGGCCGGAAACTTCCACTTTGCCCCTGGGAAG 221 S F Q Q S H V H V H D L Q S F G L D N I 661 AGCTTCCAGCAGTCCCATGTGCACGTCCATGACTTGCAGAGCTTTGGCCTTGACAACATC 241 N M T H Y I Q H L S F G E D Y P G I V N 721 AACATGACCCACTACATCCAGCACCTGTCATTTGGGGAGGACTATCCAGGCATTGTGAAC 261 P L D H T N V T A P Q A S M M F Q Y F V 781 CCCCTGGACCACACCAATGTCACTGCGCCCCAAGCCTCCATGATGTTCCAGTACTTTGTG 281 K V V P T V Y M K V D G E V L R T N Q F 841 AAGGTGGTGCCCACTGTGTACATGAAGGTGGACGGAGAGGTACTGAGGACAAATCAGTTC 301 S V T R H E K V A N G L L G D Q G L P G 901 TCTGTGACCAGACATGAGAAGGTTGCCAATGGGCTGTTGGGCGACCAAGGCCTTCCCGGA 321 V F V L Y E L S P M M V K L T E K H R S 961 GTCTTCGTCCTCTATGAGCTCTCGCCCATGATGGTGAAGCTGACGGAGAAGCACAGGTCC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		341 F T H F L T G V C A I I G G M F T V A G 1021 TTCACCCACTTCCTGACAGGTGTGTGCGCCATCATTGGGGGCATGTTCACAGTGGCTGGA 361 L I D S L I Y H S A R A I Q K K I D L G 1081 CTCATCGATTCGCTCATCTACCACTCAGCACGAGCCATCCAGAAGAAAATTGATCTAGGG 381 K T T - 1141 AAGACAACGTAG	
WBC003F02	IBR domain containing 3 (IBRDC3)	1 catgctgcgc cgctacctag cctcggaccc cgactgccgc tggtgcccgg ccccggactg 61 cggttatgct gttattgcct atggctgtgc cagctgcccg aagctaactt gtgagaggga 121 aggttgccag actgagttct gctaccactg caagcagata tggcatccaa atcagacatg 181 cgatatggcc cgtcaacaga gggcccagac tttacgagtt cggaccaaac acacttcagg 241 tctcagttat gggcaagaat ctggaccagc agatgacgtc aagccatgcc cacgatgcag 301 tgcatacatt atcaagatga atgatggaag ctgtaatcac atgacctgtg cagtgtgtgg 361 ctgtgaattc tgttggcttt gtatgaaaga gatctcagac ttgcattacc tcagcccctc 421 tggctgtaca ttctggggca agaagccatg gagccgtaag aagaaaattc tttggcagct 481 gggcacgttg attggtgctc cagtggggat ttctctcatt gctggcattg ccattcctgc 541 catggtcatt ggcattcctg tttatgttgg aaggaagatt cacagcaggt atgagggaag 601 gaaaacctcc aaacacaaga ggaatttggc tatcactgga ggagtgactt tgtcggtcat 661 tgcatcccca gttattgctg cagttagtgt tggtattggt gtccccatta tgctggcata 721 tgtttatggg gttgtgccca tttctctttg tcgtggaggc ggctgtggag ttagcacagc 781 caacggaaaa ggagtgaaaa ttgaatttga tgaagatgat ggtccaatca cagtggcaga 841 tgcctggaga gccctcaaga atcccagcat tggggaaagc agcattgaag gcctgactag 901 tgtattgagc actagtggaa gccctacaga tggacttagt gttatgcaag gtccttacag 961 cgaaacggcc agctttgcag ccctctcagg gggcacgctg agtggcggca ttctctccag 1021 tggcaaggga aaatatagca ggttagaagt tcaagccgat gtccaaaagg aaattttccc 1081 caaagacaca gccagtcttg gtgcaattag tgacaacgca agcactcgtg ctatggccgg 1141 ttccataatc agttcctaca acccacagga cagagaatgc aacaatatgg aaatccaagt 1201 ggacattgaa gccaaaccaa gccactatca gctggtgagt ggaagcagca cggaggactc 1261 gctccatgtt catgctcaga tggcagagaa tgaagaagaa ggtagtggtg gcggaggcag 1321 tgaagaggat ccccccctgca gacaccaaag ctgtgaacag aaagactgcc tggccagcaa 1381 accttgggac atcagcctgg cccagcctga aagcatccgc agtgacctag agagttctga 1441 tgcacagtca gacgatgtgc cagacatcac ctcagatgag tgtggctccc cccgctccca 1501 tactgcagcc tgcccctcga cccccagagc ccaaggtgca ccgagcccaa gtgcccatat 1561 gaacctctct gccctagccg agggacaaac tgtcttgaag ccagaaggtg gagaagccag 1621 agtatgaagt ggaatgaatg ctcctgttct gagaagcaca cttgtaactg catcttttgg 1681 aatttttttt ttttttttt ccaaggggta gagatttatg tattttattt cacagattct 1741 ctggtcacag gtttttgccc agggaaattc tgagaaattc acaatttctt accagataaa 1801 acatgaaaag tttgccgtta gttcccctcc cctcccctcc ctcttttag ttttaattta 1861 ttggttaaac tgatggcagc aatccatgag gtgtgtcaaa gagtgtacat atgtatgtgt 1921 gtatattgaa tgctaaacat attactgaaa gacacatttt aataaagatt tctgtcataa 1981 ttcaactt	SEQ ID NO:115
		1 M L R R Y L A S D P D C R W C P A P D C	SEQ ID NO:116

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1 ATGCTGCGCCGCTACCTAGCCTCGGACCCCGACTGCCGCTGGTGCCCGGCCCCGGACTGC	
		21 G Y A V I A Y G G C A S C P K L T C E R E	
		61 GGTTATGCTGTTATTGCCTATGGCTGTGCCAGCCTGCCCGAAGCTAACTTGTGAGAGGAA	
		41 G C Q T E F C Y H C K Q I W H P N Q T C	
		121 GGTTGCCAGACTGAGTTCTGCTACCACTGCAAGCAGATATGGCATCCAAATCAGACATGC	
		61 D M A R Q Q R A A Q T L R V R T K H T S G	
		181 GATATGGCCCGTCAACAGAGGGCCCAGACTTTACGAGTTCGGACCAAACACACTTCAGGT	
		81 L S Y G Q E S G P A D D V K P C P R C S	
		241 CTCAGTTATGGGCAAGAATCTGGACCAGCAGATGACGTCAAGCCATGCCCACGATGCAGT	
		101 A Y I I K M N D G S C N H M T C A V C G	
		301 GCATACATTATCAAGATGAATGATGGAAGCTGTAATCACATGACCTGTGCAGTGTGTGGC	
		121 C E F C W L C M K E I S D L H Y L S P S	
		361 TGTGAATTCTGTTGGCTTTGTATGAAAGATCTCAGACTTGCATTACCTCAGCCCCTCT	
		141 G C T F W G K K P W S R K K K I L W Q L	
		421 GGCTGTACATTCTGGGGCAAGAAGCCATGGAGCCGTAAGAAGAAAATTCTTTGGCAGCTG	
		161 G T L I G A P V G I S L I A G I A I P A	
		481 GGCACGTTGATTGGTGCTCCAGTGGGGATTTCTCTCATTGCTGGCATTGCCATTCCTGCC	
		181 M V I G I P V Y V G R K I H S R Y E G R	
		541 ATGGTCATTGGCATTCCTCTGTTTATGTTGGAAGGAAGATTCACAGCAGGTATGAGGGAAGG	
		201 K T S K H K R N L A I T G G V T L S V I	
		601 AAAACCTCCAAACACAAGAGGAATTTGCCTATCACTGGAGGAGTGACTTTGTCGGTCATT	
		221 A S P V I A A V S V G I G V P I M L A Y	
		661 GCATCCCCAGTTATTGCTGCAGTTAGTGTTGGTATTGGTGTCCCCATTATGCTGGCATAT	
		241 V Y G V V P I S L C R G G G C G V S T A	
		721 GTTTATGGGGTTGTGCCCATTTCTCTTTGTCGTGGAGGCGGCTGTGGAGTTAGCACAGCC	
		261 N G K G V K I E F D E D D G P I T V A D	
		781 AACGGAAAAGGAGTGAAAATTGAATTTGATGAAGATGATGGTCCAATCACAGTGGCAGAT	
		281 A W R A L K N P S I G E S S I E G L T S	
		841 GCCTGGAGAGCCCTCAAGAATCCCAGCATTGGGGAAAGCAGCATTGAAGGCCTGACTAGT	
		301 V L S T S G S P T D G L S V M Q G P Y S	
		901 GTATTGAGCACTAGTGGAAGCCCTACAGATGGACTTAGTGTTATGCAAGGTCCTTACAGC	
		321 E T A S F A A L S G G T L S G G I L S S	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		961 GAAACGGCCAGCTTTGCAGCCCTCTCAGGGGGCACGCTGAGTGGCGGCATTCTCTCCAGT 341 G K G K Y S R L E V Q A D V Q K E I F P 1021 GGCAAGGGAAAATATAGCAGGTTAGAAGTTCAAGCCGATGTCCAAAAGGAAATTTTCCCC 361 K D T A S L G A I S D N A S T R A M A G 1081 AAAGACACAGCCAGTCTTGGTGCAATTAGTGACAACGCAAGCACTCGTGCTATGGCCGGT 381 S I I S S Y N P Q D R E C N N M E I Q V 1141 TCCATAATCAGTTCCTACAACCCACAGGACAGAGAATGCAACAATATGGAAATCCAAGTG 401 D I E A K P S H Y Q L V S G S S T E D S 1201 GACATTGAAGCCAAACCAAGCCACTATCAGCTGGTGAGTGGAAGCAGCACGGAGGACTCG 421 L H V H A Q M A E N E E E G S G G G G S 1261 CTCCATGTTCATGCTCAGATGGCAGAGAATGAAGAAGAAGGTAGTGGTGGCGGAGGCAGT 441 E E D P P C R H Q S C E Q K D C L A S K 1321 GAAGAGGATCCCCCCTGCAGACACCAAAGCTGTGAACAGAAAGACTGCCTGGCCAGCAAA 461 P W D I S L A Q P E S I R S D L E S S D 1381 CCTTGGGACATCAGCCTGGCCCAGCCTGAAAGCATCCGCAGTGACCTAGAGAGTTCTGAT 481 A Q S D D V P D I T S D E C G S P R S H 1441 GCACAGTCAGACGATGTGCCAGACATCACCTCAGATGAGTGTGGCTCCCCCCGCTCCCAT 501 T A A C P S T P R A Q G A P S P S A H M 1501 ACTGCAGCCTGCCCCTCGACCCCCAGAGCCCAAGGTGCACCGAGCCCAAGTGCCCATATG 521 N L S A L A E G Q T V L K P E G G E A R 1561 AACCTCTCTGCCCTAGCCGAGGGACAAACTGTCTTGAAGCCAGAAGGTGGAGAAGCCAGA 541 V - 1621 GTATGA	
WBC003D11	No homology	1 GGACCTTTGGCACAAACACTGAAAAGAGTTATGTTGATAATCAGAAGTGATTGATGGAGC 61 AGAATTCCAGCGTTTCATGGAGAGTTGAAGTACATGATGACAAAACCCTTGGGAAAACCT 121 TCTAATTTCTTGGGACATTTCAAGGAAGCAACATCCCCCTTTCTTCCAGGAACTTTTTTG 181 TGACTTGACTAGGACTCGCACTGCTCCCAAAGTTATCGCCATCCCACCTTGCTCTCCGTC 241 TCCCATAAAATCTTGAGGGCCACGGAGAGAAGGAGGCGAATTTTAAATGTAGATCTCCTC 301 CCTTCCACAGCCAGTCTCAAACACACCTACTCAAGGTGTGGTCCATGGACCAGAAGCATG 361 AGCATCATTTTGTTAGAAAAGCAGCATCAAAGGTACCACCGCAGATCTTCGGAACCAGAA 421 CCTGCATTTTAACAAGATCCCCAGGGAATTTGTGTTGTACACAGGAGTGAATGTTCTGGC 481 ATATTCTAGAGTATTCTTTTGTTTTCCATGCTGACAGAAGAGCTTGTCTTTAAAACTAGG 541 CAGGAAAACATATCCTCGACTTTGGGACTTTGCATCTGCCATTCTCTCTTCCTAGGACAA 601 CTTTCCTCANAATCGGACTAATTTCTACCCTCTCTTCGAGTCTCAGCATAGTCATCAATT	SEQ ID NO:117

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		661 TCACCAGGAAGCATTCTCTGAATCTCTTGAAGTAGGATTAGGTGTCACCTCTGTGTGTCC 721 TCTAAGGCTTCATGATTTCTAGCCTTGTGTGATCATTTCTTCTCTTCTTGAGTGTCTCCA 781 ACTGGACTGTGAGCTCCATAATTACAGGGAATGGCATTCAGTTGATTCTCCATAAATAAG 841 TTGAATGAATGAATGAATGATTACTTTCCATTTTGAAGATGAAGAATTTGAGGC	
		1 ACCATTCCTGCTCTCACTATGGCTTGGCCTTGAGACTTGCTTTGGCTAATGGAATGTCAG 61 CAAGTGTGACTCAGACAGAGTGTGCATTCCTTCTTGCCCGTTACACGATAAGTCTCGCTT 121 GTTCTTGCACCCCTGCCTCCGCCATGAGAATGTGCCCAGGCTGAACTGCTGGAGGGATGT 181 GAAAAATGTATGGAAGACAGTTAAGTCATTCCATTATACCAGCTGAGGTTGTCCTTAATC 241 AGCCATCGGACCAACTTGTAGCTGACTACAGTCACATCCATGAGCCCAGTCAAGATCAGC 301 AGACCTGCCCGGGCAACCCAGACTCAGGAGCCACAATCAAGTACCATTATTTTAGGGCAC 361 AGAGTTTCAGGAGTGGTTTGTTAACGAAGTATTCTTGGTGGAAGTTGCTAACTGATTCAG 421 CAACCAATGGATTGTCAATGTTTTGCATTTGACTGCAACAATTTGGAACATACAAAGAGG 481 GTGATTCGCATCTTCATTTCCTCTTAGCTGTCAGGATCTGTAAATCTAAAACGCTTTGAA 541 TAAAGTTCTTTCTGACAGAAAAAAAAAAA	SEQ ID NO:118
WBC001H09	Activated RNA polymerase II transcription cofactor 4 variant protein (incomplete)	1 gactgctaga gccgagcgaa gcgatgccta aatcaaagga acttgtttct tcaagctctt 61 ctggcagtga ttctgacagt gaggttgaca aaaagttaaa gaggaaaaag caagttgctc 121 cagaaaaacc tgtaaagaaa caaaagacag gtgagacttc gagagccctg tcatcttcta 181 aacagagcag cagcagcaga gatgataaca tgtttcagat tgggaaaatg aggtacgtta 241 gtgttcgcga ttttaaaggc aaagtgctaa ttgatattag agaatattgg atggatcctg 301 aaggtgaaat gaaaccagga agaaaaggta tttctttaaa tccagaacaa tggagccagc 361 tgaaggaaca gatttctgac attgatgatg cagtaagaaa actgtaaaat tcgagccata 421 taaataaaac ctgtactgtt ctagttgttt taatctgtct ttttacattg gcttttgttt 481 tctaaatgtt ctccaagcta ttgtatgttt ggattgcaga agaatttgta agatgaatac 541 tttttttaa tgtgcattat taaaaatatt gagtgaagct aattgtcaac tttattaagg 601 attactttgt ctgcccacca cctagtgtaa aataaaatca agtaatacaa tcttaactgt 661 tgtggccttt tttgatcata agagttggta ctgtttaagg ccaaaagtaa cagtttttat 721 agatctttta gtttcaactc agcttttaca ataaaaagga tttgtattgc attgagttta 781 taaacttttg gtttgtgaac ttcatatttg atcttttctc ttccaatcaa atgtctaggc 841 ttgtttgact tccaccccca atggtttttc actcttttta tttacttcat tttcctttaa 901 taacttaatc tcttcatgtt cagtttttac ttcactcttt attcttttct ttgattatgg 961 tatgcttatt tggaaagtca gtgaaactgt caaaatgtta tctcaataag atacttatat 1021 gagaactaca atcaccgaat ctactgtatt caatattagc agatctaatt tgataaacaa 1081 catggcttgt gtgaaaact	SEQ ID NO:119
		< 1 L L E P S E A M P K S K E L V S S S S S 3 CTGCTAGAGCCGAGCGAAGCGATGCCTAAATCAAAGGAACTTGTTTCTTCAAGCTCTTCT 21 G S D S D S E V D K K L K R K K Q V A P 63 GGCAGTGATTCTGACAGTGAGGTTGACAAAAAGTTAAAGAGGAAAAAGCAAGTTGCTCCA 41 E K P V K K Q K T G E T S R A L S S S K 123 GAAAAACCTGTAAAGAAACAAAAGACAGGTGAGACTTCGAGAGCCCTGTCATCTTCTAAA 61 Q S S S S S R D D N M F Q I G K M R Y V S	SEQ ID NO:120

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		183 CAGAGCAGCAGCAGCAGATGATAACATGTTCAGATTGGGAAAATGAGGTAGTTAGT	
		81 V R D D F K K G K V L I I D I R R E Y Y W M D P E	
		243 GTTCGCGATTTTAAAGGCAAAGTGCTAATTGATATTAGAGAATATTGGATGGATCCTGAA	
		101 G E M K P G G R K K G G I S S L N P P E Q W S S Q L	
		303 GGTGAAATGAAACCAGGAAGAAAAGGTATTTCTTTAAATCCAGAACAATGGAGCCAGCTG	
		121 K E Q I S D D I D D A V R R K L -	
		363 AAGGAACAGATTTCTGACATTGATGATGCAGTAAGAAAACTGTAA	
WBC001F11	Retinoblastoma-like 2 (p130)		SEQ ID NO:121
		1 AGCGGGCAGCGCGCGGTCGGGCGGCGACGGGCGGCGCTTCGCCGTTTGAATGGCTGCG	
		61 GGCCCGGCCCTCACCTCACCTGAGGTCCGGCCGCCCAGGGGTGCGCTATGCCGTCGGGA	
		121 GGTGACCAGTCGCCACCGCCCCCGCCTCCCCCTCCGGCGGCGGCAGCCTCGGATGAGGAG	
		181 GAGGAGGACGACGGCGAGGCGGAAGACGCCGCCGCCGCCTGCCGAGTCGCCCACCCCTCAG	
		241 ATCCAGCAGCGGTTCGACGAGCTGTGCAGCCGCCTCAACATGGACGAGGCGGCGCGGGCC	
		301 GAGGCCTGGGACAGCTACCGCAGCATGAGCGAAAGCTACACGCTGGAGGGAAATGATCTT	
		361 CATTGGTTAGCATGTGCCTTATATGTGGCTTGCAGAAAATCTGTTCCAACTGTAAGCAAA	
		421 GGGACAGTGGAAGGAAACTATGTATCTTTAACTAGAATCCTGAAATGTTCAGAGCAGAGC	
		481 TTAATCGAATTTTTTAATAAGATGAAGAAGTGGGAAGACATGGCAAATCTACCCCCACAT	
		541 TTCAGAGAACGTACTGAGAGATTAGAAAGAACTTCACTGTTTCTGCTGTAATTTTTAAG	
		601 AAATATGAACCCATTTTTCAGGACATCTTTAAATACCCTCAAGAGGAGCAACCTCGTCAG	
		661 CAGCGAGGAAGGAAACAGCGGCGACAGCCCTGTACTGTGTCTGAAATTTTCCATTTTTGT	
		721 TGGGTGCTTTTTATATATGCAAAAGGTAATTTCCCCATGATTAGTGATGATTTGGTCAAT	
		781 TCTTATCACCTGCTGCTGTGTGCTTTGGACTTAGTTTATGGAAATGCACTTCAGTGTTCT	
		841 AATCGTAAAGAACTTGTGTGAACCCTAATTTTTAAAGGCTTATCTCAAGATTTTCATGCTAAA	
		901 GATTCTAAACCTTCCTCTGACCCCCCTTGTATCATTGAGAAACTGTGTTCCTTACATGAT	
		961 GGCCTAGTTTTGGAAGCAAAGGGGATAAAGGAACATTTCTGGAAACCCTATATTAGGAAA	
		1021 CTTTATGAAAAAAAGCTCCTTAAGGGAAAAGAAGAAAATCTCACTGGGTTTCTAGAACCT	
		1081 GGGAACTTTGGAGAGAGTTTTAAAGCCATCAATAAGGCCTATGAGGAGATGCTGAGGAGGAAATTGGGACT	
		1141 GTTGGGAATTTAGATGAGCGGATATTTCTTGGAGAGGATGCTGAGGAGGAAATTGGGACT	
		1201 CTCTCAAGGTGTCTGAACGCTGGTTCAGGAACAGAGACTGCTGAAAGGGTGCAGATGAAA	
		1261 AACATCTTACAGCAGCATTTTGACAAGTCCAAAGCACTTAGAATCTCCACACCACTAACT	
		1321 GGTGTTAGGTACATTAAGGAGAATAGCCCTTGTGTGACTCCAGTTTCTACAGCTACGCAT	
		1381 AGCTTGAGTCGTCTTCACACCATGCTGACAGGCCTCAGGAATGCACCAGTGAGAAACTG	
		1441 GAACAGATTCTCAGGACATGTTCCAGAGATCCAACCCAGGCTATTGCTAACAGACTGAAA	
		1501 GAAATGTTTGAAATATATTCTCAGCATTTCCAGCCAGACGAGGATTTCAGTAATTGTGCT	
		1561 AAAGAAATTGCCAGCAAACATTTCGTTTTGCGGAGATGCTTTACTATAAAGTATTAGAA	
		1621 TCTGTTATTGAGCAGGAACAAAAAAGACTAGGAGACATGGATTTATCTGGTATTCTGGAA	
		1681 CAAGATGCGTTCCACAGATCTCTCTTGGCCTGCTGCCTTGAGGTCGTCACTTTTCTTTAT	
		1741 AAGCCTCCTGGGAATTTCCATTATTACTGAAATATTTGATGTGCCTCTTTATCATTTT	
		1801 TATAAGGTGATAGAAGTATTCATTAGAGCAGAAGATGGCCTTTGTAGAGAGGTGGTAAAA	
		1861 CACCTTAATCAGATTGAAGAACAGATCTTAGATCATTTGGCATGGAAACCAGAGTCTCCA	
		1921 CTCTGGGAAAAAATTAGAGACAATGAAAACAGAGTTCCTACATGTGAAGAGGTCATGCCA	
		1981 CCTCAGAACCTGGAAAGGGCAGATGAAATTTGCATTGCTGGCGTCCCCCTTTGACTCCCAGA	
		2041 AGGGTGACTGAAGTTCGTGCTGATACTGGAGGACTTGGAAGGAGCATAACATCTCCAACC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2101 ACATTATACGATAGGTACAGCTCCCCACCAGCCAGCACTACCAGAAGGCGGCTATTTGTT	
		2161 GAGAATGATAGCCCCCTCTGATGGAGGGACGCCTGGGCGCATGCCCCCACAGCCCCTAGTC	
		2221 AATGCTGTCCCTGTGCAGAATGTATCTGGGGAGACTGTTTCTGTCACACCAGTTCCTGGA	
		2281 CAGACTTTGGTCACCATGGCAACCGCCACTGTCACAGCCAACACAATGGCCAAACGGTAACC	
		2341 ATTCCTGTGCAAGGTATTGCCAATGAAAATGGAGGGATAACATTCTTCCCTGTCCAAGTC	
		2401 AATGTTGGGGGCAGGCACAAGCTGTGACAGGCTCCATCCAGCCCCTCAGTGCTCAGGCC	
		2461 CTGGCTGGAAGTCTGAGCTCTCAACAGGTGACAGGAACAACTTTGCAAGTCCCTGGTCAA	
		2521 GTGGCCATTCAACAGATTTCCCCAGGTGGCCAACAGCAGGAAGCCAGGCCAGTCTGTAACC	
		2581 AGCAGTAGTAATAGACCCAGCAGAAGACCACGCTCTTTATCGCTTTCTTTAGAAAGGTATAC	
		2641 CATTTAGCAGCTGTCCGCCTTCGGGATCTCTGTGCCAAACTAGATATTTCAGATGAATTG	
		2701 AGGAAAAAAATCTGGACCTGCTTTGAATTCTCCATAATTCAGTGTCCTGAACTTATATGATG	
		2761 GACAGACATCTGGACCAGTTATTAATGTGTGCCATTTATGTGATGGCAAAGGTCACAAAA	
		2821 GAAGATAAGTCCTTCCAGAACATTATGCGTTGTTATAGGACTCAGCGCAGGCCCGGAGC	
		2881 CAGGTGTATAGAAGTGTTTTGATAAAAGGAAAAAGAAAAAGAAGAAATTCTGGCAGCAGT	
		2941 GATAGCAGAAGCCATCAGAATTCTCCAACAGAACTAAACAAAGATAGAACCAGTAGAGAC	
		3001 TCCAGTCCAGTTATGAGGTCAAGCAGCACCTTGCCAGTTCCACAGCCAGCAGTCCTCCT	
		3061 CCCACACCTACTCGCCTCACAGGTGCCAACAGTGACATGGAAGAAGAGGAGAGGGCAGAC	
		3121 CTCATTCAGTTCTACAACAACATCTACATCAAACAGATTAAGACATTTGCCATGAAGTAC	
		3181 TCACAGGCAAATATGGATGCTCCTCCGCTCTCTCCCTATCCATTTGTAAGAACAGCCTCT	
		3241 CCTCGCCGAATACAGTTGTCTCAAAATCATCCTGTCTACATTTCCCCACATAAAAATGAA	
		3301 ACAATGCTTCTCCTCGTGAAAAGATTTTCTACTACTTCAGCAACAGTCCTTCAAAGAGA	
		3361 CTAAGAGAAATTAACAGTATGATCCGGACAGGAGAAACTCCAACCAAAAAGCGAGGGATT	
		3421 CTTTTGGAACACGGAAGTGAATCACCTGCAAAAAGAATTTGCCCAGAAAATCATTCTGCC	
		3481 TTACTGCGCCGTCTACAAGATGTAGCTAATGACCGAGGTTCCCACTGAGGTTAGTCCATG	
		3541 GTATTGAAACTGTCTTCTCACAAACTCTGTTTAGCAGCATCATTTAATGCATGCTCGATT	
		3601 ATGGGGCTCTTTCCCTTAATCCTTCCAGTATCCATAGGATATTCTGACTCATCCCAACTG	
		3661 CCTTTTTCCTACCATTCAGTGCTTGCCCTCAAGGCTGCTTAGAATCCAAACTTGGATTT	
		3721 TTGACTCTGGCAAAGCTTTTAGAAATACTGCAAGAAAATGATGTCTACCCAAACGTGAGC	
		3781 ATAGGAGGCTTCTGTTGACGTACTCCAACAGAAGAACTGTTTTCAAGTTCATTCCTACCC	
		3841 GTTTTGTGGTCACCTTTGGCCCTCACAAAAAGTAAAACAAAAACTAGGTATTTTGTCCTA	
		3901 AAACACCTGGTAGGAGTGTGTGATTTTTTGCATTCCTGCACAAGGAGAGCACACCCAGGT	
		3961 TTGGAGGTCCTAGGTCATAGCCCTCGTCTCCCGTTCCCTTTGTGCACATCTTCCCTCTC	
		4021 CCCATTCGGTGTGGTGCAGTGTGAAAAGTCCTTGATTGTTCGGGTGTGCAATGTCTGAGT	
		4081 GAACCTGTATAAGTGGAGGCACTTTAGGCTGTAAAATGCATGATTTTGTATACCCAGATT	
		4141 TTGCTGTATATTTGCGATGGCACTTTCTACAATGTGAACTTTATTAAGTATATAAACTTCT	
		4201 AGGCTAAACATTCAATATCTTCTTTGATGCTTTTGTACTTTTTTAAAATTGTTAAAGCCC	
		4261 CAGTAGCCACCTTTTGGGCATATTTGAAATTCTCCAGTTTTTGATTATTAAGAGGGATCA	
		4321 GCTGGCTAAGTAAAGATTTTAAATCAAGTTGAATTAAGGGGATTAATAGGAAAATTATGA	
		4381 CCTCTTCCTTTAGGAGGCAGTTATCCNAAAGACATGTCTATTAAGGTGATATATTTTTAAA	
		4441 ATATCTTTGAGTGTGTTCCTGGCAGTTTAAGAAAATAGTTGGAGAATTTAGGTTTTTATT	
		4501 AGTACACAGTACCATTTATACAAATTAGAAAATGTTATTTAACAGCTATTGAATTATCTA	
		4561 TATACACCTTTATTAATCGCTATTGTTCCAGCAGTTTTAACGTTGAACGAATAATCTTAT	
		4621 TAGGGAGAAAATTCAATTGTAAATTGAATCAGTATAAACAAGTTACTAGGTAACTTCAC	
		4681 ATTGCTCTGAAAGAAATATGGAACTTACACTGTTCAATTAGAATAGTGTTCTGCAAAAAT	
		4741 ATTTATAAAACCTCTCAGATACTGCTACTGTAATTTTATATGAAAATAAGTGTATTTTTC	
		4801 AATAAAGCATTTATAAATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1 M P S G G D Q S P P P P P P P A A A A	SEQ ID NO:122
		1 ATGCCGTCGGGAGGTGACCAGTCGCCACCGCCCCCGCCTCCCCCTCCGGCGGCGGCAGCC	
		21 S D E E E E D D G E E A E D A A P P A E S	
		61 TCGGATGAGGAGGAGGAGGACGACGGCGAGGCGGAAGACGCCGCGCCGCCTGCCGAGTCG	
		41 P T P Q I Q Q R F D E L C S R L N M D E	
		121 CCCACCCCTCAGATCCAGCAGCGGTTCGACGAGCTGTGCAGCCGCCTCAACATGGACGAG	
		61 A A R A E A W D S Y R S M S E S Y T L E	
		181 GCGGCGCGGCCGAGGCCTGGGACAGCTACCGCAGCATGAGCGAAAGCTACACGCTGGAG	
		81 G N D L H W L A C A L Y V A C R K S V P	
		241 GGAAATGATCTTCATTGGTTAGCATGTGCCTTATATGTGGCTTGCAGAAAATCTGTTCCA	
		101 T V S K G T V E G N Y V S L T R I L K C	
		301 ACTGTAAGCAAAGGGACAGTGGAAGGAAACTATGTATCTTTAACTAGAATCCTGAAATGT	
		121 S E Q S L I E F F N K M K K W E D M A N	
		361 TCAGAGCAGAGCTTAATCGAATTTTTTAATAAGATGAAGAAGTGGCAAGACATGGCAAAT	
		141 L P P H F R E R T E E R L E R N F T V S A	
		421 CTACCCCCACATTTCAGAGAACGTACTGAGAGAATTAGAAAGAAACTTCACTGTTTCTGCT	
		161 V I F K K Y E P I F Q D I F K Y P Q E E	
		481 GTAATTTTTAAGAAATATGAACCCATTTTTCAGGACATCTTTAAATACCCTCAAGAGGAG	
		181 Q P R Q Q R G R K Q R R Q P C T V S E I	
		541 CAACCTCGTCAGCAGCGAGGAAGCAAACAGCGGCGACAGCCCTGTACTGTGTCTGAAATT	
		201 F H F C W V L F I Y A K G N F P M I S D	
		601 TTCCATTTTTTGTTGGGTGCTTTTTATATATGCAAAAGGTAATTTCCCCATGATTAGTGAT	
		221 D L V N S Y H L L C A L D L V Y G N A	
		661 GATTTGGTCAATTCTTATCACCTGCTGTGTGCTTTGGACTTAGTTTATGGAAATGCA	
		241 L Q C S N R K E L V N P N F K G L S E D	
		721 CTTCAGTGTTCTAATCGTAAAGAACTTGTGAACCCTAATTTTAAAGGCTTATCTGAAGAT	
		261 F H A K D S K P S S D P P C I I E K L C	
		781 TTTCATGCTAAAGATTCTAAACCTTCCTCTGACCCCCCTTGTATCATTGAGAAACTGTGT	
		281 S L H D G L V L E A K G I K E H F W K P	
		841 TCCTTACATGATGGCCTAGTTTTGGAAGCAAAGGGATAAAGGAACATTTCTCGAAACCC	
		301 Y I R K L Y E K K L L K G K E E N L T G	
		901 TATATTAGCAAACTTTATGAAAAAAAGCTCCTTAGGGAAAAGAAGAAAATCTCACTGGG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		321 F L E P G N F G E S F K A I N K A Y E E 961 TTTCTAGAACCTGGGAACTTTGGAGAGAGTTTTAAAGCCATCAATAAGGCCTATGAGGAG 341 Y V L S V G N L D E R I F L G E D A E E 1021 TATGTTTTATCTGTTGGGAATTTAGATGAGCGGATATTTCTTGGAGAGGATGCTGAGGAG 361 E I G T L S R C L N A G S G T E T A E R 1081 GAAATTGGGACTCTCTCAAGGTGTCTGAACGCTGGTTCAGGAACAGAGACTGCTGAAAGG 381 V Q M K N I L Q Q H F D K S K A L R I S 1141 GTGCAGATGAAAAACATCTTACAGCAGCATTTTGACAAGTCCAAAGCACTTAGAATCTCC 401 T P L T G V R Y I K E N S P C V T P V S 1201 ACACCACTAACTGGTGTTAGGTACATTAAGGAGAATAGCCCTTGTGTGACTCCAGTTTCT 421 T A T H S L S R L H T M L T G L R N A P 1261 ACAGCTACGCATAGCTTGAGTCGTCTTCACACCATGCTGACAGGCCTCAGGAATGCACCA 441 S E K L E Q I L R T C S R D P T Q A I A 1321 AGTGAGAAACTGGAACAGATTCTCAGGACATGTTCCAGAGATCCAACCCAGGCTATTGCT 461 N R L K E M F E I Y S Q H F Q P D E D F 1381 AACAGACTGAAAGAAATGTTTGAAATATATTCTCAGCATTTCCAGCCAGACGAGGATTTC 481 S N C A K E I A S K H F R F A E M L Y Y 1441 AGTAATTGTGCTAAAGAAATTGCCAGCAAACATTTTCGTTTTGCGGAGATGCTTTACTAT 501 K V L E S V I E Q E Q K R L G D M D L S 1501 AAAGTATTAGAATCTGTTATTGAGCAGGAACAAAAAAGACTAGGAGACATGGATTTATCT 521 G I L E Q D A F H R S L L A C C L E V V 1561 GGTATTCTGGAACAAGATGCGTTCCACAGATCTCTCTTGGCCTGCTGCCTTGAGGTCGTC 541 T F S Y K P P G N F P F I T E I F D V P 1621 ACTTTTTCTTATAAGCCTCCTGGGAATTTTCCATTTATTACTGAAATATTTGATGTGCCT 561 L Y H F Y K V I E V F I R A E D G L C R 1681 CTTTATCATTTTTATAAGGTGATAGAAGTATTCATTAGAGCAGAAGATGGCCTTTGTAGA 581 E V V K H L N Q I E E Q I L D H L A W K 1741 GAGGTGGTAAAACACCTTAATCAGATTGAAGAACAGATCTTAGATCATTTGGCATGGAAA 601 P E S P L W E K I R D N E N R V P T C E 1801 CCAGAGTCTCCACTCTGGGAAAAAATTAGAGACAATGAAAACAGAGTTCCTACATGTGAA 621 E V M P P Q N L E R A D E I C I A G S P 1861 GAGGTCATGCCACCTCAGAACCTGGAAAGGGCAGATGAAATTTGCATTGCTGGCTCCCCT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		641 L T P R R V T E V R R A D T G G L G R S I 1921 TTGACTCCCAGAAGGGTGACTGAAGTTCGTCGTGATACTGGAGGACTTGGAAGGAGCATA	
		661 T S P T T L Y D R Y S S P P A S T T R R 1981 ACATCTCCAACCACATTATACGATAGGTACAGCTCCCCACCAGCCAGCACTACCAGAAGG	
		681 R L F V E N D S P S D G G T P G R M P P 2041 CGGCTATTTGTTGAGAATGATAGCCCCTCTGATGGAGGGACGCCTGGGCGCATGCCCCCA	
		701 Q P L V N A V P V Q N V S G E T V S V T 2101 CAGCCCCTAGTCAATGCTGTCCCTGTGCAGAATGTATCTGGGGAGACTCTTTCTGTCACA	
		721 P V P G Q T L V T M A T A T V T A N N G 2161 CCAGTTCCTGGACAGACTTTGGTCACCATGGCAACCGCCACTGTCACAGCCAACAATGGG	
		741 Q T V T I P V Q G I A N E N G G I T F F 2221 CAAACGGTAACCATTCCTGTGCAAGGTATTGCCAATGAAAATGGAGGGATAACATTCTTC	
		761 P V Q V N V G G Q A Q A V T G S I Q P L 2281 CCTGTCCAAGTCAATGTTGGGGGGCAGGCACAAGCTGTGACAGGCTCCATCCAGCCCCTC	
		781 S A Q A L A G S L S S Q Q V T G T T L Q 2341 AGTGCTCAGGCCCTGGCTGGAAGTCTGAGCTCTCAACAGGTGACAGGAACAACTTTGCAA	
		801 V P G Q V A I Q Q I S P G G Q Q Q K Q G 2401 GTCCCTGGTCAAGTGGCCATTCAACAGATTTCCCCAGGTGGCCAACAGCAGAAGCAAGGC	
		821 Q S V T S S S N R P R K T S S L S L F F 2461 CAGTCTGTAACCAGCAGTAGTAATAGACCCAGGAAGACCAGCTCTTTATCGCTTTTCTTT	
		841 R K V Y H L A A V R L R D L C A K L D I 2521 AGAAAGGTATACCATTTAGCAGCTGTCCGCCTTCGGGATCTCTGTGCCAAACTAGATATT	
		861 S D E L R K K I W T C F E F S I I Q C P 2581 TCAGATGAATTGAGGAAAAAAATCTGGACCTGCTTTGAATTCTCCATAATTCAGTGTCCT	
		881 E L M M D R H L D Q L L M C A I Y V M A 2641 GAACTTATGATGGACAGACATCTGGACCAGTTATTAATGTGTGCCATTTATGTGATGGCA	
		901 K V T K E D K S F Q N I M R C Y R T Q P 2701 AAGGTCACAAAAGAAGATAAGTCCTTCCAGAACATTATGCGTTGTTATAGGACTCAGCCG	
		921 Q A R S Q V Y R S V L I K G K R K R R N 2761 CAGGCCCGGAGCCAGGTGTATAGAAGTGTTTTGATAAAAGGAAAAAGAAAAAGAAGAAAT	
		941 S G S S D S R S H Q N S P T E L N K D R 2821 TCTGGCAGCAGTGATAGCAGAAGCCATCAGAATTCTCCAACAGAACTAAACAAAGATAGA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		961 T S R D S S P V M R S S S T L P V P Q P 2881 ACCAGTAGAGACTCCAGTCCAGTTATGAGGTCAAGCAGCACCTTGCCAGTTCCACAGCCC 981 S S A P P T P T R L T G A N S D M E E E 2941 AGCAGTGCTCCTCCCACACCTACTCGCCTCACAGGTGCCAACAGTGACATGGAAGAAGAG 1001 E R G D L I Q F Y N N I Y I K Q I K T F 3001 GAGAGGGGAGACCTCATTCAGTTCTACAACAACATCTACATCAAACAGATTAAGACATTT 1021 A M K Y S Q A N M D A P P L S P Y P F V 3061 GCCATGAAGTACTCACAGGCAAATATGGATGCTCCCTCCGCTCTCTCCCTATCCATTTGTA 1041 R T G S P R R I Q L S Q N H P V Y I S P 3121 AGAACAGGCTCTCCTCGCCGAATACAGTTGTCTCAAAATCATCCTGTCTACATTTCCCA 1061 H K N E T M L S P R E K I F Y Y F S N S 3181 CATAAAAATGAAACAATGCTTTCTCCTCGTGAAAAGATTTTCTACTACTTCAGCAACAGT 1081 P S K R L R E I N S M I R T G E T P T K 3241 CCTTCAAAGACTAAGAGAATTAACAGTATGATCCGGACAGGAGAAACTCCAACCAAA 1101 K R G I L L E D G S E S P A K R I C P E 3301 AAGCGAGGGATTCTTTTGGAAGACGGAAGTGAATCACCTGCAAAAAGAATTTGCCCAGAA 1121 N H S A L L R R L Q D V A N D R G S H - 3361 AATCATTCTGCCTTACTGCGCCGTCTACAAGATGTAGCTAATGACCGAGGTTCCCACTGA	
WBC001F08	RAB10, member RAS oncogene family (RAB10),	1 gggggcgtg agagggcacg gggaaaaggt ggctctggcc ggggtggctc ggtttcctgg 61 ggctatgtaa ctgagctcgt cgacttaggg gtccttcttc gctgccctcg ccgcgtgcta 121 gcagggagtt tccgctcggg agagagactg tcctcacgcc cgctgcgcct cctcgacggc 181 agagcaggct tgctcgcccg tgggagcgtc ccggccgaga agccctgagg ggggagggga 241 ggccatttg tcccgaccga ctccccggaa ccgggccggag cggctgggag aggctgcgga 301 gccgcggtcg ccgccctcgg aggcactgga cgccgccact gtcgggcctt cctcaaagct 361 gttcgtaggt cgcccgccgc gtcttcgagcc ttttacccac gcttcccccgg tcctccggcc 421 tgagaacgcc cgagtgagga gttggccgta gtgagaggga ccgatccctt ggggccgccg 481 gcggcgagag cccgagccgc tcctcccaat ggcgaagaag acgtacgacc tgcttttcaa 541 gctgctcctg atcggggatt ccggagtggg gaagacctgc gtcctttttc gttttcggga 601 tgatgccttc aatactacct ttatttccac cataggaata gacttcaaga tcaaaacagt 661 tgaattacaa ggaaagaaga tcaagctaca gatatgggat acagcaggcc aggagcgatt 721 tcacaccatc acaacctcct actacagagg cgcaatgggt atcatgctag tatatgacat 781 caccaatggt aaaagtttg aaaacatcag caaatggctt agaaacatag atgagcatgc 841 caatgaagat gtggaaagaa tgttactggg aaacaagtgt gatatggacg acaaaagagt 901 tgtacctaaa ggaaaaggag gacagattgc aagggagcat ggtattaggt tttttgagac 961 tagtgcaaaa gcaaatataa acatcgaaaa ggcgttcctc acgttagctg aagatatcct 1021 tcgaaagacc cctgtaaaag agcccacag tgaaaatgta gatatcagca gtggaggagg 1081 cgtgacaggc tggaagagca aatgctgctg agcattctcc tgttccatca gttgccatcc	SEQ ID NO:123

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1141 actaccccgt tttctttct tgctgcaaaa taaccactc tgtccatttt taactctaaa 1201 cagatatttt tgtttctcat cttaactatc caagccacct attttatttg ttctttcatc 1261 tgtgactgct tgctgacttt atcataattt tcttcaaaca aaaaaatgta tagaaaaatc 1321 atgtctgtga cttcattttt aaatgtactt gctcagctca actgcatttc agttgtatta 1381 tagtccagtt cttatcaaca ttaaaaccta tagcaatcat ttcaaatcta ttctgcaaat 1441 tgtataagaa taaagttaga attaacaatt ttattttgta caacagtgga atttctgtc 1501 atggataatg tgcttgagtc cctataatct atagacatgt gatagcaaaa gaaacaaaca 1561 aaagccagga aaacactcat tttcgccttg aatatgtaaa tgggattaat tttgtcctgt 1621 gccttatgtg gaaaggaact tctttggttt tccttttttg ttctggtgga agcatgtgca 1681 ggagacatat catccaaaca taaaccatta aaatgtttgt ggtttgcttg gctgtaattt 1741 tcaaagtagt taattgagga caaaggtaa tgcagaagtg atagctttgg tttgctgagt 1801 cttgttttaa gtggccttga tatttaaaac tattcctgcc accatttctt ctccttggcc 1861 acttcttcct tgcgtctccc tgcatgctgc tttatttgct tctcccctcc caaccacctc 1921 atggtatatt taagagtgaa agggacaaac tagtaggttt gtcaagttta atataaagca 1981 ctgatgtaac ttgctaggta aacggaaaga taagttctaa ctgcctacta tccaatgtca 2041 gttaattggt gtcttcccc ctcattgct ctcttcccta aaatgtgtcc cagatgcctt 2101 catttgctgt tttacttcta tgttctgctt ttcctcctct ctttgttccc ttcctgtcta 2161 tccattgagt ttatgaaatg gaagagttaa ctgcatgcac tagtgtttgg agggtgttgt 2221 ggtttgtctt tctaattagg tgtatagcct attcactttc ctagaataaa tctcttaacc 2281 taaatttgag tagtctgcat tttggcaact cctctagcag cttggtagcc tagtacaggt 2341 tgttttttaa aaaaaggaaa agcaggaagg aggagtgaat tttattaaca tgtttgccaa 2401 atgtattgag atttggcctc tgaagaacac tttttcagtg ttaagtttct ttaccttaag 2461 attcagaaat actttagaat attattaatt ttaagtcctg tctttacatc cttttggaaa 2521 acttgtatta ccatgagttt ggaaaaagga caacgaaagg ctttttcatgt aaagataaga 2581 tcttttggcta tctctaaccc tgtcctttt tcactgcatt ttttctagtt ttgcttcatt 2641 gcttatcatt aggataggt aagtgaagtt tgctatgctg ctagcatcct aagatgatac 2701 ctttgttgaa agaattgtga atagcatgat tcatttctag cagaggctga gtttaggact 2761 gcagcttcca ttgagaagtc tttctgtgtc gtgaatagca ttttaatgac ctcttggctc 2821 acataagcaa acaacatagg gacgtatctg ctatgaaaat ccacaaattt ttcagatagt 2881 gccctaaaaa caattttata tgcctcactg gttgttattc ttaggttatt cccacacttg 2941 actttatcat tgtttactac tagtaaaaag cagcattgcc aaataatccc taattttcca 3001 ctaaaaatat aatgaaatga tgttaagctt tttgaaaagt ttagttaaa cctactgttg 3061 ttagattaat gtatttgttg cttcccttta tctggaatgt ggcattagct tttttatttt 3121 aaccctcttt aattcttatt caattccatg acttaaggtt ggagagctaa acactgggat 3181 ttttggataa cagactgaca gttttgcata attataatcg gcattgtaca tagaaaggat 3241 atggctacct tttgttaaat ctgcactttc taaatatcaa aaaagggaaa tgaagtataa 3301 atcaattttt gtataatctg tttgaaacat gagttttatt tgcttaatat tagggctttg 3361 ccccttttct gtaagtctct tgggatcctg tgtagaagct gttctcatta aacaccaaac 3421 agttaagtcc attctctggt actagctaca aattcggttt catattctac ttaacaattt 3481 aaataaactg aaatatttcc aaaaaaaaaa aaaaaaaaaa c 1 M A K K T Y D L L F K L L L I G D S G V 1 ATGGCGAAGAAGACGTACGACCTGCTTTCAAGCTGCTCCTGATCGGGGATTCCGGAGTG 21 G K T C V L F R F S D D A F N T T F I S 61 CGGAAGACCTGCGTCCTTTTCGTTTTCGGATGATGCCTTCAATACTACCTTTATTTCC 41 T I G I D F K I K T V E L Q G K K I K L	SEQ ID NO:124

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		121 ACCATAGGAATAGACTTCAAGATCAAAACAGTTGAATTACAAGGAAAGAAGATCAAGCTA 61 Q I W D T A G Q E R F H T I T T S Y Y R 181 CAGATATGGGATACAGCAGGCCAGGAGCGATTTCACACCATCACAACCTCCTACTACAGA 81 G A M G I M L V Y D I T N G K S F E N I 241 GGCGCAATGGGTATCATGCTAGTATATGACATCACCAATGGTAAAAGTTTTGAAAACATC 101 S K W L R N I D E H A N E D V E R M L L 301 AGCAAATGGCTTAGAAACATAGATGAGCATGCCAATGAAGATGTGGAAAGAATGTTACTG 121 G N K C D M D D K R V V P K G K G G Q I 361 GGAAACAAGTGTGATATGGACGACAAAAGAGTTGTACCTAAAGGAAAAGGAGGACAGATT 141 A R E H G I R F F E T S A K A N I N I E 421 GCAAGGGAGCATGGTATTAGGTTTTTTGAGACTAGTGCAAAAGCAAATATAAACATCGAA 161 K A F L T L A E D I L R K T P V K E P N 481 AAGGCGTTCCTCACGTTAGCTGAAGATATCCTTCGAAAGACCCCTGTAAAAGAGCCCAAC 181 S E N V D I S S G G G V T G W K S K C C 541 AGTGAAAATGTAGATATCAGCAGTGGAGGAGGCGTGACAGGCTGGAAGAGCAAATGCTGC 201 - 601 TGA	
WBC001C12_V1.3_at	No Homology	1 GGACCCTCGTGCCGTGGAAACTGAGAAAACATTTTTTTTCCCAAAGGCAATTACTCTGCA 61 TGGCCTTTTTACCCTGTTATAGGGCCTTCTTTCTTTCCAGATAATAACCCACAGAATCTC 121 TTTGTGTGCTCAAGTTAAGTCATTAACGGCTTGACAAAGTGTTGTTAGTGCAGAAAGCTT 181 ATTCTCTTCATTGGTTGAATGTAACTTCCAGACATTAAGTGACCCATTTTGTTGTTCCTG 241 AGGCTAAGAATCATTATTTTCTTTTGGTACCATACAGATTGTGGATTTCAGTTTAATCCA 301 GAAACTCACAACTCATGTTGAAGTAATTTCTACTGAGAAGTGATTTTTCTAGATAATTGT 361 TCAAATTTTTTGATTGAGTCAACATTAGATACAACAGTGCAACGGGCATGCTCTACTGTA 421 GAGATTATAAATGGAAGACTTTGTTCTTTTAGTTTACTTTTCCTCCTTCACTAATAGTTT 481 TTGCTGAACTGTTGGTTTTTCCTGAACATTTCTTCAGAGTTAACAACAAAGACAAGTTCA 541 ACCATTGTCTTCCCTTATAAATTATTAATACAATAACATCCAGCTTTGTTCTCCTTGTGT 601 GTACCTCCTTCTTCTTAAATGAAAACCCATATTTGTTGAAAGAAAATATGAACACTAAGA 661 AAACTTTACTTAATGATGACTAACTCTG	SEQ ID NO:125
		1 AGGAGGTGGTACCCATTTTCAGGAAAAGGAAAAAGCATTACTCACTTTTCACTTCTATCT 61 ATAGTTAGAGTTCTAAAGGGGGCTATAACCCCAACATATCGTGAATGGATTTGTGGAGAG 121 ATTGAATAATAACCAGCTTTAGGAGGCAGGTGAAAATACAGAAACAATATGAATATTTGG 181 TAAAGTAAATTTAAAAAAATACTCTTAAGGGAGAAACAGTAGCAAAGAGAGCTACAATCA 241 AGATGGAAGCTCTTATTGGGCATATCTGCTGGAGAGAATGGCAAATTTTGTGTAGGATCT 301 CAGCTAATAATGACCCAACCCTGTATTTATGCAGCTAATAATTAACATGTGGGCTCAGCA 361 TGAAGTCAACTCCAAATTCTCATTCTTCAATAATCAACAGTCTTCCCTTTCCTGTAAAAA	SEQ ID NO:126

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		421 GAATGACTGTTGGAGGCCGGCCCAGTGGCATAGTGGTTAAGTTCACATGCTGTGCTTTGG 481 TGGCCTAGGGTTCGCAGGTTTGGATCCTGGGTGTAGACCGACACAGCACGCATCAAGCCA 541 TGCTGTGGCGGCATTCCATGTAGAAAAATTAGAAGGGCTTACAACTAGGATATACAGCTA 601 TGTGCTGGGGCTTTGGAGGGGAAAAAAAAAAAA	
WBC001C11 (Same as WBC041B05)	ARP3 actin-related protein 3 homolog (yeast)	1 atcttggctt cccggggaaa ggcggcgtga ggggaagaag ttgtagggtg ggggcaggag 61 tgaggaggag ggaagagaga gggggaggag gccgcggcgg ggcagggcgg ggactgcctg 121 cctgcctggg ttgcggaagt gatagccgcc gaccgagcct gctgctttct tgctactgct 181 tcggcttccc ggctaccccc cggacggtga aggcggccca gctgtggatg gtcagatagc 241 ccttgtttcc cgccgccaat ctctggccca tagcagcacg gagcagacgg cggcagcagc 301 agcagcaggc gaggaggaag atggcgggac ggctgccggc ctgtgtggtg gactgtggca 361 cggggtatac aaaactagga tatgctggaa atacagaacc acagtttatc atcccttcct 421 gtattgctat taaggagtca gcaaaagtgg gtgatcaagc tcaaaggagg gtgatgaaag 481 gtgttgatga cctagacttc ttcattggtg atgaagcaat agaaaaacct acatatgcaa 541 caaagtggcc aatccgccat ggtatagttg aagattggga cttaatggaa aggtttatgg 601 agcaagtgat ctttaaatat ttaagggcag aacctgaaga ccattatttt cttttgactg 661 aacctccatt gaatactcca gaaaacaggg aatatactgc tgaaataatg tttgagtcct 721 tcaatgttcc aggcttgtac attgctgtgc aggctgttct tgccttagct gcatcttgga 781 cctcaagaca agtaggagaa cggacgttga ccggtacggt aatagacagt ggagatggtg 841 tcactcatgt cattcctgtg gctgaagggt atgtgattgg cagctgtatt aaacacattc 901 caatcgcagg acgagatata acatatttta ttcagcaact gctgagagac cgagaagtag 961 gaatccctcc agaacaatcc ttggaaactg ctaaggcagt aaaggagcgc tatagttatg 1021 tctgcccaga tttagtaaaa gaatttaaca agtatgatac agatgggtca aaatggatta 1081 aacagtatac tggaatcaat gctatctcaa agaaagagtt ttctatcgat gttggttatg 1141 agagattttt gggacctgaa atctttttc atccagagtt tgctaatcca gactttacac 1201 aacctatctc agaagttgta gatgaagtaa ttcagaattg tcctattgat gtcagacgtc 1261 ctctctacaa gaatattgtc ctctctggag gttcaaccat gttcagggac tttggacgtc 1321 gcttgcaaag agatttgaaa agaactgtag atgcccggct gaaattaagt gaggaattga 1381 gtggtggtag attgaagcca aaacctattg atgtacaagt cattacacac cacatgcagc 1441 gatatgcagt ttggtttgga ggatcaatgc tggcttccac gcctgagttc taccaagtat 1501 gccacaccaa aaaggattat gaagaaattg gacctagcat ttgtcgtcac aatccagtgt 1561 ttggagtcat gtcgtaaaat tggcttcata gttattgggg ttagggaggt ggggaagaga 1621 taatctttct gattacctgt tttgtctgga tggctggttt tgaggtttta aacctgactt 1681 gaaatagtaa caccaaacat gattatacag gaatatttta ataagtgtat caccatgcag 1741 atgtagaaga gagcgaaagt gattgtgttt ttctttagat tgaatatttg aatcttatgt 1801 gtaacaaaaa gaagtgggtt ttagttcttt ctgtgccctg atattttgta tattaatgaa 1861 ttatccaaga ttcgatggga tttatcagtg tgtagatagc tctataatgc ttgaattgta 1921 cacttctaag tgtgcagtgc aagagcttgt ttatatttca tacttttat actttgagga 1981 aaaaaagtca aagaaaaatt gtatttgagg gaaaaaacca tgaccaagta aaggataaat 2041 tcaaaaaata gcctcatgag acttggcata cacactcgtg ggattccagt tattatggag 2101 tgcttccatc cctctccacc ccttcccccc aaaaggtttt ctttgcaagt gcttttggaa 2161 ctaagagcta gtatcttgga ttaactgatg cctgctagtg ctttctgatt actcgcattc 2221 tgtttcttgc tttaaaagaa gagtaaagac aagagtgttg gaccagtatt gcagttctgt 2281 agtgtcattt cttataaaaa acaaaacaac aacaataatt tatcaaaatt ggcatattta 2341 aagcctaaca ttctaataaa ggcacaaatt tctttttaat acttgtttca gcctctttaa 2401 tctctttata agttaactaa taaatctatt ttcttcagac ttctgcaata gttctttaaa 2461 atcacaacag ttagcaagct gacttttgta atgtgctcaa tacaaatact tgtgaacttt	SEQ ID NO:127

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2521 taatatgttg agtgctttca ttttgataac tggatctcca tttgatattt tcatttgtat 2581 aactcatttg cagtctgaaa attttttttta gtgccagtcc ctgaacatat cattgaaagt 2641 taatttttctt tgcattttaa aatatctgga ttatgaagaa aaagtgatga aaataaatta 2701 aaactgaatt acaaaaaaaa aaaaaaaa 1 M A G R L P A C V V D C G T G Y T K L G 1 ATGGCGGGACGGCTGCCGGCCTGTGTGGTGGACTGTGGCACGGGGTATACAAAACTAGGA 21 Y A G N T E P Q F I I P S C I A I K E S 61 TATGCTGGAAATACAGAACCACAGTTTATCATCCCTTCCTGTATTGCTATTAAGGAGTCA 41 A K V G D Q A Q R R V M K G V D D L D F 121 GCAAAAGTGGGTGATCAAGCTCAAAGGAGGGTGATGAAAGGTGTTGATGACCTAGACTTC 61 F I G D E A I E K P T Y A T K W P I R H 181 TTCATTGGTGATGAAGCAATAGAAAAACCTACATATGCAACAAAGTGGCCAATCCGCCAT 81 G I V E D W D L M E R F M E Q V I F K Y 241 GGTATAGTTGAAGATTGGGACTTAATGGAAAGGTTTATGGAGCAAGTGATCTTTAAATAT 101 L R A E P E D H Y F L L T E P P L N T P 301 TTAAGGGCAGAACCTGAAGACCATTATTTTCTTTTGACTGAACCTCCATTGAATACTCCA 121 E N R E Y T A E I M F E S F N V P G L Y 361 GAAAACAGGGAATATACTGCTGAAATAATGTTTGAGTCCTTCAATGTTCCAGGCTTGTAC 141 I A V Q A V L A L A A S W T S R Q V G E 421 ATTGCTGTGCAGGCTGTTCTTGCCTTAGCTGCATCTTGGACCTCAAGACAAGTAGGAGAA 161 R T L T G T V I D S G D G V T H V I P V 481 CGGACGTTGACCGGTACGGTAATAGACAGTGGAGATGGTGTCACTCATGTCATTCCTGTG 181 A E G Y V I G S C I K H I P I A G R D I 541 GCTGAAGGGTATGTGATTGGCAGCTGTATTAAACACATTCCAATCGCAGGACGAGATATA 201 T Y F I Q Q L L R D R E V G I P P E Q S 601 ACATATTTTATTCAGCAACTGCTGAGAGACCGAGAAGTAGGAATCCCTCCAGAACAATCC 221 L E T A K A V K E R Y S Y V C P D L V K 661 TTGGAAACTGCTAAGGCAGTAAAGGAGCGCTATAGTTATGTCTGCCCAGATTTAGTAAAA 241 E F N K Y D T D G S K W I K Q Y T G I N 721 GAATTTAACAAGTATGATACAGATGGGTCAAAATGGATTAAACAGTATACTGGAATCAAT 261 A I S K K E F S I D V G Y E R F L G P E 781 GCTATCTCAAAGAAAGAGTTTTCTATCGATGTTGGTTATGAGAGATTTTTGGGACCTGAA 281 I F F H P E F A N P D F T Q P I S E V V	SEQ ID NO:128

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		841 ATCTTTTTTCATCCAGAGTTTGCTAATCCAGACTTTACACAACCTATCTCAGAAGTTGTA 301 D E V I Q N C P I D V R R P L Y K N I V 901 GATGAAGTAATTCAGAATTGTCCTATTGATGTCAGACGTCCTCTCTACAAGAATATTGTC 321 L S G G S T M F R D F G R R L Q R D L K 961 CTCTCTGGAGGTTCAACCATGTTCAGGGACTTTGGACGTCGCTTGCAAAGAGATTTGAAA 341 R T V D A R L K L S E E L S G G R L K P 1021 AGAACTGTAGATGCCCGGCTGAAATTAAGTGAGGAATTGAGTGGTGGTAGATTGAAGCCA 361 K P I D V Q V I T H H M Q R Y A V W F G 1081 AAACCTATTGATGTACAAGTCATTACACACCACATGCAGCGATATGCAGTTTGGTTTGGA 381 G S M L A S T P E F Y Q V C H T K K D Y 1141 GGATCAATGCTGGCTTCCACGCCTGAGTTCTACCAAGTATGCCACACCAAAAAGGATTAT 401 E E I G P S I C R H N P V F G V M S - 1201 GAAGAAATTGGACCTAGCATTTGTCGTCACAATCCAGTGTTTGGAGTCATGTCGTAA	
WBC001A07_V1.3_at	No Homology	1 AGCACAGCTACTACATCAAGTACAACTAATACCACTTTAACTCCAACTCCGCAGCCTGCG 61 CGGAAATCCACCTTTGATGCAGCCAGTTTCATTGGAGGAATCGTCCTTGTCTTGGGTGTG 121 CAGGCTGTTATTTTCTTTCTCTATAAATTCTGCAAATCTAAAGAACGAAACTACCACACT 181 CTGTAAACAGACCCATTAAATTAACGACTGGCATATAACTCACTGAAACCAAAATGCTAT 241 CTTTCAAGATGTCCCACATGGAAGACACTATTCCAAGAGCTTTAAATTTGCAAAGGATGC 301 ATATAGGATATTTTGGAGCATCGTCCTTGAAGAAAATTAGCTAAATCATTTTGCTCAACA 361 GGAATATTTAAAATATTCTGCATGAATCCTTGTGGCTGTCTTTTCCTTTAAATGGCTGCT 421 GCTGTGGGATTGTGTTCTCTGTTCTTGACATGCCAAATGTAACTCTGTAAGGGATGGGAA 481 ACATTGTCCTGCGCAGACAACCTCATGACTCTTTGGCAGTTTAAATTTAGTCGTTTTAAA 541 GCCTGAAAGTTGCATTATTTTCATCCTAACTCAGGATGTAGTTTAGTCCCCAGAATTGAA 601 TAGAATGTGCCAAAGGAGAATCAGGCAGATTTTTGGCTGTCATTTCAAAATGGAATAAAT 661 TTATAAATTTAGTATCTTTAGAGTACACTGTATCCTTAGAGTAAAATTTTGTGCTTGANA 721 GCAGTTATTTTTTCTACATTAGAAATAAGATGCCACACAAGGAATGACATTCCCGATTGA 781 AGAGAAATGAATAGAAAGGATACAAACCATGAAAGTGTAGCGGCTTATTGTTCATACTT 1 TATTCTAGGTACCTCACAAAAAATTTATTATGGTGCCATGGCTGGTAGCTTTTAGTGAGT 61 GCTGCAAGATACAAGATTCATTTGAAAATATACAAAATTTCCATTCCTCCCAAAGTGGCA 121 AAAGTTAGCTACAAAAATTAGCTATAATTGTCTTTACCTAGATATGAATATCTTGGCACA 181 CTTTAATGTCAACACATGGAACAGTTTTTTTTGAAAATGTAGCTAATGAAGCTTCTCATC 241 TTCTATAATTTTGAATACTACTCTAACAAAATCATAATACGGAATTAGATTTTGCAAGAA 301 GAGCTCTTAAAACAGAACTCACAGCCTTTCTCCCTGTGTCTTTGGCAATGTAGTATCTTG 361 AGCCATTGATAATTTTTGGGTTTTTTAATCCAGAAGGTATATAGAAACCTTTTCAGATTT 421 TTCATCTGATTTGTTCACGCAAATGTAGTTCTTATCAAAATACCTTATTTTACCTTACAG 481 ATATTTGTTGCACAGGCAGACACTGCTGTATTTAGAAAGTTCTATTTCAGTTCGTTAAAA 541 ACTGCAAAACCANTCTGTATTATGTACCAACTGATTTAAAATAAATCTACATGTTTATTG 601 AAAAAAAAAAAAAAAAAA	SEQ ID NO:129 SEQ ID NO:130

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
GI9717252	Equus caballus Toll-like receptor 4 mRNA	1 GGCACGAGCGGCACGAGAGCAGCAGCTCCGAGGCTGCCCTGGCGGGCAGGCTGTTACGGT 61 GCGTCATGCTTTCACAGGGCCCCTTCTGGGCACAGAAAATGCCAGCATGATGCCGCCCAC 121 CCGCCTGGCTGGGACTCTGATCCCAGCCATGGCCTTCCTCTCCTGCCTGAGACCCGAGAG 181 CTGGGACCCTTGCGTGCAGGTGGTTCCTAACACTACTTACCAATGCATGGACCTGAATCT 241 CTACAAAATCCCCTGAGAACATCCCCACATCAACCAAGGAACTGGACCTGAGCTTTAACCC 301 CTTGAAGGAGTTAGGCAGCCATAGCTTCTCCAACTTCCCAGAACTGCAGGTGCTGGATTT 361 GTCCAGGTGTGAAATTGAGATGATTGAAGATGATCATATCAGGGCCTCAACCATCTCTC 421 CACCTTGATATTGACACGGAAATCCTATCAGGAGCTTAGCCCTGGGAGCCTTTTCTGGACT 481 CTCCAGTTTACAGACGCTGGTGGCCGTGGAGACAAAGCTTTCATCTCTAGAGAAGTTCCC 541 CATTGGACATCTCAAGACCTTGAAGGAGCTTAATGTGGCTCATAATCTTATCCATTCCTT 601 CAAGTTACCCGAGTATTTTTCTAAAATGCCCCAACCTGGAGCACTTGGACCTTTCCAATAA 661 CAAGATCCAAAATATTTCTCATGAAGACTTGCGTGTGCTACATCAAATGCCCTTACTCAA 721 CCTTTCTTTAGACTTGTCCCTGAATCCTTTAGAGTTTATCCAACCAGATGCCTTTAAAGA 781 AATTAAGCTCCATAAACTGACTTTGAGAAGTAATTTTGATAGTATAGATGTAATGAAATC 841 TTGTATTCAAGGACTGGCTGGTTTAAAAGTCAATCGGTTGGTCTGGGAGAATTTAAAAA 901 TGAAAGGAAATTGGAAAGATTTGACACATCTGCCCTGCGCGGACTGCACAATTTGACGAT 961 TGAAGAATTCCGGTTAGCATACATTGATAATTACAGCTCAAAGGATTCTATTGATTTACT 1021 TAATTGTTTGGCAGATATTTCTAAAATTTCTCTGGTGAGTCTGGATTTAGGCAATCTAAA 1081 AGATTTCCTAAAGGTTTCGGATGGCAAGACTTCGAATTGGTTAACTGTAGAATTGAAGG 1141 ATTTCCCACATTGGAGCTCACCTCTCTCAAAAGGTTGGTTTTCACTTCCAACAAAGATAT 1201 GAAATCTTTAATGAAGTTAAGCTACCAAGCCTTGAGTTCTAGATCTCAGCAGAAATCG 1261 CTTGAGTTTCAAGTCCTGCTGTTCTCAGGCTGATTTGAAGACAACCAGACTGAAGCATTT 1321 AGATCTGAGCTTCAATGATGTTATTTCCATGAGTTCAAACTTCATGGGCTTAGAGCAACT 1381 AGAACATCTGGATTTCCAGCATTCCACTTTGAAACAGGCCAGTGATTTTCCAGTATTCTT 1441 ATCCCTCAAAAACCTCCGTTATCTTGATATTTCTTACACTAACACCCGAGTTGTCTTCCA 1501 TGGCATCTTTGATGGCTTGGTCAGCCTCCAAGTCTTGAAAATGGCTGGCAATTCTTTTAA 1561 GGACAACTTCCTTCCAAATATCTTCAGAGAGATGACTAACCTGACCACCCTGGACCTTTC 1621 TAAGTGTAACCTGGAACAGGTGTCCCAGGAGGCATTTTGCTTACTCCCTCGACTTCGGGT 1681 GTTAAATATGAGTCACAATAACCTCCTGTTCTTGGATATGCTTCCTTACAAACCTCTCCA 1741 TTCCCTCCAGATTCTGGATTGCAGTTTTAATCGTATTGTGGCCTTCAAGTGGCAAGAACT 1801 GCAGCATTTTCCAAGTAGTCTAGCTTCCTTAAATCTTACTCAAAATGACTTGCTTGTGT 1861 TTGTGAATACCAGAGTTTTCTGCAGTGGGTCAAGGACCAGAGGCAGCTCTTGGTGGAAGT 1921 TGAACACTTGGTGTGTGCAATACCCTTACAGATGCGGGGCATGCCCGTGCTGGGTTTTAA 1981 CAATGCCACCTGTCAGATTAGCAAGCACTATCGTTGGCGGGTCGGTTTTCAGTATACTCAT 2041 GGTTTCTGTCATAGCAGTTCTGGTCTATAAGTTCTATTTCCACCTGATGCTTCTTGCTGG 2101 CTGCAAAAAGTATGGGAGAGGTGAAAGCATCTATGATGCCTTTGTTATCTACTCAAGCCA 2161 GGACGAAGACTGGGTGAGGAATGAATTGGTAAAGAACTTGGAGGAGGGGGTGCCCCCCTT 2221 TCAACTCTGCCTTCACTACAGAGACTTCATTCCTGGTGTGGCCATCGCCGCCAACATCAT 2281 CCAGGAAGGTTTCCACAAAAGCCGCAAAGTTATTGTCGTGGTGTCCCAGCACTTCATTCA 2341 GAGCCGATGGTGTATCTTGAGTATGAGATTGCCCAGACCTGCCAGTTTCTGAGCAGTCG 2401 TGCTGGCATCATCTTCATCGTCCTGCACAAGCTGGAGAAGTCCCTGCTCCGGCAGCAGGT 2461 GGAGCTGTATCGCCTTCTCAACAGGAACACTTACCTGGAGTGGGAGGACACTGTCCTGGG 2521 GCGGCACATCTTCTGGAGACGACTCAGGAAAGCCTTGCTGGATGGTAAACCGTGGAGTCC 2581 AGCAGGAACAGCAGATGCAGCAGAAAGCAGACAACATGATGCAGAAACCTCTACCTGAGG 2641 AGGAAAAACTCCTGAGGTGCTTCTTGCCCAGCTGGACCCAATACTTGTTCAGTTAACAAC	SEQ ID NO:131

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2701 TATTAAATGCTGCAACATACCAGGCATTGTGCTAGGGGCAGGTGATTCTGTCGTGCACAA 2761 GATACACAGGACTGCTAATCCCTTTGAGTTTACAGTGCAGAGGGAATAAATGCCGTGCTA 2821 AAATACAGAACCTCCAGGGGGATGTTTTAACCAAGTCAGCTAAGGAGTCCGTGCCAGGGA 2881 AAGTCAACTCAACTCTTACCCCATCAAAATGAATCAGAACTGAGACACTGGGCCCCAGTG 2941 AGTTCAGAAAAGGACATCGTCTCCCAAGTCTTTTGAATGGAAACCATCTCATCTTTGACA 3001 TCTTAGCCATCCTAAAACAAAACAAAGCAGTTTTGGTACTTTCAACTGAACAGCGTCTCT 3061 GTTCAATTTTCCCTTTTCTACTGAACACAATTTAAATTTTACTTGATGACTCAGAAGGCT 3121 CCTGATTCAGATCCTCCCTCCTCTTTAAGGCAGTTTCCTTATGAAGGTTAAACTCTTACG 3181 ACTAATTCCTAAGGAAATCTGATTGATACATATTCACAAACATCCTGGTCATTCTTTAGC 3241 GTGCTCTATTTATTAATAAATAGCAGGTTCTATTTAAAAAAAAAAAAAAAAA	
		1 M M P P T R L A G T L I P A M A F L S C 1 ATGATGCCGCCCACCCGCCTGGCTGGGACTCTGATCCCAGCCATGGCCTTCCTCTCCTGC	SEQ ID NO:132
		21 L R P E S W D P C V Q V V P N T T Y Q C 61 CTGAGACCCGACAGCTGGGACCCTTGCGTGCAGGTGGTTCCTAACACTACTTACCAATGC	
		41 M D L N L Y K I P E N I P T S T K E L D 121 ATGGACCTGAATCTCTACAAAATCCCTGAGAACATCCCCACATCAACCAAGGAACTGGAC	
		61 L S F N P L K E L G S H S F S N F P E L 181 CTGAGCTTTAACCCCTTGAAGGAGTTAGGCAGCCATAGCTTCTCCAACTTCCCAGAACTG	
		81 Q V L D L S R C E I E M I E D D A Y Q G 241 CAGGTGCTGGATTTGTCCAGGTGTGAAATTGAGATGATTGAAGATGATGCATATCAGGGC	
		101 L N H L S T L I L T G N P I R S L A L G 301 CTCAACCATCTCTCCACCTTGATATTGACAGGAAATCCTATCAGGAGCTTAGCCCTGGGA	
		121 A F S G L S S L Q T L V A V E T K L S S 361 GCCTTTTCTGGACTCTCCAGTTTACAGACGCTGGTGGCCGTGGAGACAAAGCTTTCATCT	
		141 L E K F P I G H L K T L K E L N V A H N 421 CTAGAGAAGTTCCCCATTGGACATCTCAAGACCTTGAAGGAGCTTAATGTGGCTCATAAT	
		161 L I H S F K L P E Y F S K M P N L E H L 481 CTTATCCATTCCTTCAAGTTACCCGAGTATTTTTCTAAAATGCCCAACCTGGAGCACTTG	
		181 D L S N N K I Q N I S H E D L R V L H Q 541 GACCTTTCCAATAACAAGATCCAAAATATTTCTCATGAAGACTTGCGTGTGCTACATCAA	
		201 M P L L N L S L D L S L N P L E F I Q P 601 ATGCCCTTACTCAACCTTTCTTTAGACTTGTCCCTGAATCCTTTAGAGTTTATCCAACCA	
		221 D A F K E I K L H K L T L R S N F D S I 661 GATGCCTTTAAAGAAATTAAGCTCCATAAACTGACTTTGAGAAGTAATTTTGATAGTATA	
		241 D V M K S C I Q G L A G L K V N R L V L	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		721 GATGTAATGAAATCTTGTATTCAAGGACTGGCTGGTTTAAAAGTCAATCGGTTGGTTCTG	
		261 G E E F K K N E E R K K L E E R R F D D T S A L R R G L L	
		781 GGAGAATTTAAAAATGAAAGGAAATTGGAAAGATTTGACACATCTGCCCTGCCGCGGACTG	
		281 H N L T I I E E E F R R L L A A Y Y I I D D N N Y Y S S S K K D	
		841 CACAATTTGACGATTGAAGAATTCCGGTTAGCATACATTGATAATTACAGCTCAAAGGAT	
		301 S I I D D L L L N N C C L L A A D D I I S S K K I I S S L L V V S S L L D D	
		901 TCTATTTGATTTACTTAATTGTTTGGCAGATATTTCTAAAATTTCTCTGGTGAGTCTGGAT	
		321 L L G G N N L L K K D D F F P P K K G G F F G G W W Q Q D D F F E E L L V V N N	
		961 TTAGGCAATCTAAAAGATTTTCCTAAAGGTTTCGGATGGCAAGACTTCGAATTGGTTAAC	
		341 C C R R I I E E G G F F P P T T L L E E L L T T S S L L K K R R L L V V F F T T	
		1021 TGTAGAATTGAAGGATTTCCCACATTGGAGCTCACCTCTCTCAAAAGGTTGGTTTTCACT	
		361 S S N N K K D D M M K K S S F F N N E E V V K K L L P P S S L L E E F F L L D D	
		1081 TCCAACAAAGATATGAAATCTTTTAATGAAGTTAAGCTACCAAGCCTTGAGTTTCTAGAT	
		381 L L S S R R N N R R L L S S F F K K S S C C C C S S E E A A D D L L K K T T T T	
		1141 CTCAGCAGAAATCGCTTGAGTTTCAAGTCCTGCTGTTCTGAGGCTGATTTGAAGACAACC	
		401 R R L L K K H H L L D D L L S S F F N N D D V V I I S S M M S S S N N F F M M	
		1201 AGACTGAAGCATTTAGATCTGAGCTTCAATGATGTTTATTTCCATGAGTTCAAACTTCATG	
		421 G G L L E E Q Q L L E E H H L L D D F F Q Q H H S S T T L L K K Q Q A A S S D D	
		1261 GGCTTAGAGCAACTAGAACATCTGGATTTCCAGCATTCCACTTTGAAACAGGCCAGTGAT	
		441 F F P P V V F F L L S S L L K K N N L L R R Y Y L L D D I I S S Y Y T T N N T T	
		1321 TTTCCAGTATTCTTATCCCTCAAAAACCTCCGTTATCTTGATATTTCTTACACTAACACC	
		461 R R V V V V F F H H G G I I F F D D G G L L V V S S L L Q Q V V L L K K M M A A	
		1381 CGAGTTGTCTTCCATGGCATCTTTGATGGCTTGGTCAGCCTCCAAGTCTTGAAAATGGCT	
		481 G G N N S S F F K K D D N N F F L L P P N N I I F F R R E E M M T T N N L L T T	
		1441 GGCAATTCTTTTAAGGACAACTTCCTTCCAAATATCTTCAGAGAGATGACTAACCTGACC	
		501 T T L L D D L L S S K K C C N N L L E E Q Q V V S S Q Q E E A A F F C C L L L L	
		1501 ACCCTGGACCTTTCTAAGTGTAACCTGGAACAGGTGTCCCAGGAGGCATTTTGCTTACTC	
		521 P P R R L L R R V V L L N N M M S S H H N N N N L L L L F F L L D D M M L L P P	
		1561 CCTCGACTTCGGGTGTTAAATATGAGTCACAATAACCTCCTGTTCTTGGATATGCTTCCT	
		541 Y Y K K P P L L H H S S L L Q Q I I L L D D C C S S F F N N R R I I V V A A F F	
		1621 TACAAACCTCTCCATTCCCTCCAGATTCTGGATTGCAGTTTTAATCGTATTGTGGCCTTC	
		561 K K W W Q Q E E L L Q Q H H F F P P S S S S L L A A S S L L N N L L T T Q Q N N	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1681 AAGTGGCAAGAACTGCAGCATTTTCCAAGTAGTCTAGCTTCCTTAAATCTTACTCAAAAT 581 D F A C V C E Y Q S F L Q W V K D Q R Q 1741 GACTTTGCTTGTGTTTGTGAATACCAGAGTTTTCTGCAGTGGGTCAAGGACCAGAGGCAG 601 L L V E V E H L V C A I P L Q M R G M P 1801 CTCTTGGTGGAAGTTGAACACTTGGTGTGTGCAATACCCTTACAGATGCGGGGCATGCCC 621 V L G F N N A T C Q I S K T I V G G S V 1861 GTGCTGGGTTTTAACAATGCCACCTGTCAGATTAGCAAGACTATCGTTGGCGGGTCGGTT 641 F S I L M V S V I A V L V Y K F Y F H L 1921 TTCAGTATACTCATGGTTTCTGTCATAGCAGTTCTGGTCTATAAGTTCTATTTCCACCTG 661 M L L A G C K K Y G R G E S I Y D A F V 1981 ATGCTTCTTGCTGGCTGCAAAAAGTATGGGAGAGGTGAAAGCATCTATGATGCCTTTGTT 681 I Y S S Q D E D W V R N E L V K N L E E 2041 ATCTACTCAAGCCAGGACGAAGACTGGGTGAGGAATGAATTGGTAAAGAACTTGGAGGAG 701 G V P P F Q L C L H Y R D F I P G V A I 2101 GGGGTGCCCCCCTTTCAACTCTGCCTTCACTACAGAGACTTCATTCCTGGTGTGGCCATC 721 A A N I I Q E G F H K S R K V I V V V S 2161 GCCGCCAACATCATCCAGGAAGGTTTCCACAAAAGCCGGAAAGTTATTGTCGTGGTGTCC 741 Q H F I Q S R W C I F E Y E I A Q T W Q 2221 CAGCACTTCATTCAGAGCCGATGGTGTATCTTTGAGTATGAGATTGCCCAGACCTGGCAG 761 F L S S R A G I I F I V L H K L E K S L 2281 TTTCTGAGCAGTCGTGCTGGCATCATCTTCATCGTCCTGCACAAGCTGGAGAAGTCCCTG 781 L R Q Q V E L Y R L L N R N T Y L E W E 2341 CTCCGGCAGCAGGTGGAGCTGTATCGCCTTCTCAACAGGAACACTTACCTGGAGTGGGAG 801 D S V L G R H I F W R R L R K A L L D G 2401 GACAGTGTCCTGGGGCGGCACATCTTCTGGAGACGACTCAGGAAAGCCTTGCTGGATGGT 821 K P W S P A G T A D A A E S R Q H D A E 2461 AAACCGTGGAGTCCAGCAGGAACAGCAGATGCAGCAGAAAGCAGACAACATGATGCAGAA 841 T S T - 2521 ACCTCTACCTGA	
GI1592834	Equus caballus gelsolin mRNA	1 CCCAGCAG**CAT**GGTGGTAGAACACCCCGAGTTCCTCAAGGCGGGGAAGGAGCCTGGCCTG 61 CAGATCTGGCGCGTGGAGAAGTTCGACCTGGTGCCCGTGCCCCCCAACCTTTACGGAGAC	SEQ ID NO:133

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		121 TTCTTCACAGGTGACGCCTATGTCATCCTGAAGACGGTGCAGCTGAGGAACGGGATCCTG	
		181 CAGTACGACCTCCACTACTGGCTGGGCAATGAGTGCAGCCAGGATGAGAGCGGCGCGGCC	
		241 GCCATCTTCACCGTGCAGCTGGATGACTACCTGAACGGTCGGGCTGTGCAGCACCGCGAG	
		301 GTCCAGGGCTTTGAGTCGGCCACCTTCCTTGGCTACTTCAAGTCTGGCCTCAAGTACAAG	
		361 AAAGGAGGTGTGGCATCAGGATTCAAGCATGTGGTGCCCAATGAGGTGGTGGTGCAGAGG	
		421 CTCCTCCAGGTCAAAGGGCGGCGTGTGGTCCGTGCTACCGAGGTGCCCGTATCCTGGGAG	
		481 AGCTTCAACAATGGCGACTGCTTCATCCTGGACCTGGGCAACAACATCTATCAGTGGTGC	
		541 GGCTCCAAAAGCAACCGATTTGAGAGGCTGAAGGCCACACAGGTGTCCAAGGGCATCGGG	
		601 GACAACGAGCGGAGCGGCCGGGCCCAAGTGTCCGTGTTTGAGGAAGGCGCTGAGCCCGAG	
		661 GCCATGCTCCAGGTGCTGGCCCCAAGCCAACTCTGCCCGAAGCGACTGAGGACCAGTC	
		721 AAGGAGGATGCGGCCAACCGCAAGCTGGCCAAGCTCTACAAGGTCTCCAATGGCGCGGGC	
		781 CCCATGGTGGTCTCCCTTGTGGCTGATGAGAATCCCTTCGCCCAGGGGCCTTGAGGTCA	
		841 GAGGACTGCTTCATCCTGGACCACGGCAAAGATGGGAAAATCTTTGTCTGGAAAGGCAAG	
		901 CAAGCCAACATGGAGGAGAAGGCTGCCCTCAAAACGGCCTCCGACTTCATCTCCAAG	
		961 ATGGACTACCCCAAGCAGACCCAGGTCTCCGTCCTTCCCGAGGGCGGTGAGACCCCGCTG	
		1021 TTCAGGCAGTTCTTCAAGAACTGGCGGGACCCGGACCAGACGGAAGGCCTGGGCTTGGCC	
		1081 TATCTCTCCAGCCACATCGCCGAGCGCGTGCCTTTCGATGCCGCCACCCTGCAC	
		1141 ACCTCCACTGCCATGGCCGCCCAGCATGGCATGATGACGACGGCCACAGGCCAGAAACAG	
		1201 ATCTGGAGAGTCGAAGGGTCCAACAAAGTGCCCGTGGACCCCGCCACCTACGGGCAGTTC	
		1261 TACGGTGGGGACAGCTACATCATTCTGTACAACTACCGCCACGGCAGCCGTCAGGGACAG	
		1321 ATCATCTACAACTGGCAGGGCGCCCAGTCCACCCAGGATGAGGTCGCTGCGTCTGCCATC	
		1381 CTGACCGCCCAGCTAGATGAGGAACTGGGAGGTACCCCTGTCCAGAGCCGTGTGGTCCAA	
		1441 GGCAAGGAGCCTGCCCATCTCATGAGTCTATTTGGCGGCAAGCCCATGATCGTCTACAAG	
		1501 GGTGGCACCTCCCGCGAGGGTGGGCAGACGGCCCCCGCCAGTACTCGCCTCTTCCAGGTC	
		1561 CGGGCCAGCAGCTCTGGAGCCACCCGAGCCGTTGAGATAATCCCCAAGGCCGGCGCGCTG	
		1621 AACTCCAACGATGCCTTTGTCCTGAAAACTCCCTCGGCTGCCTACCTGTGGGTGGGTGCA	
		1681 GGAGCCAGCGGAGAAGACGGGGCCCAGGAGCTGCTCAGGGTGCTGCGGGCCCAA	
		1741 CCTGTGCAGGTGGCAGAAGGCAGCGAGCCAGACAGCTTCTGGGAGGCCTTGGGTGGGAAG	
		1801 GCCACCTACGGCACGTCCCGCGGCTGAAGGACAAGAAGATGGACGCCCACCCTCCTCGC	
		1861 CTCTTTGCCTGCTCCAACAAGATTGGACGTTTTGTGATCGAAGAGGTCCCTGGCGAGTTC	
		1921 ATGCAGGAAGACCTGGCCACTGATGACGTCATGCTCCTGGACACCTGGGACCAGGTCTTT	
		1981 GTCTGGGTCGGAAAGGATTCTCAAGACGAGGAAAAGACGGAAGCCTTGACCTCTGCTAAG	
		2041 CGGTATATCGACACAGACCCAGCTCATCGCGATAGGCGTACCCCCATCACCGTCGTGAAG	
		2101 CAAGGCTTTGAGCCTCCGTCCTTCGTGGCGCTGGTTCCTCGGCTGGGATGACAGCTACTGG	
		2161 TCTGTGGATCCCTTGGACAGGGCCTTGGCTGAGCTGGCTGCCTGA	
		1 M V V E H P E F L K A G K E P G L Q I W	SEQ ID NO:134
		1 ATGGTGGTAGAACACCCCGAGTTCCTCAAGGCGGGAAGGAGCCTGGCCTGCAGATCTGG	
		21 R V E K F D L V P V P P N L Y G D F F T	
		61 CGCGTGGAGAAGTTCGACCTGGTGCCGTGCCCCCCAACCTTTACGGAGACTTCTTCACA	
		41 G D A Y V I L K T V Q L R N G I L Q Y D	
		121 GGTGACGCCTATGTCATCCTGAAGACGGTGCAGCTGAGGAACGGGATCCTGCAGTACGAC	
		61 L H Y W L G N E C S Q D E S G A A A I F	
		181 CTCCACTACTGGCTGGGCAATGAGTGCAGCCAGGATGAGAGCGGCGGCCGCCATCTTC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		81 T V Q L D D Y L N G R A V Q H R E V Q G 241 ACCGTGCAGCTGGATGACTACCTGAACGGTCGGGCTGTGCAGCACCGCGAGGTCCAGGGC	
		101 E S A T F L G Y F K S G L K Y K K G G 301 TTTGAGTCGGCCACCTTCCTTGGCTACTTCAAGTCTGGCCTCAAGTACAAGAAAGGAGGT	
		121 V A S G F K H V V P N E V V V Q R L L Q 361 GTGGCATCAGGATTCAAGCATGTGGTGCCCAATGAGGTGGTGGTCACAGAGGCTCCTCCAG	
		141 V K G R R V V R A T E V P V S W E S F N 421 GTCAAAGGGCGGCGTGTGGTCCGTGCTACCGAGGTGCCCGTATCCTGGGAGAGCTTCAAC	
		161 N G D C F I L D L G N N I Y Q W C G S K 481 AATGGCGACTGCTTCATCCTGGACCTGGGCAACAACATCTATCAGTGGTGCGGCTCCAAA	
		181 S N R F E R L K A T Q V S K G I R D N E 541 AGCAACCGATTTGAGAGGCTGAAGGCCACACAGGTGTCCAAGGGCATCCGGGACAACGAG	
		201 R S G R A Q V S V F E E G A E P E A M L 601 CGGAGCGGCCGGCCCAAGTGTCCGTGTTTGAGGAAGCGCTGAGCCCGAGGCGATGCTC	
		221 Q V L G P K P T L P E A T E D T V K E D 661 CAGGTGCTGGGCCCCAAGCCAACTCTGCCCGAAGCGACTGAGGACACAGTCAAGGAGGAT	
		241 A A N R K L A K L Y K V S N G A G P M V 721 GCGGCCAACCGCAAGCTGGCCAAGCTCTACAAGGTCTCCAATGGCGCGGGCCCCATGGTG	
		261 V S L V A D E N P F A Q G A L R S E D C 781 GTCTCCCTTGTGGCTGATGAGAATCCCTTCGCCCAGGGGGCCTTGAGGTCAGAGGACTGC	
		281 F I L D H G K D G K I F V W K G K Q A N 841 TTCATCCTGGACCACGGCAAAGATGGGAAAATCTTTGTCTGGAAAGGCAAGCAAGCCAAC	
		301 M E E R K A A L K T A S D F I S K M D Y 901 ATGGAGGACAGGAAGGCTGCCCTCAAAACGGCCTCCGACTTCATCTCCAAGATGGACTAC	
		321 P K Q T Q V S V L P E G G E T P L F R Q 961 CCCAAGCAGACCCAGGTCTCCGTCCTTCCCGAGGGCGGTGAGACCCCGCTGTTCAGGCAG	
		341 F F K N W R D P D Q T E G L G L A Y L S 1021 TTCTTCAAGAACTGGCGGGACCCGGACCAGACGGAAGGCCTGGGCTTGGCCTATCTCTCC	
		361 S H I A H V E R V P F D A A T L H T S T 1081 AGCCACATCGCCCACGTGGAGCGCGTGCCTTTCGATGCCGCCACCCTGCACACCTCCACT	
		381 A M A A Q H G M D D D G T G Q K Q I W R 1141 GCCATGGCGCCCAGCATGGCATGGATGACGACGGCACAGGCCAGAAACAGATCTGGAGA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		401 V E G S N K V P V D P A T Y G Q F Y G G 1201 GTCGAAGGGTCCAACAAAGTGCCCGTGGACCCGCCACCTACGGGCAGTTCTACGGTGGG	
		421 D S Y I I L Y N Y R H G S R Q G Q I I Y 1261 GACAGCTACATCATTCTGTACAACTACCGCCACGGCAGCCGTCAGGGACAGATCATCTAC	
		441 N W Q G A Q S T Q D E V A A S A I L T A 1321 AACTGGCAGGGCGCCCAGTCCACCCAGGATGAGGTCGCTGCGTCTGCCATCCTGACCGCC	
		461 Q L D E E L G G T P V Q S R V V Q G K E 1381 CAGCTAGATGAGGAACTGGGAGGTACCCCTGTCCAGAGCCGTGTGGTCCAAGGCAAGGAG	
		481 P A H L M S L F G G K P M I V Y K G G T 1441 CCTGCCCATCTCATGAGTCTATTTGGCGGGAAGCCCATGATCGTCTACAAGGGTGGCACC	
		501 S R E G G Q T A P A S T R L F Q V R A S 1501 TCCCGCGAGGGTGGGCAGACGGCCCCCCCCCAGTACTCGCCTCTTCCAGGTCCGGCCAGC	
		521 S S G A T R A V E I I P K A G A L N S N 1561 AGCTCTGGAGCCACCCGAGCCGTTGAGATAATCCCCAAGGCCGGCGCGCTGAACTCCAAC	
		541 D A F V L K T P S A A Y L W V G A G A S 1621 GATGCCTTTGTCCTGAAAACTCCCTCGGCTGCCTACCTGTGGGTGGGTGCAGGAGCCAGC	
		561 E A E K T G A Q E L L R V L R A Q P V Q 1681 GAGGCGGAGAAGACGGGGGCCCAGGAGCTGCTCAGGGTGCTGCGGCCCCAACCTGTGCAG	
		581 V A E G S E P D S F W E A L G G K A T Y 1741 GTGGCAGAAGGCAGCGAGCCAGACAGCTTCTGGGAGGCCTTGGGTGGGAAGGCCACCTAC	
		601 R T S P R L K D K K M D A H P P R L F A 1801 CGCACGTCCCCGCGGCTGAAGGACAAGAAGATGGACGCCCACCCTCCTCGCCTCTTTGCC	
		621 C S N K I G R F V I E E V P G E F M Q E 1861 TGCTCCAACAAGATTGGACGTTTTGTGATCGAAGAGGTCCCTGGCGAGTTCATGCAGGAA	
		641 D L A T D D V M L L D T W D Q V F V W V 1921 GACCTGCCCACTGATGACGTCATGCTCCTGGACACCTGGGACCAGGTCTTTGTCTGGGTC	
		661 G K D S Q D E E K T E A L T S A K R Y I 1981 GGAAAGATTCTCAAGACGAGGAAAAGACGGAAGCCTTGACCTCTGCTAAGCGGTATATC	
		681 D T D P A H R D R R T P I T V V K Q G F 2041 GACACAGACCCAGCTCATCGCGATAGGCGTACCCCCATCACCGTCGTGAAGCAAGGCTTT	
		701 E P P S F V G W F L G W D D S Y W S V D 2101 GAGCCTCCGTCCTTCGTGGGCTGGTTCCTCGGCTGGGATGACAGCTACTGGTCTGTGGAT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		721 P L D R A L A E L A A - 2161 CCCTTGGACAGGGCCTTGGCTGAGCTGGCTGCCTGA	
Gi576646	Equus caballus Ig epsilon heavy chain (partial)	1 ggcacgagga atcacctgtg gttcttccta gttctggtgg ccgctcctac atgtgccccg 61 tcccaggtgc aactgaagga gtcaggacct ggcctggtga agccctcgca gaccctgtcc 121 ctcacctgca ctgtctctgg attctctttg actagttaca ctgtaggctg ggtcgccagg 181 ctccaggaaa aggactggaa tatgttgcgg ctatacgtaa tagtgggagt gcaaacttca 241 acccagaccc tgaagtcccg agccagcatc accagggacg cctcaaagag ccaagtttat 301 ctgacgctga acagcctgac agtcgaggac acggccgtct attactgtgc gaggtctctg 361 ccagtctctg gtaatggtta tagtttggtg aactattggg gccaggcatc tgtcaccgtc 421 tcatcagtct ccaagcagag ccccattatc ttgcccttgg ctgcctgctg caaagacacc 481 aagactacta acatcacact gggctgcctg gtcaagggct acttcccgga gccagtgacc 541 gtgacctggg atgcagggtc ccttaaccgg agcaccataa ccttccctgc cgtctttgac 601 caaacctctg gcctctacac caccatcagc agggtggtcg cctcggggaa gtgggccaag 661 cagaagttca cctgcaacgt ggtgcactcc caggagacct tcaacaagac cttcaacgca 721 tgcatcgtga ccttcacccc acccaccgtg aagctcttcc actcctcctg cgaccccggc 781 ggcgactccc ataccaccat ccagctcctg tgcctcatct ccgactacac ccctggcgac 841 atcgacatcg tttggctgat agacgggcag aaggtcgacg agcagttccc tcaacacggc 901 ctcgtgaagc aggagggcaa gctggcctcc acacacagcg agctcaacat cacccagggc 961 cagtgggcgt ccgaaaacac ctacacctgc caggtcactt acaaaagaca tgatctttta 1021 aggaccaggc cccgcaagtg cacagagtct gaaccccgcg gtgtgagcgt ctacctgagc 1081 ccgcccagcc ccctggacct gtacgtctct aaatcgccca agatcacctg cctggtggtg 1141 gacctggcca acgtgcaggg cttaagcctg aactggtccc gggagagcgg ggagcccctg 1201 cagaagcaca cactggcgac cagcgaacaa tttaacaaga cattctcggt cacgtccacc 1261 ctgcctgtgg acaccaccga ctggatcgag ggcgagactt acaagtgcac cgtgtcccac 1321 ccagacctgc ccagggaagt cgtgcgctcc atcgccaagg cccctggcaa gcgtttgtcc 1381 cccgaggtct acgtgttcct gccgcctgag gaggaccaga gctccaagga caaggtcacc 1441 ctcacctgcc tgatccagaa cttcttcccc gcggacatct ccgtacagtg gctgcgtaac 1501 aatgtcctaa tccagacaga ccagcaagcc accacacgcc ccaaaagcca atggccccga 1561 cccgccttct tcgtcttcag ccgcctagag gtcagccggg cggaatggga gcagaagaac 1621 aaatttgcct gcaaggtggt ccacgaggcg ctgtcccaaa ggaccctcca gaaagaggtg 1681 tccaaagacc ctggtaaatg atgccctctg cccgccgcct cccaccctcc caggctccct 1741 cctgctgggg tggaggtggg ggccagccag acctgctccg gtc	SEQ ID NO:135
		1 G T R N H L W F F L V L V A A P T C A P 1 GGCACGAGGAATCACCTGTGGTTCTTCCTAGTTCTGGTGGCCGCTCCTACATGTGCCCCG 21 S Q V Q L K E S G P G L V K P S Q T L S 61 TCCCAGGTGCAACTGAAGGAGTCAGGACCTGGCCTGGTGAAGCCCTCGCAGACCCTGTCC 41 L T C T V S G F S L T S Y T V G W V A R 121 CTCACCTGCACTGTCTCTGGATTCTCTTTGACTAGTTACACTGTAGGCTGGGTCGCCAGG 61 L Q E K D W N M L R L Y V I V G V Q T S	SEQ ID NO:136

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		181 CTCCAGGAAAAGGACTGGAATATGTTGCGGCTATACGTAATAGTGGGAGTGCAAACTTCA	
		81 T Q T L K S S R A S I T R D A S K S Q V Y	
		241 ACCCAGACCCTGAAGTCCCGAGCCAGCATCACCAGGGACGCCTCAAAGAGCCAACTTTAT	
		101 L T L N S L T V E D T A V Y Y C A R S L	
		301 CTGACGCTGAACAGCCTGACAGTCGAGGACACGGCCGTCTATTACTGTGCGAGGTCTCTG	
		121 P V S G N G Y S L V N Y W G Q A S V T V	
		361 CCAGTCTCTGGTAATGGTTATAGTTTGGTGAACTATTGGGGCCAGGCATCTGTCACCGTC	
		141 S S V S K Q S P I I L P L A A C C K D T	
		421 TCATCAGTCTCCAAGCAGAGCCCCATTATCTTGCCCTTGGCTGCCTGCTGCAAAGACACC	
		161 K T T N I T L G C L V K G Y F P E P V T	
		481 AAGACTACTAACATCACACTGGGCTGCCTGGTCAAGGCTACTTCCCGGAGCCAGTGACC	
		181 V T W D A G S L N R S T I T F P A V F D	
		541 GTGACCTGGGATGCAGGGTCCCTTAACCGGAGCACCATAACCTTCCCTGCCGTCTTTGAC	
		201 Q T S G L Y T T I S R V V A S G K W A K	
		601 CAAACCTCTGGCCTCTACACCACCATCAGCAGGGTGGTCGCCTCGGGAAGTGGGCCAAG	
		221 Q K F T C N V V H S Q E T F N K T F N A	
		661 CAGAAGTTCACCTGCAACGTGGTGCACTCCCAGGAGACCTTCAACAAGACCTTCAACGCA	
		241 C I V T F T P P T V K L F H S S C D P G	
		721 TGCATCGTGACCTTCACCCCACCCACCGTGAAGCTCTTCCACTCCTCCTGCGACCCCGGC	
		261 G D S H T T I Q L L C L I S D Y T P G D	
		781 GGCGACTCCCATACCACCATCCAGCTCCTGTGCCTCATCTCCGACTACACCCCTGGCGAC	
		281 I D I V W L I D G Q K V D E Q F P Q H G	
		841 ATCGACATCGTTTGGCTGATAGACGGGCAGAAGGTCGACGAGCAGTTCCCTCAACACGGC	
		301 L V K Q E G K L A S T H S E L N I T Q G	
		901 CTCGTGAAGCAGGAGGGCAAGCTGGCCTCCACACAGCGAGCTCAACATCACCCAGGGC	
		321 Q W A S E N T Y T C Q V T Y K R H D L L	
		961 CAGTGGGCGTCCGAAAACACCTACACCTGCCAGGTCACTTACAAAAGACATGATCTTTTA	
		341 R T R P R K C T E S E P R G V S V Y L S	
		1021 AGGACCAGGCCCCCGCAAGTGCACAGAGTCTGAACCCCGCGGTGTGAGCGTCTACCTGAGC	
		361 P P S P L D L Y V S K S P K I T C L V V	
		1081 CCGCCCAGCCCCCTGGACCTGTACGTCTCTAAATCGCCCAAGATCACCTGCCTGGTGGTG	
		381 D L A N V Q G L S L N W S R E S G E P L	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1141 GACCTGGCCAACGTGCAGGGCTTAAGCCTGAACTGGTCCCGGGAGAGCGGGGAGCCCCTG	
		401 Q K H T L A T S E Q F N K T F S V T S T	
		1201 CAGAAGCACACACTGGCGACCAGCGAACAATTTAACAAGACATTCTCGGTCACGTCCACC	
		421 L P V D T T D W I E G E T Y K C T V S H	
		1261 CTGCCTGTGGACACCACCGACTGGATCGAGGGCGAGACTTACAAGTGCACCGTGTCCCAC	
		441 P D L P R E V V R S I A K A P G K R L S	
		1321 CCAGACCTGCCCAGGGAAGTCGTGCGCTCCATCGCCAAGGCCCCTGGCAAGCGTTTGTCC	
		461 P E V Y V F L P P E E D Q S S K D K V T	
		1381 CCCGAGGTCTACGTGTTCCTGCCGCCTGAGGAGGACCAGAGCTCCAAGGACAAGGTCACC	
		481 L T C L I Q N F F P A D I S V Q W L R N	
		1441 CTCACCTGCCTGATCCAGAACTTCTTCCCCGCGGACATCTCCGTACAGTGGCTGCGTAAC	
		501 N V L I Q T D Q Q A T T R P K S Q W P R	
		1501 AATGTCCTAATCCAGACAGACCAGCAAGGCCACCACACCCCCAAAAGCCAATGGCCCGA	
		521 P A F F V F S R L E V S R A E W E Q K N	
		1561 CCCGCCTTCTTCGTCTTCAGCCGCCTAGAGGTCAGCCGGGCGGAATGGGAGCAGAAGAAC	
		541 K F A C K V V H E A L S Q R T L Q K E V	
		1621 AAATTTGCCTGCAAGGTGGTCCACGAGGCCCTGTCCCAAAGGACCCTCCAGAAAGAGGTG	
		561 S K D P G K -	
		1681 TCCAAAGACCCTGGTAAATGA	
Foe 545	Homo sapiens mRNA; cDNA DKFZp666I186 (from clone DKFZp666I186)		SEQ ID NO:137
		1 ggctagcaag gggcaagatt tacccacccc tgaccaggat aatggctacc acagcctgga	
		61 ggaggaacac agccttctcc ggatggatcc aaaacactgc agagataacc caacacagtt	
		121 tgttcctgct gctggagaca ttcctggaaa cacccaggaa tccactgaag aaaaaataga	
		181 attattaact acagaggttc cacttgcttt ggaagaagag agcccttctg aggctgtcc	
		241 atctagtgag atacctatgg aaaaggagcc tggagagggc cgaataagtg tagttgatta	
		301 ctcataccta gaaggtgacc ttcccatttc tgccagacca gcttgtagta acaaactgat	
		361 agattatatt ttgggaggtg catccagtga cctggaaaca agttctgatc cagaaggtga	
		421 ggattgggat gaggaagctg aggatgtgg tttgatagt gatagctcac tgtcagactc	
		481 agaccttgaa caagaccctg aagggcttca cctttgaac tctttctgca gtgtagatcc	
		541 ttataatccc cagaacttta cagcaacaat tcagactgct gccagaattg ttcctgaaga	
		601 gccttctgat tcagagaagg atttgtctgg caagtctgat ctagagaatt cctcccagtc	
		661 tggaagcctt cctgagaccc ctgagcatag ttctgcggag gaagatgact gggaatctag	
		721 tgcagatgaa gcagagagtc tcaaactgtg gaactcattc tgtaattctg atgacccta	
		781 caacccttta aatttaagg ctccttttca aacatcaggg gaaaatgaga aaggctgtcg	
		841 tgactcaaag accccatctg agtccattgt ggccatttct gagtgtcaca ccttactttc	
		901 ttgtaaggtg cagctgttgg ggagccaaga aagtgaatgt ccagactcgg tacagcgtga	
		961 cgttctttct ggaggaagac acacacatgt caaaagaaaa aaggtaacct tccttgaaga	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1021 agttactgag tattatataa gtggtgatga ggatcgcaaa ggaccatggg aagaattgc	
		1081 aagggatgga tgcaggttcc agaaacgaat tcaagaaaca gaagatgcta ttggatattg	
		1141 cttgacattt gaacacagag aaagaatgtt taatagactc cagggaacat gcttcaaagg	
		1201 acttaatgtt ctcaagcaat gttgagttgg cagcctgtag tcctagctag catacactac	
		1261 ctcttacctg agaggtgtct tttaaaaaca aatcttggca gctgtccttt gacatttttt	
		1321 ttttagagga aatgtaactt ggatctagtt taatttttt tttgcaaca tatcccactc	
		1381 agaaacattc aggtttgaag ccagccctga taatgaagga tgaactagtg tgatttctaa	
		1441 tcctcccttt tttgatttag ttggatgtgc ttttaaatgt cctttgcctg catgaggtgg	
		1501 aaagggacc tttttgagtt gtcatttgc actttcaaaa cttatttttct tggaaaacaa	
		1561 tatttatagg gcttaaagcc catttcatt tctaatctaa attatgtgtg cctatctgaa	
		1621 aacttgggc tctttcttgt ttctttccca aaattcagaa gttaatgggc ttttatgttt	
		1681 ttctatattt tttttatttc aatgatttgg cctgtctatg ttaggctaaa aaataacctt	
		1741 gtgtatgcta ccaacttaaa gtgcattatt ttgtgtcact ttttttttttc ttgtaaaaat	
		1801 gacttggatt gaaaatatgt ggtagccttt ttatttctac attaagttct acctaggata	
		1861 tttccaagga ctgccacaaa acccatatgt gcagtacttt actactttgg gaaagctgca	
		1921 tctttctacc acattttaac atctaatata tttaatttct ttgaagaggg ttctgtgtac	
		1981 gttattgtag ttcccagttt aatatagttc tttgtatctc ttaacaggtt gaagttattg	
		2041 caaaacactc tggaaagtaa taattacatc ataatcattt attttttaaa cttaaaagcc	
		2101 tagaaatttc ctagaaagaa aataggagac atctcagagc aatttggttt tggtgtatat	
		2161 gttctcaaca gaaaaccagt gttaatgaat atcatgcctc agcactgtca cttttaaaac	
		2221 ctgtcaggat cccactgtaa aattggaaat gggcagttct gaattttcac gtttgaaatg	
		2281 taaaatataa acttcagtca atatccaggt ttattgtgtc ctactattta ataatgagag	
		2341 aagtaatggc aaggccttta ctttcaggaa aggatagaag tatagattaa tgactggaaa	
		2401 gttttaatat atttagccca aaggttactt tgaattgaag tctttgcatt gactgtttgt	
		2461 gtttggttta tttgtttagc tttacaaggt acacataagt taggttgagg ggttgttaac	
		2521 ccttccgtgg tctgctttca ttccgtgtgc ttcctgtcac aggtaatgga aaacataagt	
		2581 agaataggtg acctcttagt tttgaactta tttaagtgtg gggatgaatt tttcatcaga	
		2641 agtgcttaca gggttactac ctcagtttac aatctacctg gtcattattt tatttctatc	
		2701 cagttctaag aactgcctcc actgtttata tattcataat taaacacatt gagaatgcaa	
		2761 cactataaaa gctggtcaaa ttttttgcaga gcccttattc tgtgtgtttt ttgttttttt	
		2821 ctttttttg agacagagtc tcgttcggtc ccccagcttg gagtgcagtg gcgcgatctc	
		2881 ggctcactgc aacctccgcc tcctgggttc acgcgattct cctgcctcag cctcccgagt	
		2941 agctgggatt acaggcacac accaccacgc ccggctaatt ttttgtgtct ttttagtaga	
		3001 gacggggttt cgctatgttg gccagactgg tcttgaactg ctgacctcgt gatccgcccg	
		3061 cctcggcctc tcaaagtgct gggattctgt gtgttttgtg cacctccact ttaggtaatc	
		3121 ataggagca catttacagg atggtctaat aacatgaaaa caggctagtt tcaagcaaca	
		3181 gcaatgtcgg ttggaaagca ggcgtcattt gccttgaaaa aagccttttg acaacataca	
		3241 ggcattcttt taaaaccagg ctgaaacatt ttatttccga gacttaacgt tgtgtttcct	
		3301 gtttcttaaa cctagcacct ctgtgtattt gaaaataatg agacatcttt cattggattt	
		3361 tggaaaattg ttccccatgg gattctaacc tcactaccaa atgagtgaaa gcttgattaa	
		3421 gagttcttcc atatactagc ctccttggaa gaagtgatca gaaggtgata agaaggacag	
		3481 aaaggactat tttaaagttg gactgaagga gaaaaaagca aaattcttgt ttcatcccaa	
		3541 ttctagttag aacaaagtta aaccccccgta atcttaaaga gaaaatcttt ggaggtttta	
		3601 attaaacatt ttatacattt aaagtcttgt taatggtgct ttaagtgtca atgtagcatg	
		3661 taaaaggctt tgtacagaca ggtaaaagtt ccatttctga gtgatgaaat gtaacacttc	
		3721 ttcatcttta acttgaaatc aaaactatca gatttttattt ttgtataatt taaggaaggt	
		3781 aaagttaggg gactagaaga ctctaaattg gcttctacag atcaataatt taaatgtaac	
		3841 tagttgggat tttatagtta aaattatatt tgtgtatata acataactaa tctgtaaatt	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		3901 gtaataaata tatttgcaat tatcaaaaaa aaaaaaaaaa a 1 A S K G Q D L P T P D Q D N G Y H S L E 2 GCTAGCAAGGGGCAAGATTTACCCACCCCTGACCAGGATAATGGCTACCACAGCCTGGAG 21 E E H S L L R M D P K H C R D N P T Q F 62 GAGGAACACAGCCTTCTCCGGATGGATCCAAAACACTGCAGAGATAACCCAACACAGTTT 41 V P A A G D I P G N T Q E S T E E K I E 122 GTTCCTGCTGCTGGAGACATTCCTGGAAACACCCAGGAATCCACTGAAGAAAAAATAGAA 61 L L T T E V P L A L E E E S P S E G C P 182 TTATTAACTACAGAGGTTCCACTTGCTTTGGAAGAAGAGAGCCCTTCTGAGGGCTGTCCA 81 S S E I P M E K E P G E G R I S V V D Y 242 TCTAGTGAGATACCTATGGAAAAGGAGCCTGGAGAGGGCCGAATAAGTGTAGTTGATTAC 101 S Y L E G D L P I S A R P A C S N K L I 302 TCATACCTAGAAGGTGACCTTCCCATTTCTGCCAGACCAGCTTGTAGTAACAAACTGATA 121 D Y I L G G A S S D L E T S S D P E G E 362 GATTATATTTTGGGAGGTGCATCCAGTGACCTGGAAACAAGTTCTGATCCAGAAGGTGAG 141 D W D E E A E D D G F D S D S S L S D S 422 GATTGGGATGAGGAAGCTGAGGATGATGGTTTTGATAGTGATAGCTCACTGTCAGACTCA 161 D L E Q D P E G L H L W N S F C S V D P 482 GACCTTGAACAAGACCCTGAAGGGCTTCACCTTTGGAACTCTTTCTGCAGTGTAGATCCT 181 Y N P Q N F T A T I Q T A A R I V P E E 542 TATAATCCCCAGAACTTTACAGCAACAATTCAGACTGCTGCCAGAATTGTTCCTGAAGAG 201 P S D S E K D L S G K S D L E N S S Q S 602 CCTTCTGATTCAGAGAAGGATTTGTCTGGCAAGTCTGATCTAGAGAATTCCTCCCAGTCT 221 G S L P E T P E H S S G E E D D W E S S 662 GGAAGCCTTCCTGAGACCCCTGAGCATAGTTCTGGGGAGGAAGATGACTGGGAATCTAGT 241 A D E A E S L K L W N S F C N S D D P Y 722 GCAGATGAAGCAGAGAGTCTCAAACTGTGGAACTCATTCTGTAATTCTGATGACCCCTAC 261 N P L N F K A P F Q T S G E N E K G C R 782 AACCCTTTAAATTTTAAGGCTCCTTTTCAAACATCAGGGGAAAATGAGAAAGGCTGTCGT 281 D S K T P S E S I V A I S E C H T L L S 842 GACTCAAAGACCCCATCTGAGTCCATTGTGGCCATTTCTGAGTGTCACACCTTACTTTCT 301 C K V Q L L G S Q E S E C P D S V Q R D	SEQ ID NO:138

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		902 TGTAAGGTGCAGCTGTTGGGGAGCCAAGAAAGTGAATGTCCAGACTCGGTACAGCGTGAC 321 V L S G G R H T H V K R K K V T F L E E 962 GTTCTTTCTGGAGGAAGACACACACATGTCAAAAGAAAAAAGGTAACCTTCCTTGAAGAA 341 V T E Y Y I S G D E D R K G P W E E F A 1022 GTTACTGAGTATTATATAAGTGGTGATGAGGATCGCAAAGGACCATGGGAAGAATTTGCA 361 R D G C R F Q K R I Q E T E D A I G Y C 1082 AGGGATGGATGCAGGTTCCAGAAACGAATTCAAGAAACAGAAGATGCTATTGGATATTGC 381 L T F E H R E R M F N R L Q G T C F K G 1142 TTGACATTTGAACACAGAGAAAGAATGTTTAATAGACTCCAGGGAACATGCTTCAAAGGA 401 L N V L K Q C - 1202 CTTAATGTTCTCAAGCAATGTTGA	
Foe 1072	Transducin (beta)-like 1X-linked receptor 1	1 gttttaggat taaatacctt ttacagatac tgaaagtgcc tccttttgtg gtgtaaaaaa 61 caaattatgg tgcaaaaagt aatcactaga ttgaaataca tgaaggtttt ttgctttttg 121 acatacgaaa atgtcaagag aaaggccaaa gatttgtact ttttcactta caaagcactc 181 ctttttccct taaacttctt tctgtcaaat tagatttaat gagagagtac tatttttaag 241 gagctatctg tttatgtaga atgattttgt taagagtaat gtaaactatt attgagtaga 301 ggcctaaaga ggactgtgca tttttgctat ttaaaggaat cacaaatgat catacttaag 361 tgagcaaaaa tgacaagttt tactagctaa gtagagaaat aaatctcaaa tgcagcgcta 421 caatttttcat tatcttaagt acattgtaca tttctacaga acctgtgatt attctcgcat 481 gataaggatg gtacttgcat atggtgaatt actactgttg acagtttccg cagaaatcct 541 atttcagtgg accaacattg tggcatggca gcaaatgcca acattttgtg gaatagcagc 601 aaatctacaa gagaccctgg ttggtttttc gttttgtttt ctttgttttt tccccttct 661 cctgaatcag cagggatgga aggagggtag ggaagttatg aattactcct tccagtagta 721 gctctgaagt gtcacattta atatcagttt tttttaaaca tgattctagt taaatgtaga 781 agagagaaga aagaggaagt gttcactttt ttaatacact gatttagaaa tttgatgtct 841 tatatcagta gttctgaggt attgatagct tgctttattt ctgcctttac gttgacagtg 901 ttgaagcagg gtgaataact agggcatata ttttttttt tttgtaagct gtttcatgat 961 gttttctttg gaatttccgg ataagttcag gaaaacattc tgcatgttgt atctagtctg 1021 atgtacttat ccatctcatt acaaacaaaa acacacagac tgcatttgta gctctgtaat 1081 ccttgaatac ggaagtaaat tttcttcttt cctgactttg acattgtagc tatactgttt 1141 ccatttttgt ttttacaaat cctttgggtc taattctgtg agcctaccta tagcactgga 1201 ttaaaatgtc tgcatcattt ctttagttat ccagttaact ttaaaactgt tgtaaaagtg 1261 taaaccagcc catgacaggt ttttgtacat gttaaagaac ttcattgttc agttttcatg 1321 attattgtgt aaggaagact gatgtagatg ttctgtgctg tcctggacca tgttaattac 1381 acttacgacg tattttagtt ccacatcaca atgatttgtc cccagtgacc cttttatcct 1441 ttctaggcac atttcttgtt gttgttgttg ttgcagttcc cctttgcatt gtattgcttt 1501 gacaactgta atttgaatca gatctgaaag aggtccagaa taaaatatat tttgatatta 1561 aaaaaaaaaa aaaaaaaaca aaaaaaaaaa aaaaaaaaa 1 M Q R Y N F H Y L K Y I V H F Y R T C D	SEQ ID NO:139 SEQ ID NO:140

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1 ATGCAGCGCTACAATTTTCATTATCTTAAGTACATTGTACATTTCTACAGAACCTGTGAT 21 Y S R M I R M V L A Y G E L L L L T V S 61 TATTCTCGCATGATAAGGATGGTACTTGCATATGGTGAATTACTACTGTTGACAGTTTCC 41 A E I L F Q W T N I V A W Q Q M P T F C 121 GCAGAAATCCTATTTCAGTGGACCAACATTGTGGCATGGCAGCAAATGCCAACATTTTGT 61 G I A A N L Q E T L V G F S F C F L C F 181 GGAATAGCAGCAAATCTACAAGAGACCCTGGTTGGTTTTTCGTTTTGTTTTCTTTGTTTT 81 F P L L L N Q Q G W K E G R E V M N Y S 241 TTCCCCCTTCTCCTGAATCAGCAGGGATGGAAGGAGGGTAGGGAAGTTATGAATTACTCC 101 F Q - 301 TTCCAGTAG	
Foe 1060	Homo sapiens 15 kDa selenoprotein, transcript variant 1	1 gcagccagaa acctgcggaa aatggtagcg atggcggctg ggccgagtgg gtgtctggtg 61 ccggcgtttg ggctacggtt gttgttggcg actgtgcttc aagcggtgtc tgcttttggg 121 gcagagtttt catcggaggc atgcagagag ttaggctttt ctagcaactt gctttgcagc 181 tcttgtgatc ttctcggaca gttcaacctg cttcagctgg atcctgattg cagaggatgc 241 tgtcaggagg aagcacaatt tgaaaccaaa aagctgtatg caggagctat tcttgaagtt 301 tgtggatgaa aattgggaag gttccctcaa gtccaagctt ttgttaggag tgataaaccc 361 aaactgttca gaggactgca aatcaagtat gtccgtggtt cagaccctgt attaaagctt 421 ttggacgaca atgggaacat tgctgaagaa ctgagcattc tcaaatggaa cacagacagt 481 gtagaagaat tcctgagtga aaagttggaa cgcatataaa tcttgcttaa attttgtcct 541 atccttttgt taccttatca aatgaaatat tacagcacct agaaaataat ttagttttgc 601 ttgcttccat tgatcagtct tttacttgag gcattaaata tctaattaaa tcgtgaaatg 661 gcagtatagt ccatgatatc taaggagttg gcaagcttaa caaaacccat tttttataaa 721 tgtccatcct cctgcatttg ttgataccac taacaaaatg ctttgtaaca gacttgcggt 781 taattatgca aatgatagtt tgtgataatt ggtccagttt tacgaacaac agatttttaa 841 attagagagg ttaacaagac agatgattac tatgcctcat gtgctgtgtg ctctttgaaa 901 ggaatgacag cagactacaa agcaaataag atatactgag cctcaacaga ttgcctgctc 961 ctcagagtct ctcctatttt tgtattaccc agctttcttt ttaatacaaa tgttatttat 1021 agtttacaat gaatgcactg cataaaaact ttgtagcttc attattgtaa aacatattca 1081 agatcctaca gtaagagtga aacattcaca aagatttgcg ttaatgaaga ctacacagaa 1141 aacctttcta aggatttgtg tggatcagat acatacttgg caaatttttg agttttacat 1201 tcttacagaa aagtccattt aaaagtgatc atttgtaaga ccaaaatata aataaaaagt 1261 ttcaaaaacc aaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1 M V A M A A G P S G C L V P A F G L R L 1 ATGGTAGCGATGGCGGCTGGGCCGAGTGGGTGTCTGGTGCCGGCGTTTGGGCTACGGTTG 21 L L A T V L Q A V S A F G A E F S S E A 61 TTGTTGGCGACTGTGCTTCAAGCGGTGTCTGCTTTTGGGGCAGAGTTTTCATCGGAGGCA	SEQ ID NO:141 SEQ ID NO:142

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		41 C R E L G F S S N L L C S S C D L L G Q 121 TGCAGAGAGTTAGGCTTTTCTAGCAACTTGCTTTGCAGCTCTTGTGATCTTCTCGGACAG 61 F N L L Q L D P D C R G C C Q E E A Q F 181 TTCAACCTGCTTCAGCTGGATCCTGATTGCAGAGGATGCTGTCAGGAGGAAGCACAATTT 81 E T K K L Y A G A I L E V C G U K L G R 241 GAAACCAAAAAGCTGTATGCAGGAGCTATTCTTGAAGTTTGTGGATGNAAATTGGGAAGG 101 F P Q V Q A F V R S D K P K L F R G L Q 301 TTCCCTCAAGTCCAAGCTTTTGTTAGGAGTGATAAACCCAAACTGTTCAGAGGACTGCAA 121 I K Y V R G S D P V L K L L D D N G N I 361 ATCAAGTATGTCCGTGGTTCAGACCCTGTATTAAAGCTTTTGGACGACAATGGGAACATT 141 A E E L S I L K W N T D S V E E F L S E 421 GCTGAAGAACTGAGCATTCTCAAATGGAACACAGACAGTGTAGAAGAATTCCTGAGTGAA 161 K L E R I - 481 AAGTTGGAACGCATATAA	
BM781417	No homology	1 GGCACGAGTCTGAAGTCACTGATTATAAAGAATATGCAATCCATTTGGGATTTATTGCAT 61 TTAAAGAAAGCAGATTATTAAAACAGTAGGTATGATAAATACAGTAAGAAAATAACTTTA 121 AATTTCAAACAAAACAAAGTAAATGAAGGACAGAATTCAGTCAATAAGAATAAGCAATGT 181 AAAGGCAATAAAGTAGCTAAATCACTTAGTGCTTAATTAGATCAAAGAAGGAAAAAGCAA 241 CTGATTCTTCCTCATGACAGTTTCCCAGCTAGATCTGAGGATTGAAGTTATTTAGAAAGT 301 ATGTTTTATAACAATTAGAAATATAATAAAGATGTAAATCATGTTTATTAAAAGTTAAAG 361 TTATTTGCTTAGTGGTACATAAAAGGCTTCAGAAAATTCAAGTTTAACAAAAAATGGAAG 421 TGTAATCAAAGAAAGTGCACTTAAAGCTGTTTGTCAGCAATTAAAAAGTAGCTTACTATT 481 ACTATACTGGTTACTAGGAGACGACTTTTCAATCGCAAAGAGCGTAATAATAACAATTCT 541 CTTTCAAAAGT	SEQ ID NO:143
BM781334	No homology	1 GGCACGAGATTGCATTCCTTTTGGAGACCTGTTTCCCTGGTGACACCTCTGGACTTTCCA 61 GGACCTGCCTGGCAGCCTGAGGGCACCTGGGGGCAGGGGGCCCTGAGCATGTGGGGCCAC 121 GTGCAGGCGCGGGTGTGGCCCAAATACGGGGCAGAGGTGACATGCAGTCACCTGATGACT 181 TGAAATCAGCCAGTGGCTGCAGAGGCCTCGCGCTGTGGCCTCATTCAGTCAGACTTGACT 241 CTGTTCTGCCTGAGCTAGGGGCTTCGGGTCTGAAGGGGACGTTGGCTCACTGGCGCCCGG 301 CCTTGGGGGCGCCCTGGTTGCATGGGTAGAAGTGCCTGACGAGGTCCCTCTTGTTGACCT 361 TCCCCATCTGGTTCCGCGGGATCTCTTCCACCAGCAGAAGCTCCGAGGGCACCACGTACG 421 GGGCCATGACGTCTCTTGCCCACTCTTTGAGCTCCCTGTGGGACAGCGAGTGTCCCTCTT 481 GAAGGGTCACTACTGCAGTGACCCGCTGGCCCCACGTCATGTCCGGAACTCCAATCACAG 541 CCACATCTNGTGA	SEQ ID NO:144

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
BM781186	Membrane-spanning 4-domains, subfamily A, member 6A, transcript variant 1	1 GGGAGGTAAGTAGAAACCGTTGATGGGACTGAGAAACCAGAGTTAAAACCTCTTTGGAGC 61 TTCTGAGGGCTCAGCTGGAACCAACGGGCACAGTTGGCAGCACCATCATGATGTCACAAC 121 CCAAGACCAATGAGACCTTCATAGCTCTCACACCAAATGGCATCAGCTTCCTCCAAACAG 181 AGGATCCCAAACTTACCAACAAGAGGCAGGACAGCCTGAAGAAACATCTAAAGGCAGAGG 241 TCAAAGTTCTCGGGACTATCCAGATCCTGTGTGGGATGATGGTGTTGAGTTTGGGAATTA 301 TTTTGGCATCGGCTTCCTTCTCTCAGCATTTTACCCAAGCGTTTTCTATTCTGTTGAAGG 361 CTGCTTACCCATTCATAGGAGCCTTGTGTTTTGTCATCTCTGGATCTCTATCAATCATCA 421 CAGAGAAAAAGTCCACTAAGCCTTTGGTTCAGAGCAGCCTAGCTGCAAACATTCTGAGCT 481 CTCTATCAGCTCTGGTGGGTTTCATCCTCCTTTCTGTCAAACAGGCCACCTTAAATCCTG 541 CCTCACTGCAGTGTGAGTTGGACAAAAATAATATACCAACAAGAAGTTATGTTTCTTACT 601 TTTATCATGATTCACTTTATACCACGGACTGCTATACAGCCAAAGCCAGTCTGGCTGGAT 661 CCCTCTCTCTGATGCTGATTTGCACTCTGCTGGAATTCTGCCTAGCTGTGCTCACTGCTG 721 TGCTGCGGTGGAAACAGGCTTACTCTGACTTCCCTGGGAGTGTACTTTTCCTGCCTCACA 781 GTTACATTGGTAATTCTGGCATGTCCTCAAAAATGACTCATGACTGTGGATATGAAGAAC 841 TATTGACTTCTTAAGAAAAAAGGGAGAAATATTAATCAGAAAGTTGATTCTTATGATAAT 901 ATGGAAAAGTTAACCATTATAGAAAAGCAAAGCTTGAGTTTCCTAAATGTAAGCTTTTAA 961 AGTAATGAACATTAAAAAAAACCATTATTTCACTGTCATTTAAGATATGTGTTCATTGGG 1021 GATCTCTTGATTTGCCTGACATTGACTTCAGCAAAAGCACGGGGCTGTAAATTACCATTT 1081 ACTAGATTAGCCAAATAGTCTGAATTTCCAGAAAACAAGGCAGAATGATCATTCCCAGAA 1141 ACATTTCCCAGAAAATGTTTCCCAGAAAACTAGACAGAATGATCATTCAATGGATCACAG 1201 TGAAGCAAAGGACACAACTTTTTATTGTACCCCTTAATTGTCAACAGGAGTTAACTGATT 1261 TGTTGTGGTGCTCAGACTTTTTTATACAGGTGCTAGTGTTTTATCCTATGTATTTTAACT 1321 CATTAGTGCATAAAGGCAAGCCCCATATAATGAAGTCTCAGGGTATATGAAAGTAGCTGG 1381 CTTCAAAATAAAATTTTTGAGTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	SEQ ID NO:145
		1 M M S Q P K T N E T F I A L T P N G I S 1 ATGATGTCACAACCCAAGACCAATGAGACCTTCATAGCTCTCACACCAAATGGCATCAGC 21 F L Q T E D P K L T N K R Q D S L K K H 61 TTCCTCCAAACAGAGGATCCCAAACTTACCAACAAGAGGCAGGACAGCCTGAAGAAACAT 41 L K A E V K V L G T I Q I L C G M M V L 121 CTAAAGGCAGAGGTCAAAGTTCTCGGGACTATCCAGATCCTGTGTGGGATGATGGTGTTG 61 S L G I I L A S A S F S Q H F T Q A F S 181 AGTTTGGGAATTATTTTGGCATCGGCTTCCTTCTCTCAGCATTTTACCCAAGCGTTTTCT 81 I L L K A A Y P F I G A L C F V I S G S 241 ATTCTGTTGAAGGCTGCTTACCCATTCATAGGAGCCTTGTGTTTTGTCATCTCTGGATCT 101 L S I I T E K K S T K P L V Q S S L A A 301 CTATCAATCATCACAGAGAAAAAGTCCACTAAGCCTTTGGTTCAGAGCAGCCTAGCTGCA 121 N I L S S L S A L V G F I L L S V K Q A 361 AACATTCTGAGCTCTCTATCAGCTCTGGTGGGTTTCATCCTCCTTTCTGTCAAACAGGCC 141 T L N P A S L Q C E L D K N N I P T R S	SEQ ID NO:146

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		421 ACCTTAAATCCTGCCTCACTGCAGTGTGAGTTGGACAAAAATAATATACCAACAAGAAGT	
		161 Y V S Y F Y H D S L Y T T D C Y T A K A	
		481 TATGTTTCTTACTTTTATCATGATTCACTTTATACCACGGACTGCTATACAGCCAAAGCC	
		181 S L A G S L S L M L I C T L L E F C L A	
		541 AGTCTGGCTGGATCCCCTCTCTCTGATGCTGATTTGCACTCTGCTGGAATTCTGCCTAGCT	
		201 V L T A V L R W K Q A Y S D F P G S V L	
		601 GTGCTCACTGCTGTGCTGCGGTGGAAACAGGCTTACTCTGACTTCCCTGGGAGTGTACTT	
		221 F L P H S Y I G N S G M S S K M T H D C	
		661 TTCCTGCCTCACAGTTACATTGGTAATTCTGGCATGTCCTCAAAAATGACTCATGACTGT	
		241 G Y E E L L T S -	
		721 GGATATGAAGAACTATTGACTTCTTAA	
BM781178	No homology		
		1 GCAGTCATATTTTATTCATTGCTTGGGCAATTCGAAATTGCCATCGCCCCCGTCTGTCCC	SEQ ID NO:147
		61 CACCATTGATTCTAAGGTGACATAAGAACTGGTGATAAATCTAAACTGTTTTACCTCTTA	
		121 AATGCCACATCATAGATCACAGTTGCCAAAGAGAAGATAACGAACCATCTATTGAAGGAA	
		181 ATGGAGGCTATCGTCATGGCAGGGGAGCAGTCCTGTGCGGGTGTTTAAGGCATCCCACTG	
		241 TAGACTCTTCTCTCG	
BM781174	GM2 ganglioside activator		
		1 GTTAACTCCGCCCTGACCCACCCTTCCCGATGCAGTCCCTGATGCAGGCTCCGTTCCTGA	SEQ ID NO:148
		61 TCGCCCTGGGCTTGCTTCTCGCGGCCCTGCGCCAAGCCCACCTGAAAAAGCCATCCCAGC	
		121 TCCGTAGCTTTCCTGGGATAACTGTGATGAGGGGAAGGACCCTATGGTGCTCAAAAGCC	
		181 TGACTCTGGAACCTGACCCCATTGCCGTTCCTGGGAACGTGACCCTCAGTGTCGTGGGCA	
		241 GCACCAGTGTCCCCCTGAGTTCTCCTCTGAAGGTGGATTTAGTTTTGGAGAAGGAGGTGG	
		301 CTGGCCTCTGGATCAAGATCCCATGCACAGACTACATTGGCAGCTGTACCTTTGAACACT	
		361 TCTGTGATGTGCTTGACATGTTAATTCCTACTGGGCAGCCCTGCCCAGAGCCCCTGCACA	
		421 CCTTTGGGCTTCCCTGCCACTGTCCCTTCAAAGAAGGCACCTACTCACTGCCCAAGAGTA	
		481 CTTTCCCCTTGCCTGACCTGGAGCTGCCCAGCTGGCTCAGCAACGCGGAACTACCGTGTCC	
		541 AGAGCATCCTGAGCAGCGGTGGGAAACGTCTGGGCTGTGTCAAGATCACTGCCTCTCTAA	
		601 AGGGCATATAGCATGGCATCTGCCACAGCAGAATGGAGCGGTGTGAGGAAGGTCCCTTTT	
		661 CCTCTGTTTTGTGTTTGCCAAGGCCAAACTCCCACTCTCTGCCCCCCTTTAATCCCCTTT	
		721 CTACAGTGAGTCCACTACCCTCACTGAAAATCATTTTGTACCACTTACATTTTAGGCTGG	
		781 GGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTTCTTGATAGCCCAGGGCATC	
		841 TGCTGGGCTGACCACGTTACTCATCCCCGTTAACATTCTCTCTAAAGAGCCTCGTTCATT	
		901 TCCAAAGCAGTTAAGGAATGGGAACCAGAGTGTTTTAGGACCTGAAGAATCTTTATGACT	
		-961 CTCTCTCTTTCACTCTTTTTTTTTTGTCACTAACGTTAAAAGCGAAGTGAGAGTATTAAC	
		1021 GTTTTTGTTCTCCTCCGGCCCCCTGTTACAATGAAGGGGCAAAAGTATTTGCTCTTAGTC	
		1081 TATTCCTCCCTTAACTTCTGTGACTAATTTTTATTTCCTTTCTAGATTTGCCCAATTAAT	
		1141 ACTAGGGTGCAGTGTATCCTGGAGAGGTAGGGTGTGTGGGGGGACGCAATCCCTTGGGGGAG	
		1201 ATATTAGGAGTGCTCTGTTGTTTACAAACTCAGGTACCCGCAGGGCCTAGCAAGAGACTT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1261 AAATGACTGATAAGAACCGTGAGAAACATGTTGCTTCCAGGCTTGATTTCGATTTTTCGC 1321 TTTTTTTTTTTGGGACGGAGTCTCGCTTTGTCACCAGGCTGGAGTGCAGTGGTGCAATCT 1381 CACCTCACTGCAACCTCCGCCTCCTGGGTTCAAGCAATTCTCCTGCCTCAGCCTCCCAAG 1441 TAGCTTGGACTACAGGCCCTGCCACCACGCCCGGCTAATTTGTGTATTTTTAGTAGAGAT 1501 GGGGTTTCACCATGTTGGCCAGGATGGTCTCGATCTCTTGACCTCGTGATCCGTCCACCT 1561 TGGCCTTGCAAAGCGCTGGATTACAGGCATGAGCCACTACACCCAGCCGATTTTTCCTTT 1621 TTGATTAAAGATGCTATTACAATGTAAATATTTCTTACACAGAAAGTCACAGCACATGTG 1681 CCCATTGATACAAGGCTGCTGAGGCCTGGTCTCCAGTTGGAAATATAATTAAGGGTGGCA 1741 GGGACTGGAGTCAGTTGGAGAGTGCATAGCCAGTCTGTGAAGACAACTGCCAGATACTGG 1801 CAATACTCCAGCCTGGTGACAGAGTGAGACTCTGTCTCAAAAAAAAAGTTTCAATGTTTA 1861 CTCCTAGAGAAGCCAAAAATCCAGATTTGTATATGAAATCTTACCATTTTAAAAGATTGG 1921 CAGCTAATTATTTTTTTAAAAAGCTGTGCAGTGTGATGTGTCCCAAACGGACTGGCTCAT 1981 GGGTGGCCACGTCACAACCTCTGATCTCAGACCGTGCATGCCTTGTCCTCTTAAGACAAC 2041 TCCTGTGGCACCGTTTCTCCCTCCACAGGGCCAAAGCCATAGTGTCCGGTCCCAAGGACA 2101 AGGCTCTTCCAGTGCTAGGAGAGGTATGAGCAGCCTCTCACCTGTGAGCTGTGGGGATCA 2161 CAAGGCTGCCTGCCTCAGTCTTGGAGTCCTGTTGGGTGAATGAGGCAGATGGGAAAGAGC 2221 CTCACCAGCAGCTGCTTTTGGAGCAGGGGTCCAAGGAAGAGAGGGTGGCCTCGACATCAA 2281 ACTGCCTGGATTTTTCTACCACCCTGTTACATCATAACAACTTCTGAAACACACACCAGC 2341 CCTGAGTTCTGGGCTCATTTGAAGCCTGGAATAGCAATAAATCTTTTTAACTTGCAAAAA 2401 AAAAAAAAAAAA	
		1 M Q S L M Q A P F L I A L G L L L A A P 1 ATGCAGTCCCTGATGCAGGCTCCGTTCCTGATCGCCCTGGGCTTGCTTCTCGCGGCCCCT	SEQ ID NO:149
		21 A Q A H L K K P S Q L R S F S W D N C D 61 GCGCAAGCCCACCTGAAAAAGCCATCCCAGCTCCGTAGCTTTTCCTGGGATAACTGTGAT	
		41 E G K D P M V L K S L T L E P D P I A V 121 GAGGGGAAGGACCCTATGGTGCTCAAAAGCCTGACTCTGGAACCTGACCCCATTGCCGTT	
		61 P G N V T L S V V G S T S V P L S S P L 181 CCTGGGAACGTGACCCTCAGTGTCGTGGGCAGCACCAGTGTCCCCCTGAGTTCTCCTCTG	
		81 K V D L V L E K E V A G L W I K I P C T 241 AAGGTGGATTTAGTTTTGGAGAAGGAGGTGGCTGGCCTCTGGATCAAGATCCCATGCACA	
		101 D Y I G S C T F E H F C D V L D M L I P 301 GACTACATTGGCAGCTGTACCTTTGAACACTTCTGTGATGTGCTTGACATGTTAATTCCT	
		121 T G Q P C P E P L H T F G L P C H C P F 361 ACTGGGCAGCCCTGCCCAGAGCCCCTGCACACCTTTGGGCTTCCCTGCCACTGTCCCTTC	
		141 K E G T Y S L P K S T F P L P D L E L P 421 AAAGAAGGCACCTACTCACTGCCCAAGAGTACTTTCCCCTTGCCTGACCTGGAGCTGCCC	
		161 S W L S N G N Y R V Q S I L S S G G K R 481 AGCTGGCTCAGCAACGGGAACTACCGTGTCCAGAGCATCCTGAGCAGCGGTGGGAAACGT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		181 L G C V K I T A S L K G I - 541 CTGGGCTGTGTCAAGATCACTGCCTCTCTAAAGGGCATATAG	
BM780906.V1.3_at	No Homology	1 GGGGTTTCTCCCCTCCTTTCCCTTTACCCGCAGTATCAAGCACAAGAATTGTTGGATTAA 61 AAAAAGAACTGATATCTTAGAACCCGAAAGAATCAATTGAATAGGATAAATCAGTACGTC 121 AGTGGTGGAGCTTTTGCCTGTAGCTTGAGAGGGGAAAGGTGGGAGGGAAAGGAGAAAACG 181 AAAGCTGAAACACATCTCTTGGGTCCTCCTGTTCCGTTTTCAAGGACCAGTCAGCTTCCC 241 ATCATAGTTTTGCCG	SEQ ID NO:150
BM735585	Fc-epsilon-receptor gamma-chain	1 CAGAACGGCCGATCTCCAGCCCAAGATGATTCCAGCAGTGGTCTTGCTCTTACTCCTTTT 61 GGTTGAACAAGCAGCGGCCCTGGGAGAGCCTCAGCTTTGCTATATTCTGGATGCCATCCT 121 GTTCTTGTATGGTATTGTCCTCACCCTGCTCTACTGTCGACTCAAGATCCAGGTGCGAAA 181 GGCAGCTATAGCCAGCTATGAGAAATCAGATGCCGTTTACACGGGCTTGAGTACCCGGAC 241 CCAGGAGACTTATGAGACTCTGAAGCATGAGAAACCGCCACAGTAACTTTAGAATAGATG 301 CGGTCATATTCTTCTTTGGCTTCTGGTTCTTCCAGCCCTCATGGTTGGCATCACACATGT 361 CTCCCTGCCATTAATGCTAGCTGACCCTACCCCTGTAATGATGCTATGCCCCCCATTAAC 421 GGACATCAGTGGTTCCTCTTCCCTGTTAAACACCTATGCTCAGATGCTATTCATTAATGT 481 TTATATTCTAGTCTCACTCTCTTGTCCCACCCTTCTTCTCTTCCCCATTCCCAACTCCAG 541 CTAAAATATGGGAAGGGAGAACCCCCAATAAAACTGCCATGGACTGGACTC 1 M I P A V V L L L L L L V E Q A A A L G 1 ATGATTCCAGCAGTGGTCTTGCTCTTACTCCTTTTGGTTGAACAAGCAGCGGCCCTGGGA 21 E P Q L C Y I L D A I L F L Y G I V L T 61 GAGCCTCAGCTTTGCTATATTCTGGATGCCATCCTGTTCTTGTATGGTATTGTCCTCACC 41 L L Y C R L K I Q V R K A A I A S Y E K 121 CTGCTCTACTGTCGACTCAAGATCCAGGTGCGAAAGGCAGCTATAGCCAGCTATGAGAAA 61 S D A V Y T G L S T R T Q E T Y E T L K 181 TCAGATGCCGTTTACACGGGCTTGAGTACCCGGACCCAGGAGACTTATGAGACTCTGAAG 81 H E K P P Q - 241 CATGAGAAACCGCCACAGTAA	SEQ ID NO:151 SEQ ID NO:152
BM735576	Minor histocompatibility antigen H13 isoform 1 (H13)	1 cgtggctttc cctgcagagc cggtgtctcc gcctgcgtcc ctgctgcagc aaccggagct 61 ggagtcggat cccgaacgca ccctcgccat ggactcggcc ctcagcgatc cgcataacgg 121 cagtgccgag gcaggcggcc ccaccaacag cactacgcgg ccgccttcca cgcccgaggg 181 catcgcgctg gcctacggca gcctcctgct catggcgctg ctgcccatct tcttcggcgc 241 cctgcgctcc gtacgctgcg cccgcggcaa gaatgcttca gacatgcctg aaacaatcac 301 cagccgggat gccgcccgct tccccatcat cgccagctgc acactcttgg ggctctacct 361 ctttttcaaa atattctccc aggagtacat caacctcctg ctgtccatgt atttcttcgt	SEQ ID NO:153

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		421 gctgggaatc ctggccctgt cccacaccat cagcccttc atgataagt ttttccagc 481 cagctttcca aatcgacagt accagctgct cttcacacag ggttctgggg aaaacaagga 541 agagatcatc aattatgaat ttgacaccaa ggacctggtg tgcctgggcc tgagcagcat 601 cgttggcgtc tggtacctgc tgaggaagca ctggattgcc aacaacctt ttggcctggc 661 ctcctccctt aatggagtag agctcctgca cctcaacaat gtcagcactg gctgcatcct 721 gctgggcgga ctcttcatct acgatgtctt ctgggtattt ggcaccaatg tgatggtgac 781 agtggccaag tccttcgagg caccaataaa attggtgttt ccccaggatc tgctggagaa 841 aggcctcgaa gcaaacaact ttgccatgct gggacttgga gatgtcgtca ttccagggat 901 ctccattgcc ttgctgctgc gctttgacat cagcttgaag aagaataccc acacctactt 961 ctacaccagc tttgcagcct acatcttcgg cctgggcctt accatcttca tcatgcacat 1021 cttcaagcat gctcagcctg ccctcctata cctggtcccc gcctgcatcg gttttcctgt 1081 cctggtggcg ctggccaagg gagaagtgac agagatgttc agttatgagg agtcaaatcc 1141 taaggatcca gcggcagtga cagaatccaa agagggaaca gaggcatcag catcgaaggg 1201 gctggagaag aaagagaaat gatgcagctg gtgcccgagc ctctcagggc cagaccagac 1261 agatgggggc tgggcccaca caggcgtgca ccggtagagg gcacaggagg ccaagggcag 1321 ctccaggaca gggcaggggg cagcaggata cctccagcca ggcctctgtg gcctctgttt 1381 cctttcccct ttcttggccc tcctctgctc ctccccacac cctgcaggca aaagaaccc 1441 ccagcttccc ccctccccgg gagccaggtg ggaaaagtgg gtgtgatttt tagatttgt 1501 attgtggact gattttgcct cacattaaaa actcatccca tggccagggc gggccactgt 1561 gctcctgg	SEQ ID NO:154
		1 M D S A L S D P H N G S A E A G G P T N 1 ATGGACTCGGCCCTCAGCGATCCGCATAACGGCAGTGCCGAGGCAGGCGGCCCCACCAAC 21 S T T R P P S T P E G I A L A Y G S L L 61 AGCACTACGCGGCCGCCTTCCACGCCGAGGGCATCGCGCTGGCCTACGGCAGCCTCCTG 41 L M A L L P I F F G A L R S V R C A R G 121 CTCATGGCGCTGCTGCCCATCTTCTTCGGCGCCCTCCGCTCCGTACGCTGCGCCCGCGGC 61 K N A S D M P E T I T S R D A A R F P I 181 AAGAATGCTTCAGACATGCCTGAAACAATCACCAGCCGGGATGCCGCCCGCTTCCCCATC 81 I A S C T L L G L Y L F F K I F S Q E Y 241 ATCGCCAGCTGCACACTCTTGGGCTCTACCTCTTTTTCAAAATATTCTCCCAGGAGTAC 101 I N L L L S M Y F F V L G I L A L S H T 301 ATCAACCTCCTGCTGTCCATGTATTTCTTCGTGCTGGGAATCCTGGCCCTGTCCCACACC 121 I S P F M N K F F P A S F P N R Q Y Q L 361 ATCAGCCCCTTCATGAATAAGTTTTTCCAGCCAGCTTTCCAAATCGACACGATACCAGCTG 141 L F T Q G S G E N K E E I I N Y E F D T 421 CTCTTCACACAGGGTTCTGGGGAAAACAAGGAAGAGATCATCAATTATGAATTTGACACC 161 K D L V C L G L S S I V G V W Y L L R K 481 AAGGACCTGGTGTGCCTGGGCCTGAGCAGCATCGTTGGCGTCTGGTACCTGCTGAGGAAG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		181 H W I A N N L F G L A F S L N G V E L L 541 CACTGGATTGCCAACAACCTTTTTGGCCTGGCCTTCTCCCTTAATGGAGTAGAGCTCCTG 201 H L N N V S T G C I L L G G L F I Y D V 601 CACCTCAACAATGTCAGCACTGGCTGCATCCTGCTGGGCGGACTCTTCATCTACGATGTC 221 F W V F G T N V M V T V A K S F E A P I 661 TTCTGGGTATTTGGCACCAATGTGATGGTGACAGTGGCCAAGTCCTTCGAGGCACCAATA 241 K L V F P Q D L L E K G L E A N N F A M 721 AAATTGGTGTTTCCCCAGGATCTGCTGGAGAAAGGCCTCGAAGCAAACAACTTTGCCATG 261 L G L G D V V I P G I F I A L L L R F D 781 CTGGGACTTGGAGATGTCGTCATTCCAGGGATCTTCATTGCCTTGCTGCTGCGCTTTGAC 281 I S L K K N T H T Y F Y T S F A A Y I F 841 ATCAGCTTGAAGAAGAATACCCACACCTACTTCTACACCAGCTTTGCAGCCTACATCTTC 301 G L G L T I F I M H I F K H A Q P A L L 901 GGCCTGGGCCTTACCATCTTCATCATGCACATCTTCAAGCATGCTCAGCCTGCCCTCCTA 321 Y L V P A C I G F P V L V A L A K G E V 961 TACCTGGTCCCCGCCTGCATCGGTTTTCCTGTCCTGGTGGCGCTGGCCAAGGGAGAAGTG 341 T E M F S Y E E S N P K D P A A V T E S 1021 ACAGAGATGTTCAGTTATGAGGAGTCAAATCCTAAGGATCCAGCGGCAGTGACAGAATCC 361 K E G T E A S A S K G L E K K E K - 1081 AAAGAGGGAACAGAGGCATCAGCATCGAAGGGGCTGGAGAAGAAAGAGAAATGA	
BM735573	No Homology	1 GCACGAGCTCGTGCCGAATTCGGCACGAGGAAATTCCTAACAAGAGAAATTCCCATGCAT 61 CGGTGGTAGGTCTAAACAAGCAGCTTTCCAGATTTGGAATCAGTTGAGAAGAGAAATAGT 121 GGGGCGGGCAGCTCTTTGGAGAAAGCCACGTTCTCCTAGGGCCCCTGCATCTACTGAGCT 181 TTGCCCTGTTGCTAACCATCTCTAGTCTTGTCCTTGGCATGATTCTTTTGTAATAGAAGT 241 TTTATTTTTTGTGCACCTCAGCTGATCATGTGAAAGAGAGTCTGATCATTGGAAGAGCCG 301 TGCTAGTTTCACAGATGGGCTCCTTAAATTAAAACTGGGTGGTTATGATTGGGCTGATCT 361 GACCTCTGATACTACAGTGAAACTAGTGTGGGAGAAACCAGCTTTTACTGTTTAAAAATC 421 ACTGCTTTACTCTGTTAATTTACAAGGAAAGGAATGACTGTGCCAATAAAAGTGTTCTCC 481 TTC	SEQ ID NO:155
BM735545	CD68 protein	1 AGCAGCTGGTACTGAGACGAGCCTAGCTGAACTTTGGGTGAGGCTGGTCTGTCATGAGGC 61 TGGCTGTGCTTTTCTCAGGGGCCTTGCTGGGGCTACTAGCAGCCCAGGAGACAGGGAATG 121 ACTGTCCTCATAAAAAATCAGCCACTCTGCTGCCATCCTTCACGGTGACCCCTACAGCTA 181 CAGAAAGCACAGCAAGCCCTGGAACAACGAGCCACCAAACTACCCAGAGCCACAGAACCA	SEQ ID NO:156

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		241 CCACCACAGGCACCACCAGCGACCACCCCACAACAGCCACTCACAATCCTACCACCACCA 301 GTCATGGAAACACCACAGTTCATCCAACGACAAGCAACAGTACTGTCACCAGCCCAGGAT 361 CAGCCAGCAGTTCCCCCCCACCCAAGACCACCTCCGCCCTCTCCAAGTCCTAGTCCAGGCT 421 CCAAGGAGGCTATAGGAGATTACATTTGGACTAATGGTTCCCAGCCCTGCGTCCGCTCC 481 AAGCCCAGATTCAGATTCGAGTTCTGTACCCAACCCTGGGTGGAGGAAAGGCCTGGGGCA 541 TCTCTGTACTGAACCCCAACAAACCAAGGCCCAGGGGGGCTGTGCCCATCCCCACTTAC 601 TTCTCTCATTCCCCCTACGGACAGCTCAGCTTTGGATTCAAGCAGGAGCCACTGCAGAGCA 661 CTGTCTACCTGAACTATATCGCTGTGGAGTACAACGTGTCCTTCCCACAGGCAGCGCCAGT 721 GGACATTCTTGGTTCAGAATTCATCCCTTCGAGATCTCCAAGCCCCCCTAGGCCAGAGAT 781 TCAGTTGCAGAAACGCAAGCATCGCTCTTTCACCAGCTTTCCACCTTGACCTGCTCTCCC 841 TGAAGCTACAAGCTGCTCAGCTGACCCCCACAGGAGCCTTTGGGCCAAGTTTCTCTTGTC 901 CCAGTGACCAGTCCCATCTTGCTGCCTCTCATCATCGGCCTGATCCTCCTCGGCCTCTTCG 961 CCCTGGTCCTCATTACCTTCTGTGTCATCCGGAGACGCCCCACCCACCTACCAGCCACTCT 1021 GA	SEQ ID NO:157
		1 M R L A V L F S G A L L G L L A A Q E T 1 ATGAGGCTGGCTGTGCTTTTCTCAGGGCCTTGCTGGGGCTACTAGCAGCCCAGCAGACA	
		21 G N D C P H K K S A T L L P S F T V T P 61 GGGAATGACTGTCCTCATAAAAAATCAGCCACTCTGCTGCCATCCTTCACGGTGACCCCT	
		41 T A T E S T A S P G T T S H Q T T T Q S H 121 ACAGCTACAGAAAGCACAGCCAAGCCCTGGAACAACGAGCCACCAAACTACCCAGAGCCAC	
		61 R T T T T G T T S D H P T T T A T H H N P T 181 AGAACCACCACCACAGGCACCACCAGCGACCACCCCACACCCAGCCACTCACAATCCTACC	
		81 T T S H G N T T V H P T T T S N S T V T S 241 ACCACCAGTCATGGAAACACCACAGTTCATCCAACGACAAGCAACAGTACTGTCACCAGC	
		101 P G S A S S S P H P P R P P P P P S P S P S 301 CCAGGATCAGCCAGCAGTTCCCCCCCACCCCAAGACCACCTCCGCCCTCTCCAACTCCTAGT	
		121 P G S K E A I G D Y I W T N G S Q P C V 361 CCAGGCTCCAAGGAGGCTATAGGAGATTACATTTGGACTAATGGTTCCCAGCCCTGCGTC	
		141 R L Q A Q I Q I R V L Y P T L G G G K A 421 CGGCTCCAAGCCCAGATTCAGATTCGAGTTCTGTACCCAACCCTGGGTGGAGGAAAGGCC	
		161 W G I S V L N P N K T K A Q G G C A H P 481 TGGGGCATCTCTGTACTGAACCCCAACAAACCAAGGCCCAGGGGGGCTGTGCCCATCCC	
		181 H L L L S F P Y G Q L S F G F K Q E P L 541 CACTTACTTCTCATTCCCCTACGGACAGCTCAGCTTTGGATTCAAGCAGGAGCCCACTG	
		201 Q S T V Y L N Y I A V E Y N V S F P Q A 601 CAGAGCACTGTCTACCTGAACTATATCGCTGTGGAGTACAACGTGTCCTTCCCACAGGCA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		221 A Q W T F L V Q N S S L R D L Q A P L G 661 GCGCAGTGACATTCTTGGTTCAGAATTCATCCCTTCGAGATCTCCAAGCCCCCCTAGGC	
		241 Q R F S C R N A S I A L S P A F H L D L 721 CAGAGATTCAGTTGCAGAAACGCAAGCATCGCTCTTTCACCAGCTTTCCACCTTGACCTG	
		261 L S L K L Q A A Q L T P T G A F G P S F 781 CTCTCCCTGAAGCTACAAGCTGCTCAGCCTGACCCCCACAGGAGCCTTTGGGCCAAGTTTC	
		281 S C P S D Q S I L L P L I I G L I L L G 841 TCTTGTCCCAGTGACCAGTCCATCTTGCTGCCTCTCATCATCGGCCTGATCCTCCTCGGC	
		301 L F A L V L I T F C V I R R R P P T Y Q 901 CTCTTCGCCCTGGTCCTCATTACCTTCTGTGTCATCCGGAGACGCCCACCCACCTACCAG	
		321 P L - 961 CCACTCTGA	
BM735536	Transglutaminase E3 (TGASE3)	1 CCTTTAGAGGAGCCTGAGAAGAGGCAGAGGAAGGGCGAAACATGGCTGCTCTAGGAGTCC 61 AGAGTATCAACTGGCAGAAGGCCTTCAACCGACAAGCGCATCACACAGACAAGTTCTCCA 121 GCCAGGAGCTCATCTTGCGGAGAGGCCAAAACTTCCAGGTCTTAATGATCATGAACAAAG 181 GCCTTGGCTCTAACGAAAGACTGGAGTTCATTGACACCACAGGCCTTACCCCTCAGAGT 241 CGGCCATGACGAAGGCTGTGTTTCCACTCTCCAATGGCAGTAGTGGTGGCTGGAGTGCGG 301 TGCTTCAGGCCAGCAATGGCAATACTCTGACTATCAGCATCTCCAGTCCTGCCAGCGCAC 361 CCATAGGACGGTACACACAATGGCCCTCCAGATCTTCTCCCAGGGCGGCATCTCCTCTGTGA 421 AACTTGGGACGTTCATACTGCTTTTAACCCCTGGCTGAATGTGGATAGCGTCTTTATGG 481 GTAACCATGCTGAGAGAGAAGATATGTTCAGGAAGATGCCGCATCATCTTTGTGGGAA 541 GCACAAACCGAATTGGCATGATTGGCTGGAACTTTGGACAGTTTGAAGACATTCTCA 601 GCATCTGCCTCTCAATCTTGGATAGGAGTCTGAATTTCCGCCGTGACGCTGCTACTGATG 661 TGGCCAGCAGAAATGACCCCAAATACGTTGGCCGGGTGCTGAGTGCCATGATCAATAGCA 721 ATGATGACAATGGTGTGCTTGCTGGGAATTGGAGCGGCACTTACACCGGTGGCCGGGACC 781 CAAGGAGCTGGGACGGCAGCCGTGGAGATCCTCAAAAATTGGAAAAAATCTGGCTTCAGCC 841 CAGTCCGATATGGCCAGTGCTGGGTCTTTGCTGGGACCCTCAACACAGCGCTGCGGTCTT 901 TGGGGATTCCTTCCCGGGTGATCACCAACTTCAACTCAGCTCATGACACAGACCGAAATC 961 TCAGTGTGGATGTGTACTACGACCCCATGGGAAACCCCCTGGACAAGGGTAGTGATAGCG 1021 TATGGAATTTCCATGTCTGGAATGAAGCGCTGGTTTGTGAGGTCTGACCTGGGCCCCCGT 1081 ACGGTGGATGGCAGGTGTTGGATGCCTACCCCGCAGGAAAGAAGCCAAGGGGTGTTCCAGT 1141 GCGGCCCCGCTTCGGTCATTGGTGTTCGAGAGGGTGATGTGCAGCTGAACTTCGACATGC 1201 CCTTTATCTTCGCGGAGGTTAATGCCGACCGCATCACCTGGCTGTACGACAACACCACTG 1261 GCAAACAGTGGAAGAATTCCGTGAACAGTCACACCATTGGCAGGTACATCAGCACCAAGG 1321 CGGTGGCAGCAATGCTCGCATGGACGTCACGGACAAGTACCAAGAAGGCTCTG 1381 ACCAGGAAAGACAAGTGTTCCAAAAGCCTTTGGGGAAACTTAAACCCAACACGCCATTTG 1441 CCGCGACGTCTTCGATGGGTTTGGAAACAGAGGAACAGGAGCCCAGCATCATCGGGAAGC 1501 TGAAGGTCGCCTGGCATGCTGGCAGTAGGCAAAGAAGTCAACCTGGTCCTACTGCTCAAAA 1561 ACCTGAGCAGGGATACGAAGACAGTGACAGTGAACATGACGAGCCTGGACCATCATCTACA 1621 ACGGCACGCTTGTACATGAAGTGTGGAAGGACTCTGCCACAATGTCCCTGGACCCTGAGG	SEQ ID NO:158

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1681 AAGAGGCAGAACATCCCATAAAGATCTCGTACGCTCAGTATGAGAGGTACCTGAAGTCAG 1741 ACAACATGATCCGGATCACAGCGGTGTGCAAGGTCCCAGATGAGTCTGAGGTGGTGGTGG 1801 AGCGGGACATCATCCTGGACAACCCCACCTTGACCCTGGAGGTGCTGAACGAGGCTCGTG 1861 TGCGGAAGCCTGTGAACGTGCAGATGCTCTTCTCCAATCCACTGGATGAGCCGGTGAGGG 1921 ACTGCGTGCTGATGGTGGAGGGAAGCGGCCTGCTGTTGGGTAACCTGAAGATCGACGTGC 1981 CGACCCTAGGGCCCAAGGAGCGGTCCCGGGTACGTTTTGAGATCCTGCCCACCCGGAGTG 2041 GCACCAAGCAGCTGCTTGCTGACTTCTCCTGCGACAAGTTCCCTGCAATCAAGGCCATGC 2101 TGTCCATCGACGTGGCTGAGTGAAGGGCTCAGGCGGCCCCCATACAAACTTGGGTAACAC 2161 AGAGCAGGCAGGGCTCACCTGTGGAGTGAGCCCCCTGCCCATGCTGTCCAGCCTGGGAAA 2221 CCCACTCCGTCCCCCAAGGCTGCCAGACATGGACTCCGGGCTCCAGCACATCCCCCTCTC 2281 CTCTCCCCCAGGTTGGGGCTGGCTTCACCCTGGCCCGTGACTTGATCACTTTTGCACATT 2341 CCCTGGCTGTTTCTCCCCGAGGCTGCCTGCTCTGTGAGCCCCACAGCCCTGCTCATTCCT 2401 CACGCCCATCAATGCTGCAGGACAGAGTGGCACCTGACCCAGCGACCCTCCGAATGGATG 2461 CTCAGGGAGAAGTCGGTCTGGACTGTTTGCTGATCCCCAGCCTGCAGTTGGGACATTCGT 2521 GCTACTCCCTCAGGCCACTGTGGAGGGGAGGGGATGGTTAGTCACCTGCCCCAGCACTCA 2581 CACCCTAACTCAAAATAAATGTTAAATAAGTGCGATCACAC 1 M A A L G V Q S I N W Q K A F N R Q A H 1 ATGGCTGCTCTAGGAGTCCAGAGTATCAACTGGCAGAAGGCCTTCAACCGACAAGCGCAT 21 H T D K F S S Q E L I L R R G Q N F Q V 61 CACACAGACAAGTTCTCCAGCCAGGAGCTCATCTTGCGGAGAGGCCAAAACTTCCAGGTC 41 L M I M N K G L G S N E R L E F I D T T 121 TTAATGATCATGAACAAAGGCCTTGGCTCTAACGAAAGACTGGAGTTCATTGACACCACA 61 G P Y P S E S A M T K A V F P L S N G S 181 GGGCCTTACCCCTCAGAGTCGGCCATGACGAAGGCTGTGTTTCCACTCTCCAATGGCAGT 81 S G G W S A V L Q A S N G N T L T I S I 241 AGTGGTGGCTGGAGTGCGGTGCTTCAGGCCAGCAATGGCAATACTCTGACTATCAGCATC 101 S S P A S A P I G R Y T M A L Q I F S Q 301 TCCAGTCCTGCCAGCGCACCCATAGGACGGTACACAATGGCCCTCCAGATCTTCTCCCAG 121 G G I S S V K L G T F I L L F N P W L N 361 GGCGGCATCTCCTCTGTGAAACTTGGGACGTTCATACTGCTTTTTAACCCCTGGCTGAAT 141 V D S V F M G N H A E R E E Y V Q E D A 421 GTGGATAGCGTCTTTATGGGTAACCATGCTGAGAGAGAAGAGTATGTTCAGGAAGATGCC 161 G I I F V G S T N R I G M I G W N F G Q 481 GGCATCATCTTTGTGGGAAGCACAAACCGAATTGGCATGATTGGCTGGAACTTTGGACAG 181 F E E D I L S I C L S I L D R S L N F R 541 TTTGAAGAAGACATTCTCAGCATCTGCCTCTCAATCTTGGATAGGAGTCTGAATTTCCGC 201 R D A A T D V A S R N D P K Y V G R V L	SEQ ID NO:159

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		601 CGTGACGCTGCTACTGATGTGGCCAGCAGAAATGACCCCAAATACGTTGGCCGGGTGCTG	
		221 S A M I N S N D D N G V L A G N W S G T	
		661 AGTGCCATGATCAATAGCAATGATGACAATGGTGTGCTTGCTGGGAATTGGAGCGGCACT	
		241 Y T G G R D P R S W D G S V E I L K N W	
		721 TACACCGGTGGCCGGGACCCAAGGAGCTGGGACGGCAGCGTGGAGATCCTCAAAAATTGG	
		261 K K S G F S P V R Y G Q C W V F A G T L	
		781 AAAAAATCTGGCTTCAGCCCAGTCCGATATGGCCAGTGCTGGGTCTTTGCTGGGACCCTC	
		281 N T A L R S L G I P S R V I T N F N S A	
		841 AACACAGCGCTGCGGTCTTTGGGGATTCCTTCCCGGGTGATCACCAACTTCAACTCAGCT	
		301 H D T D R N L S V D D V Y Y D P M G N P L	
		901 CATGACACAGACCGAAATCTCAGTGTGGATGTGTACTACGACCCCATGGGAAACCCCCTG	
		321 D K G S D S V W N F H V W N E G W F V R	
		961 GACAAGGGTAGTGATAGCGTATGGAATTTCCATGTCTGGAATGAAGGCTGGTTTGTGAGG	
		341 S D L G P P Y G G W Q V L D A T P Q E R	
		1021 TCTGACCTGGGCCCCCCGTACGGTGGATGGCAGGTGTTGGATGCTACCCCGCAGGAAGA	
		361 S Q G V F Q C G P A S V I G V R E G D V	
		1081 AGCCAAGGGGTGTTCCAGTGCGGCCCCGCTTCGGTCATTGGTGTTCGAGAGGGTGATGTG	
		381 Q L N F D M P F I F A E V N N A D R I T W	
		1141 CAGCTGAACTTCGACATGCCCTTTATCTTCGCGGAGGTTAATGCCGACCGCATCACCTGG	
		401 L Y D N T T G K Q W K N S V N S H T T I G	
		1201 CTGTACGACAACACCACTGGCAAACAGTGGAAGAATTCCGTGAACAGTCACACCATTGGC	
		421 R Y I S T K A V G S N A R M D V T D K Y	
		1261 AGGTACATCAGCACCAAGGCGGTGGGCAGCAATGCTCGCATGGACGTCACGGACAAGTAC	
		441 K Y P E G S D Q E R Q V F Q K A L G K L	
		1321 AAGTACCCAGAAGGCTCTGACCAGGAAAGACACAGTGTTCCAAAGGCTTTGGGGAAACTT	
		461 K P N T P F A A T S S M G L E T E E Q E	
		1381 AAACCCAACACGCCATTTGCCGCGACGTCTTCGATGGGTTTGGAAACAGAGGAACAGGAG	
		481 P S I I G K L K V A G M L A V G K E V N	
		1441 CCCAGCATCATCGGGAAGCTGAAGGTCGCTGGCATGCTGGCAGTAGGCAAAGAAGTCAAC	
		501 L V L L L K N L S R D T K T V T V N M T	
		1501 CTGGTCCTACTGCTCAAAAACCTGAGCAGGGATACGAAGACAGTGACAGTGAACATGACA	
		521 A W T I I Y N G T L V H E V W K D S A T	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1561 GCCTGGACCATCATCTACAACGGCACGCTTGTACATGAAGTGTGGAAGGACTCTGCCACA 541 M S L D D P E E E A E E H P I K I S Y A Q Y 1621 ATGTCCCTGGACCCTGAGGAAGAGGCAGAACATCCCATAAAGATCTCGTACGCTCAGTAT 561 E R Y L K S D N M I R I T A V C K V P D 1681 GAGAGGTACCTGAAGTCAGACAACATGATCCGGATCACAGCGGTGTGCAAGGTCCCAGAT 581 E S E V V V E R D I I L L D N P T L T L E 1741 GAGTCTGAGGTGGTGGTGGAGCGGGACATCATCCTGGACAACCCCACCTTGACCCTGGAG 601 V L N E A R V R K P Y N V Q M L F S N P 1801 GTGCTGAACGAGGCTCGTGTGCGGAAGCCTGTGAACGTGCAGATGCTCTTCTCCAATCCA 621 L D E P V R D C V L M V E G S G L L L G 1861 CTGGATGAGCCGGTGAGGGACTGCGTGCTGATGGTGGAGGGAAGCGGCCTGCTGTTGGGT 641 N L K I D V P T L G P K E E R S R V R F E 1921 AACCTGAAGATCGACGTGCCGACCCTAGGGCCCAAGGAGCGGTCCCGGGTACGTTTGAG 661 I L P T R S G T K Q L L A D F S C D K F 1981 ATCCTGCCCACCCGGAGTGGCACCAAGCAGCTGCTTGCTGACTTCCTCCTGCGACAAGTTC 681 P A I K A M L S I D V A E - 2041 CCTGCAATCAAGGCCATGCTGTCCATCGACGTGGCTGAGTGA	
BM735534	PREDICTED: Bos taurus similar to hypothetical protein (LOC515494),	1 gaggcactgt ggcccaccca gataggatta ttttcccgaa tcctgcctgt gaggacccac 61 cagcggtgct cttggaagtg caaggcacct tacagaggcc tgtgggccgg gacagccgca 121 gctcccctgc caactgtacc tggctcatcc tgggcaggaa ggagcagacg gtaacggtca 181 ggttccaaaa actgcatctg gcctgtggct cagagcgctt aaccctgcgc tcccccatcc 241 agccgcagat ctccctgtgc gaggcacctg ccagcctct gcaactgcct ggaggcaacg 301 tcaccatcac ctacagctat gtcgggggcca gagctcccat gggccagggc ttcctgctct 361 cttacagcca agattggctg atgtgcctgc aggaggagtt ccagtgcctg aaccaccgct 421 gtgtgcccct gctccagcgc tgtgatgggg tcgacgcctg tggcgatggc tctgacgagg 481 caggttgcag ctcagacccc ttcctgact tggccctagc ccctgtcctc acccaccct 541 gcaatcacac cttagaagac ttctatgggg tcttctcctc cttcggatac tcacacctgg 601 cctcagtctc ccacccccag tcttgccgct ggctgctgga cccacgtgat ggccggcgcc 661 tggcagtgcg cttcacggcc ttggatctag gctatgacga tgcagtgcgt gtatatgacg 721 gcgcgggggc cctcgagacc ctccgactgc tgcgcagcct cacccgcttc agtaatggca 781 aggctgtcac tgtggagacg ctgtctggcc aggccacagt ggactaccgc acagtccctt 841 ggagcactgg tcgggcttc aatgccacct accatgtgcg gggctactgc ttgccttggg 901 accgaccgtg cggcttaagc tctggcttgg gggctagcga aggcctcggc gagcgctgct 961 acagcgaggc acagcgctgc gacggctcat gggactgtgc agatggcacg gacgaggaga 1021 actgccccag ctgcccacct ggacactacc cctgtggggc cgccggcacc cctgggccca 1081 cagcctgcta cctgcccact gaccgctgta actaccagac cttctgtgcc gatggagcag 1141 atgagagacg ctgtcgccac tgccagccag gcaacttccg gtgccgggat gagaagtgcg	SEQ ID NO:160

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1201 tgtatgagac gtgggtgtgc gacgggcagc cggactgtgc tgatggcagt gacgagtggg 1261 actgctccta cgcctgccc cgcaagtca ttaccgctgc cgtcattggc agccttgtgt 1321 gcggcttgct gctggtcatc gccctgggct gcacctgcaa gctctatgcc attcgcaccc 1381 aggagtacag catcttcgcc ccctctcccc ggatggaggc cgagattgtg cagcagcagg 1441 cgcctccctc ctacgggcag ctcattgccc agggcgccat ccctcctgta gaggacttcc 1501 ctacagagaa ccctaatgat aactctgttc tgggcaatct gcgttctctg ctacagatcc 1561 tgcgccagga catgactcca gggagcacct ctggtgcccg ccgccgccag cggggccgct 1621 ctatgcgccg cctggtgcgc cgtcttcgcc gctgggcttt gcttccccga accaacccc 1681 cagcccggac ccctgaaacc agatcccagg ccacaccatc cactgctcct cctgagacct 1741 tagatggcag cacaggtcca gcccatgagg gcgggcagt ggtgtggcaa gatgggatc 1801 aggcaccccc gctgcctgtc aaggctccac tgccacctgc cagcacatcc ccagcctgtc 1861 ctactgtccc tgaagcccca gggccactgc ctgcggtgcc cttggagcca tcactgctgt 1921 ctggagtggt acaggccctg cgaggccgcc tcctgcccag cctgcggccc cctggaccaa 1981 cccgggcgtc acctggaccc cacacaacag tcctgtcccc agaggatgag gacgatgtgc 2041 tgctggtgcc actggctgaa cctgggtct gggtggtcga agcggaggat gagccactgc 2101 tggcctgagg tgacctagct ccctgggca ttctgttcac agggacagca accctataga 2161 gggcagctca gcttcccatc cactacttcc ttccttgtcc ctcagtctga ggggacttga 2221 tgggcctcct gttgatccca ggtagctgct atcaagttag gtgtcctca gacagggaga 2281 gggccctcac agagctcccc ctgcgcatgg ccagagacca cagtccacca ccaccctctc 2341 cccacactgc caccggttgg tggctgtttt taaaaagtaa agttcttaaa gggtcatggg 2401 cctggacact ccatccttgc caaacccatc caaaagtggc cttaagcacc agaatgccaa 2461 ctggctggag acctccagcc cccaagggag gatttgggca gggcctgagg ttttgccaac 2521 agtgatccct cctacaaggc ctggctcata aaaagagcac aacaaatgct tctgtcccat 2581 agctaggttg ttgcccagga agccaaggtt gaaaaataaa ggaatcagaa atttca	
BM735519	Ring finger protein 10	1 cgactcgtcg ccattcccgg agcaggtcgg cctcggccca ggggcgagta tccgttgctg 61 tgtcggagac actagtcccc gacaccgaga cagccagccc tctcccctgc ctcgcggcgg 121 gagagcgtgt ccggccggcc ggccggcggg gctcgcgcaa cctccctcgc ctcccgttcc 181 ccgcagcct ccgccccgcc aggccccggc cggactcccg agccccggcc tcctcgtcct 241 cggtcgccgc tgccgccggg cttaacagcc ccgtccgccg cttctcttcc tagtttgaga 301 agccaaggaa ggaaacaggg aaaaatgtcg ccatgaaggc cgagaaccgc tgccgccgcc 361 gaccccgcgc ggccctgaac gccatgagcc tgggtccccg ccgcgcccgc tccgctccga 421 ctgccgtcgc cgccgaggcc cccgttgatg ccgctgagct ccccaacgc cgccgccacc 481 gcctccgaca tggacaagaa cagcggctcc aacagctcct ccgcctcttc gggcagcagc 541 aaagggcaac agccgccccg ctccgcctcg gcgggccagg ccggcgagtc taaacccaag 601 agcgatggaa agaactccag tggatccaag cgttataatc gcaaacgtga actttcctac 661 cccaaaaatg aaagtttaa caaccagtcc cgtcgctcca gttcacagaa aagcaagact 721 tttaacaaga tgcctcctca aaggggcggc ggcagcagca aactctttag ctctttcttt 781 aatggtggaa gacgagatga ggtagcagag gctcaacggg cagagtttag ccctgcccag 841 ttctctggtc ctaagaagat caacctgaac cacttgttga atttcacttt tgaaccccgt 901 ggccagacgg gtcactttga aggcagtgga catggtagct ggggaaagag gaacaagtgg 961 ggacataagc ctttaacaa ggaactcttt ttacaggcca actgccaatt tgtggtgtct 1021 gaagaccaag actacacagc tcatttgct gatcctgata cattagttaa ctgggacttt 1081 gtggaacaag tgcgcatttg tagccatgaa gtgccatctt gcccaatatg cctctatcca 1141 cctactgcag ccaagataac ccgttgtgga cacatcttct gctgggcatg catcctgcac 1201 tatctttcac tgagtgagaa gacgtggagt aaatgtccca tcgttacag ttctgtgcat	SEQ ID NO:161

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1261 aagaaggatc tcaagagtgt tgttgccaca gagtcacatc agtatgttgt tggtgatacc 1321 attacgatgc agctgatgaa gagggagaaa gggtgttggg tggctttgcc caaatccaaa 1381 tggatgaatg tagaccatcc catcatcta ggagatgaac agcacagcca gtactccaag 1441 tttctgctgg cctctaagga gcagtgctg caccggtag ttctggagga gaaagtagca 1501 ctagagcagc agctggcaga ggagaagcac actcccgagt cctgctttat tgaggcagct 1561 atccaggagc tcaagactcg ggaagaggct ctgtcgggat tggccggaag cagaagggag 1621 gtcactggtg ttgtggctgc tctggaacaa ctggtgctga tggctccctt ggcgaaggag 1681 tctgtttttc aacccaggaa gggtgtgctg gagtatctgt ctgccttcga tgaagaaacc 1741 acggaagttt gttctctgga cactccttct agacctcttg ctctccctct ggtagaagag 1801 gaggaagcag tgtctgaacc agagcctgag gggttgccag aggcctgtga tgacttggag 1861 ttagcagatg acaatcttaa agagggacc atttgcactg agtccagcca gcaggaaccc 1921 atcaccaagt caggcttcac acgcctcagc agctctcctt gttactactt ttaccaagcg 1981 gaagatggac agcatatgtt cctgcaccct gtgaatgtgc gctgcctcgt gcgggagtac 2041 ggcagcctgg agaggagccc cgagaagatc tcagcaactg tggtggagat tgctggctac 2101 tccatgtcctg aggatgttcg acagcgtcac agatatctct ctcacttgcc actcacctgt 2161 gagttcagca tctgtgaact ggctttgcaa cctcctgtgg tctctaagga aaccctagag 2221 atgttctcag atgacattga gaagaggaaa cgtcagcgcc aaaagaaggc tcgggaggaa 2281 cgccgccgag agcgcaggat tgagatagag gagaacaaga aacagggcaa gtacccagaa 2341 gtccacattc ccctcgagaa tctacagcag tttcctgcct tcaattctta tacctgctcc 2401 tctgattctg ctttgggtcc caccagcacc gagggccatg gggccctctc catttctcct 2461 ctcagcagaa gtccaggttc ccatgcagac tttctgctga ccccctctgtc acccactgcc 2521 agtcagggca gtccctcatt ctgcgttggg agtctggaag aagactctcc cttccttcc 2581 tttgcccaga tgctgaggct tggaaaagca aaagcagatg tgtggcccaa aactgctcca 2641 aagaaagatg agaacagctt agttcctcct gcccctgtgg acagcgacgg ggagagtgat 2701 aattcagacc gtgttcctgt gcccagtttt caaaattcct tcagccaagc tattgaagca 2761 gccttcatga aactggacac accagctact tcagatcccc tctctgaaga gaaaggagga 2821 aagaaaagaa aaaaacagaa acagaagctc ctgttcagca cctcagtcgt ccacaccaag 2881 tgacactact ggcccaggct accttctcca tctggttttt gtttttgttt ttttttcccc 2941 catgcttttg tttggctgct gtaatttta agtatttgag tttgaacaga ttagctctgg 3001 gggagggggg tttccacaat gtgaggggga accaagaaaa ttttaaatac agtgtatttt 3061 ccagcttcct gtctttacac caaaataaag tattgacaca agaggaaaaa aaaaaaaaaa 3121 aaaaaaaaa 1 M P L S S P N A A A T A S D M D K N S G 1 ATGCCGCTGAGCTCCCCCAACGCCGCCCCACCGCCTCCGACATGGACAAGAACAGCGGC 21 S N S S S A S S G S S S K G Q Q P P R S A 61 TCCAACAGCTCCTCCGCCTCTTCGGGCAGCAAAGGGCAACAGCCGCCCCGCTCCGCC 41 S A G P A G E S K P K S D G K N S S G S 121 TCGGCGGGGCCAGCCGGCGAGTCTAAACCCAAGAGCCATGGAAAGAACTCCAGTGGATCC 61 K R Y N R K R E L S Y P K N E S F N N Q 181 AAGCGTTATAATCGCAAACGTGAACTTTCCTACCCCAAAAATGAAAGTTTTAACAACCAG 81 S R R R S S S Q K S K T F N K M P P Q R G 241 TCCCGTCGCTCCAGTTCACAGAAAAGCAAGACTTTTAACAAGATGCCTCCTCAAAGGGGC	SEQ ID NO:162

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		101 G G S S K L F S S S F N G G R R D E V A 301 GGCGGCAGCAAACTCTTTAGCTCTTCTTTTAATGGTGGAAGACGAGATGAGGTAGCA 121 E A Q R A E F S P A Q F S G P K K I N L 361 GAGGCTCAACGGGCAGAGTTTAGCCCTGCCCAGTTCTCTGGTCCTAAGAAGATCAACCTG 141 N H L L N F T F E P R G Q T G H F E G S 421 AACCACTTGTTGAATTTCACTTTTGAACCCCGTGGCCAGACGGGTCACTTTGAAGGCAGT 161 G H G S W G K R N K W G H K P F N K E L 481 GGACATGGTAGCTGGGGAAAGAGGAACAAGTGGGGACATAAGCCTTTTAACAAGGAACTC 181 F L Q A N C Q F V V S E D Q D Y T A H F 541 TTTTTACAGGCCAACTGCCAATTTGTGGTGTCTGAAGACCAAGACTACACAGCTCATTTT 201 A D P D T L V N W D F V E Q V R I C S H 601 GCTGATCCTGATACATTAGTTAACTGGGACTTTGTGGAACAAGTGCGCATTTGTAGCCAT 221 E V P S C P I C L Y P P T A A K I T R C 661 GAAGTGCCATCTTGCCCAATATGCCTCTATCCACCTACTGCAGCCAAGATAACCGTTGT 241 G H I F C W A C I L H Y L S L S E K T W 721 GGACACATCTTCTGCTGGGCATGCATCCTGCACTATCTTCACTGAGTGAGAAGACGTGG 261 S K C P I C Y S S V H K K D L K S V V A 781 AGTAAATGTCCCATCTGTTACAGTTCTGTGCATAAGAAGGATCTCAAGAGTGTTGTTGCC 281 T E S H Q Y V V G D T I T M Q L M K R E 841 ACAGAGTCACATCAGTATGTTGTTGGTGATACCATTACGATGCAGCTGATGAAGAGGAG 301 K G V L V A L P K S K W M N V D H P I H 901 AAAGGGGTGTTGGTGGCTTTGCCCAAATCCAAATGGATGAATGTAGACCATCCCATTCAT 321 L G D E Q H S Q Y S K L L L A S K E Q V 961 CTAGGACATGAACAGCACAGCCAGTACTCCAAGTTGCTGCTGGCCTCTAAGGAGCAGGTG 341 L H R V V L E E K V A L E Q Q L A E E K 1021 CTGCACCGGGTAGTTCTGGAGGAGAAAGTAGCACTAGAGCAGCAGCTGGCAGAGGAGAAG 361 H T P E S C F I E A A I Q E L K T R E E 1081 CACACTCCCGAGTCCTGCTTTATTGAGGCAGCTATCCAGGAGCTCAAGACTCGGGAAGAG 381 A L S G L A G S R R E E V T G V V A A L E 1141 GCTCTGTCGGGATTGGCCGGAAGCAGAAGGGAGGTCACTGGTGTTGTGGCTGCTCTGGAA 401 Q L V L M A P L A K E S V F Q P R K G V 1201 CAACTGGTGCTGATGGCTCCCCTTGGCGAAGGAGTCTGTTTTTCAACCCAGGAAGGGTGTG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		421 L E Y L S A F D E E T T E V C S L D T P	
		1261 CTGGAGTATCTGTCTGCCTTCGATGAAGAAACCACGGAAGTTTGTTCTCTGGACACTCCT	
		441 S R P L A L P L V E E E E A V S E E P E P	
		1321 TCTAGACCTCTTGCTCTCCCTCTGGTAGAAGAGGAGGAAGCAGTGTCTGAACCAGAGCCT	
		461 E G L P E A C D D L E L A D D N L K E G	
		1381 GAGGGGTTGCCAGAGGCCTGTGATGACTTGGAGTTAGCAGATGACAATCTTAAAGAGGGG	
		481 T I C T E S S Q Q E P I T K S G F T R L	
		1441 ACCATTTGCACTGAGTCCAGCCAGGAACCCATCACCAAGTCAGGCTTCACACGCCTC	
		501 S S S P C Y Y F Y Q A E D G Q H M F L H	
		1501 AGCAGCTCTCCTTGTTACTATTTACCAAGCGGAAGATGGACAGCATATGTTCCTGCAC	
		521 P V N V R C L V R E Y G S L E R S P E K	
		1561 CCTGTGAATGTGCGCTGCCTCGTGCGGAGTACGGCAGCCTGGAGAGGAGCCCCGAGAAG	
		541 I S A T V V E I A G Y S M S E D V R Q R	
		1621 ATCTCAGCAACTGTGGTGGAGATTGCTGCTACTCCATGTCTGAGGATGTTCGACAGCGT	
		561 H R Y L S H L P L T C E F S I C E L A L	
		1681 CACAGATATCTCTCACTTGCCACTCACCTGTGAGTTCAGCATCTGTGAACTGGCTTTG	
		581 Q P P V V S K E T L E M F S D D I E K R	
		1741 CAACCTCCTGTGGTCTCTAAGGAAACCTAGAGATGTTCTCAGATGACATTGAGAAGAGG	
		601 K R Q R Q K K A R E E E R R R E R R I E I	
		1801 AAACGTCAGCGCCAAAAGAAGGCTCGGGAGGAACGCCGCCGAGAGCGCAGGATTGAGATA	
		621 E E N K K Q G K Y P E V H I P L E N L Q	
		1861 GAGGAGAACAAGAAACAGGGCAAGTACCCAGAAGTCCACATTCCCCTCGAGAATCTACAG	
		641 Q F P A F N S Y T C S S D S A L G P T S	
		1921 CAGTTTCCTGCCTTCAATTCTTATACCTGCTCCTCNGATTCTGCTTTGGGTCCCACCAGC	
		661 T E G H G A L S I S P L S R S P G S H A	
		1981 ACCGAGGGCCATGGGGCCCTCTCCATTTCTCCTCTCAGCAGAACTCCAGGTTCCCATGCA	
		681 D F L L T P L S P T A S Q G S P S F C V	
		2041 GACTTTCTGCTGACCCCTCTGTCACCCACTGCCAGTCAGGGCAGTCCCTCATTCTGCGTT	
		701 G S L E E D S P F P S F A Q M L R V G K	
		2101 GGGAGTCTGGAAGAAGACTCTCCCTTCCCTTCCTTTGCCCAGATGCTGAGGGTTGGAAAA	
		721 A K A D V W P K T A P K K D E N S L V P	
		2161 GCAAAAGCAGATGTGTGGCCCAAAACTGCTCCAAAGAAAGATGAGAACAGCTTAGTTCCT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		741 P A P V D S D G E S D N S D R V P V P S 2221 CCTGCCCCTGTGGACAGCGACGGGGAGAGTGATAATTCAGACCGTGTTCCTGTGCCCAGT 761 F Q N S F S Q A I E A A F M K L D T P A 2281 TTTCAAAATTCCTTCAGCCAAGCTATTGAAGCAGCCTTCATGAAACTGGACACACCAGCT 781 T S D P L S E E K G G K K R K K Q K Q K 2341 ACTTCAGATCCCCTCTCTGAAGAGAAAGGAGGAAAGAAAAGAAAAAAACAGAAACAGAAG 801 L L F S T S V V H T K - 2401 CTCCTGTTCAGCACCTCAGTCGTCCACACCAAGTGA	
BM735487.V1.3_at	No Homology	1 CTGGCCATAGCATTAACCCCTCGCCCGGCCCGGACACAAGGAGGAAGCTCCTAGGGGCCA 61 GGGGCAGGACTGTGGAGGGACAGGCTTCCCCTCACNCCACCCACTCCCTCCTTCTGCCCC 121 CTCCCACATGCCCGCCTCGCCTCCCACCAGGACTCTAGCCCCAGAGTGGCTCCAGAAGGT 181 CCCCCGGGCGTCTGACCCCAGCGAAGGGCCAGCCTTGCTTGGTTCAGCTGGGGGTGCTTG 241 CTTGGGAGTTCGAAGTCACCCTAATCACGTAAATGGAACTCTCCTTTTCGAGCATCTCTC 301 CCTTCCCACACCTTCCTCCGTTAGCTTCCCCAAAAGAATTGTGTTATTAAACTTATTCTC 361 AATGAGTCCTCCTGC	SEQ ID NO:163
BM735457	No homology	1 CACTGCNCAGGACCCAACTCTGAATACATTTTTGAAATGTTAACTCCCTTTTGCAGAAGG 61 GAAACCTAAGTATCAGAGAGGTTGCCCTACGAACAGACAGCATGCCAGGGACAGAATTAG 121 GATTGAGATTCAACCTGGCCTTACCCCAATTTGACCCATTCCCACCCAGGAAGCTGAAGA 181 TAAAAGATTAGGGAAAATGCAAAGAACAAGGGCAGTTTTCTTTGCCCAAGCCTTCGGTGC 241 TAGTTAGCTCTCACCCACTCAGCCTGCACATCTTCTCAGCAAAAACTTGGAATGAAGGAG 301 GTGACACAAGGAAGTCAATGGGAGGGGGGAGGCAATAATCCCCACCTGTCTAAAAACCAC 361 AGGAACCTAACCTGATGCTCTTTCGGCCCCATCTGCATCAACACTAAACAACTACCAACT 421 CCCTTAATCTTTCACACATGCCAAGTGAACATTTTTGAAGATTTCTCTCTGTGACTGCAA 481 CCACCTGCAAACCAGGACGAATCTAGAAGTTCTCTTTTTTTTTTTTTGGTTTAATTTCTA 541 ATCTCTTGTTGTTTATGAGGTGTGGGGTTTATAAGGGACTGAATCAAATGAATGT	SEQ ID NO:164
BM735450	Lymphocyte surface antigen precursor CD44	1 tctaaagcgg gacccccagc tccactggct cggcttcgcc gtcgctccca caccatggac 61 aagttttggt ggcgcgcagc ctggggactc tgcctcgtgc cgctgagcct ggcgcagatc 121 gatttgaaca taacctgccg atacgcaggg gtattccatg tggagaaaaa tggccgctac 181 agcatctcgc ggacggaggc cgcggacctg tgcaaggctt tcaacagcac cctgcccacc 241 atggcccaga tgcagaaagc actgaacatt ggctttgaga cctgcaggat cgggttcata 301 gaagggcacg tggtcatccc cccgatccac cccaactcca tctgtgccgc caacaacacg 361 ggcgtgtaca tcctcacgtc caacacctct cagtacgaca cctattgctt caatgcctca 421 gctccgcccg aagaagactg cacctcggtc acagacctgc ccaacgcctt cgagggaccc 481 attaccataa ctatcgttaa ccgtgatggc actcgctaca ccaagaaagg cgagtacaga 541 actaaccctg aagacatcaa ccccagcacc cctgcggatg acgacgtgag cagtgggtcc 601 tccagcgaaa gaagcacttc aggaggctac agcatcttcc acacccacct tccaaccact	SEQ ID NO:165

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		661 cgcccaccc aagaccagag cagtccctgg gtgtctgaca gcccagagaa gactcccact 721 accaaagacc gagcctctgg cgggagggcc cagaccaccc acggatctga aacaagtgga 781 cactcgactg ggagtcaaga aggtgggca agcacaacct cgggtcccat acggagacct 841 caaattccag aatggctgat catcttggcg tccctcctgg ccctggctct gattctcgca 901 gtttgcattg ctgtcaacag tcgaagaagg tgtggacaga agaagaagct ggtgatcaac 961 aatggcaatg gagctgtgga cgacagaaag gcaagtgggc tcaatggaga ggccagcagg 1021 tctcaggaga tggtgcactt ggtgaacaag gagtcgtcag agacccaaga ccagtttatg 1081 acagccgacg agacacggaa cctgcagaat gtggacatga agattgtggt gtagcacctg 1141 caccttgacc ttggaacaaa ccacagtcag agacagacaa tcacagtggg ctgggacatt 1201 tcacagatgt gatgtgctac tgactgcttc attcgggtct ttttttaaca taaaatttcc 1261 tactccttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1321 aaaaaaaact ttagagca 1 M D K F W W R A A W G L C L V P L S L A 1 ATGGACAAGTTTTGGTGGCGCGCAGCCTGGGGACTCTGCCTCGTGCCGCTGAGCCTGGCG 21 Q I D L N I T C R Y A G V F H V E K N G 61 CAGATCGATTTGAACATAACCTGCCGATACGCAGGGGTATTCCATGTGGAGAAAAATGGC 41 R Y S I S R T E A A D L C K A F N S T L 121 CGCTACAGCATCTCGCGGACGGAGGCCGCGGACCTGTGCAAGGCTTTCAACAGCACCCTG 61 P T M A Q M Q K A L N I G F E T C R I G 181 CCCACCATGGCCCAGATGCAGAAAGCACTGAACATTGGCTTTGAGACCTGCAGGATCGGG 81 F I E G H V V I P P I H P N S I C A A N 241 TTCATAGAAGGGCACGTGGTCATCCCCCGATCCACCCCAACTCCATCTGTGCCGCCAAC 101 N T G V Y I L T S N T S Q Y D T Y C F N 301 AACACGGGCGTGTACATCCTCACGTCCAACACCTCTCAGTACGACACCTATTGCTTCAAT 121 A S A P P E E D C T S V T D L P N N A F E 361 GCCTCAGCTCCGCCCGAAGAAGACTGCACCTCGGTCACAGACCTGCCCAACGCCTTCGAG 141 G P I T I I V N R D G T R Y T K K G E 421 GGACCCATTACCATAACTATCGTTAACCGTGATGGCACTCGCTACACCAAGAAAGGCGAG 161 Y R T N P E D I N P S T P A D D D V S S 481 TACAGAACTAACCCTGAAGACATCAACCCCAGCACCCCTGCCGATGACGACGTGAGCAGT 181 G S S S E R S T S G G Y S I F H T H L P 541 GGGTCCTCCAGCGAAAGAAGCACTTCAGGAGGCTACAGCATCTTCCACACCCACCTTCCA 201 T T R P T Q D Q S S P W V S D S P E K T 601 ACCACTCGCCCCACCCAAGACCAGAGCAGTCCCTGGGTGTCTGACAGCCCAGAGAAGACT 221 P T T K D R A S G G R A Q T T H G S E T 661 CCCACTACCAAGACCGAGCCTCTGGCGGGAGGGCCCAGACCACCCACGGATCTGAAACA	SEQ ID NO:166

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		241 S G H S T G S Q E G G A S T T S G P I R 721 AGTGGACACTCGACTGGGAGTCAAGAAGGTGGGGCAAGCACAACCTCGGGTCCCATACGG 261 R P Q I P E W L I I L A S L L A L A L I 781 AGACCTCAAATTCCAGAATGGCTGATCATCTTGGCGTCCCTCCTGGCCCTGGCTCTGATT 281 L A V C I A V N S R R R C G Q K K K L V 841 CTCGCAGTTTGCATTGCTGTCAACAGTCGAAGAAGGTGTGGACAGAAGAAGAAGCTGGTG 301 I N N G N G A V D D R K A S G L N G E A 901 ATCAACAATGGCAATGGAGCTGTGGACGACAGAAAGGCAAGTGGGCTCAATGGAGAGGCC 321 S R S Q E M V H L V N K E S S E T Q D Q 961 AGCAGGTCTCAGGAGATGGTGCACTTGGTGAACAAGGAGTCGTCAGAGACCCAAGACCAG 341 F M T A D E T R N L Q N V D M K I G V - 1021 TTTATGACAGCCGACGAGACACGGAACCTGCAGAATGTGGACATGAAGATTGGGGTGTAG	
BM735441	WD repeat domain 1, transcript variant 2	1 tccggacgcg tgggtcgacg cagcgcgggc cggccccgga ggctctcggc gagcgcggcg 61 cggtaacaag tgggcgagga tgccgtacga gatcaagaag gtgttcgcca gcctcccgca 121 ggtggagagg ggcgtctcca agatcatcgg cggcgaccct aagggcaaca attttctgta 181 caccaatgga aagtgcgtca tcctaaggaa catcgacgac cacagccgct ttgtcaactg 241 tgtgcgattc tctcctgatg ggaacagatt tgccacagcc agtgctgacg gccagatata 301 catctatgac gggaagactg gggagaaggt gtgcgcgctg ggcggaagca aggcccacga 361 cggtgggatt tacgcaatta gttggagtcc cgacagcacc catttgcttt ctgcttctgg 421 ggacaaaact tccaagattt gggacgtcag cgtgaactcc gtggtcagca catttcccat 481 gggctccacg gttctggacc agcagctggg ctgcctatgg cagaaggacc acctgctcag 541 tgtctccctg tccgggtaca tcaactatct ggacagaaac aaccccagca agcccctgca 601 cgtcatcaag ggtcacagta aatcgatcca gtgtctgacg gtgcataaaa acggcggcaa 661 gtcctacatt tactctggga gccacgacgg acacattaat tactgggatt cagagacggg 721 ggagaacgac tccttcgctg ggaaaggcca cacgaaccag gtgtccagga tgaccgtgga 781 tgagtcgggg cagctcatca gctgcagcat ggacgacacc gtgcggtaca ccagcctcat 841 gctgcgggac tacagcggac aaggagttgt gaaactggac gttcagccaa agtgcgtagc 901 cgtcggcccc gggggatacg ccgtggtcgt gtgcattgga cagattgtcc tgctgaagga 961 tcagaggaag tgcttcagca tcgacaaccc cggctacgag cccgaagttg tggcagtgca 1021 ccccggcggg gacacggtgg caattggggg tgtggacggc aacgtccgcc tgtattccat 1081 cctgggcacc acgctgaagg atgagggcaa gctcctagag gccaagggcc ccgtgaccga 1141 cgtggcctac tcccacgacg gcgccttcct cgcggtgtgc gacgccagca aggtggtcac 1201 agtgttcagc gttgctgacg gctactcgga gaacaatgtt ttttatggac accatgcaaa 1261 aatcgtctgc ctggcctggt ccccagacaa tgaacacttt gcctccggtg gcatggacat 1321 gatggtgtat gtttggaccc tgagtgaccc ggaaaccaga gtcaagatcc aagatgcaca 1381 ccggctgcac catgtcagca gcctggcctg gctggacgag cacacgctgg tcacgacctc 1441 ccatgatgcc tctgtcaagg agtggacaat cacctactga ggagccccac ccccgcctct 1501 ggatggaccg aatcagggac tagagtttaa ctgcagcgga acatgtcatt tctctatttc 1561 tgtgacgcgc ccccatgccc ccaccccacc acaagaggca ggagggccca gtcatgaccc	SEQ ID NO:167

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1621 tcgtctctgc agggtgtctg tacacgttct tctgaaagct ttagacagta acagtttgca 1681 catgaaaaat aaagcgagca cctaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1 M P Y E I K K V F A S L P Q V E R G V S 1 ATGCCGTACGAGATCAAGAAGGTGTTCGCCAGCCTCCCGCAGGTGGAGAGGGGCGTCTCC 21 K I I G G D P K G N N F L Y T N G K C V 61 AAGATCATCGGCGGCGACCCTAAGGGCAACAATTTTCTGTACACCAATGGAAAGTGCGTC 41 I L R N I D D H S R F V N C V R F S P D 121 ATCCTAAGGAACATCGACGACCACAGCCGCTTTGTCAACTGTGTGCGATTCTCTCCTGAT 61 G N R F A T A S A D G Q I Y I Y D G K T 181 GGGAACAGATTTGCCACAGCCAGTGCTGACGGCCAGATATACATCTATGACGGGAAGACT 81 G E K V C A L G G S K A H D G G I Y A I 241 GGGGAGAAGGTGTGCGCGCTGGGCGGAAGCAAGGCCCACGACGGTGGGATTTACGCAATT 101 S W S P D S T H L L S A S G D K T S K I 301 AGTTGGAGTCCCGACAGCACCCATTTGCTTTCTGCTTCTGGGGACAAAACTTCCAAGATT 121 W D V S V N S V V S T F P M G S T V L D 361 TGGGACGTCAGCGTGAACTCCGTGGTCAGCACATTTCCCATGGGCTCCACGGTTCTGGAC 141 Q Q L G C L W Q K D H L L S V S L S G Y 421 CAGCAGCTGGGCTGCCTATGGCAGAAGGACCACCTGCTCAGTGTCTCCCTGTCCGGGTAC 161 I N Y L D R N N P S K P L H V I K G H S 481 ATCAACTATCTGGACAGAAACAACCCCAGCAAGCCCCTGCACGTCATCAAGGGTCACAGT 181 K S I Q C L T V H K N G G K S Y I Y S G 541 AAATCGATCCAGTGTCTGACGGTGCATAAAAACGGCGGCAAGTCCTACATTTACTCTGGG 201 S H D G H I N Y W D S E T G E N D S F A 601 AGCCACGACGGACACATTAATTACTGGGATTCAGAGACGGGGGAGAACGACTCCTTCGCT 221 G K G H T N Q V S R M T V D E S G Q L I 661 GGGAAAGGCCACACGAACCAGGTGTCCAGGATGACCGTGGATGAGTCGGGGCAGCTCATC 241 S C S M D D T V R Y T S L M L R D Y S G 721 AGCTGCAGCATGGACGACACCGTGCGGTACACCAGCCTCATGCTGCGGGACTACAGCGGA 261 Q G V V K L D V Q P K C V A V G P G G Y 781 CAAGGAGTTGTGAAACTGGACGTTCAGCCAAAGTGCGTAGCCGTCGGCCCCGGGGGATAC 281 A V V V C I G Q I V L L K D Q R K C F S 841 GCCGTGGTCGTGTGCATTGGACAGATTGTCCTGCTGAAGGATCAGAGGAAGTGCTTCAGC	SEQ ID NO:168

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		301 I D N P G Y E P E V V A V H P G G D T V 901 ATCGACAACCCCGGCTACGAGCCCGAAGTTGTGGCAGTGCACCCCGGCGGGGACACGGTG 321 A I G G V D G N V R L Y S I L G T T L K 961 GCAATTGGGGGTGTGGACGGCAACGTCCGCCTGTATTCCATCCTGGGCACCACGCTGAAG 341 D E G K L L E A K G P V T D V A Y S H D 1021 GATGAGGGCAAGCTCCTAGAGGCCAAGGGCCCCGTGACCGACGTGGCCTACTCCCACGAC 361 G A F L A V C D A S K V V T V F S V A D 1081 GGCGCCTTCCTCGCGGTGTGCGACGCCAGCAAGGTGGTCACAGTGTTCAGCGTTGCTGAC 381 G Y S E N N V F Y G H H A K I V C L A W 1141 GGCTACTCGGAGAACAATGTTTTTTATGGACACCATGCAAAAATCGTCTGCCTGGCCTGG 401 S P D N E H F A S G G M D M M V Y V W T 1201 TCCCCAGACAATGAACACTTTGCCTCCGGTGGCATGGACATGATGGTGTATGTTTGGACC 421 L S D P E T R V K I Q D A H R L H H V S 1261 CTGAGTGACCCGGAAACCAGAGTCAAGATCCAAGATGCACACCGGCTGCACCATGTCAGC 441 S L A W L D E H T L V T T S H D A S V K 1321 AGCCTGGCCTGGCTGGACGAGCACACGCTGGTCACGACCTCCCATGATGCCTCTGTCAAG 461 E W T I T Y - 1381 GAGTGGACAATCACCTACTGA	
BM735409	No homology	1 GATGGAAGTCAGAAGCCAAGCTTTCTCCCCACCCTCTGTGGGCCGCACGTACACACACAC 61 ACACACACACACACACAGGCGCACACACACACACACACTTTGCGTATCTGAGCGCGCCCC 121 TCGCACTGGGTCTTATCTTGCACCTTCTTCAGGATTTTATATGTGAAGAGATTTTTATAT 181 AGAATTTTTTCCCCAAAACACTTTATACCTTTTAAAAAGCAGTACCTGGTGGCCGTGTGC 241 CTCCACACTGGCCTGGGCTCTGTCTACAGCCACCTGCCTGGGCTTCTGGGCCTGTGGCCC 301 TGCCCGGGGTCTGGTGGGGGCCCAGCAGCGGCCATGGCAGGGTGGACTCTGTGGGAGAGG 361 CAGGGGGCCAGCCACCCTACCTCCCACTAACTACTTCCTGCCCTGGGGGACCCACACCCT 421 GGGGCTCTGGCGGAGGGACAGATGGACAGAGGGAGCCAGCAGCTGTCCCCAGGCCGTACC 481 TCCTCCTCTGGAGGTGCTGGGCGTGGAAGCGCTGGAGCCACCCCGTGAAGGTGCCTCTCC 541 TCTGCTCCATGAGCCTTCTTAACTTAATAAAATGTTCCGGC	SEQ ID NO:169
BM735352	No homology	1 CTCTGGACGGAGCAAGCTCTTGCCATCAGACTGCACTGCCTGCGGGAGGAAGAGAGTCTA 61 ATGGCTTTAGGTGTCTGGGGGCTCGTTATGGCCTAATGCCCACTTTTGTCCTGATCCTCC 121 TCCTGCGCAGAATAGAGAACTGCACTGAATAATAGTTAATACTTAATGTTCTCTATTAAC 181 TTACTGCTCACACGTAACAGTCTGGTGGGGAAATGCGATTCATTCATTTAAATCCCGAGT 241 AAGCCTCGGGGGTATTGACTGAAGATGCCATAAGCAGTCAAACCAAAGCATTCCATTTGT 301 AGAGTTAGATGGGACGCTCCAGATATTTGAATCTCTTCACTTGATAGGAAAGGAAACAGA	SEQ ID NO:170

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		361 CCCAGGGAGAGAACGTCGCTGCTGTATACTGTAACGTCTGTGTTCAAGTACCTCACGGGA 421 TAGAGGAAAGATGGTCTTAAGTTTTGGGAATTAAAAGAAAAATATCTTTTAATAAATATA 481 TATTTTT	
BM735286	Ferritin light chain	1 ATGAGCTCCCAGATTCGTCAGAATTATTCTACTGAAGTGGAGGCCGCCGTCAACCGCCTG 61 GTCAACCTGTACCTGCGGGCCTCCTACACCTACCTCTCTCTGGGCTTCTATTTCGACCGC 121 GACGATGTGGCTCTGGAGGGCGTATGCCACTTCTTCCGCGAGTTGGCGGAGGAGAAGCGC 181 GAGGGTGCCGAGCGTCTCTTGAAGATGCAAAACCAGCGCGGCGGCCGCGCTCTCTTCCAG 241 GACTTGCAGAAGCCGTCCCAGGATGAATGGGGTACAACCCTGGATGCCATGAAAGCCGCC 301 ATTGTCCTGGAGAAGAGCCTGAACCAGGCCCTTTTGGATCTGCATGCCCTGGGTTCTGCC 361 CAGGCAGACCCCCATCTCTGTGACTTCTTGGAGAGCCACTTCCTAGACGAGGAGGTGAAA 421 CTCATCAAGAAGATGGGCGACCATCTGACCAACATCCAGAGGCTCGTTGGCTCCCAAGCT 481 GGGCTGGGCGAGTATCTCTTTGAAAGGCTCACCCTCAAGCACGACTAA	SEQ ID NO:171
		1 M S S Q I R Q N Y S T E V E A A V N R L 1 ATGAGCTCCCAGATTCGTCAGAATTATTCTACTGAAGTGGAGGCCGCCGTCAACCGCCTG 21 V N L Y L R A S Y T Y L S L G F Y F D R 61 GTCAACCTGTACCTGCGGGCCTCCTACACCTACCTCTCTCTGGGCTTCTATTTCGACCGC 41 D D V A L E G V C H F F R E L A E E K R 121 GACGATGTGGCTCTGGAGGGCGTATGCCACTTCTTCCGCGAGTTGGCGGAGGAGAAGCGC 61 E G A E R L L K M Q N Q R G G R A L F Q 181 GAGGGTGCCGAGCGTCTCTTGAAGATGCAAAACCAGCGCGGCGGCCGCGCTCTCTTCCAG 81 D L Q K P S Q D E W G T T L D A M K A A 241 GACTTGCAGAAGCCGTCCCAGGATGAATGGGGTACAACCCTGGATGCCATGAAAGCCGCC 101 I V L E K S L N Q A L L D L H A L G S A 301 ATTGTCCTGGAGAAGAGCCTGAACCAGGCCCTTTTGGATCTGCATGCCCTGGGTTCTGCC 121 Q A D P H L C D F L E S H F L D E E V K 361 CAGGCAGACCCCCATCTCTGTGACTTCTTGGAGAGCCACTTCCTAGACGAGGAGGTGAAA 141 L I K K M G D H L T N I Q R L V G S Q A 421 CTCATCAAGAAGATGGGCGACCATCTGACCAACATCCAGAGGCTCGTTGGCTCCCAAGCT 161 G L G E Y L F E R L T L K H D - 481 GGGCTGGGCGAGTATCTCTTTGAAAGGCTCACCCTCAAGCACGACTAA	SEQ ID NO:172
BM735167	TAP2E	1 GTTGGGAGAGACGGAGCGGACCTCAGCGCTGAAGCAGAAGTCCCCGGAGCTGCGGTCTCC 61 CCGCCGCGGCTGAGCCATGCGGCTCCCTGACCTGAGACCCTGGACCTCCCTGCTGCTGGT 121 GGACGCGGCTTTACTGTGGCTGCTTCAGGGCCCTCTGGGGACTTTGCTTCCTCAAGGGCT	SEQ ID NO:173

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		181 GCCAGGACTATGGCTGGAGGGGACCCTCGCGGCTGGGAGGGCTGTGGGGGCTGCTAAAGCT	
		241 AAGAGGGCTGCTGGGATTTGTGGGGACACTGCTGCTCCCGCTCTGTCTGGCCACCCCCCT	
		301 GACTGTCTCCCTGAGAGCCCTGGTCGCGGGGGCCTCACGTGCTCCCCCAGCCAGAGTCGC	
		361 TTCAGCCCCTTGGAGCTGGCTGCTGGTGGGGTACGGGGCTGCGGGGCTCAGCTGGTCACT	
		421 GTGGGCTGTTCTGAGCCCTCCTGGAGCCCAGGAGAAGGAGCCAGGACCAGGTGAACAACAA	
		481 AGTCTTGATGTGGAGGCTGCTGAAGCTCTCCAGGCCGGACCTGCCTCTCCTCGTTGCCGC	
		541 CTTCTCTTCCTTGTCCTTGCTGTTTTCGGTGAGACATTAATCCCTCACTATTCTCGTCG	
		601 TGTGATTGACATCCTGGGAGGTGATTTTGACCCCCATGCCTTTGCCAGTGCCATCTTCTT	
		661 CATGTGCCTCTTCTCCTTTGGCAGCTCACTGTCTGCAGGCTGCCGAGGAGGCTGCTTCAC	
		721 CTACACCATGTCTCGAATCAACTTGCGGATCCGGGACGCAGCTTTCTCCTCCCTGCTGCG	
		781 CCAGGACCTCGGTTCTTCCAGGAGACTAAGACAGGGGAGCTGAACTCACGGCTGGAGCTC	
		841 GGATACCACCCTGATGAGTAACTGGCTCCTTTAAATGCCAATGTGCTCTTGCGAAGCCT	
		901 GGTGAAAGTGGTGGGGCTGTATGGCTTCATGCTCAGCATATCGCCTCGACTCACCCTCCT	
		961 TTCTCTGCTGCACATGCCCTTCACAATAGCAGCCGGAGAAGGTGTACAACACCCGCCATCA	
		1021 GGAAGTGCTTCGGGAGATCCAGGATGCAGTGGCCAGGGCGGGGCAGGTGGTGCGGGAAGC	
		1081 CGTTGGAGGGCTGCAGACCGTTCGCAGTTTGGGGCCGAGGAGCATGAAGTCTGTCGCTA	
		1141 TAAAGAGGCCCTTGAACAATGTCGGCAGCTGTATTGGCGGAGAGACCTGGAACCGCGCCTT	
		1201 GTACCTGCTCGTAAGGAGGGTGCTGCACTTGGGTGTGCAGATGCTGATGCTGAGCTGTGG	
		1261 GCTGCAGCAGATGCAGGATGGGGAGCTCACCCAGGGCAGCCTGCTTTCCTTTATGATCTA	
		1321 CCAGGAGAGCGTGGGGAGCTATGTGCAGACCCTGGTATACATATATGGGGATATGCTCAG	
		1381 CAACGTGGGAGCTGCAGAGAAGGTTTCTCCTACATGGACCGACAGCCAAATCTGCCTTC	
		1441 ACCTGGCACGCTTGCCCCCCACCACTCTGCAGGGGGTTGTGAAATTCCAAGACGTCTCCTT	
		1501 TGCATATCCCAATCGCCCTGACAGGCCTGTGCTCAAGGGGCTGACGTTTACCCTACGTCC	
		1561 TGGTGAGGTGACGGCGCTGGTGGGACCCAATGGGTCTGGGAAGAGCACAGTGGCTGCCCT	
		1621 GCTGCAGAATCTGTACCAGCCCCACAGGGGGACAGGTGCTGCTGGATGAAAAGCCCATCTC	
		1681 ACAGTATGAACACTGCTACCTGCACACCAGGTGGTTTCAGTTGGCCAGGAGCCTGTGCT	
		1741 GTTCTCCGGTTCTGTGAGGAACAACATTACTTATGGGCTGCAGAGCTGCGAAGATGATAA	
		1801 GGTGATGGCGCTGCCCAGGCTGCCCACGCAGATGACTTCATCAAAGAAATGGAGCATGG	
		1861 ACTACAAACAGATGTAGGGGAGAAAGGAAGCCAGTTGGCTGTGGCACAGAAACAATGTCT	
		1921 GGCCATTGCTCGGGCCCTTGTGCGGAACCCACGAGTCCTCATCCTGGATGAAGCCACCAG	
		1981 TGCCCTGGACGTCCAGTGTGAGCAGGCTCTGCAGGACTGGATATCCCGTGGGGACCGAAC	
		2041 GGTGCTGGTGATCGCTCACAGGCTGCAGACGGTTCAGAACGCTGACCAGATCCTGGTGCT	
		2101 CAGGCAGGGAGAGCTGGTGGATCATGCCCAGCTCATGGAGGGGGAGGACCTCTATTCCCG	
		2161 CCTGGTGCAGCAGTGTCTGGAGGACTGAGGCTGAAGGGACACTGGGCCCTTCTCATGGCT	
		2221 GTCTTCATGACCTGGAGTAGCTCCTGCTTTGAGTTTCCCTGGGGCTGTTCCCCTGGGTAG	
		2281 TTTTTCCTGGAGTTGGACACATGATGGAGATTTGGACCTTGTGTGCTTTTGGTGGGGTAG	
		2341 AGAGGTGGGGTGGGGTGGGGGCTGTCTGTGTCCAGGAAACTTAATTCCCTGGGTGA	
		2401 CTAGAGCTTTGCCTGGTGATGAGGAGTATTTTGTGGCATAATACATATATTTTAAAATAT	
		2461 TTTCCTTCTTACATGAACTGTATACATTCATATAGAAAATTTAGACAATATAAAAAAAAA	
		2521 A	
		1 M R L P D L R R P W T S L L L V D A A L L	SEQ ID NO:174
		1 ATGCGGCTCCCTGACCTGAGACCCTGGACCTCCCTGCTGGTGGACGCGGCTTTACTG	
		21 W L L Q G P L G T L L P Q G L P G L W L	
		61 TGGCTGCTTCAGGGCCCTCTGGGGACTTTGCTTCCTCAAGGGCTGCCAGGACTATGGCTG	
		41 E G T L R L G G L W G L L K L R G L L G	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		121 GAGGGGACCCTGCGGCTGGGAGGGCTGTGGGGGGCTGCTAAAGCTAAGAGGGCTGCTGGGA	
		61 F V G G T L L L L P L C L A A T P P L T T V S L L R	
		181 TTTGTGGGGACACTGCTGCTCCCGCTCTGTCTGGCCACCCCCCTGACTGTCTCCCTGAGA	
		81 A L V A G G A S S R A A P P P A A R V A S A A P P W S	
		241 GCCCTGGTCGCGGGGGGCCTCACGTGCTCCCCCAGCCAGAGTCGCTTCAGCCCCTTGGAGC	
		101 W L L L V G G Y G G A A A G G L S S W S L L W A A V L L S	
		301 TGGCTGCTGGTGGGGTACGGGGGCTGCGGGGCTCAGCTGGTCACTGTGGGCTGTTCTGAGC	
		121 P P G G A Q Q E K E Q D D Q V N N N K V V L M W W R	
		361 CCTCCTGGAGCCCAGGAGAAGGAGCAGGACCAGGTGAACACAAACAAAGTCTTGATGTGGAGG	
		141 L L K L L S R P P D L L P P L L L V A A A F F F F L L V	
		421 CTGCTCAAGCTCTCCAGGCCGGACCTGCCTCTCCTCGTTGCCGCCTTCTTCTTCCTTCTTGTC	
		161 L A A V L L G G E T T L L I P P H Y Y S S G G R V V I D D I I L	
		481 CTTGCTGTTTTGGGTGAGACATTAATCCCTCACTATTCTGGTCGTGTGATTGACATCCTTG	
		181 G G G D F D P P H A F F A S A A I F F F M C L L F F S	
		541 GGAGGTGATTTTGACCCCCATGCCTTTGCCAGTGCCATCTTCTTCATGTGCCTCTTCTTCTCC	
		201 F G G S S L L S S A G G C R G G G C C F F T Y Y T T M S S R	
		601 TTTGGCAGCTCACTGTCTGCAGGCTGCCGAGGAGGCTGCTTCACCTACCTACACCATGTCTCGA	
		221 I N N L R R I R R E E Q Q L F F S S S L L L R R Q Q D D L L G G F	
		661 ATCAACTTGCGGATCCGGGAGCAGCTTTTCTCCTCCCTGCTGCGCCAGGACCTCGGTTTC	
		241 F Q Q E E T T K K T T G G E E L L N N S S R R L L S S S S D D T T T T L L M M	
		721 TTCCAGCAGACTAAGACAGGGGAGCTGAACTCACGGCTGAGCTCGGATACCACCCCTGATG	
		261 S S N N W W L L P P L L N N A A N N V V L L L L R R S S L L V V K K V V V V G G	
		781 AGTAACTGGCTTCCTTTAAATGCCAATGTGCTCTTGCCGAAGCCTGGTGAAAGTGGTGGGG	
		281 L L Y Y G G F F M M L L S S I I S S P P R R L L T T L L L S S L L L H H M M	
		841 CTGTATGGCTTCATGCTCAGCATATCGCCTCGACTCACCCTCCTTTCTCTGCTGCACATG	
		301 P P F F T T I I A A A E E K K V V Y Y N N T T R R H H Q Q E E V V L L R R E E	
		901 CCCTTCACAATAGCAGCGGAGAAGGTGTACAACACCCGCCATCAGGAAGTGCTTCGGGAG	
		321 I I Q Q D D A A V V A A R R A A G G Q Q V V V V R R E E A A V V G G G G L L Q Q	
		961 ATCCAGGATGCAGTGGCCAGGGCGGGCAGGTGGTGCGGGAAGCCGTTGGAGGGCTGCAG	
		341 T T V V R R S S F F G G A A E E E E H H E E V V C C R R Y Y K K E E A A L L E E	
		1021 ACCGTTCGCAGTTTTGGGGCCGAGGAGCATGAAGTCTGTCGCTATAAAGAGGCCCTTGAA	
		361 Q Q C C R R Q Q L L Y Y W W R R R R D D L L E E R R A A L L Y Y L L V V R R	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1081 CAATGTCGGCAGCCTGTATTGCCGGAGACCTGGAACGGCGCCTTGTACCTGCTCGTAAGG	
		381 R V L H L G V Q M L M L S C G L L Q Q M Q	
		1141 AGGGTGCTGCACTTGGGTGTCCAGATGCTGATGCTGACCTGTGGGCTGCCAGCAGATGCAG	
		401 D G E L T Q G S L L S F M I Y Q E S V G	
		1201 GATGGGGAGCTCACCCAGGGCAGCCTGCTTTCCTTTATGATCTACCAGGAGAGCGTGGGG	
		421 S Y V Q T L V Y I Y G D M L S N V G A A	
		1261 AGCTATGTGCAGACCCTGGTATACATATATGGGGATATGCTCAGCAACGTGGGAGCTGCA	
		441 E K V F S Y M D R Q P N L P S P G T L A	
		1321 GAGAAGGTTTTCTCCTACATGGACCGACAGCCAAATCTGCCTTCACCTGGCACGCTTGCC	
		461 P T T L Q G V V K F Q D V S F A Y P N R	
		1381 CCCACCACTCTGCAGGGGGTTGTGAAATTCCAAGACGTCTCCTTTGCATATCCCAATCGC	
		481 P D R P V L K G L T F T L R P G E V T A	
		1441 CCTGACAGGCCTGTGCTCAAGGGGCTGACGTTTACCCTACGTCCTGGTGAGGTGACGGCG	
		501 L V G P N G S G K S T V A A L L Q N L Y	
		1501 CTGGTGGGACCCAATGGGTCTGGGAAGAGCACAGTGGCTGCCCTGCTGCAGAATCTGTAC	
		521 Q P T G G Q V L L D E K P I S Q Y E H C	
		1561 CAGCCCACAGGGGGACAGGTGCTGCTGGATGAAAAGCCCATCTCACAGTATGAACACTGC	
		541 Y L H S Q V V S V G Q E P V L F S G S V	
		1621 TACCTGCACAGCCAGGTGGTTTCAGTTGGGCAGGAGCCTGTGCTGTTCTCCGGTTCTGTG	
		561 R N N I T Y G L Q S C E D D K V M A A A	
		1681 AGGAACAACATTACTTATGGGCTGCAGCTGCGAAGATGATAAGGTGATGGCGGCTGCC	
		581 Q A A H A D E F I K E M E H G L Q T D V	
		1741 CAGGCTGCCCACGCAGATGAGTTCATCAAAGAAATGGAGCATGGACTACACAAACAGATGTA	
		601 G E K G S Q L A V G Q K Q C L A I A R A	
		1801 GGGGAGAAAGGAAGCCAGTTGGCTGTGGGACAGAAACAATGTCTGGCCATTGCTCGGGCC	
		621 L V R N P R V L I L D E A T S A L D V Q	
		1861 CTTGTGCGGAACCCACGAGTCCTCATCCTGGATGAAGCCACCAGTGCCCTGGACGTCCAG	
		641 C E Q A L Q D W I S R G D R T V L V I A	
		1921 TGTGAGCAGGCTCTGCAGGACTGGATATCCCGTGGGGACCGAACGGTGCTGGTGATCGCT	
		661 H R L Q T V Q N A D Q I I L V L R Q G E L	
		1981 CACAGGCTGCAGACGGTTCAGAACGCTGACCAGATCCTGGTGCTCAGGCAGGGAGAGCTG	
		681 V D H A Q L M E G E D L Y S R L V Q Q C	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2041 GTGGATCATGCCCAGCTCATGGAGGGGGAGGACCTCTATTCCCGCCTGGTGCAGCAGTGT 701 L E D - 2101 CTGGAGGACTGA	
BM735166	No homology	1 CTGTGCGGACAAGCAGCCACTGATCAGGCAGGATGCCCAGTGGCCAATACAGGCACAGGG 61 TGGCAGGTACGGGGCAGTGTATGGGGGGCATGAGGGGCATGGGCTGACAGGGAGCTGGAT 121 GGGTTGGGGGTCATGAGGGCACCCAGCATGGTTGAGTCTGGAGTGGACAGGTGTGGGGAA 181 GGCCTTCCTTGAAGGAGCCCATCCAGAGCCTCTCTCAACCTCTGCTGACCACTGAGTGAC 241 CAGACCCCCAGCCTGGGTGCTCAGGACAGGTGTGGGGAGCAGGTTGGGCCAGGCTGGGCT 301 GGGAGAGGGAAGTAGAGGGAGGAACCCACAGGCAGATGCTCACCCTGCAGACCCTCCCAC 361 TTCCCAGGAGGACACCTCCTCCTCCCCCGACAGACACTCGCAGGCAGGTCTGTGGGTTCA 421 GGTTCATGTTTATTATTACCCCGTGGCGGTCACGTAGCTCAGGGCCTTGTAGTGCAGGTT 481 GCCTGTGGCATCCATGGTCGCCAACTGGAACGTCTGGTCCACCTGCGAGTGGGTTTGGTC 541 TGGAAGTCAGGCCCAGGCAGAGGGAGGGAGCAAAGGCTCCGCGGGGCCTGCAGCCACTGG 601 GGGAATTACACGCGCTGAACTCCAGGG	SEQ ID NO:175
BM735102	COP9 constitutive photomorphogenic homolog subunit 7A	1 gcccggtgcg ctggaggtcg aagcttccag gtagcggccc gcagagcctg acccaggctc 61 tggacatcct gagcccaagt cccccacact cagtgcagtg atgagtgcgg aagtgaaggt 121 gacagggcag aaccaggagc aatttctgct cctagccaag tcggccaagg gggcagcgct 181 ggccacactc atccatcagg tgctggaggc ccctggtgtc tacgtgtttg gagaactgct 241 ggacatgccc aatgttagag agctggctga gagtgacttt gcctctacct tccggctgct 301 cacagtgttt gcttatggga catacgctga ctacttagct gaagcccgga atcttcctcc 361 actaacagag gctcagaaga ataagcttcg acacctctca gttgtcaccc tggctgctaa 421 agtaaagtgt atcccatatg cagtgttgct ggaggctctt gccctgcgta atgtgcggca 481 gctggaagac cttgtgattg aggctgtgta tgctgacgtg cttcgtggct ccctggacca 541 gcgcaaccag cggctcgagg ttgactacag catcgggcgg gacatccagc gccaggacct 601 cagtgccatt gcccgaaccc tgcaggaatg gtgtgtgggc tgtgaggtcg tgctgtcagg 661 cattgaggag caggtgagcc gtgccaacca acacaaggag cagcagctgg gcctgaagca 721 gcagattgag agtgaggttg ccaaccttaa aaaaaccatt aaagttacga cggcagcagc 781 agccgcagcc acatctcagg accctgagca acacctgact gagctgaggg aaccagctcc 841 tggcaccaac cagcgccagc ccagcaagaa agcctcaaag ggcaaggggc tccgagggag 901 cgccaagatt tggtccaagt cgaattgaaa ggactgtcgt ttcctccctg gggatgtggg 961 gtcccagctg cctgcctgcc tcttaggagt cctcagagag ccttctgtgc ccctggccag 1021 ctgataatcc taggttcatg acccttcacc tcccctaacc ccaaacatag atcacacctt 1081 ctctagggag gaggcaaatg taggtcatgt ttttgttggt actttctgtt ttttgtgact 1141 tcatgtgttc cattgctccc cgctgccatg ctctctccct tgtttcctta agagctcagc 1201 atctgtccct gttcattaca tgtcattgag taggtgggta gccctgatgg gggtcgctct 1261 gtctggagca taacccacag gcgtttttc tgccacccca tccctgcatg cctgatcccc 1321 agttcctata ccctaccct gacctattga gcagcctctg aagagccata gggcccccac 1381 ctttactcac accctgagaa ttctgggagc cagtctgcca tgccaggagt cactggacat 1441 gttcatccta gaatcctgtc acactacagt catttctttt cctctctctg gcccttgggt 1501 cctgggaatg ctgctgcttc aaccccagag cctaagaatg gcagccgttt cttaacatgt 1561 tgagagatga ttctttcttg gccctggcca tctcgggaag cttgatggca atcctggaag	SEQ ID NO:176

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1621 ggtttaatct ccttttgtga gtttggtggg gaagggaagg gtatatagat tgtattaaaa 1681 aaaaaaaggt atatatgcat atatctatat ataatatgac gcagaaataa atctatgaga 1741 aatctaaaaa aaaaaaaaaa aaa	
		1 M S A E V K V T G Q N Q E Q F L L L A K 1 ATGAGTGCGGAAGTGAAGGTGACAGGGCAGAACCAGGAGCAATTTCTGCTCCTAGCCAAG	SEQ ID NO:177
		21 S A K G A A L A T L I H Q V L E A P G V 61 TCGGCCAAGGGGGCAGCGCTGGCCACACTCATCCATCAGGTGCTGGAGGCCCCTGGTGTC	
		41 Y V F G E L L D M P N V R E L A E S D F 121 TACGTGTTTGGAGAACTGCTGGACATGCCCAATGTTAGAGAGCTGGCTGAGAGTGACTTT	
		61 A S T F R L L T V F A Y G T Y A D Y L A 181 GCCTCTACCTTCCGGCTGCTCACAGTGTTTGCTTATGGGACATACGCTGACTACTTAGCT	
		81 E A R N L P P L T E A Q K N K L R H L S 241 GAAGCCCGGAATCTTCCTCCACTAACAGAGGCTCAGAAGAATAAGCTTCGACACCTCTCA	
		101 V V T L A A K V K C I P Y A V L L E A L 301 GTTGTCACCCTGGCTGCTAAAGTAAAGTGTATCCCATATGCAGTGTTGCTGGAGGCTCTT	
		121 A L R N V R Q L E D L V I E A V Y A D V 361 GCCCTGCGTAATGTGCGGCAGCTGGAAGACCTTGTGATTGAGGCTGTGTATGCTGACGTG	
		141 L R G S L D Q R N Q R L E V D Y S I G R 421 CTTCGTGGCTCCCTGGACCAGCGCAACCAGCGGCTCGAGGTTGACTACAGCATCGGGCGG	
		161 D I Q R Q D L S A I A R T L Q E W C V G 481 GACATCCAGCGCCAGGACCTCAGTGCCATTGCCCGAACCCTGCAGGAATGGTGTGTGGGC	
		181 C E V V L S G I E E Q V S R A N Q H K E 541 TGTGAGGTCGTGCTGTCAGGCATTGAGGAGCAGGTGAGCCGTGCCAACCAACACAAGGAG	
		201 Q Q L G L K Q Q I E S E V A N L K K T I 601 CAGCAGCTGGGCCTGAAGCAGCAGATTGAGAGTGAGGTTGCCAACCTTAAAAAAACCATT	
		221 K V T T A A A A A A T S Q D P E Q H L T 661 AAAGTTACGACGGCAGCAGCAGCCGCAGCCACATCTCAGGACCCTGAGCAACACCTGACT	
		241 E L R E P A P G T N Q R Q P S K K A S K 721 GAGCTGAGGGAACCAGCTCCTGGCACCAACCAGCGCCAGCCCAGCAAGAAAGCCTCAAAG	
		261 G K G L R G S A K I W S K S N - 781 GGCAAGGGGCTCCGAGGGAGCGCCAAGATTTGGTCCAAGTCGAATTGA	
BM734889.V1.3_at	Equus caballus		

Gene Name	GenBank HomoLogy	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
	lipopolysaccharide receptor (CD14) mRNA	1 GGCACGAGGGAATCTGCAGCTGCCAGCATTAATTAGCCTTCCTCTTTCTAACCTCTTGT 61 ACAGACTGTTGTCAGTGACAGTGCAGCTCTCCTCCCTGATTCGGCCATCCTGGGTGATGTTCA 121 CGCAAGAACCATTTTCCCTGGGGACCATCTTACTTCTAATGGGGCCAAAGAATGGAAGGC 181 AAATGTGTAGACGACCTTTAGATTACAGGGCAGTCTTCTCCTGGAGCATCTTCTCCTGGC 241 CCTGCCCCCTTCCCATGCTGTTTGAATTAGCCCAGCAGGAGGCTGTGACCGGGCTAGTA 301 GGCAGTGGCGACATGGTCCTCTCTCGTGCCGCTCGTGCCGAATTCGCCACGAGTGGAAGCCA 361 GCGAGCGCCGCTGTATAGGAAAGAAGCCGCAGCTCTTTCCAGAGTCCACCGGGAGGCAG 421 AGGCTCTGAGGACCTATAGACC**ATG**GTGCGCGCCCTGCCTGCTGCTGCTGCCACT 481 GCTGCGCTTCTCTGCGGCCACACTAGACCCTGTGAGGTGGACGATGAGAACTTCCGCTG 541 CGTCTGTAACTTCACGGGTCCTCAGCCCGACTGGTCCAGCGCCTTCCAGTGCATGACTGC 601 CGTCGAGGTGGAGATCCCTGGCGGCGGCCGCAACCTGGAACAGTTTCTAAAAGGCGCCTC 661 CGCCGACCCGAAGCAGTATGCTGACATTGTCAAGGCCTGCGCAGCGGCTCACAGT 721 GGGCGCCGTACAGGTTCCTGCCCCGCTTCTGGTCGCCCTCCTACGTGCGCTCGGTACTC 781 CCGCCTCAAGGAACTGACGCTGGAGGACCTAGAGGTAACCGGCACGATGCAGCCGCCGCC 841 TCTAGAAGCCACTGGGCCTCCGCTCTCCTCCCTCGTCTCCGCAACGTGTCGTGGGCGAC 901 AGGAGGTGCCTGGCTCGCCGAACTGCAGCAGTGGCTCAAGCCGGGCCTCAAGATATTGAG 961 CATTGCGCAAGCTCACTCACTCGCCTTTCCTGCGCGCAGCTCCACAGTTTCTCGGCCCT 1021 CCACACCCTAGACCTGTCTGACAATCCTGGACTGGGCGAGCGCGGACTGATTGCAGCTCT 1081 CTGTCCGCACAAGTTCCCGGCCCTCCGAGATCTAGCGCTCCCGCAACGCGGGGATGCAGAC 1141 ACCCAACGGCGTGTGCGCGGCGATGGCGGCGGCGGTGTGCAGCCCCATAGCCTGGACCT 1201 CAGCCACAACTCGCTGAGCGCCGCCTGCTCCGGGCGCTCCCAGGTGTGACTGGCCCAGCGC 1261 ACTGAGTTCTCTCAACTTGTCCTTCGCTGGGCTGGAGCAGGTGCCTAAAGGACTACCGGG 1321 CAAGCTTAGCGTGCTTGATCTCAGCTGCAACACAGGCTCAACAAGGCGCCGCGAGCAGACGA 1381 GCTGCCCGTGGTGAGTAATCTGATACTGGACAGGAATCCCTATCTGGACCCTGAAGCGTC 1441 CAAGCAGCAAGACCAGAACTCCGGCGTGGTCGCCGCCTGTGCGCACTCAGCCCTGACCGT 1501 GGGGATATCAGGAACCCTGGCGCTGCTTCGAGGAGCCGGGGACTTCGCC**TAA**GCCCCAGG 1561 GGAGAAGAATGCAATTGACTCAGATTGCCCTGGCTCCAGGGGAGCCTCATTAGGACGTCTT 1621 AACCAACCCGACCCTCTGCCCCCATCTTCATTAAAATCTTAACACAACAAAAAAAAAAAAA 1681 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	SEQ ID NO:178
		1 M V R A P C L L L L L P L L R F S A A T 1 ATGGTGCGCGCCGCCCTGCCTGCTGCTGCTGCCACTGCTGCGCTTCTCTGCCGCCACA 21 L E P C E V D D E N F R C V C N F T G P 61 CTAGAGCCCTGTGAGGTGGACGATGAGAACTTCCGCTGCGTCTGTAACTTCACGGGTCCT 41 Q P D W S S A F Q C M T A V E E V E I R G 121 CAGCCCGACTGGTCCAGCGCCTTCCAGTGCATGACTGCCGTCGAGGTGGAGATCCGTGGC 61 G G R N L E Q F L K G A S A D P K Q Y A 181 GGCGGCCGCAACCTGGAACAGTTTCTAAAAGGCGCCTCCGCCGACCCGAAGCAGTATGCT 81 D I V K A L R L Q R L T V G A V Q V P A 241 GACATTGTCAAGGCCCTGCGCCTGCAGCGCCTCACAGTGGGCGCCGTACAGGTTCCTGCC 101 P L L V A L L R A L G Y S R L K E L T L 301 CCGCTTCTGGTCGCCCTCCTACGTGCGCTCGGGTACTCCCGCCTCAAGGAACTGACGCTG	SEQ ID NO:179

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		121 E D L E V T G T M Q P P P L E A T G P P 361 GAGGACCTAGAGGTAACCGGCACGATGCAGCCGCCGCCTCTAGAAGCCACTGGGCCTCCG 141 L S S L R L R N V S W A T G G A W L A E 421 CTCTCCTCCCTCCGTCTCCGCAACGTGTCGTGGGCGACAGGAGGTGCCTGGCTCGCCGAA 161 L Q Q W L K P G L K I L S I A Q A H S L 481 CTGCAGCAGTGGCTCAAGCCGGGCCTCAAGATATTGAGCATTGCGCAAGCTCACTCACTC 181 A F S C A Q L H S F S A L H T L D L S D 541 GCCTTTTCCTGCGCGCAGCTCCACAGTTTCTCGGCCCTCCACACCCTAGACCTGTCTGAC 201 N P G L G E R G L I A A L C P H K F P A 601 AATCCTGGACTGGGCGAGCGCGGACTGATTGCAGCTCTCTGTCCGCACAAGTTCCCGGCC 221 L R D L A L R N A G M Q T P N G V C A A 661 CTCCGAGATCTAGCGCTCCGCAACGCGGGGATGCAGACACCCAACGGCGTGTGCGCGGCG 241 M A A A G V Q P H S L D L S H N S L S A 721 ATGGCGGCGGCGGGTGTGCAGCCCCATAGCCTGGACCTCAGCCACAACTCGCTGAGCGCC 261 A A P G A P R C D W P S A L S S L N L S 781 GCTGCTCCGGGCGCTCCCAGGTGTGACTGGCCCAGCGCACTGAGTTCTCTCAACTTGTCC 281 F A G L E Q V P K G L P G K L S V L D L 841 TTCGCTGGGCTGGAGCAGGTGCCTAAAGGACTACCGGGCAAGCTTAGCGTGCTTGATCTC 301 S C N R L N K A P R A D E L P V V S N L 901 AGCTGCAACAGGCTCAACAAGGCGCCGCGAGCAGACGAGCTGCCCGTGGTGAGTAATCTG 321 I L D R N P Y L D P E A S K Q Q D Q N S 961 ATACTGGACAGGAATCCCTATCTGGACCCTGAAGCGTCCAAGCAGCAAGACCAGAACTCC 341 G V V A A C A H S A L T V G I S G T L A 1021 GGCGTGGTCGCCGCCTGTGCGCACTCAGCCCTGACCGTGGGGATATCAGGAACCCTGGCG 361 L L R G A G D F A - 1081 CTGCTTCGAGGAGCCGGGGACTTCGCCTAA	
BM734865	Nuclear receptor binding factor 1	1 GCTCTGTGTTGGTTGGAGCGAGCATGTGGGTCTGCAGTACCCTGTGGCGGGTGCGAACCC 61 CCGCCCGGCAGTGGCGGGGGCTGCTCCCAGCTTCTGGCTGTCACGGACCTGCCGCCTCCT 121 CCTACTCCGCATCCGCCGAGCCTGCCCGGGTCCGGGCGCTTGTCTATGGGCACCACGGGG 181 ATCCAGCCAAGGTCGTCGAACTCAAGAACCTGGAGCTAGCTGCTGTGAGAGGATCAGATG 241 TCCGTGTGAAGATGCTGGCGGCCCCTATCAATCCATCTGACATAAATATGATCCAAGGAA 301 ACTACGGACTCCTTCCTGAACTGCCTGCTGTTGGAGGGAACGAAGGTGTTGCACAGGTGG 361 TAGCGGTGGGCAGCAATGTGACCGGGCTGAAGCCAGGAGACTGGGTGATTCCAGCAAATG	SEQ ID NO:180

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		421 CTGGTTTAGGAACCTGGCGGACCGAGGCTGTGTTCAGCGAGGAAGCACTGATCCAAGTTC 481 CGAGTGACATCCCTCTTCAGAGCGCTGCCACCCTGGGTGTCAATCCCTGCACAGCCTACA 541 GGATGTTGATGGACTTCGAGCAACTGCAGCCAGGGATTCTGTCATCCAGAATGCATCCA 601 ACAGCGCAGTGGGGCAAGCGGTCATCCAGATCGCCGCAGCCCTGGGCCTAAGAACCATCA 661 ATGTGGTCCGAGACAGACCTGATATCCAGAAGCTGAGTGACAGACTGAAGAAAATGGGGG 721 CTGAGCATGTTATCACTGAAGAGGAATTAAGAAAACATGAGATGAAAAACTTCTTTAAGG 781 ATGTGCCCCGGCCGCGCTTGCTCTCAACTGCGTCGGTGGGAAAAGCTCCACAGAGCTGC 841 TGCGACATTTAGCGCCCGGAGGAACCATGGTGACCTACGGGGGGATGGCCAAGCAGCCTG 901 TCATAGCCTCTGTGAGCCTGTTCATTTTTAAGATGTCAAACTGCGGGGCTTTTGGTTGT 961 CCCAGTGCAAGAAGGACCACAGTCCAGAGCAGTTCCAGGGCTGATCCTCACGCTGTGCG 1021 ATCTCATCCGCCAAGGCCAGCTCATGGCCCCCATCTGCTCTGAGCTCCCGCTGCAGGACT 1081 ACCAGCGTGCCTTGGAAACTGCGATGCAGCCCTTCGTGTCTTCCAAGCAGATTCTCACCA 1141 TGTGATCATCCCCAAAAGAGCTGGAGTGACATGGGAGGGGAGGCGGATCTGAGGGGCTGGG 1201 TGCAGGCCCCTCAGTTGGGGCTCCCACCTTCCCCAGACTACTGTTCTCCTCACTGCCTCT 1261 TCCTATTAGGAGGATGGTGAAGCCAGCCAAGGCTTTTCCCAGGGCCAGCCTCAGGGTATC 1321 TAATAAAGTCTGAACTCTCCCTTCCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAA	
		1 M W V C S T L W R V R T P A R Q W R G L 1 ATGTGGTCTGCAGTACCCTGTGGCGGGTGCGAACCCCCGCCCGGCAGTGGCGGGGGCTG	SEQ ID NO:181
		21 L P A S G C H G P A A S S Y S A S A E P 61 CTCCCAGCTTCTGGCTGTCACGGACCTGCCGCCTCCTCCTACTCCGCATCCGCCGAGCCT	
		41 A R V R A L V Y G H H G D P A K V V E L 121 GCCCGGGTCCGGGCGCTTGTCTATGGCCACCACGGGATCCAGCCAAGGTCGTCGAACTC	
		61 K N L E L A A V R G S D V R V K M L A A 181 AAGAACCTGGAGCTAGCTGCTGTGAGAGGATCAGATGTCCGTGTGAAGATGCTGGCGGCC	
		81 P I N P S D I N M I Q G N Y G L L P E L 241 CCTATCAATCCATCTGACATAAATATGATCCAAGGAAACTACGGACTCCTTCCTGAACTG	
		101 P A V G G N E G V A Q V V A V G S N V T 301 CCTGCTGTTGGAGGGAACGAAGGTGTTGCACAGGTGGTAGCGGTGGGCAGCAATGTGACC	
		121 G L K P G D W V I P A N A G L G T W R T 361 GGGCTGAAGCCAGGAGACTGGGTGATTCCAGCAAATGCTGGTTTAGGAACCTGGCGGACC	
		141 E A V F S E E A L I Q V P S D I P L Q S 421 GAGGCTCTGTTCAGCGAGGAAGCACTGATCCAAGTTCCGAGTGACATCCCTCTTCAGAGC	
		161 A A T L G V N P C T A Y R M L M D F E Q 481 GCTGCCACCCTGGGTGTCAATCCCTGCACAGCCTACAGGATGTTGATGGACTTCGAGCAA	
		181 L Q P G D S V I Q N A S N S G V G Q A V 541 CTGCAGCCAGGGGATTCTGTCATCCAGAATGCATCCAACAGCGGAGTGGGGCAAGCGGTC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		201 I Q I A A A L G L R R T I N V V R R D R R P D 601 ATCCAGATCGCCGCCAGCCCTGGGCCTAAGAACCATCAATGTGGTCCGAGACAGACCTGAT 221 I Q K L S D R L K K M G A E H V I T E E 661 ATCCAGAAGCTGAGTGACAGACTGAAGAAAATGGGGGCCTCAGCATGTTATCACTGAAGAG 241 E L R K H E M K N F F K D V P R P R L A 721 GAATTAAGAAAACATGAGATGAAAAACTTCTTTAAGGATGTGCCCCGCGGCCGGCTTGCT 261 L N C V G G K S S T E L L R H L A P G G 781 CTCAACTGCGTCGGTGGGAAAAGCTCCACAGAGCTGCTGCGACATTTAGCGCCCGGAGGA 281 T M V T Y G G M A K Q P V I A S V S L F 841 ACCATGGTGACCTACGGGGGGGATGGCCAAGCAGCCTGTCATAGCCTCTGTGAGCCTGTTC 301 I F K D V K L R G F W L S Q W K K D H S 901 ATTTTTAAGGATGTCAAACTGCGGGGCTTTTGGTTGTCCCAGTGGAAGAAGGACCACAGT 321 P E Q F Q G L I L T L C D L I R Q G Q L 961 CCAGAGCAGTTCCAGGGGCTGATCCTCACGCTGTGCGATCTCATCCGCCAAGGCCAGCTC 341 M A P I C S E L P L Q D Y Q R A L E T A 1021 ATGGCCCCCATCTGCTCTGAGCTCCCGCTGCAGGACTACCAGCGTGCCTTGGAAACTGCG 361 M Q P F V S S K Q I L T M - 1081 ATGCAGCCCTTCGTGTCTTCCAAGCAGATTCTCACCATGTGA	
BM734862.V1.3_at	Triggering receptor expressed on myeloid cells 1	1 GTCCCGGGAGCCCTCAGCAGCAGTTGGAGCTGGTGCACAGGAAGCATGAGGAAGACCAGG 61 CTCTGGGGGCTGCTGTGGATGCTCTTTGTCTCAGAACTCCGAGCTGCAACTAAATTAACT 121 GAGGAAAAGTATGAACTGAAAGAGGGGCAGACCCTGGATGTGAATGTGACTACACGCTA 181 GAGAAGTTTGCCAGCAGCCAGAAAGCTTGGCAGATAATAAGGGACGGAGATGCCCAAG 241 ACCCTGGCATGCACAGAGAGGCCTTCAAAGAATTCCCATCCAGTCCAAGTGGGAGGATC 301 ATACTAGAAGACTACCATGATCATGGTTTACTGCGCGTCCGAATGGTCAACCTTCAAGTG 361 GAAGATTCTGGACTGTATCAGTGTGTGATCTACCAGCCTCCCAAGGAGCCTCACATGCTG 421 TTCGATCGCATCCCGCTTGGTGGTGACCAAGGGTTTTTCAGGGACCCCTGGCTCCAATGAG 481 AATTCTACCCAGAATGTGTATAAGATTCCTCCTACCACCACTAAGGCCTTGTGCCCACTC 541 TATACCAGCCCCAGAACTGTGACCCAACCCCCACCCAAGTCAACTGCCGGTGTCTCCCGC 601 CCTGGACTTGAAGTCAACCCCACACATGTGACAGACGTCACCAGGATCTCTGTGTTCAGC 661 ATTGTCATTCCTGTGGCGTGCGCACTCGTGACTAAGAGCCTGGTCCTTACTGTCCTGTTT 721 GCTGTCACACAGAAGTCATTTGCATCCTAGGCCCATGGACCCATGAGGATGACCTCTGAT 781 CTCCATCTACATCCCATCTGGCAGTTGTGCCAAGGGAGGGAGGGAGGAGGTAAAAGGCAGGG 841 AGTTAATAACATGAATTAAATCTGTAATCACCGCCAAAAAAAAAAAAAAAAAAAAAAAAA 901 AAAAA 1 M R K T R L W G L L W M L F V S E L R A	SEQ ID NO:182 SEQ ID NO:183

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1 ATGAGGAAGACCAGGCTCTGGGGGCTGCTGTGGATGCTCTTTGTCTCAGAACTCCGAGCT 21 A T K L T E E K Y E L K E G Q T L D V K 61 GCAACTAAATTAACTGAGGAAAAGTATGAACTGAAAGAGGGGCAGACCCTGGATGTGAAA 41 C D Y T L E K F A S S Q K A W Q I I R D 121 TGTGACTACACGCTAGAGAAGTTTGCCAGCAGCCAGAAAGCTTGGCAGATAATAAGGGAC 61 G E M P K T L A C T E R P S K N S H P V 181 GGAGAGATGCCCAAGACCCTGGCATGCACAGAGAGGCCTTCAAAGAATTCCCATCCAGTC 81 Q V G R I I L E D Y H D H G L L R V R M 241 CAAGTGGGGAGGATCATACTAGAAGACTACCATGATCATGGTTTACTGCGCGTCCGAATG 101 V N L Q V E D S G L Y Q C V I Y Q P P K 301 GTCAACCTTCAAGTGGAAGATTCTGGACTGTATCAGTGTGTGATCTACCAGCCTCCCAAG 121 E P H M L F D R I R L V V T K G F S G T 361 GAGCCTCACATGCTGTTCGATCGCATCCGCTTGGTGGTGACCAAGGGTTTTTCAGGGACC 141 P G S N E N S T Q N V Y K I P P T T T K 421 CCTGGCTCCAATGAGAATTCTACCCAGAATGTGTATAAGATTCCTCCTACCACCACTAAG 161 A L C P L Y T S P R T V T Q P P P K S T 481 GCCTTGTGCCCACTCTATACCAGCCCCAGAACTGTGACCCAACCCCCACCCAAGTCAACT 181 A G V S R P G L E V N P T H V T D V T R 541 GCCGGTGTCTCCCGCCCTGGACTTGAAGTCAACCCCACACATGTGACAGACGTCACCAGG 201 I S V F S I V I P V A C A L V T K S L V 601 ATCTCTGTGTTCAGCATTGTCATTCCTGTGGCGTGCGCACTCGTGACTAAGAGCCTGGTC 221 L T V L F A V T Q K S F G S - 661 CTTACTGTCCTGTTTGCTGTCACACAGAAGTCATTTGGATCCTAG	
BM734722	No homology	1 ACCGCGACTTCCAGTACGAGCTGGTCATCCAGAGACAGAGGATCGAGGTGCCGGGCGACT 61 CGCAGAATCAATACATTTTCCCGAGTCTGGAGCCCAGACCGAAGCACACGGTGAAGATCA 121 GGACGGGGGACGCCCGGGACGCCCAGGACCCCCGCTGGGGCGCCTGGAGCCGGCCCGTCG 181 AGTTCGGCTCCGAGGACCCGGATGCGGGGGTCGTGCACGTGTACGTGCTCGTCGTGCTGG 241 GGACCCTGGGCTGCGCGCTGGCGCTCGGCTGCCTGGTGAAGAGGTTCCTCCGGAGACACA 301 GTCTGTTCCAGCCGGTCCCGCGCATCAAAGACAAACTGAACGATAACCATCCGACCGACC 361 TCCAGGACGTCTGGGAGGAATTCCCGGCGGGGGCCGGAAAAGCCGAGCACGAAGAGGTGG 421 TGACCGTCCAGGAGGTCGACAGAGCCCCGGTCAGCGGGTGAAAGGTCACGGGCACCTCCG 481 GCCCCCAGACACCCCGGAAGCCGCCCGGGTTTTCTCAAAACCGTTTTAAGCGTTTCTGCA 541 GCTATTTTTCTACTTTTTATTAAAAAAATAAATGTGAAGTTTGGCCAAGAGGCTTCCCGA 601 CGGGGGGCCGGAAAAAAGGCCCAAAGCTT	SEQ ID NO:184

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
BM734719	No homology	1 AGTCCTCTCGATGAAGCTTCTTCCCACCTAGAAAGAAGTCCTCTCTGAGACTCAAGGGCT 61 AAGGCAAGGTCTTCCAGAAAACAAGGCTTTGACTCCAAGAACAGAGGTGATGGGCAGACT 121 TCTTGGCTCGCCGGGGAAAGGAGGACGCCAATGGGTCAAACTAACTCTGAATCCCTCCCT 181 CCATCTCTCTTTTTCCACTGTCGTCAGAGCCAACAAGAAATGACAGCCTCCAAGCCTTCC 241 TAAAAGCACACTTGCCCCCGCCTGCCACCTCTCCTCAGGCTGCTGCCCTCCCAGGCGCTC 301 CACAGCGAAGGGGTGTGGTGTTTCCTGCAGGCCAGCTGCCTCAGCCCCGCCAAAA 361 CTGTGTTCCCAGCCACGCTCTGGAGCAGGATGACGTGTGGCCAGCCCTTCTCAGGTCT 421 CAGCTCTGCTGGGATGGGAGCAGAGGCCAGGGAGAAAGGTTAGGGGCCCAGGGGTGGGTG 481 ACAACGCTGGCTGCTGAAAGCCCATGAGCTGCTTCTTTGTTCTCTGTCACGGGACAAAAA 541 TCTCTCATCCTATTCTGCTTTCAGTTCATTAAGAGAGCACACATTTTACTCATACACAAATA 601 AAAGTTTTCCCTTGTGGAAACAACAGCTTTAAAAGAAAGG	SEQ ID NO:185
BM734654	No homology	1 AGGGCGTCACGCTGACCGTGATGGTCAACACCAGCCAAACGCAGGTTTCGGAGAAGCTCG 61 TCTACACCAACCCAGGTGGTGAGGGCACCGCCGCCCCAGAACTTCTCATGCTTCATCTACA 121 TCGTGCACTTCATGATCTGCACTTGGCCCCCGGCCCGCGCGGCCCCCGACGACGTCCAGT 181 ATTTCCTGTATATACGAGACTCCCAAGAAGCGGGAGAGGGAATGTCCCGTTACATGAGCG 241 ACTCGGGGACCCACGTGGGCTGCCACCTAGACGACCTCTCGGGATTGACCTCTTACAATT 301 ACTTCGTGGTGAACGGGACCAGCCAAACGACGGGGATCCAGTTCTTCGATTCCGTTATGC 361 GGTCCAAGCAAATAGAGAGGTACAGCCCCCCCCGCCCAACATCAGCGTCCAGGTAAAC	SEQ ID NO:186
BM734531	No homology	1 TCCTCATCAGAGTCACCCAAGGAACTTATGCAGATGCCATGTCCTCACTCCGAATCCTCA 61 CTCTGGGAGTGGAGCCAGGTGTCTGCATTTGAACAGGGTGAGGGGGTGGGTTGCCTGCTG 121 GACAAGGGAGCTGAGCCAGCAGCTCCGGACTCTGTCCTGTGGCTTTTGTGTCTCTCCC 181 ATGTTCTCCCTCCCAGGGCCCACCACTTCATGTTCTCTACAGAGCTAAGATGATGGCCT 241 TGCTTGAGACAGGTCCATCCCCCGTGGTTGGGGTCACTTAGCAGCGACTTCTTGGACTGC 301 CATCCAGCCACAGTGGCCCCACAGAGCTGTCCAGAGCCGAGGCTGTGGGCTGCAGTCCCA 361 GTGAGCAGGGACGTTGCCCGCTGTTGGTCATGACAACCAAACGACGTCCGAGGGCACAGCC 421 AGGTGTCTTCCACCAGCCCATGAGCTGAGAATGCTAAGTCACCAGACAACCAGAAATTGA 481 GTCTCTGTCAGGATCCTTTTGAAGTGTAAGGAGAGAGAAACTTACACTTTGAAAGGTTTT 541 GAGCCTCATCCAGGACAATAAAAATAACTGT	SEQ ID NO:187
BM734457	High-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 beta mRNA	1 ggtgtggacg ttgtctaaat ttcggtagcc atggcacaag aatataagaa agcatgggat 61 tatggcaacc acagaatctc agtagtacaa gttccattca gtttttctg aaagaaagcc 121 ctctgttaaa gtgaagcaaa gaaactgttg tggattataa cgtttagaag ttccaatttt 181 tcagtgcttt acaaataaag catcatttaa ccttttaaat gaaaaagatt aagatctcat 241 gcaactgttg tatttttctgg aagccattct ccaaaaggga agtgcacatt taaaacacag 301 atatgatggt ccttgctgca gggatttaag tctacttgct ttacatcat gaccagcttg 361 aaacggtcac agacagaaag gcctcttgcc actgacaggg cctctgttgt tggcacagac 421 ggcaccccca aagtccacac tgatgatttc tacatgcggc gcttccggtc ccaaaatggc	SEQ ID NO:188

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		481 agcttaggat catcagttat ggctcctgta ggaccccccc gaagtgaagg ttctcaccat 541 ataacctcaa cccccggagt cccaaaaatg gggtaaggg caaggattgc agattggccc 601 ccaagaaagg aaaacataaa agaatctagc cgttcaagcc aggaaataga aacctcaagt 661 tgccttgata gcctgtcctc caaaagcagt cctgtgagtc agggaagttc tgttagcctc 721 aattccaatg actcagccat gctgaaaagc atacagaaca cgctgaaaaa caagacaaga 781 ccgtcggaga acatggactc cagatttctc atgcctgaag cctaccccag ctcccccaga 841 aaagctcttc gcagaatacg ccagcgaagc aacagtgata tcaccataag tgaacttgat 901 gtggatagct ttgatgaatg tatctcacct acatacaaga ctggaccatc actgcacagg 961 gaatatggta gcacatcttc aattgataaa caggaacat ctggagaaag ctttttgat 1021 ttgttaaagg gctacaaaga tgacaaatct gatcgaggtc caactccaac caagctcagt 1081 gacttttcta ttactggtgg tggcaagggt tctgttttct ctttgatgt aatagacggg 1141 cctatctcac agagagagaa cctcaggctt tttaaggaaa gggaaaaacc actcaagcga 1201 cgttcaaaat ctgaaactgg agactcctct attttcgta aattgcgcaa tgccaaaggt 1261 gaagaacttg ggaagtcatc agatcttgaa gataaccgat cagaagactc tgtcaggccc 1321 tggacatgtc caaagtgctt tgcccactat gatgtccaga gtatattatt tgatttgaat 1381 gaggcaatta tgaacaggca caatgttatt aagaggagaa acaccaccac tggagcttcc 1441 gcagctgccg tggcatcctt ggtctctgga cctctgtctc attcagccag ttttagctcc 1501 ccaatgggca gcacagagga cctgaattcc aaaggaagcc tcagcatgga ccagggagat 1561 gataaaagca atgagcttgt aatgagctgt ccatatttcc ggaatgagat aggtggagaa 1621 ggggagagga aaatcagcct ttcaaaatca aattctggct cctttagtgg atgtgaaagt 1681 gcctcctttg agtctaccct tagttcccat tgcacaaatg caggagtggc agtacttgaa 1741 gtgcccaagg agaacttggt gttgcaccta gatagagtga aaagatacat cgtggaacac 1801 gtagatctgg gtgcatacta ttatagaaaa ttttctacc agaaggaaca ctggaactat 1861 tttgggctg atgagaatct tggtccagtg gctgtgagca ttcgaaggga aaaaccagat 1921 gaaatgaaag aaaatggatc tccgtacaac taccgaataa ttttagaac tagtgagctc 1981 atgacactga gaggttcggt cctggaggac gccattccgt cgacagccaa gcactcgaca 2041 gccagaggcc tgcctctcaa agaagtgctg gagcacgtgg ttcctgagct caatgtccag 2101 tgcctgcggt tggccttcaa cacaccaag gtcacagagc agctcatgaa actggatgaa 2161 caagggctga actaccagca gaaagtaggc atcatgtact gcaaagctgg acagagcact 2221 gaagaagaga tgtacaacaa tgagtcagct ggcccagcct ttgaagaatt ccttcaacta 2281 ttgggagagc gagttcggct caaaggattt gagaagtatc gagcacagct tgataccaaa 2341 actgactcca ctggaaccca ttctctgtac acaacataca aagattatga aattatgttc 2401 catgtttcta ccatgctgcc atacacaccc aacaacaaac aacagctcct gaggaagcgg 2461 cacattggaa atgatatcgt aacaatgttt ttccaagagc ctggagcaca gccattcagc 2521 ccaaaaaaca tccgatccca cttccagcac gttttcgtca tcgtcagggt gcacaatccg 2581 tgctctgaca gtgtctgtta tagtgtggct gttaccaggt ccagagatgt gccttcttt 2641 ggcctcccca ttcctaaagg ggtcacttcc cctaagtcaa atgtgttcag ggacttcctt 2701 ttggcgaaag tgattaatgc agaaaatgct gctcataaat cggagaagtt tcgggccatg 2761 gcaactcgga cccgccagga atacctgaaa gatctggcag aaaagaatgt caccaacacc 2821 cctatcgacc cttctggcaa gtttccgttc atctctctgg cttccaagaa gaaggaaaag 2881 tctaagccat atccaggagc cgagctcagc agcatggggg ccattgtatg ggcagtccgg 2941 gctgaagact acaacaaggc catggaacta gactgccttt tagggatctc caatgagttc 3001 attgtgctca ttgaacagga aacaaagagc gtggtcttca atgttcctg tagagatgtg 3061 atagggtgga cttcaactga caccagcctc aaaatcttct atgaacgagg agaatgtgtt 3121 tcagtgggta gttttattaa cattgaggag atcaaagaga ttgtcaaaag gttgcagttt 3181 gtttcaaaag gctgtgaatc ggtggagatg actctgcgaa gaaatgggct aggacagctt 3241 ggcttccatg tcaactatga gggcattgtg gcggatgtgg agccctacgg ttatgccttgg 3301 caggcagggc tgaggcaggg cagtcgcctg gtggagatct gcaaggtggc ggtagccact	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		3361 ctgagccatg agcagatgat cgacctcctg agaacatctg tcacggtgaa ggttgtcatc 3421 attcccccgc atgatgactg cacccgcgg aggagttgct ctgaaaccta ccgcatgcca 3481 gtgatggagt acaaaatgaa tgaaggtgtt tcatacgaat tcaagtttcc cttccgaaat 3541 aataacaagt ggcagaggaa cgccagcaag gggcctcatt cacctcaagt cccgtcccag 3601 gtgcagagtc ccatgacctc gcggctgaat gctggaaaag gagatggaa gatgcctcct 3661 ccagaaagag ccgccaacat ccctcgaagc atctccagtg acggcgccc actagaggag 3721 cggctgtctc ctggttcgga catctatgtg acggtctcat ccatggcttt agcaagatcc 3781 cagtgtcgga actctcctag caacttgtct tcatccagtg atactgttc tgtgggggc 3841 acttacaggc agaagtccat gcccgaaggg tttggagtga gccgtagatc cccagcctcc 3901 attgcaggc agaacaccca gtcagatatt ggtggcagcg gaaaatccac gcctagctgg 3961 caaagaagtg aggatagcat tgctgaccag atggcttaca gttatagagg acctcaggat 4021 ttcaattctt ttgtcctcga gcagcatgaa tatacagagc caacatgcca tctcccagca 4081 gtatcaaagg tactgccagc tttccgagag agccccagtg ggagattaat gcggcaggat 4141 ccagtggttc atttgtctcc aaacaaacaa gggcattctg atagccacta ctcgagccac 4201 tccagtagca atactctctc cagcaatgcg tcaagtgccc atagtgatga gaagtggtac 4261 gatgggacc gcacagaatc cgaactcaac agctataact atctgcaagg cacctctgct 4321 gacagtggca ttgacaccac ctctttatggc cccagccacg gcagcacagc ctcgctgggg 4381 gctgccacat cgtcacctcg ctcagggcca ggcaaggaga aagtggcacc cctatggcac 4441 agctccagtg aagtaatctc catggcagat cggactttgg agacagagag ccacggcctg 4501 gaccggaaaa cagagtcttc cctgagctta gacatacaca gcaagagcca agccggctcg 4561 acccctctga caagggagaa cagcaccttc agtataaacg atgctgcttc ccacacaagt 4621 accatgagct cccgacactc tgccagccca gtggttttca ccagtgcccg gagttcacct 4681 aaagaagagc ttcatccagc tgccccctca cagctcgcac catccttctc ctcctcttcc 4741 tcctcctcct ctggtcctag gagttttttac cctcgccagg gcgctactag caagtacctg 4801 attggatgga aaaaaccega aggaaccata aactccgtgg gatttatgga cacgagaaag 4861 cgtcatcaga gcgatggcaa tgaaatagcc cacaccaggc tgcgtgcctc aaccagagac 4921 ctccgggcat ctcctaagcc aacctccaag tccaccattg aagaagatct aaagaaacta 4981 attgatcttg aaagcccaac tcctgaatca cagaagagtt ttaagttcca cgcactctcc 5041 tctcctcagt ctcctttccc cagcacccca acctcacggc gggccttgca cagaacactg 5101 tcggacgaga gcatttacaa tagccagagg gagcactttt tcacctccag ggcgtcactt 5161 ctggaccaag ccctgcccaa cgacgtcctc ttcagtagca cgtaccctc tctccccaag 5221 tcgctcccgt tgaggaggcc ttcttacacc ttaggaatga aatcgctgca tggagagttc 5281 tcagcctcgg acagctccct cactgacatc caggagaccc gcaggcagcc tatgcccgac 5341 cctggcctga tgccctgcc tgacactgct gcagacttgg attggtccaa cctggtagat 5401 gctgccaaag cctatgaggt ccagagagcc tcatttttg ctgctagtga tgaaaaccat 5461 cgcccttga gtgctgcatc caacagtgat cagctggagg accaggctct ggcccagatg 5521 aagccttaca gcagcagtaa agactcctct cccactctgg cttctaaagt ggacccagctg 5581 gaaggtatgc tgaagatgct tcgggaagat ttgaagaagg aaaaagaaga caaagctcac 5641 cttcaggcgg aggtgcagca cctgcgagag gacaacctga ggctacagga ggagtcccag 5701 aacgcctcgg acaagctgaa gaagttcaca gaatggtct tcaacaccat agacatgagc 5761 tagggaaggc tgaggaggac aggagaaggg cccagacact ccctccagtg agtgtcctgc 5821 agcccttatt ccctccatag aaagcatcct cagagcacct tccctggctt cctactctgc 5881 ccccttccgg ggagtgcaca acacaatagt tgcagatcaa caatcatcac ctgccttttg 5941 tagaaaagaa aaacaaaaaa agtaaataaa aatttaaac agtaaaataa aagtttaact 6001 gctaaaaaaa aaaaaaaaaa aaaaaaaa 1 M T S L K R S Q T E E R P L A T D R A S V 1 ATGACCAGCTTGAAACGGTCACAGACAGAAAGGCCTCTTGCCACTGACAGGGCCTCTCTT	SEQ ID NO:189

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		21 V G T D G T P K V H T D D F Y M R R F R 61 GTTGGCACAGACGGCACCCCCAAAGTCCACACTGATGATTTCTACATGCGGCGCTTCCGG 41 S Q N G S L G S S V M A P V G P P R S E 121 TCCCAAAATGGCAGCTTAGGATCATCAGTTATGGCTCCTGTAGGACCCCCCCGAAGTGAA 61 G S H H I T S T P G V P K M G V R A R I 181 GGTTCTCACCATATAACCTCAACCCCCGGAGTCCCAAAAATGGGGGTAAGGGCAAGGATT 81 A D W P P R K E N I K E S S R S S Q E I 241 GCAGATTGGCCCCCAAGAAAGGAAAACATAAAAGAATCTAGCCGTTCAAGCCAGGAAATA 101 E T S S C L D S L S S K S S P V S Q G S 301 GAAACCTCAAGTTGCCTTGATAGCCTGTCCTCCAAAAGCAGTCCTGTGAGTCAGGGAAGT 121 S V S L N S N D S A M L K S I Q N T L K 361 TCTGTTAGCCTCAATTCCAATGACTCAGCCATGCTGAAAAGCATACAGAACACGCTGAAA 141 N K T R P S E N M D S R F L M P E A Y P 421 AACAAGACAAGACCGTCGGAGAACATGGACTCCAGATTTCTCATGCCTGAAGCCTACCCC 161 S S P R K A L R R I R Q R S N S D I T I 481 AGCTCCCCCAGAAAAGCTCTTCGCAGAATACGCCAGCGAAGCAACAGTGATATCACCATA 181 S E L D V D S F D E C I S P T Y K T G P 541 AGTGAACTTGATGTGGATAGCTTTGATGAATGTATCTCACCTACATACAAGACTGGACCA 201 S L H R E Y G S T S S I D K Q G T S G E 601 TCACTGCACAGGGAATATGGTAGCACATCTTCAATTGATAAACAGGGAACATCTGGAGAA 221 S F F D L L K G Y K D D K S D R G P T P 661 AGCTTTTTTGATTTGTTAAAGGGCTACAAAGATGACAAATCTGATCGAGGTCCAACTCCA 241 T K L S D F L I T G G G K G S G F S L D 721 ACCAAGCTCAGTGACTTTCTCATTACTGGTGGTGGCAAGGGTTCTGGTTTCTCTTTGGAT 261 V I D G P I S Q R E N L R L F K E R E K 781 GTAATAGACGGGCCTATCTCACAGAGAGAGAACCTCAGGCTTTTTAAGGAAAGGGAAAAA 281 P L K R R S K S E T G D S S I F R K L R 841 CCACTCAAGCGACGTTCAAAATCTGAAACTGGAGACTCCTCTATTTTTCGTAAATTGCGC 301 N A K G E E L G K S S D L E D N R S E D 901 AATGCCAAAGGTGAAGAACTTGGGAAGTCATCAGATCTTGAAGATAACCGATCAGAAGAC 321 S V R P W T C P K C F A H Y D V Q S I L 961 TCTGTCAGGCCCTGGACATGTCCAAAGTGCTTTGCCCACTATGATGTCCAGAGTATATTA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		341 F D L N E A I M N R H N V I K R R N T T 1021 TTTGATTTGAATGAGGCAATTATGAACAGGCACAATGTTATTAAGAGGAGAAACCACC	
		361 T G A S A A A V A S L V S G P L S H S A 1081 ACTGGAGCTTCCGCAGCTGCCGTGGCATCCTTGGTCTCTGGACCTCTGTCTCATTCAGCC	
		381 S F S S P M G S T E D L N S K G S L S M 1141 AGTTTTAGCTCCCCAATGGCCAGCACAGAGGACCTGAATTCCAAAGGAAGCCTCAGCATG	
		401 D Q G D D K S N E L V M S C P Y F R N E 1201 GACCAGGGAGATGATAAAAGCAATGAGCTTGTAATGAGCTGTCCATATTTTCGGAATGAG	
		421 I G G E G E R K I S L S K S N S G S F S 1261 ATAGGTGGAGAAGGGGAGAGGAAAATCAGCCTTTCAAAATCAAATTCTGGCTCCTTTAGT	
		441 G C E S A S F E S T L S S H C T N A G V 1321 GGATGTGAAAGTGCCTCCTTTGAGTCTACCCTTAGTTCCCATTGCACAAATGCAGGAGTG	
		461 A V L E V P K E N L V L H L D R V K R Y 1381 GCAGTACTTGAAGTGCCCAAGGAGAACTTGGTGTTGCACCTAGATAGAGTGAAAAGATAC	
		481 I V E H V D L G A Y Y Y Y R K F F Y Q K E 1441 ATCGTGGAACACGTAGATCTGGGTGCATACTATTATATAGAAAATTTTTCTACCAGAAGGAA	
		501 H W N Y F G A D E N L G P V A V S I R R 1501 CACTGGAACTATTTTGGGGCTGATGAGAATCTTGGTCCAGTGGCTCTGTGAGCATTCGAAGG	
		521 E K P D E M K E N G S P Y N Y R I I F R 1561 GAAAAACCAGATGAAATGAAAGAAATGGATCTCCGTACAACTACCGAATAATTTTTAGA	
		541 T S E L M T L R G S V L E D A I P S T A 1621 ACTAGTGAGCTCATGACACTGAGAGGTTCGGTCCTGGAGGACGCCATTCCGTCGACAGCC	
		561 K H S T A R G L P L K E V L E H V V P E 1681 AAGCACTCGACAGCCAGAGGCCTGCCTCTCAAAGAAGTGCTGGAGCACGTGGTTCCTGAG	
		581 L N V Q C L R L A F N T P K V T E Q L M 1741 CTCAATGTCCAGTGCCTGCGGTTGCCTTCAACACACCCAAGGTCACAGAGCAGCTCATG	
		601 K L D E Q G L N Y Q Q K V G I M Y C K A 1801 AAACTGGATGAACAAGGCTGAACTACCAGCAGAAAGTAGGCATCATGTACTGCAAAGCT	
		621 G Q S T E E E M Y N N E S A G P A F E E 1861 GGACAGAGCACTGAAGAAGATGTACAACAATGAGTCAGCTGGCCCAGCCTTTGAAGAA	
		641 F L Q L L G E R V R L K G F E K Y R A Q 1921 TTCCTTCAACTATTGGGAGAGCGAGTTCGGCTCAAAGGATTTGAGAAGTATCGAGCACAG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		661 L D T K T D S T G T H S L Y T T Y K D Y 1981 CTTGATACCAAAACTGACTCCACTGGAACCCATTCTCTGTACACAACATACAAAGATTAT 681 E I M F H V S T M L P Y T P N N K Q Q L 2041 GAAATTATGTTCCATGTTTCTACCATGCTGCCATACACACCCAACAACAAACAACAGCTC 701 L R K R H I G N D I V T I V F Q E P G A 2101 CTGAGGAAGCGGCACATTGGAAATGATATCGTAACAATTGTTTTCCAAGAGCCTGGAGCA 721 Q P F S P K N I R S H F Q H V F V I V R 2161 CAGCCATTCAGCCCAAAAAACATCCGATCCCACTTCCAGCACGTTTTCGTCATCGTCAGG 741 V H N P C S D S V C Y S V A V T R S R D 2221 GTGCACAATCCGTGCTCTGACAGTGTCTGTTATAGTGTGGCTGTTACCAGGTCCAGAGAT 761 V P S F G P P I P K G V T F P K S N V F 2281 GTGCCTTCCTTTGGGCCTCCCATTCCTAAAGGGGTCACTTTCCCTAAGTCAAATGTGTTC 781 R D F L L A K V I N A E N A A H K S E K 2341 AGGGACTTCCTTTTGGCGAAAGTGATTAATGCAGAAAATGCTGCTCATAAATCGGAGAAG 801 F R A M A T R T R Q E Y L K D L A E K N 2401 TTTCGGGCCATGGCAACTCGGACCCGCCAGGAATACCTGAAAGATCTGGCAGAAAAGAAT 821 V T N T P I D P S G K F P F I S L A S K 2461 GTCACCAACACCCCTATCGACCCTTCTGGCAAGTTTCCGTTCATCTCTCTGGCTTCCAAG 841 K K E K S K P Y P G A E L S S M G A I V 2521 AAGAAGGAAAAGTCTAAGCCATATCCAGGAGCCGAGCTCAGCAGCATGGGGGCCATTGTA 861 W A V R A E D Y N K A M E L D C L L G I 2581 TGGGCAGTCCGGGCTGAAGACTACAACAAGGCCATGGAACTAGACTGCCTTTTAGGGATC 881 S N E F I V L I E Q E T K S V V F N C S 2641 TCCAATGAGTTCATTGTGCTCATTGAACAGGAAACAAAGAGCGTGGTCTTCAATTGTTCC 901 C R D V I G W T S T D T S L K I F Y E R 2701 TGTAGAGATGTGATAGGGTGGACTTCAACTGACACCAGCCTCAAAATCTTCTATGAACGA 921 G E C V S V G S F I N I E E I K E I V K 2761 GGAGAATGTGTTTCAGTGGGTAGTTTTATTAACATTGAGGAGATCAAAGAGATTGTCAAA 941 R L Q F V S K G C E S V E M T L R R N G 2821 AGGTTGCAGTTTGTTTCAAAAGGCTGTGAATCGGTGGAGATGACTCTGCGAAGAAATGGG 961 L G Q L G F H V N Y E G I V A D V E P Y 2881 CTAGGACAGCTTGGCTTCCATGTCAACTATGAGGGCATTGTGGCGGATGTGGAGCCCTAC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		981 G Y A W Q A G L R R Q G S R L V E I C K V 2941 GGTTATGCCTGGCAGGCAGGGCTGAGGCAGGGCAGTCGCCTGGTGGAGATCTGCAAGGTG	
		1001 A V A T L S H E Q M I D L L R T S V T V 3001 GCGGTACCCACTCTGAGCCATGAGCAGATGATCGACCTCCTGACAACATCTGTCACGGTG	
		1021 K V V L I P P H D D C T P R R S C S E T 3061 AAGGTTGTCATCATTCCCCCGCATGATGACTGCACCCCGCGGAGGAGTTGCTCTGAAACC	
		1041 Y R M P V M E Y K M N E G V S Y E F K F 3121 TACCGCATGCCAGTGATGGAGTACAAAATGAATGAAGGTGTTTCATACGAATTCAAGTTT	
		1061 P F R N N N K W Q R N A S K G P H S P Q 3181 CCCTTCCGAAATAATAACAAGTGGCAGAGGAACGCCAGCAAGGGCCTCATTCACCTCAA	
		1081 V P S Q V Q S P M T S R L N A G K G D G 3241 GTCCCGTCCCAGGTGCAGAGTCCCATGACCTCGCGGCTGAATGCTGGAAAAGGAGATGGG	
		1101 K M P P P E R A A N I P R S I S S D G R 3301 AAGATGCCTCCTCCAGAAAGAGCCGCCAACATCCCTCGAAGCATCTCCAGTGACGGGCGC	
		1121 P L E R R L S P G S D I Y V T V S S M A 3361 CCACTAGAGAGGCGGCTGTCTCCTGGTTCGGACATCTATGTGACGGTCTCATCCATGGCT	
		1141 L A R S Q C R N S P S N L S S S S D T G 3421 TTAGCAAGATCCCCAGTGTCGGAACTCTCCTAGCAACTTGTCTCTTCATCCAGTGATACTGGT	
		1161 S V G G T Y R Q K S M P E G F G V S R R 3481 TCTGTGGGGGCACTTACAGGCAGAAGTCCATGCCCGAAGGGTTTGGAGTGAGCCGTAGA	
		1181 S P A S I D R Q N T Q S D I G G S G K S 3541 TCCCCAGCCTCCATTGACAGGCAGAACACCCAGTCAGATATTGGTGGCAGCGGAAAATCC	
		1201 T P S W Q R S E D S I A D Q M A Y S Y R 3601 ACGCCTAGCTGGCAAAGAAGTGAGGATAGCATTGCTGACCAGATGGCTTACAGTTATAGA	
		1221 G P Q D F N S F V L E Q H E Y T E P T C 3661 GGACCTCAGGATTTCAATTCTTTGTCCTCGAGCAGCATGAATATACAGAGCCAACATGC	
		1241 H L P A V S K V L P A F R E S P S G R L 3721 CATCTCCCAGCAGTATCAAAGGTACTGCCAGCTTTCCGAGAGAGCCCCAGTGGGAGATTA	
		1261 M R Q D P V V H L S P N K Q G H S D S H 3781 ATGCGGCAGGATCCAGTGGTTCATTTGTCTCCAAACAAACACAAGGCATTCTGATAGCCAC	
		1281 Y S S H S S S N T L S S N A S S A H S D 3841 TACTCGAGCCACTCCAGTAGCAATACTCTCTCCAGCAATGCGTCAAGTGCCCATAGTGAT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1301 E K W Y D G D R T E S E L N S Y N Y L Q 3901 GAGAAGTGGTACGATGGGGACCGCACAGAATCCGAACTCAACAGCTATAACTATCTGCAA 1321 G T S A D S G I D T T S Y G P S H G S T 3961 GGCACCTCTGCTGACAGTGGCATTGACACCACCTCTTATGGCCCCAGCCACGGCAGCACA 1341 A S L G A A T S S P R S G P G K E K V A 4021 GCCTCGCTGGGGGCTGCCACATCGTCACCTCGCTCAGGGCCAGGCAAGGAGAAAGTGGCA 1361 P L W H S S S E V I S M A D R T L E T E 4081 CCCCTATGGCACAGCTCCAGTGAAGTAATCTCCATGGCAGATCGGACTTTGGAGACAGAG 1381 S H G L D R K T E S S L S L D I H S K S 4141 AGCCACGGCCTGGACCGGAAAACAGAGTCTTCCCTGAGCTTAGACATACACAGCAAGAGC 1401 Q A G S T P L T R E N S T F S I N D A A 4201 CAAGCCGGCTCGACCCCTCTGACAAGGGAGAACAGCACCTTCAGTATAAACGATGCTGCT 1421 S H T S T M S S R H S A S P V V F T S A 4261 TCCCACACAAGTACCATGAGCTCCCGACACTCTGCCAGCCCAGTGGTTTTCACCAGTGCC 1441 R S S P K E E L H P A A P S Q L A P S F 4321 CGGAGTTCACCTAAAGAAGAGCTTCATCCAGCTGCCCCCTCACAGCTCGCACCATCCTTC 1461 S S S S S S S S G P R S F Y P R Q G A T 4381 TCCTCCTCTTCCTCCTCCTCCTCTGGTCCTAGGAGTTTTTACCCTCGCCAGGGCGCTACT 1481 S K Y L I G W K K P E G T I N S V G F M 4441 AGCAAGTACCTGATTGGATGGAAAAAACCCCAAGGAACCATAAACTCCGTGGGATTTATG 1501 D T R K R H Q S D G N E I A H T R L R A 4501 GACACGAGAAAGCGTCATCAGAGCGATGGCAATGAAATAGCCCACACCAGGCTGCGTGCC 1521 S T R D L R A S P K P T S K S T I E E D 4561 TCAACCAGAGACCTCCGGGCATCTCCTAAGCCAACCTCCAAGTCCACCATTGAAGAAGAT 1541 L K K L I D L E S P T P E S Q K S F K F 4621 CTAAAGAAACTAATTGATCTTGAAAGCCCAACTCCTGAATCACAGAAGAGTTTTAAGTTC 1561 H A L S S P Q S P F P S T P T S R R A L 4681 CACGCACTCTCCTCTCCTCAGTCTCCTTTCCCCAGCACCCCCACCTCACGGCGGGCCTTG 1581 H R T L S D E S I Y N S Q R E H F F T S 4741 CACAGAACACTGTCGGACGAGAGCATTTACAATAGCCAGAGGGAGCACTTTTTCACCTCC 1601 R A S L L D Q A L P N D V L F S S T Y P 4801 AGGGCGTCACTTCTGGACCAAGCCCTGCCCAACGACGTCCTCTTCAGTAGCACGTACCCT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1621 S L P K S L P L R R P S Y T L G M K S L 4861 TCTCTCCCCAAGTCGCTCCCGTTGAGGAGGCCTTCTTACACCTTAGGAATGAAATCGCTG	
		1641 H G E F S A S D S S L T D I Q E T R R Q 4921 CATGGAGAGTTCTCAGCCTCGGACAGCTCCCTCACTCGACATCCAGGAGACCCGCAGGCAG	
		1661 P M P D P G L M P L P D T A A D L D W S 4981 CCTATGCCCGACCCTGGCCTGATGCCCCTGCCTGACACTGCTGCAGACTTGGATTGGTCC	
		1681 N L V D A A K A Y E V Q R A S F F A A S 5041 AACCTGGTAGATGCTGCCAAAGCCTATGAGGTCCAGAGAGCCTCATTTTTTGCTGCTAGT	
		1701 D E N H R P L S A A S N S D Q L E D Q A 5101 GATGAAAACCATCGCCCCTTGAGTGCTGCATCCAACAGTGATCAGCTGGAGGACCAGGCT	
		1721 L A Q M K P Y S S S S K D S S P T L A S K 5161 CTGGCCCAGATGAAGCCTTACAGCAGCAGTAAAGACTCCTCTCCCACTCTGGCTTCTAAA	
		1741 V D Q L E G M L K M L R E D L K K E K E 5221 GTGGACCAGCTGGAAGGTATGCTGAAGATGCTTCGGGAAGATTTGAAGAAGGAAAAAGAA	
		1761 D K A H L Q A E V Q H L R E D N L R L Q 5281 GACAAAGCTCACCTTCAGGCGGAGGTGCAGCACCTGCGAGAGGACAACCTGAGGCTACAG	
		1781 E E S Q N A S D K L K K F T E W V F N T 5341 GAGGAGTCCCAGAACGCCTCGGACAAGCTGAAGAAGTTCACAGAATGGGTCTTCAACACC	
		1801 I D M S - 5401 ATAGACATGAGCTAG	
B1961941	Fibroblast mRNA for aldolase A	1 GGGGAACCACACTCCGTCCACGGACTCTCCGTTATTTTAGGAGGTCCCTGGCCAAAGATT 61 TATTTCTCTTGACAACCAAGGGCCTCCGTCTGGATTTCCAGGAAGAATTTCCTCTGAAG 121 CACCGGAACTTGCTACTACCAGCACCACTGCCCTACCAATATCCACCACTGACCCCGGAGC 181 AGAAGAAGGAGCTGTCTGACATCGCTCACCGCATCGTGGCACCTGGCAAGGGCATCCTGG 241 CTGCAGATGAGTCCCACTGGGAGCATTGCCAAGCGGCTGCAGTCCATTGGCACCGAGACA 301 CCGAGGAGAACCGGCGCTTCTACCGCCAGCTGCTGCTGACAGCTGACGACCGCCTGAACC 361 CCTGCATTGGGGGTGTCATCCTCTTCCATGAGACACTCTACCAGAAGGCGGATGATGGGC 421 GTCCCTTCCCCCAAGTTATCAAATCCAAGGGCGGTGTTGTGGGCATCAAGGTAGACAAGG 481 GCGTGGTCCCCCTGGCAGGGACAAATGGCGAGACTACCACCCCAAGGGTTGGATGGGCTGT 541 CTGAGCGCTGTGCCCAGTACAAGAAGGACGGAGCTGACTTTGCCAAGTGGCGCTGTGTGC 601 TGAAGATTGGGGAGCACACTCCCTCATCCCTTGCCATCATGGAAAATGCCAATGTTCTGG 661 CCCGTTATGCCAGCATCTGCCAGCAGAATGGCATTGTGCCCATCGTGGAGCCTGAGATCC 721 TCCCTGATGGGGACCATGACTTGAAGCGCTGTCAGTATGTAACCGAGAAGGTGCTGGCTG 781 CTGTTTACAAGGCTCTGAGTGACCACCACATCTACCTGGAAGGCACCTTGCTGAAGCCCA 841 ATATGGTAACCCCAGGCCACGCCTGCACCCACAAATATTCTCATGAGGAGATTGCCATGG	SEQ ID NO:190

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		901 CAACTGTCACGGCACTGCGTCGCACGGTGCCCCCTGCTGTCACTGGATCACCTTCCTAT 961 CTGGAGGCCAGAGTGAGGAGGAGGCATCCATCAACCTCAACGCCATCAACAAGTGCCCCC 1021 TGCTGAAGCCGTGGGCCCTGACCTTCTCCTATGGCCGAGCCCTGCAGGCCTCTGCCCTGA 1081 AGGCCTGGGGTGGGAAGAAGGAGAACCTGAAGGCTGCCCAGGAGGAATATGTCAAGCGAG 1141 CCCTGGCCAACAGCCTCGCCTGCCAAGGAAAATACACCCCAAGTGGTCACGCTGGGGCTG 1201 CAGCCAGCCGAGTCCCTCTTCATCTCTAACCATGCCTACTAAGTGGAGGTATTCTAAGGCT 1261 GCCCCCTCAACACTCCAGGCCCTGCCTCCTCCCACTCTCACTCTTGAAGAGGGGCCTCA 1321 TCCAGGGCTTTAGGCTGTTCTTTCCCATTCTCCTTGCCTCCCTGGTGACATTGGTCTGTG 1381 GTATTGTCTGTGTATGCTAACTCCATCACCCTTTCGAGCCCACTGCCAAATAAACAGCTA 1441 TTTAAGGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAATAAAAAAAAAAAAAA 1501 AAAAAAAAAAAAAA	SEQ ID NO:191
		1 M P Y Q Y P A L T P E· Q K K E L S D I A 1 ATGCCCTACCAATATCCAGCACTGACCCCGGAGCAGAAGAGGAGCTGTCTGACATCGCT 21 H R I V A P G K G I L A A D E S T G S I 61 CACCGCATCGTGGCACCTGGCAAGGGCATCCTGGCTGCAGATGACTCCACTGGGAGCATT 41 A K R L Q S I G T E E N T E E N R R F Y R 121 GCCAAGCGGCTGCAGTCCATTGGCACCGAGAACACCGAGGAGAACCGGCGCTTCTACCGC 61 Q L L L T A D D R V N P C I G G V I L F 181 CAGCTGCTGCTGACAGCTGACGACCGCGTGAACCCCTGCATTGGGGGTGTCATCCTCTTC 81 H E T L Y Q K A D D G R P P F P Q V I K S 241 CATGAGACACTCTACCAGAAGGCGGATGATGGGCGTCCCTTCCCCCAAGTTATCAAATCC 101 K G G V V G I K V D K G V V P L A G T N 301 AAGGGCGGTGTTGTGGGCATCAAGGTAGACAAGGGCGTGGTCCCCCTGGCAGGGACAAAT 121 G E T T T Q G L D G L S E R C A Q Y K K· 361 GGCGAGACTACCACCCAAGGGTTGGATGGGCTGTCTGAGCGCTGTGCCCAGTACAAGAAG 141 D G A D F A K W R C V L K I G E H T P S 421 GACGGAGCTGACTTTGCCAAGTGGCGCTGTGTGCTGAAGATTGGGGAGCACACTCCCTCA 161 S L A I M E N A N V L A R Y A S I C Q Q 481 TCCCTTGCCATCATGGAAAATGCCAATGTTCTGGCCCGTTATGCCAGCATCTGCCAGCAG 181 N G I V P I V E P E I·L P D G D H D L K 541 AATGGCATTGTGCCCATCGTGGAGCCTGAGATCCTCCCTGATGGGGACCATGACTTGAAG 201 R C Q Y V T E K V L A A V Y K A L S D H 601 CGCTGTCAGTATGTAACCGAGAAGGTGCTGGCTGCTGTTTACAAGGCTCTGAGTGACCAC 221 H I Y L E G T L L K P N M V T P G H A C 661 CACATCTACCTGGAAGGCACCTTGCTGAAGCCCAATATGGTAACCCCAGGCCACGCCTGC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		241 T H K Y S H E E E I A M A A T V V T A L R R R T 721 ACCCACAAATATTCTCATGAGGAGATTGCCATGGCAACTGTCACGGCACTGCGTCGCACG	
		261 V P P A V T G G I T T F L S G G G Q S S E E E E A 781 GTGCCCCCTGCTGTCACTGGGATCACCTTCCTATCTGGAGGCCAGAGTGAGGAGGAGGCA	
		281 S I N L N N A I N K K C P L L K P W A L T F 841 TCCATCAACCTCAACGCCATCAACAAGTGCCCCCTGCTGAAGCCGTGGGCCCTGACCTTC	
		301 S Y G G R A L Q A S A L K K A W G G G K K E E N 901 TCCTATGGCGGAGCCCTGCAGGCCTCTGCCCTGAAGGCCTGGGGTGGGAAGAAGGAGAAC	
		321 L K A A Q E E E Y V K K R A L L A N N S L A A C Q 961 CTGAAGGCTGCCCCAGGAGGAATATGTCAAGCGAGCCCTGGCCAACAGCCTCGCCTGCCAA	
		341 G K Y T P S G G H A G G A A A S E S S L F I S 1021 GGAAAATACACCCCAAGTGGTCACGCTGGGGCTGCAGCCAGCGAGTCCCTCTTCATCTCT	
		361 N H A Y - 1081 AACCATGCCTACTAA	
B1961885	Tumor necrosis factor-inducible (TSG-6) mRNA fragment, adhesion receptor CD44 putative .CDS	1 GAATTCGCACTGCTCTGAGAATTTGTGAGCAGCCCCTAACAGGCTGTTACTTCACTACAA 61 CTGACGATATGATCATCTTAATTTACTTATTTCTCTTGCTATGGCAAGACACTCAAGGAT 121 GGGGATTCAAGGATGGAATTTTTCATAACTCCATATGGCTTGAACGAGCAGCCGGTGTGT 181 ACCACAGAGAGCACGGTCTGGCAAATACAAGCTCACCTACGCAGAAGCTAAGGCGGTGT 241 GTGAATTTGAAGGCGGCCATCTCGCAACTTACAAGCAGCTAGAGGCAGCCAGAAAAATTG 301 GATTTCATGTCTGTGCTGCTGGATGGATGGCTAAGGGCAGAGTTGCATACCCCATTCTGA 361 AGCCAGGGCCCAACTGATGATTTGGAAAAACTGGCATTATTGATTATGGAATCCGTCTCA 421 ATAGGAGTGAAAGATGGGATGCCTACTGCTACAACACCCACATGCAAAGGAATGCGGTGGCA 481 TCTTTACAGATACAAAGAGAATTTTTAAATCTCCAGGCTTCCCAAATGAATATGATGATA 541 ACCAAGTCTGCTACTGGCACATCAGACTCAAGTATGGTCAGCGTATTCACCTGAGTTTTC 601 TGGACTTTGATCTTGAACGACGATACAGGTTGCTTGGCTGACTATGTTGAAATATATGACA 661 GTTATGATGATGTCCATGGCTTTGTGGGAAGATACTGTGGAGATGAGCTTCCAGAAGACA 721 TCATTTGCACAGGAAATGTCATGACTTTGAAGTTTCTAAGCGATGCTTCGGTGACCGCAG 781 GAGGTTTCCAAATCAACGTACGTGGCAGTGGATCCCCCCATCCAAACCCAGTCAAGGAAAAA 841 ATACAAGCACTACTTCTACGGGAAATAAAAGCTTTTTAGCTGGAAGATTTACCCATTTAT 901 AAAAAAAAAAAAGGATCAAAACACACAGTGTTTATGGTTGTCTCTTTGGAACCCCT 961 TTGATCTCACTGTTATTATTAACATTTATTTATTATTTTTCTAAATGTGAAAGAAATACA 1021 TAATTTAGGGAAAATTCGAAAATATAGGAAACTTTAAACGAGAAAATGAAACCTCTCATA 1081 ATCCCACTGCATAGAAATAACAAGCGTTAACATTTCATATTTTTTTCTTTCAGTCATTT 1141 TTGTATTTGTGGTATATGTATATATGTACCTATATGTATTTGCATTTGAAATTTTGGAAT 1201 CCTGCTCTATGTACAGTTTTGTATTATACTTTTTAAATCTTGAACTTTATGAACATTTTC 1261 TGAAATCATTGATTATTCTACAAAAACATGATTTTAAACAGCTGTAAAATATTCTATGAT 1321 ATGAATGTTTTATGCATTATTTAAGCCTGTCTCTATTTGTTGGAATTTCAGGTCATTTTCA 1381 TAAATATTGTTGCAATAAATATCCTTCGGAATTC	SEQ ID NO:192

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1 M I I L I Y L F L L L W E D T Q G W G F 1 ATGATCATCTTAATTTACTTATTTCTCTTGCTATGGGAAGACACTCAAGGATGGGGATTC 21 K D G I F H N S I W L E R A A G V Y H R 61 AAGGATGGAATTTTTCATAACTCCATATGGCTTGAACGAGCAGCCGGTGTGTACCACAGA 41 E A R S G K Y K L T Y A E A K A V C E F 121 GAAGCACGGTCTGGCAAATACAAGCTCACCTACGCAGAAGCTAAGGCGGTGTGTGAATTT 61 E G G H L A T Y K Q L E A A R K I G F H 181 GAAGGCGGCCATCTCGCAACTTACAAGCAGCTAGAGGCAGCCAGAAAAATTGGATTTCAT 81 V C A A G W M A K G R V G Y P I V K P G 241 GTCTGTGCTGCTGGATGGATGGCTAAGGGCAGAGTTGGATACCCCATTGTGAAGCCAGGG 101 P N - - F G K T G I I D Y G I R L N R S 301 CCCAACTGATGATTTGGAAAAACTGGCATTATTGATTATGGAATCCGTCTCAATAGGAGT 121 E R W D A Y C Y N P H A K E C G G V F T 361 GAAAGATGGGATGCCTATTGCTACAACCCACACGCAAAGGAGTGTGGTGGCGTCTTTACA 141 D P K R I F K S P G F P N E Y E D N Q I 421 GATCCAAAGCGAATTTTTAAATCTCCAGGCTTCCCAAATGAGTACGAAGATAACCAAATC 161 C Y W H I R L K Y G Q R I H L S F L D F 481 TGCTACTGGCACATTAGACTCAAGTATGGTCAGCGTATTCACCTGAGTTTTTTAGATTTT 181 D L E D D P G C L A D Y V E I Y D S Y D 541 GACCTTGAAGATGACCCAGGTTGCTTGGCTGATTATGTTGAAATATATGACAGTTACGAT 201 D V H G F V G R Y C G D E L P D D I I S 601 GATGTCCATGGCTTTGTGGGAAGATACTGTGGAGATGAGCTTCCAGATGACATCATCAGT 221 T G N V M T L K F L S D A S V T A G G F 661 ACAGGAAATGTCATGACCTTGAAGTTTCTAAGTGATGCTTCAGTGACAGCTGGAGGTTTC 241 Q I K Y V A M D P V S K S S Q G K N T S 721 CAAATCAAATATGTTGCAATGGATCCTGTATCCAAATCCAGTCAAGGAAAAAATACAAGT 261 T T S T G N K N F L A G R F S H L - 781 ACTACTTCTACTGGAAATAAAAACTTTTTAGCTGGAAGATTTAGCCACTTATAA	SEQ ID NO:193
B1961711.V1.3_at	No Homology	1 TTCGGCACGAGCTCGTGCCGTTCGCGTGCACCCAGGGAGGACTCGGAGTCCCCCGCCCTG 61 ACTCCCATTTTCTTCTGGTCGCCGTGGTCACCCACAGGAAGGGGGCATTCAGGAGGAGTG 121 CTGGGCCCCGGAGGCCATCTCCTGCCGCTCCCCTATTTGGGGCAGCCTGGGTTTTCTCGG 181 GCGGCTCCCCAGGTCTCAGCCTGTGAGGACTGCGGCGAGTCTGGAGACCCCAGGGCTGCC	SEQ ID NO:194

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		241 CCCTTCTTCGGGACTGTGTGGACCCACGAGGGCCATCTGCTGACAGAGCAACCCCCTCCT 301 GCCCCCTCTTGCCTTCCCCCGCAGCCAGCCACGTTTCGGGGGTGGGCTCTGTCTGGTTCACAGA 361 GCCACCCCACTGCCCCGGCCCATCCTCCGATGCAGCGCAGACACCCAATAAATATTGATGG 421 TTGACTGAAAAAAAAAAAAAAAAA	
		1 TTCGGCACGAGCTCGTGCCGTTCGCGTGCACCCAGGGAGGACTCGGAGTCCCCCGCCCTG 61 ACTCCCATTTTCTTCTGGTCGCCGTGGTCACCCACAGCAAGGGGCCATTCAGGAGCAGTG 121 CTGGGCCCCGGAGGCCATGTCCTGCCGCTCCCCTATTTGGGGCAGCCTGGGTTTTCTCGG 181 GCGGCTCCCCAGGTCTCAGCCTGTGAGGACTGCGGCCAGTCTGGACACCCCAGGGCTGCC 241 CCCTTCTTCGGGACTGTGTGGACCCACGAGGGCCATCTGCTGACAGAGCAACCCCCTCCT 301 GCCCCCTCTTGCCTTCCCCCGCAGCCACGTTTCGGGGTGGGCTCTGTCTGGTTCACAGAG 361 CCACCCCACTGCCCCGGCCCATCCTCCGATGCAGCGCAGACACCCAATAAA	SEQ ID NO:195
B1961682.V1.3_at	Formin homology 2 domain containing 1	1 AGAAGCTGCACTGGGGCCGGGACTCGGAGGCGCGCTGCGTGAGCCGGCCGCAGACCCATG 61 GCGGGCGGGCGAAGACCGCCGGGGACGGAGACCCGGTATCAGTGGTCACCGTGAGGGTGCAG 121 TACCTGGAAGACACCGACCCCTTCGCATGTGCCAACTTTCCGGAGCCGCGCCGGCCCCC 181 ACCTGCAGCCTGGACGGGGCGCTGCCCTTGGGCGCGCAGATACCCGCGGTGCACCGCCTG 241 CTGGGAGCGCCGCTCAAGTTGGAGGATTGTGCTCTGCAAGTGTCTCCCTCCGGATACTAC 301 CTGGACACCGAGCTGTCCCTGGAAGAGCAGCGGGAGATGCTGGAGGGCTTCTATGAAGAG 361 ATCAGCAAAGGGCGGAAGCCCACGCTGATCCTTCGGACCCAGCTCTCTGTGAGGGTCAAC 421 GCTATCTTGGAAAAGCTGTATAGCTCCAGTGGTCCTGAGCTCCGCCGCTCCCTCTTCTCA 481 CTGAAGCAGATCTTCCAGGAGGACAAAGACCTGGTGCCTGAATTTGTGCATTCAGAGGGG 541 CTGAGCTGCCTGATCCGTGTGGGTGCTCGCTGCCGACCACACTACCAGAGCTACATCCTT 601 AGAGCGCTCGGCCAGCTGATGCTCTTTGTGGATGGAATGCTGGGGGTGGTGGCCCACAGT 661 GACACTATTCAGTGGCTGTACACATTGTGTGCCAGCCTGTCCCGCTTGGTGGTGTGAAGACA 721 GCCCTGAAGCTGCTGTTGGTGTTTGTAGCAATACTCCGAAAACAACGCACCGCTGTTCATC 781 CGTGCAGTGAACTCTGTGGCCAGCACCACCGGTGCTCCTCCCTGGCCCAATCTGGTGTCC 841 ATCCTGGAGGAGAAGAATGGCGCTGACCCTGAGTTGTTGGTGTACACGGTCACCCTCATC 901 AACAAGACGCTGGCGGCGCTCCCGGACCAGGACTCCTTCTACGATGTGACGGATGCACTG 961 GAGCAGCAGGGCATGGAAGCGCTGGTCCAGCGCCACCTGGGCACTGCGGGCACTGACGTC 1021 GACCTGCGCACGGCAGCTTGTGCTCTACAGAGAACGCCCTGAAATTGGAGGATGGAGACATC 1081 GAAGAAGCCCCAGGCGCTGGTGGCGGCGGGAACGACGAAAGCCTTCTTCTGAGGAGGGC 1141 AAGAGGAGCCGCCGTTCTCTGGAAGGCGGGGCTGCCCCGCGGTGCCCCGGAACCTGGC 1201 CCCACAGGCCCGCCTCACGGTAGGCCCCACCTCTTCCACCGGCCCCGCCCTGCTGACA 1261 GGCCCCGCCTCCAGCCCTGTGGGCCCTCCCTCCGGTCTCCAAGCTTCAGTGAACCTTTTT 1321 CCTACCATCTCTGTGGCACCCTCAGCTGACACCTCCAGCGAGAGGAGCATCTACAAAGCC 1381 CGGTTCCTGGAGAATGTGGCGGCAGCAGAAACAGAGAAGCAGGTTGCGCTGGCCCAGGGC 1441 CGGGCAGAGACACTTGCCGGGGCCATGCCCAATGAGGCGGGTGGACACCCAGATGCCCGG 1501 CAACTCTGGGACTCCCCAGAGACAGCCCTGCAGCCAGAACACCCCAGAGCCCTGCCCCC 1561 TGTGTCCTGCTCCGGGCCCAGCGAAGCCTTGCACCAGAGCCCAAGGAGCCACTGATACCA 1621 GCAAGCCCCAAGGCTGAGCCCATCTGGGAGCTCCCTACCCGTGCACCCAGGCTCTCTATT 1681 GGGGACCTGGACTTTTCAGATCTAGGGAGGATGAAGACCAGGACATGCTGAATGTAGAG 1741 TCTGTGGAGGCTGGGAAAGACATCCCAGCTCCCTCACCCCCACTGCCCCTGCTCTCGGGA 1801 GTACCCCCCCCTCCCCCACTTCCACCTCCCCCCACCCATCAAAGGCCCCTTCCCACCACCT 1861 CCACCTCTACCTCTGGCTGCCCCTCTTCCCCATTCAGTGCCTCAGCTCAGCCCTCCCC 1921 ACTAAGAGGAAGACAGTAAAACTTTTCTGGCGTGAGCTGAAGCTGGCTGGGGCCATGGA	SEQ ID NO:196

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1981 GTCTCTGCAAGCCGCTTTGGGCCCTGCGCCACCCTCTGGGCTTCACTGGACCCTGTCTCA	
		2041 GTGGACACGGCCCGACTGGAACACCTCTTTGAGTCTCGTGCCAAGAGGTGCTGCCCTCC	
		2101 AAGAAAGCTGGAGAGGCGCCGCCGGACAATGACCACAGTGCTGGACCCCAAGCGCAGCAAC	
		2161 GCCATCAACATCGGCCTAACCACACTGCCACCTGTGCATGTCATTAAGGCTGCTCTGCTC	
		2221 AACTTTGATGAGTTTTGCTGTCAGCAAGCATGGCATTGAGAAGCTACTGACCATGATGCCC	
		2281 ACGGAGGAAGAGCGGCACGAAGATTGAGCAAGCCCAGCTGGCCCAACCCTGACATACCCCTG	
		2341 GGCCCAGCCGAGAACTTCCTGATGACTCTTGCCTCCATTGGCGGCCTCGCTGCTCGTCTA	
		2401 CAACTCTGGGCCTTCAAGCTGGACTATCAGACATGGAGCGGGAAATTGCTGAGCCACTG	
		2461 TTTGACCTGAAAGTGGGTATGGAACAGCTGGTACACAGAATGCCACCTTCCGCTGCATCCTG	
		2521 GCTACCCTCCTAGCTGTGGCCAACTTCCTCAATGGCTCCCCAGAGCGAGCGGCTTTGAGCTG	
		2581 AGCTACCTGGAGAAGGTGTCAGAGGTGAAGGACACGGTGCGTCGACAGTCACTGCTACAC	
		2641 CATCTCTGCTCCCTAGTGCTCCAGACCGGCCTGAGTCCTCTGACCTCTATTCAGAAATC	
		2701 CCTGCCCTGACCCGCTGTGCCAAGGTGACTTTGAACAGCTGACTGAGAACCTGGGGCAG	
		2761 CTGGAGCGCCGGAGCCGGCAGCCGAGGAGAGCCTGCGGAGCTTGGCCAAGCATGAGCTG	
		2821 GCCCCAGCCCTGCGTGCCCGCCTCACCCACTTCCTGGACCAGTGTGCCCGCCGTGTTGCC	
		2881 ATGCTAAGGATAGTAGTGCACCGCCGTGTCTGCAATAGGTTCCATGCCTTCCTGCTCTACCTG	
		2941 GGCTACACCCCGCAGGCGCCCCGTGAAGTGCGCATCATGCAGTTCTGCCACACCGCTGCGG	
		3001 GAATTTGCGCTTGAGTATCGGACTTGCCGGGAACGAGTGCTACAGCAGCAGCAGAAGCAG	
		3061 GCCACATACCGTGAGCGCAACAAGACCCGGGGACGCATGATCACCGAGACAGAGAAGTTC	
		3121 TCAGGTGTGGCTGGGGAAGCCCCCAGCAACCCCTCTGTCCCAGTAGCAGTGAGCAGCGGG	
		3181 CCAGGCCGGGGTGATGCTGACAGTCATCCCAGCATGAAGATTCTGCTCACCAGCAAGCCT	
		3241 GAGGACACCACACATGGTCGCCGCAGCAGAGGCATGGTCCAGAACAGCTCCCCAGTCGTG	
		3301 CCCACAGCAGTGGGGCCCTCCACTGTACCCCCAGAAGAATCCCCAGGCTCCAGTTTACCC	
		3361 AGTGACACTTCAGATGAGATCATGGACCTGCTAGTGCAGTCAGTGACCAAGAGCAGTCCT	
		3421 CGCGCCTTAGCTGCTCCAGAACGCAACGCTTCCCGTGGCAACCGCAAGTCTTCGAGCGCG	
		3481 ACATTGAAGAGCGGGCTCGGAGAGGACCTGGTGCAGGCACTGGGACTGAGCAAGGGTTCT	
		3541 GACCTGGAGGTGTGAAGGCGCTGCCTCCAGGACATCTATATGGGCCCCGGTATGCAGTGC	
		3601 AAGAGACTGTAGAGTGAGGAGGGACCAGACGCAGAATTCTGGCCCCAGAACTCTGTGCCCA	
		3661 GGAGCCATGCCTTGAGCACTATTAGCCCTGTGTGTATGCATGTGAGTGTGTGTCTATGTG	
		3721 TGTGTGTGCATGCATATGCATGTGCATGTGTGTGAGCTCCTTGAACGCACGGAGCAAAAT	
		3781 AAAATTTCTTAGCTAAAAAAAAAAAAAAAAAAA	
			SEQ ID NO:197
		1 M A G G E D R G D D G E P V S V V T V R V	
		1 ATGGCGGGCGGGGAGACCGCGGGGACGGAGAGCCGGTATCAGTGGTGACCGTGAGGGTG	
		21 Q Y L E D T D P F A C A N F P E P R R A	
		61 CAGTACCTGGAAGACACCGACCCCTTCGCATGTGCCAACTTTCCGGAGCCGCGCCGGGCC	
		41 P T C S L D G A L P L G A Q I P A V H R	
		121 CCCACCTGCAGCCTGGACGGGGCGCTGCCCTTGGGCGCGCAGATACCCGCGGTGCACCGC	
		61 L L G A P L K L E D C A L Q V S P S G Y	
		181 CTGCTGGGAGCGCCCGCTCAAGTTGGAGGATTGTGCTCTGCAGTGTCTCCCTCCGGATAC	
		81 Y L D T E L S L E E Q R E M L E G F Y E	
		241 TACCTGGACACCGAGCTGTCCCTGGAAGAGCAGCGGGAGATGCTGGAGGGGCTTCTATGAA	
		101 E I S K G R K P T L I L R T Q L S V R V	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		301 GAGATCAGCAAAGGGCGGAAGCCCAGCGCTGATCCTTCGGACCCAGCTCTCTGTGAGGGTC	
		121 N A I L E K L Y S S S G P E L R R S L F	
		361 AACGCTATCTTGGAAAAGCTGTATAGCTCCAGTGGTCCTGAGCTCCGCCGCTCCCTCTTC	
		141 S L K Q I F Q E D K D L V P E F V H S E	
		421 TCACTGAAGCAGATCTTCCAGGAGGACAAAGACCTGGTGCCTGAATTTGTGCATTCAGAG	
		161 G L S C L I R V G A A A D H N Y Q S Y I	
		481 GGGCTGAGCTGCCTGATCCGTGTGGCTGCTGCCGACCACAACTACCAGAGCTACATC	
		181 L R A L G Q L M L F V D G M L G V V A H	
		541 CTTAGAGCGCTCGGCCAGCTGATGCTCTTTGTGGATGGAATGCTGGGGGTGGTGGCCCAC	
		201 S D T I Q W L Y T L C A S L S R L V V K	
		601 AGTGACACTATTCAGTGGCTGTACACATTGTGTGCCAGCCTGTCCCGCTTGGTGGTGAAG	
		221 T A L K L L L V F V E Y S E N N A P L F	
		661 ACAGCCCTGAAGCTGCTGTTGGTGTTTGTAGAATACTCCGAAAACAACGCACCGCTGTTC	
		241 I R A V N S V A S T T G A P P W A N L V	
		721 ATCCGTGCAGTGAACTCTGTGGCCACACCACCGGTGCTCCTCCCTGGGCCAATCTGGTG	
		261 S I L E E K N G A D P E L L V Y T V T L	
		781 TCCATCCTGGAGGAGAAGAATGGCGCTGACCCTGAGTTGTTGGTGTACACGGTCACCCTC	
		281 I N K T L A A L P D Q D S F Y D V T D A	
		841 ATCAACAAGACGCTGGCGGCGCTCCCGGACCAGGACTCCTTCTACGATGTGACGGATGCA	
		301 L E Q Q G M E A L V Q R H L G T A G T D	
		901 CTGGAGCAGCAGGGCATGGAAGCGCTGGTCCAGCGCCACCTGGGCACTGCGGGCACTGAC	
		321 V D L R T Q L V L Y E N A L K L E D G D	
		961 GTCGACCTGCGCACAGCAGCTTGTGCTCTACGAGAACGCCCTGAAATTGGAGGATGGAGAC	
		341 I E E A P G A G G R R E R R K P S S E E	
		1021 ATCGAAGAAGCCCCAGGCGCTGGTGGGCGGCGGGAACGACGAAAGCCTTCTTCTGAGGAG	
		361 G K R S R R S L E G G G G C P A R A P E P	
		1081 GGCAAGAGGAGCCGCCGTTCTCTGGAAGGCGGGGGCTGCCCCGCGCGTGCCCCGGAACCT	
		381 G P T G P A S S P V G P P T S S T G P A L L	
		1141 GGCCCCACAGGCCCCGCCTCACCGGTAGGCCCCACCTCTTCCACCGGCCCCGCCCTGCTG	
		401 T G P A S S P V G P P S G L Q A S V N L	
		1201 ACAGGCCCCGCCTCCAGCCCTGTGGCCCTCCCTCCGGTCTCCAAGCTTCAGTGAACCTT	
		421 F P T I S V A P S A D T S S E R S I Y K	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1261 TTTCCTACCATCTCTGTGGCACCCTCAGCTGACACCTCCAGCGAGAGGAGCATCTACAAA	
		441 A R F L E N V A A A A E T E K Q V A L A Q	
		1321 GCCCGGTTCCTGGAGAATGTGGCGGCAGCAGAAACAGAGAAGCAGGTTGCGCTGGCCCAG	
		461 G R A E T L A G A M P N E A G G H P D A	
		1381 GGCCGGGCAGACACTTGCCGGGGCCATGCCCAATGAGGCGGGTGGCACACCCAGATGCC	
		481 R Q L W D S P E T A P A A R T P Q S P A	
		1441 CGGCAACTCTGGGACTCCCCAGAGACAGCCCCTGCAGCCAGAACACCCCAGAGCCCTGCC	
		501 P C V L L R A Q R S L A P E P K E P L I	
		1501 CCCTGTGTCCTGCTCCGGGCCCAGCGAAGCCTTGCACCAGAGCCCAAGGAGCCACTGATA	
		521 P A S P K A E P I W E L P T R A P R L S	
		1561 CCAGCAAGCCCCAAGGCTGAGCCCATCTGGGAGCTCCCTACCCGTGCACCCAGGCTCTCT	
		541 I G D L D F S D L G E D E D Q D M L N V	
		1621 ATTGGGGACCTGGACTTTTCAGATCTAGGGGAGGATGAAGACCAGGCACATGCTGAATGTA	
		561 E S V E A G K D I P A P S P P L P L L S	
		1681 GAGTCTGTGGAGGCTGGGAAAGACATCCCAGCTCCCTCACCCCCACTGCCCCCTGCTCTCG	
		581 G V P P P P P L P P P P P P I K G P P F P P	
		1741 GGAGTACCCCCCCCCTCCCCCACTTCCACCTCCCCCCACCCATCAAAGGCCCCCTTCCCACCA	
		601 P P P L P L A A P L P H S V P D S S A L	
		1801 CCTCCACCTCTACCTCTGGCTGCCCCCTCTTCCCCATTCAGTGCCTGACAGCTCAGCCCCTC	
		621 P T K R K T V K L F W R E L K L A G G H	
		1861 CCCACTAAGAGGAAGACAGTAAAACTTTTCTGGCGTGAGCTGAAGCTGGCTGGGGGCCAT	
		641 G V S A S R F G P C A T L W A S L D P V	
		1921 GGAGTCTCTGCAAGCCGCTTTGGGCCCTGCGCCACCCTCTGGGCTTCACTGGACCCTGTC	
		661 S V D T A R L E H L F E S R A K E V L P	
		1981 TCAGTGGACACGGGCCCGACTGGAACACCTCTTTGAGTCTCGTGCCAAAGAGGTGCTGCCC	
		681 S K K A G E G R R T M T T V L D P K R S	
		2041 TCCAAGAAAGCTGGAGAGGGCCGCCGGACAATGACCACAGTGCTGGACCCCAAGCGCAGC	
		701 N A I N I G L T T L P P V H H V I K A A L	
		2101 AACGCCATCAACATCGGCCTAACCACACTGCCACCTGTGCATGTCATTAAGGCTGCTCTG	
		721 L N F D E F A V S K D G I E K L L T M M	
		2161 CTCAACTTTGATGAGTTTGCTGTCAGCAAGGATGGCATTGAGAAGCTACTGACCATGATG	
		741 P T E E E R Q K I E E A Q L A N P D I P	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2221 CCCACGGAGGAAGAGCGGCAGAAGATTGAGCAAGCCCAGCTGGCCAACCCTGACATACCC	
		761 L G P A E N F L M T T L A S I G G L A A R	
		2281 CTGGGCCCAGCCGAGAACTTCCTGATGACTCTTGCCTCCATTGGCGGCCTCGCTGCTCGT	
		781 L Q L W A F K L D Y D S M E E R E I A E E P	
		2341 CTACAACTCTGGGCCTTCAAGCTGGACATGACAGCATGGAGCGGGAAATTGCTGAGCCA	
		801 L F D L K V G M E Q L V Q N A T F R C I	
		2401 CTGTTTGACCTGAAAGTGGGTATGGAACAGCTGGTACAGAATGCCACCTTCCGCTGCATC	
		821 L A T L L A V G N F L N G S Q S S G F E	
		2461 CTGGCTACCCTCCTAGCTGTGGGCAACTTCCTCAATGGCTCCCAGACGCAGCGGCTTTGAG	
		841 L S Y L E K V S E V K D T V R R Q S L L	
		2521 CTGAGCTACCTGGAGAAGGTGTCAGAGGTGAAGGACACGGTGCGTCGACAGTCACTGCTA	
		861 H H L C S L V L Q T R P E S S D L Y S E	
		2581 CACCATCTCTGCTCCCTAGTGCTCCAGACCCGGCCTGAGTCCTCTGACCTCTATTCAGAA	
		881 I P A L T R C A K V D F E Q L T E N L G	
		2641 ATCCCTGCCCTGACCCGCTGTGCCAAGGTGGACTTTCAACAGCTGACTGAGAACCTGGGG	
		901 Q L E R R S R A A E E S L R S L A K H E	
		2701 CAGCTGGAGCGCCGGAGCCGGGCAGCCGAGGAGAGCCTGCGGAGCTTGGCCAAGCATGAG	
		921 L A P A L R A R L T H F L D Q C A R R V	
		2761 CTGGCCCCAGCCCTGCGTGCCCGCCTCACCCACTTCCTGGACCAGTGTGCCCGCCGTGTT	
		941 A M L R I V H R R V C N R F H A F L L Y	
		2821 GCCATGCTAAGGATAGTGCACCGCCGTGTCTGCAATAGGTTCCATGCCTTCCTGCTCTAC	
		961 L G Y T P Q A A R E V R I M Q F C H T L	
		2881 CTGGGCTACACCCCGCAGGCGGCCCGTGAAGTGCGCATCATGCAGTTCTGCCACACGCTG	
		981 R E F A L E Y R T C R E R V L Q Q Q Q K	
		2941 CGGGAATTTGCGCTTGAGTATCGGACTTGCCGGGAACCAGTGCTACAGCAGCAGCAGAAG	
		1001 Q A T Y R E R N K T R G R M I T E T E K	
		3001 CAGGCCACATACCGTGAGCGCAACAAGACCCGGGGACGCATGATCACCGAGACAGAGAAG	
		1021 F S G V A G E A P S N P S V P V A V S S	
		3061 TTCTCAGGTGTGGCTGGGGAAGCCCCCAGCAACCCCTCTGTCCCAGTAGCAGTGAGCAGC	
		1041 G P G R G D A D S H A S M K I L L T S K	
		3121 GGGCCAGGCCGGGGTGATGCTGACAGTCATGCCAGCATGAAGATTCTGCTCACCAGCAAG	
		1061 P E D T T H G R R S R G M V Q N S S P V	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		3181 CCTGAGGACACCACACATGGTCGCCGCAGCAGAGGCATGGTCCAGAACAGCTCCCCAGTC	
		1081 V P T A V G P S T V P P E E S P G S S L	
		3241 GTGCCCACAGCAGTGGGCCCTCCACTGTACCCCCAGAGAATCCCCAGGCTCCAGTTTA	
		1101 P S D T S D E I M D L L V Q S V T K S S	
		3301 CCCAGTGACACTTCAGATGAGATCATGGACCTGCTAGTGCAGTCAGTGACCAAGAGCAGT	
		1121 P R A L A A R E R K R S R G N R K S L R	
		3361 CCTCGCGCCTTAGCTGCTCGAGAACGCAAGCGTTCCGTGGCAACCGCAAGTCTTTGAGG	
		1141 R T L K S G L G E D L V Q A L G L S K G	
		3421 CGGACATTGAAGAGCGGGCTCGGAGAGGACCTGGTGCAGGCACTGGGACTGAGCAAGGGT	
		1161 S D L E V -	
		3481 TCTGACCTGGAGGTGTGA	
B1961671	NAD synthetase 1		SEQ ID NO:198
		1 ggaaggtccg gcgtcccagc cgcctacctc gctgggaccc tggtcttgct gtcccccgct	
		61 ggcctcctgc ccaagcgact gcggccagga tgggccggaa ggtgaccgtg gccacctgcg	
		121 cactcaacca gtgggccctg gacttcgagg gcaatttgca aagaatttta aagagtattg	
		181 aaattgccaa aaacagagga gcaagataca ggcttggacc agagctggaa atatgcggct	
		241 acggatgttg ggatcattat tacgagtcgg acaccctctt gcactcgttt caagtcctag	
		301 cggcccttct ggagtctccc gtcactcagg acatcatctg cgacgtgggg atgcctgtaa	
		361 tgcaccgaaa cgtccgctac aactgcagag tgatattcct caacaggaag atcctgctca	
		421 tcagacccaa gatggccttg gccaatgaag gcaactaccg cgagctgcgc tggttcaccc	
		481 cgtggtcgag gagtcggcac acagaggagt actttctgcc tcggatgata caggacctga	
		541 caaagcagga aaccgtaccc ttcggagatg cggtgctggt gacatgggac acctgcattg	
		601 gaagtgagat ctgtgaggag ctctggacac cccacagccc gcacatcgac atgggcctgg	
		661 atggcgtgga gatcatcacc aacgcctcgg gcagccacca cgtgctgcgc aaagccaaca	
		721 ccagggtgga tctcgtgact atggtcacca gcaagaacgg tgggatttac ttgctggcca	
		781 accagaaggg ttgcgacggg gaccgcctgt actacgacgg ctgtgccatg atcgccatga	
		841 acggaagcgt ctttgctcaa ggatcccagt tttctctgga tgacgtggaa gtcctgacgg	
		901 ccacgctgga tctggaggac gtccggagct acagggcgga gatttcatct cgaaacctgg	
		961 cggccagcag ggcgagcccc taccccagag tgaaggtgga ctttgccctc tcgtgccacg	
		1021 aggacttgct ggcacccatc tctgagccca tcgagtggaa ataccacagc cctgaggagg	
		1081 agataagcct tggacctgcc tgctggctct gggatttttt aagacgaagt caacaggcag	
		1141 ggttttgct gccttgagt ggcgggtgg acagcgcagc caccgcctgc ctcatctact	
		1201 ccatgtgctg ccaggtctgc gaggccgtga ggagtgggaa tgacggaagtg ctggctgatg	
		1261 tccgcaccat cgtgaaccag atcagctaca ccccccagga tccccgagac ctctgtggac	
		1321 gcatactgac cacctgctac atggccagca agaactcctc ccaggagacg tgcacccggg	
		1381 ccagagagtt ggcccagcag attggaagcc accacatcag tctcaacatc gatccagccg	
		1441 tgaaggccgt catgggcatc ttcagcctgg tgacgggaaa gagccctctg tttgcagctc	
		1501 atggaggaag cagcagggaa aacctggcgc tgcaaaatgt gcaggctcga atacggatgg	
		1561 tcctcgccta tctgtttgct cagttgagcc tctggctctcg gggtgtccac ggtgggctcc	
		1621 tcgtgctggg atccgccaac gtggatgaga gtctcctggg ctacctgacc aagtacgact	
		1681 gctccagtgc ggacatcaac cccataggcg ggatcagcaa gacggacctc agggccttcg	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1741 tccagttctg catccagcgc ttccagcttc ctgccctgca gagcatcctg ttggcgccgg 1801 ccaccgcaga gctggagccc ttggctgatg gacaggtgtc ccagaccgac gaggaagata 1861 tggggatgac atatgcggag ctctcggtct atgggaaact caggaaggtg gccaagatgg 1921 ggccctacag catgttctgc aaactcctcg gcatgtggag acacatctgc accccgagac 1981 aggtcgctga caaagtgaag cggtttttct ccaagtactc catgaacaga cacaagatga 2041 ccacgctcac acccgcgtac cacgccgaga actacagccc tgaggacaac aggtttgatc 2101 tgcgaccatt tctgtacaac acaagctggc cttggcagtt tcggtgcata gaaaatcagg 2161 tgctacagct cgagagggca gagccacagt ccctggacgg cgtggactga ggccggttcc 2221 ttcctggagg cctcctgtcc tcggggaccc cagcacctca tcatcagcat tgctggagcc 2281 aagggtagga gccctacact aggagcccag gatgggacgg cgcatcagcc gagagggagg 2341 gaacttttca gtcaaattcc tcaaaaagag gctggaataa agcctgggct taaaaaaaaa 2401 aaaaaaaaaa aaaaaaa	
		1 M G R K V T V A T C A L N Q W A L D F E 1 ATGGGCCGGAAGGTGACCGTGGCCACCTGCGCACTCAACCAGTGGGCCCTGGACTTCGAG	SEQ ID NO:199
		21 G N L Q R I L K S I E I A K N R G A R Y 61 GGCAATTTGCAAAGAATTTTAAAGAGTATTGAAATTGCCAAAAACAGAGGAGCAAGATAC	
		41 R L G P E L E I C G Y G C W D H Y Y E S 121 AGGCTTGGACCAGAGCTGGAAATATGCGGCTACGGATGTTGGGATCATTATTACGAGTCG	
		61 D T L L H S F Q V L A A L L E S P V T Q 181 GACACCCTCTTGCACTCGTTTCAAGTCCTAGCGGCCCTTCTGGAGTCTCCCGTCACTCAG	
		81 D I I C D V G M P V M H R N V R Y N C R 241 GACATCATCTGCGACGTGGGGATGCCTGTAATGCACCGAAACGTCCGCTACAACTGCAGA	
		101 V I F L N R K I L L I R P K M A L A N E 301 GTGATATTCCTCAACAGGAAGATCCTGCTCATCAGACCCAAGATGGCCTTGGCCAATGAA	
		121 G N Y R E L R W F T P W S R S R H T E E 361 GGCAACTACCGCGAGCTGCGCTGGTTCACCCCGTGGTCGAGGAGTCGGCACACAGAGGAG	
		141 Y F L P R M I Q D L T K Q E T V P F G D 421 TACTTTCTGCCTCGGATGATACAGGACCTGACAAAGCAGGAAACCGTACCCTTCGGAGAT	
		161 A V L V T W D T C I G S E I C E E L W T 481 GCGGTGCTGGTGACATGGGACACCTGCATTGGAAGTGAGATCTGTGAGGAGCTCTGGACA	
		181 P H S P H I D M G L D G V E I I T N A S 541 CCCCACAGCCCGCACATCGACATGGGCCTGGATGGCGTGGAGATCATCACCAACGCCTCG	
		201 G S H H V L R K A N T R V D L V T M V T 601 GGCAGCCACCACGTGCTGCGCAAAGCCAACACCAGGGTGGATCTCGTGACTATGGTCACC	
		221 S K N G G I Y L L A N Q K G C D G D R L 661 AGCAAGAACGGTGGGATTTACTTGCTGGCCAACCAGAAGGGTTGCGACGGGGACCGCCTG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		241 Y Y D G C A M I A M N G S V F A Q G S Q 721 TACTACGACGGCTGTGCCATGATCGCCATGAACGGAAGCGTCTTTGCTCAAGGATCCCAG	
		261 F S L D D V E V L T A T L D L E D V R S 781 TTTTCTCTGGATGACGTGGAAGTCCTGACGGCCACGCTGGATCTGGAGGACGTCCGGAGC	
		281 Y R A E I S S R N L A A S R A S P Y P R 841 TACAGGGCGGAGATTTCATCTCGAAACCTGGCGGCCAGCAGGGCGAGCCCCTACCCCAGA	
		301 V K V D F A L S C H E D L L A P I S E P 901 GTGAAGGTGGACTTTGCCCTCTCGTGCCACGAGGACTTGCTGGCACCCATCTCTGAGCCC	
		321 I E W K Y H S P E E E I S L G P A C W L 961 ATCGAGTGGAAATACCACACGCCCTGAGGAGGAGATAAGCCTTGGACCTGCCTGCTGGCTC	
		341 W D F L R R S Q Q A G F L L P L S G G G V 1021 TGGGATTTTTTAAGACGAACGTCAACAGGCAGGGTTTTTGCTGCCCTTGAGTGGCGGGGTG	
		361 D S A A T A C L I Y S M C C Q V C E A V 1081 GACAGCGCAGCCCACCGCCTGCCTCATCTACTCCATGTGCTGCCAGGTCTGCGAGGCCGTG	
		381 R S G N E E V L A D V R T I V N Q I S Y 1141 AGGAGTGGAAATGAGGAAGTGCTGGCTGATGTCCGCACCATCGTGAACCAGATCAGCTAC	
		401 T P Q D P R D L C G R I L T T C Y M A S 1201 ACCCCCCAGATCCCCGAGACCTCTGTGGACGCATACTGACCACCTGCTACATGGCCAGC	
		421 K N S S Q E T C T R A R E L A Q Q I G S 1261 AAGAACTCCTCCCAGGACGTGCACCCGGCCAGAGAGTTGGCCCAGCAGATTGGAAGC	
		441 H H I S L N I D P A V K A V M G I F S L 1321 CACCACATCAGTCTCAACATCGATCCACCGTGAAGGCCGTCATGGCATCTTCAGCCTG	
		461 V T G K S P L F A A H G G S S R E N L A 1381 GTGACGGGGAAGAGCCCTCTGTTTGCACCTCATGGAGGAAGCAGCAGGGAAAACCTGGCG	
		481 L Q N V Q A R I R M V L A Y L F A Q L S 1441 CTGCAAAATGTGCAGGCTCGAATACGGATGGTCCTCGCCTATCTGTTTGCTCAGTTGAGC	
		501 L W S R G V H G G L L V L G S A N V D E 1501 CTCTGGTCTCGGGGTGTCCACGGTGGGCTCCTCGTGCTGGGATCCGCCAACGTGGATGAG	
		521 S L L G Y L T K Y D C S S A D I N P I G 1561 AGTCTCCTGGGCTACCTGACCAAGTACGACTGCTCCAGTGCGGACATCAACCCCATAGGC	
		541 G I S K T D L R A F V Q F C I Q R F Q L 1621 GGGATCAGCAAGACGGACCTCAGGGCCTTCGTCCAGTTCTGCATCCAGCGCTTCCAGCTT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		561 P A L Q S I L L A P A T A E L E P L A D 1681 CCTGCCCTGCAGAGCATCCTGTTGGCGCCGGCCACCGCAGAGCTGGAGCCCTTGGCTGAT 581 G Q V S Q T D E E D M G M T Y A E L S V 1741 GGACAGGTGTCCCAGACCGACGAGGAAGATATGGGGATGACATATGCGGAGCTCTCGGTC 601 Y G K L R K V A K M G P Y S M F C K L L 1801 TATGGGAAACTCAGGAAGGTGGCCAAGATGGGGCCCTACAGCATGTTCTGCAAACTCCTC 621 G M W R H I C T P R Q V A D K V K R F F 1861 GGCATGTGGAGACACATCTGCACCCCGAGACAGGTCGCTGACAAAGTGAAGCGGTTTTTC 641 S K Y S M N R H K M T T L T P A Y H A E 1921 TCCAAGTACTCCATGAACAGACACAAGATGACCACGCTCACACCCGCGTACCACGCCGAG 661 N Y S P E D N R F D L R P F L Y N T S W 1981 AACTACAGCCCTGAGGACAACAGGTTTGATCTGCGACCATTTCTGTACAACACAAGCTGG 681 P W Q F R C I E N Q V L Q L E R A E P Q 2041 CCTTGGCAGTTTCGGTGCATAGAAAATCAGGTGCTACAGCTCGAGAGGGCAGAGCCACAG 701 S L D G V D - 2101 TCCCTGGACGGCGTGGACTGA	
B1961637	Mn-SOD mRNA for manganese superoxide dismutase	1 GACGCGCGTCCGCCGCGGGCCGTGTGTGCGGCGCGATCTCCGAGGTGCTTTGCCTTCTGG 61 ACGGTCACCATGTTGTGCCGGGCGGCGTGCAGCACGAGCAGGAAGCTGGTGCCAGCTCTG 121 GGGTCTCTGGGGTCCCGGCAGAAGCACAGCCTCCCCGACTTGCAGTATGATTATGGCGCT 181 CTGGAGCCCTACATCAACGCCCAGATCATGCAGCTGCACCACAGCAAGCACCACGCGGCC 241 TATGTGAACAACCTGAACGTCACCGAGGAGAAGTACCAGGAGGCGCTGGCCAAGGGGGAC 301 GTGACAGCTCACATTGCTCTGCAGCCTGCACTCAAGTTCAATGGTGGAGGCCATATCAAT 361 CATACCATTTTCTGGACAAACCTGAGCCCCAATGGCGGGGGAGAACCCAAAGGGAAATTG 421 CTGGACGCCATCAAACGTGACTTTGGTTCCTTCGACAAATTTAAAGAGAAGTTGACTGCT 481 GTATCGGCTGGTGTCCAAGGCTCGGGTTGGGGTTGGCTTGGTTTCAATAAGGACCAGGGA 541 CGCCTCCAGATTGTTGCCTGTCCTAACCAGGATCCCCTGCAGGGAACAACAGGTCTTATT 601 CCCCTGCTGGGGATTGACGTGTGGGAGCACGCTTATTACCTTCAGTATAAAAATGTCAGG 661 CCTGATTATCTGAAAGCCATTTGGAATGTGATCAACTGGGAGAATGTATCTGAGAGATAC 721 ATGGCTTGCAAAAAGTAAAGCATTATCGTTACACCGAGTGCATTAAGCAATTTCCAACTA 781 TTTTTGTAGTAGCTCGAAGTACCACAGTATACCAGTAAGCTGCTCTAGGATAGCATTTCT 841 GAATGTGGCTTATTCAGATATTTGATAAACGTAATGCTATGAATAATTTCCTGTTTTACA 901 ATTTTGTTATTGGGCAACTGTTTGAAAATATTAAATGCTTTGTATGATTCGGTT 1 M L C R A A C S T S R K L V P A L G S L 1 ATGTTGTGCCGGGCGGCGTGCAGCACGAGCAGGAAGCTGGTGCCAGCTCTGGGGTCTCTG 21 G S R Q K H S L P D L Q Y D Y G A L E P	SEQ ID NO:200 SEQ ID NO:201

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		61 GGGTCCCGGCAGAAGCACAGCCTCCCCGACTTGCAGTATGATTATGGCGCTCTGGAGCCC 41 Y I N A Q I M Q L H H S K H H A A Y V N 121 TACATCAACGCCCAGATCATGCAGCTGCACCACAGCAAGCACCACGCGGCCTATGTGAAC 61 N L N V T E E K Y Q E A L A K G D V T A 181 AACCTGAACGTCACCGAGGAGAAGTACCAGGAGGCGCTGGCCAAGGGGGACGTGACAGCT 81 Q I A L Q P A L K F N G G G H I N H T I 241 CAGATTGCTCTGCAGCCTGCACTCAAGTTCAATGGTGGAGGCCATATCAATCATACCATT 101 F W T N L S P N G G G E P K G K L L D A 301 TTCTGGACAAACCTGAGCCCCAATGGCGGGGGAGAACCCAAAGGGAAATTGCTGGACGCC 121 I K R D F G S F D K F K E K L T A V S A 361 ATCAAACGTGACTTTGGTTCCTTCGACAAATTTAAAGAGAAGTTGACTGCTGTATCGGCT 141 G V Q G S G W G W L G F N K D Q G R L Q 421 GGTGTCCAAGGCTCGGGTTGGGGTTGGCTTGGTTTCAATAAGGACCAGGGACGCCTCCAG 161 I V A C P N Q D P L Q G T T G L I P L L 481 ATTGTTGCCTGTCCTAACCAGGATCCCCTGCAGGGAACAACAGGTCTTATTCCCCTGCTG 181 G I D V W E H A Y Y L Q Y K N V R P D Y 541 GGGATTGACGTGTGGGAGCACGCTTATTACCTTCAGTATAAAAATGTCAGGCCTGATTAT 201 L K A I W N V I N W E N V S E R Y M A C 601 CTGAAAGCCATTTGGAATGTGATCAACTGGGAGAATGTATCTGAGAGATACATGGCTTGC 221 K K - 661 AAAAAGTAA	
B1961620	ILT11A mRNA for immunoglobulin-like transcript 11 protein	1 cacggctgga gaccatggga agcagtgccg ggacaccttc cctcattgcc tttcagtgac 61 ttgggctgag tatggacccg aggaccccag tgcaggcaga cactctcccc aaacccacca 121 tctgggctga gccaggctct gtgatccctc gggggaagcc tgtggccatc aggtgtcaag 181 ggacactgga gacccaagag tatcgtctgc ataaagagcg aaatccagtg ccttgggacc 241 aaaagagccc tctggagccc ggggaaaagg ccaatttctc catcccacac atgacagaga 301 aatattcagg gacatatcac tgttactatc tcggccccac tggctggtca gagcacagtg 361 acccccтcga gctggtggtg acaggattct acaccaaacc caccctctca gccctgccga 421 gcccactggt gatctcagga gggaatgtga ccctccagtg tggctcaaag cttggatttg 481 ccaggtttgt tctcactaag gaaggagaaa acaagacctc ctggaccctg gattcacagc 541 gacaacccaa tgggcagttc caggccctgt tccctgtggg ccctgtgatc cccttccaca 601 agtggatgtt cagctgctat ggcttttaca ggaactaccc tcacgtgtgg tcacatccta 661 gtgacccctt ggagctcctg gtctcagcct cacaccctca agattacaca gtggagaatc 721 tcatccggat gagtgcagct ggcttgatcc tggtggtcct tgggattctg ctatttcagg 781 ctcaacacag ccagaaaaga ccccaagagg cagacaggaa gtaaacacaa gtgagaaaaa	SEQ ID NO:202

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		841 tgcacagttc agagtagtag agccttgaaa gtaaatcttg tgcacccagg aggttcctga 901 agagcatctg tggtgtatga tcagtgaact gtctgcaggt cattgtgagg tgtagtagtt 961 atcgttcatg tgcagggaca atgtccgctc ctttctgcca ttaaactgag ggacattcct 1021 tcacaagcac ttttgagtta tcttggtggg tttgtaactt tctctctttt tgtgaaatca 1081 gcatgtatcc caaaggacag atttgggtcc acacttcctt gcactttcat gctgtggtac 1141 aatttcatgt aatacatata tttttaaatt 1 M D P R T P V Q A G F Y T K P T L S A L 1 ATGGACCCGAGGACCCCAGTGCAGGCAGGATTCTACACCAAACCCACCCTCTCAGCCCTG 21 P S P L V I S G G N V T L Q C G S K L G 61 CCGAGCCCACTGGTGATCTCAGGAGGGAATGTGACCCTCCAGTGTGGCTCAAAGCTTGGA 41 F A R F V L T K E G E N K T S W T L D S 121 TTTGCCAGGTTTGTTCTCACTAAGGAAGGAGAAAACAAGACCTCCTGGACCCTGGATTCA 61 Q R Q P N G Q F Q A L F P V G P V I P F 181 CAGCGACAACCCAATGGGCAGTTCCAGGCCCTGTTCCCTGTGGGCCCTGTGATCCCCTTC 81 H K W M F S C Y G F Y R N Y P H V W S H 241 CACAAGTGGATGTTCAGCTGCTATGGCTTTTACAGGAACTACCCTCACGTGTGGTCACAT 101 P S D P L E L L V S A S H P Q D Y T V E 301 CCTAGTGACCCCTTGGAGCTCCTGGTCTCAGCCTCACACCCTCAAGATTACACAGTGGAG 121 N L I R M S A A G L I L V V L G I L L F 361 AATCTCATCCGGATGAGTGCAGCTGGCTTGATCCTGGTGGTCCTTGGGATTCTGCTATTT 141 Q A Q H S Q K R P Q E A D R K - 421 CAGGCTCAACACAGCCAGAAAAGACCCCAAGAGGCAGACAGGAAGTAA	SEQ ID NO:203
B1961494	HREV107-3	1 acatctacgc agcgaaatcg agcctggcct tgagggtcca caccgcgagg gaagatgcgt 61 gcgcccattc cagagcctaa gcctggagac ctgattgaga ttttcgccc tttctacaga 121 cactgggcca tctatgttgg cgatggatat gtggttcatc tggcccctcc aagtgaggtc 181 gcaggagctg gtgcagccag tgtcatgtcc gccctgactg acaaggccat cgtgaagaag 241 gaattgctgt atgatgtggc cgggagtgac aagtaccagg tcaacaacaa acatgatgac 301 aagtactcgc cgctgccctg cagcaaaatc atccagcggg cggaggagct ggtggggcag 361 gaggtgctct acaagctgac cagtgagaac tgcgagcact ttgtgaatga gctgcgctat 421 ggagtcgccc gcagtgacca ggtcagagat gtcatcatcg ctgcaagcgt tgcaggaatg 481 ggcttggcag ccatgagcct tattggagtc atgttctcaa gaaacaagcg acaaaagcaa 541 taactgaaaa agactgtcct gtcagcgatg actttataca tcaaggggtt cttgttttgc 601 tagagagttt ggggtttggt ttgtggattt cattgtgatt tataataagg cttattttca 661 cagaataaaa taaagc 1 M R A P I P E P K P G D L I E I F R P F 1 ATGCGTGCGCCCATTCCAGAGCCTAAGCCTGGAGACCTGATTGAGATTTTTCGCCCTTTC	SEQ ID NO:204 SEQ ID NO:205

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		21 Y R H W A I Y V G D G Y V V H L A P P S 61 TACAGACACTGGGCCATCTATGTTGGCGATGGATATGTGGTTCATCTGGCCCCTCCAAGT 41 E V A G A G A A S V M S A L T D K A I V 121 GAGGTCGCAGGAGCTGGTGCAGCCAGTGTCATGTCCGCCCTGACTGACAAGGCCATCGTG 61 K K E L L Y D V A G S D K Y Q V N N K H 181 AAGAAGGAATTGCTGTATGATGTGGCCGGGAGTGACAAGTACCAGGTCAACAACAAACAT 81 D D K Y S P L P C S K I I Q R A E E L V 241 GATGACAAGTACTCGCCGCTGCCCTGCAGCAAAATCATCCAGCGGGCGGAGGAGCTGGTG 101 G Q E V L Y K L T S E N C E H F V N E L 301 GGGCAGGAGGTGCTCTACAAGCTGACCAGTGAGAACTGCGAGCACTTTGTGAATGAGCTG 121 R Y G V A R S D Q V R D V I I A A S V A 361 CGCTATGGAGTCGCCCGCAGTGACCAGGTCAGAGATGTCATCATCGCTGCAAGCGTTGCA 141 G M G L A A M S L I G V M F S R N K R Q 421 GGAATGGGCTTGGCAGCCATGAGCCTTATTGGAGTCATGTTCTCAAGAAACAAGCGACAA 161 K Q - 481 AAGCAATAA	
B1961443	PREDICTED: Homo sapiens steroid receptor RNA activator 1 (SRA1)	1 atgacgcgct gccccgctgg ccaagcggaa gtggagatgg cggagctgta cgtgaagccg 61 ggcaacaagg aacgcggctg gaacgacccg ccgcagttct catacgggct gcagacccag 121 gccggcggac ccaggcgctc gctgcttacc aagagggtcg ccgcacccca ggatggatcc 181 cccagagtcc ccgcatcaga gacttctcct gggcctcccc caatggggcc tccacctcct 241 tcaagtaagg ctcccaggtc cccacctgtg gggagtggtc ctgcctctgg cgtggagccc 301 acaagtttcc cagtcgagtc tgaggctgtg atggaggatg tgctgagacc tttggaacag 361 gcattggaag actgccgtgg ccacacaagg aagcaggtat gtgatgacat cagccgacgc 421 ctggcactgc tgcaggaaca gtgggctgga ggaaagttgt caatacctgt aaagaagaga 481 atggctctac tggtgcaaga gctttcaagc caccggtggg acgcagcaga tgacatccac 541 cgctccctca tggttgacca tgtgactgag gtcagtcagt ggatggtagg agttaaaaga 601 ttaattgcag aaaagaggag tctgttttca gaggaggcag ccaatgaaga gaaatctgca 661 gccacagctg agaagaacca taccatacca ggcttccagc aggcttcata a 1 M T R C P A G Q A E V E M A E L Y V K P 1 ATGACGCGCTGCCCCGCTGGCCAAGCGGAAGTGGAGATGGCGGAGCTGTACGTGAAGCCG 21 G N K E R G W N D P P Q F S Y G L Q T Q 61 GGCAACAAGGAACGCGGCTGGAACGACCCGCCGCAGTTCTCATACGGGCTGCAGACCCAG 41 A G G P R R S L L T K R V A A P Q D G S 121 GCCGGCGGACCCAGGCGCTCGCTGCTTACCAAGAGGGTCGCCGCACCCCAGGATGGATCC	SEQ ID NO:206 SEQ ID NO:207

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		61 P R V P A S E T S P G P P P M G P P P P 181 CCCAGAGTCCCCGCATCAGAGACTTCTCCTGGGCCTCCCCCAATGGGGCCTCCACCTCCT 81 S S K A P R S P P V G S G P A S G V E P 241 TCAAGTAAGGCTCCCAGGTCCCCACCTGTGGGGAGTGGTCCTGCCTCTGGCGTGGAGCCC 101 T S F P V E S E A V M E D V L R P L E Q 301 ACAAGTTTCCCAGTCGAGTCTGAGGCTGTGATGGAGGATGTGCTGAGACCTTTGGAACAG 121 A L E D C R G H T R K Q V C D D I S R R 361 GCATTGGAAGACTGCCGTGGCCACACAAGGAAGCAGGTATGTGATGACATCAGCCGACGC 141 L A L L Q E Q W A G G K L S I P V K K R 421 CTGGCACTGCTGCAGGAACAGTGGGCTGGAGGAAAGTTGTCAATACCTGTAAAGAAGAGA 161 M A L L V Q E L S S H R W D A A D D I H 481 ATGGCTCTACTGGTGCAAGAGCTTTCAAGCCACCGGTGGGACGCAGCAGATGACATCCAC 181 R S L M V D H V T E V S Q W M V G V K R 541 CGCTCCCTCATGGTTGACCATGTGACTGAGGTCAGTCAGTGGATGGTAGGAGTTAAAAGA 201 L I A E K R S L F S E E A A N E E K S A 601 TTAATTGCAGAAAAGAGGAGTCTGTTTTCAGAGGAGGCAGCCAATGAAGAGAAATCTGCA 221 A T A E K N H T I P G F Q Q A S - 661 GCCACAGCTGAGAAGAACCATACCATACCAGGCTTCCAGCAGGCTTCATAA	
B1961009	G protein-coupled receptor HM74a	1 cgccactttg ctggagcatt cactaggcga ggcgctccat cggactcact agccgcactc 61 atgaatcggc accatctgca ggatcacttt ctggaaatag acaagaagaa ctgctgtgtg 121 ttccgagatg acttcattgt caaggtgttg ccgccggtgt tggggctgga gtttatcttc 181 gggcttctgg gcaatggcct tgccctgtgg attttctgtt tccacctcaa gtcctggaaa 241 tccagccgga ttttcctgtt caacctggca gtggctgact ttctactgat catctgcctg 301 cccttcctga tggacaacta tgtgaggcgt tgggactgga agtttgggga catcccttgc 361 cggctgatgc tcttcatgtt ggctatgaac cgccagggca gcatcatctt cctcacggtg 421 gtggcggtag acaggtattt ccgggtggtc catccccacc acgccctgaa caagatctcc 481 aatcggacag cagccatcat ctcttgcctt ctgtggggca tcactattgg cctgacagtc 541 cacctcctga agaagaagat gccgatccag aatggcggtg caaatttgtg cagcagcttc 601 agcatctgcc ataccttcca gtggcacgaa gccatgttcc tcctggagtt cttcctgccc 661 ctgggcatca tcctgttctg ctcagccaga attatctgga gcctgcggca gagacaaatg 721 gaccggcatg ccaagatcaa gagagccatc accttcatca tggtggtggc catcgtcttt 781 gtcatctgct tccttcccag cgtggttgtg cggatccgca tcttctggct cctgcacact 841 tcgggcacgc agaattgtga agtgtaccgc tcggtggacc tggcgttctt tatcactctc 901 agcttcacct acatgaacag catgctggac cccgtggtgt actatttttc cagcccatcc 961 tttcccaact tcttctccac tttgatcaac cgctgcctcc agaggaagat gacaggtgag 1021 ccagataata accgcagcac gagcgtcgag ctcacagggg accccaacaa aaccagaggc	SEQ ID NO:208

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1081 gctccagagg cgttaatggc caactccggt gagccatgga gcccctctta tctgggccca 1141 acctctcctt aaataaccat gccaagaagg gacattgtca ccaagaacca gcatctctgg 1201 agaaacagtt gggctgttgc atcgagtaat gtcactggac tcggcctaag gtttcctgga 1261 acttccagat tcagagaatc tgatttaggg aaact 1 M N R H H L Q D H F L E I D K K N C C V 1 ATGAATCGGCACCATCTGCAGGATCACTTTCTGGAAATAGACAAGAAGAACTGCTGTGTG 21 F R D D F I V K V L P P V L G L E F I F 61 TTCCGAGATGACTTCATTGTCAAGGTGTTGCCGCCGGTGTTGGGGCTGGAGTTTATCTTC 41 G L L G N G L A L W I F C F H L K S W K 121 GGGCTTCTGGGCAATGGCCTTGCCCTGTGGATTTTCTGTTTCCACCTCAAGTCCTGGAAA 61 S S R I F L F N L A V A D F L L I I C L 181 TCCAGCCGGATTTTCCTGTTCAACCTGGCAGTGGCTGACTTTCTACTGATCATCTGCCTG 81 P F L M D N Y V R R W D W K F G D I P C 241 CCCTTCCTGATGGACAACTATGTGAGGCGTTGGGACTGGAAGTTTGGGGACATCCCTTGC 101 R L M L F M L A M N R Q G S I I F L T V 301 CGGCTGATGCTCTTCATGTTGGCTATGAACCGCCAGGGCAGCATCATCTTCCTCACGGTG 121 V A V D R Y F R V V H P H H A L N K I S 361 GTGGCGGTAGACAGGTATTTCCGGGTGGTCCATCCCCACCACGCCCTGAACAAGATCTCC 141 N R T A A I I S C L L W G I T I G L T V 421 AATCGGACAGCAGCCATCATCTCTTGCCTTCTGTGGGGCATCACTATTGGCCTGACAGTC 161 H L L K K K M P I Q N G G A N L C S S F 481 CACCTCCTGAAGAAGAAGATGCCGATCCAGAATGGCGGTGCAAATTTGTGCAGCAGCTTC 181 S I C H T F Q W H E A M F L L E F F L P 541 AGCATCTGCCATACCTTCCAGTGGCACGAAGCCATGTTCCTCCTGGAGTTCTTCCTGCCC 201 L G I I L F C S A R I I W S L R Q R Q M 601 CTGGGCATCATCCTGTTCTGCTCAGCCAGAATTATCTGGAGCCTGCGGCAGAGACAAATG 221 D R H A K I K R A I T F I M V V A I V F 661 GACCGGCATGCCAAGATCAAGAGAGCCATCACCTTCATCATGGTGGTGGCCATCGTCTTT 241 V I C F L P S V V V R I R I F W L L H T 721 GTCATCTGCTTCCTTCCCAGCGTGGTTGTGCGGATCCGCATCTTCTGGCTCCTGCACACT 261 S G T Q N C E V Y R S V D L A F F I T L 781 TCGGGCACGCAGAATTGTGAAGTGTACCGCTCGGTGGACCTGGCGTTCTTTATCACTCTC 281 S F T Y M N S M L D P V V Y Y F S S P S	SEQ ID NO:209

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		841 AGCTTCACCTACATGAACAGCATGCTGGACCCCGTGGTGTACTATTTTTCCAGCCCATCC	
		301 F P N F F S T L I N R C L Q R K M T G E 901 TTTCCCAACTTCTTCTCCACTTTGATCAACCGCTGCCTCCAGAGGAAGATGACAGCTGAG	
		321 P D N N R S T S V E L T G D P N K T R G 961 CCAGATAATAACCGCAGCACGAGCGTCGAGCTCACAGGGACCCCAACAAAACCACAGGC	
		341 A P E A L M A N S G E P W S P S Y L G P 1021 GCTCCAGAGGCGTTAATGGCCAACTCCGGTGAGCCATGGAGCCCCTCTTATCTGGCCCA	
		361 T S P - 1081 ACCTCTCCTTAA	
B1960933	Pleckstrin		SEQ ID NO:210
		1 gcagaggagg cccagctgct gagaggagtt gcctgagagt gaccttgca tctgcctgtc 61 cagccagcat ggaaccaaag cggatcagag agggctacct tgtgaagaag gggagcgtgt 121 tcaatacgtg gaaacccatg tgggttgtat tgttagaaga tggaattgaa ttctatagaa 181 agaaaagtga caacagcccc aaaggaatga tcccgctgaa agggagcact ctgactagcc 241 cttgtcaaga ctttggcaaa aggatgtttg tgtttaagat cactacgacc aaacagcagg 301 accacttctt ccaggcagcc ttcctggagg agagagatgc ctgggttcgg gatatcaaga 361 aggccattaa atgcattgaa ggaggccaga aatttgccag gaaatctacc aggaggtcca 421 ttcgactgcc agaaaccatt gacttaggtg ccttatattt gtccatgaaa gacactgaaa 481 aaggaataaa agaactgaat ctagagaagg acaagaagat ttttaatcac tgcttcacag 541 gtaactgcgt cattgattgg ctggtatcca accagtctgt taggaatcgc caggaaggcc 601 tcatgattgc ttcatcgctg ctcaatgagg ggtatctgca gcctgctgga gacatgtcca 661 agagtgcagt ggatggaact gctgaaaacc cttccctgga caaccctgat gccttctact 721 actttccaga cagtggttc ttctgtgaag agaattccag tgatgatgat gtgattctga 781 aagaagaatt cagagggctc attatcaagc agggatgttt actgaagcag gggcatagaa 841 ggaaaaactg gaaagtgagg aagttcatct tgagagaaga ccctgcctac ctgcactact 901 atgaccctgc tggggcagaa gatccctgg gagcaattca cttgagaggc tgtgtggtga 961 cttcagtgga gagcaactca aatggcagga agagtgagga agagaacctt tttgagatca 1021 tcacagcaga tgaagtgcac tatttcttgc aagcagccac ccccaaggag cgcacagagt 1081 ggatcaaagc catccagatg gcctcccgaa ctgggaagta aagacactcc tgcattcctc 1141 ctccctcctt gagggaagcc cacggacaag ctcagtccag gacctgtcca cttctgtgac 1201 aaatcaacgg gaaacagccc agggtgggga agttttcatt tgcagggggg tctgaatgta 1261 actcaccatg tggtgtgcaa ggttcccctg cattgtattg ctcactgcag ccctctgct 1321 cctatccatg acccccaagc agatataaca agctgtgcag cctcagtagg ctgcttgccc 1381 tctccaggcc tcagggcctc ttctggaaaa tgaagaaatt caactagtag attcctgagg 1441 tcccccccagc ttaaaaaaaa aaaatctgcc ccgtgattct aacactcgca gtagtgatag 1501 tgtatctagt tgttctgctg gtgtcctcc ttggctaagt cttggccttc agttatcttc 1561 aaatgtacca gaacctgagc caacgcctcc ctgtgaaact gttgctgatc tgtagtacag 1621 taccaggaag aaacctcttt tgttctcttt agacatcttc tacttgctct tggccttgag 1681 atcgtgtaac aaaatgaagg agggctctct tctttcttcc tcatcctact caaaaacttc 1741 ccgagagcag tggtggtttt gagggttttg acttctatta ctttttggcag cctggaaagt 1801 tgtgtcttct gggaaagaga cccgggagg ccaggagtag ctgagggtcc tttctgtgcc 1861 cttaaaccgc ccagaggagc cctattccac tctggtttta ggctgatctg agagggtctc	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1921 cctttgttcc tttctggagc atttctctaa cgtttattac aattaggagg gggaccccac 1981 atctgtgaga ttctgtttca tttgaggttt acagaaaaaa aaagtggcca gatgtgttcc 2041 ccccatgggt gagaggcctg ggcaactgcc tggtgaatgt gtctcgcggc agctgcagca 2101 agtggagggg ctgaactact ggccagctca ctggatgatg ggttaataca acaactgcac 2161 tgtaaggact cagagccaca cagaacttct gagaggggct gttagcattg cgcagcatct 2221 tcagttctcc agtaaatgat attgcgttcg tgcctcagct ttaagcacaa gtagcagcag 2281 ctcctgcttg agttctgagg gcatcatggc cctatgatta accagagtga tctaacctag 2341 actaaaattg ggaacttatt tgcaattttt gaccctgacc actaactagt gattcttctc 2401 caaaattgag aaagacagca cccattgaaa cagataigtg tgtgaaagta tatttttcaa 2461 ttccagattt ttaatttttaa ggctccagga aagaaaggag agtagaacat ttttcctcat 2521 tttatcaaat cctcttctgc cctccctcaa ttcccctgta acattcctga agctgttccc 2581 actcccagat ggttttatca atagcctaga ggtaaagaac tgtctttttc tctgattctt 2641 taataaatta tctttatага atatgcacaa gttttttctac actcagtgtt aaagtattta 2701 ttaatgggaa gtcaacttaa tgttttgaaa taaatatatg actctgttta atgcaaaaaa 2761 aaaaaaaaa 1 M E P K R I R E G Y L V K K G S V F N T 1 ATGGAACCAAAGCGGATCAGAGAGGGCTACCTTGTGAAGAAGGGGAGCGTGTTCAATACG 21 W K P M W V V L L E D G I E F Y K K K S 61 TGGAAACCCATGTGGGTTGTATTGTTAGAAGATGGAATTGAATTCTATAAGAAGAAAAGT 41 D N S P K G M I P L K G S T L T S P C Q 121 GACAACAGCCCCAAAGGAATGATCCCGCTGAAAGCGAGCACTCTGACTAGCCCTTGTCAA 61 D F G K R M F V F K I T T T K Q Q D H F 181 GACTTTGGCAAAAGGATGTTTGTGTTTAAGATCACTACGACCAAACAGCAGGACCACTTC 81 F Q A A F L E E R D A W V R D I K K A I 241 TTCCAGGCAGCCTTCCTGGAGGAGAGATGCCTGGTTCGGGATATCAAGAAGGCCATT 101 K C I E G G Q K F A R K S T R R S I R L 301 AAATGCATTGAAGGAGGCCAGAAATTGCCAGGAAATCTACCAGGAGGTCCATTCGACTG 121 P E T I D L G A L Y L S M K D T E K G I 361 CCAGAAACCATTGACTTAGGTGCCTTATATTTGTCCATGAAAGACACTGAAAAAGGAATA 141 K E L N L E K D K K I F N H C F T G N C 421 AAAGAACTGAATCTAGAAGAAGGACAAGAAGATTTTTAATCACTGCTTCACAGGTAACTGC 161 V I D W L V S N Q S V R N R Q E G L M I 481 GTCATTGATTGGCTGGTATCCAACCAGTCTGTTAGGAATCGCCAGGAAGGCCTCATGATT 181 A S S L L N E G Y L Q P A G D M S K S A 541 GCTTCATCGCTGCTCAATGAGGGGTATCTGCAGCCTGCTGGAGACATGTCCAAGAGTGCA 201 V D G T A E N P F L D N P D A F Y Y F P 601 GTGGATGGAACTGCTGAAAACCCTTTCCTGGACAACCCTGATGCCTTCTACTACTTTCCA	SEQ ID NO:211

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		221 D S G F F C E E N S S D D D V I L K E E 661 GACAGTGGGTTCTTCTGTGAAGAGAATTCCAGTGATGATGTGATTCTGAAAGAAGAA 241 F R G V I I K Q G C L L K Q G H R R K N 721 TTCAGAGGGGTCATTATCAAGCAGGGATGTTTACTGAAGCAGGGGCATAGAAGGAAAAAC 261 W K V R K F I L R E D P A Y L H Y Y D P 781 TGGAAAGTGAGGAAGTTCATCTTGAGAAGACCCTGCCTACCTGCACTACTATGACCCT 281 A G A E D P L G A I H L R G C V V T S V 841 GCTGGGGCAGAAGATCCCCTGGGAGCAATTCACTTGAGAGGCTGTGTGGTGACTTCAGTG 301 E S N S N G R K S E E E N L F E I I T A 901 GAGAGCAACTCAAATGGCAGGAAGAGTGAGGAAGAACCTTTTTGAGATCATCACAGCA 321 D E V H Y F L Q A A T P K E R T E W I K 961 GATGAAGTGCACTATTTCTTGCAAGCAGCCACCCCCAAGGAGCGCACAGAGTGGATCAAA 341 A I Q M A S R T G K - 1021 GCCATCCAGATGGCCTCCCGAACTGGGAAGTAA	
WBC037F12	Selenoprotein P	1 gtggagctgc cagagtaaag caaagagaaa ggaagcaggc ccgttggaag tggttgtgac 61 aaccccagca atgtggagaa gcctgggggct tgccctggct ctctgtctcc tcccatcggg 121 aggaacagag agccaggacc aaagctcctt atgtaagcaa cccccagcct ggagcataag 181 agatcaagat ccaatgctaa actccaatgg ttcagtgact gtggttgctc ttcttcaagc 241 cagctgatac ctgtgcatac tgcaggcatc taaattagaa gacctgcgag taaaactgaa 301 gaaagaagga tatctaata ttttctatat tgttgttaat catcaaggaa tctcttctcg 361 attaaaatac acacatctta agaataaggt ttcagagcat attcctgttt atcaacaaga 421 agaaaaccaa acagatgtct ggactctttt aaatggaagc aaagatgact tcctcatata 481 tgatagatgt ggccgtcttg tatatcatct tggtttgcct tttcccttcc taactttccc 541 atatgtagaa gaagccatta agattgctta ctgtgaaaag aaatgtggaa actgctctct 601 cacgactctc aaagatgaag actttgtaa acgtgtatct ttggctactg tggataaaac 661 agttgaaact ccatcgcctc attaccatca tgagcatcat cacaatcatg gacatcagca 721 ccttggcagc agtgagcttt cagagaatca gcaaccagga gcaccaaata ctcctactca 781 tcctgctcct ccaggccttc atcaccacca taagcacaag ggtcagcata ggcagggtca 841 cccagagaac cgagatatgc cagcaagtga agatttacaa gatttacaaa agaagctctg 901 tcgaaagaga tgtataaatc aattactctg taaattgccc acagattcag agttggctcc 961 taggagctga tgctgccatt gtcgacatct gatatttgaa aaaacagggt ctgcaatcac 1021 ctgacagtgt aaagaaaacc tcccatcttt atgtagctga cagggacttc gggcagagga 1081 gaacataact gaatcttgtc agtgacgttt gcctccagct gcctgacaaa taagtcagca 1141 gcttataccc acagaagcca gtgccagttg acgctgaaag aatcaggcaa aaaagtgaga 1201 atgaccttca aactaaatat ttaaaatagg acatactccc caatttagtc tagacacaat 1261 ttcatttcca gcatttttat aaactaccaa attagtgaac caaaaataga aatcagattt 1321 gtgcaaacat ggagaaatct actgaattgg cttccagatt ttaaatttta tgtcatagaa	SEQ ID NO:212

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1381 atattgactc aaaccatatt ttttatgatg gagcaactga aaggtgattg cagcttttgg 1441 ttaatatgtc ttttttttttc tttttccagt gttctatttg ctttaatgag aatagaaacg 1501 taaactatga cctaggggtt tctgttggat aattagcagt ttagaatgga ggaagaacaa 1561 caaagacatg ctttccattt ttttctttac ttatctctca aaacaatatt actttgtctt 1621 ttcaatcttc tacttttaac taataaaata agtggatttt gtattttaag atccagaaat 1681 acttaacacg tgaatatttt gctaaaaaag catatataac tattttaaat atccatttat 1741 cttttgtata tctaagactc atcctgattt ttactatcac acatgaataa agcctttgta 1801 tctttctttc tctaatgttg tatcatactc ttctaaaact tgagtggctg tcttaaaaga 1861 tataagggga aagataatat tgtctgtctc tatattgctt agtaagtatt tccatagtca 1921 atgatggttt aataggtaaa ccaaacccta taaacctgac ctcctttatg gttaatacta 1981 ttaagcaaga atgcagtaca gaattggata cagtacggat ttgtccaaat aaattcaata 2041 aaaaccaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1 M W R S L G L A L A L C L L P S G G T E 1 ATGTGGAGAAGCCTGGGGCTTGCCCTGGCTCTCTGTCTCCTCCCATCGGGAGGAACAGAG 21 S Q D Q S S L C K Q P P A W S I R D Q D 61 AGCCAGGACCAAAGCTCCTTATGTAAGCAACCCCCAGCCTGGAGCATAAGAGATCAAGAT 41 P M L N S N G S V T V V A L L Q A S U Y 121 CCAATGCTAAACTCCAATGGTTCAGTGACTGTGGTTGCTCTTCTTCAAGCCAGCTGATAC 61 L C I L Q A S K L E D L R V K L K K E G 181 CTGTGCATACTGCAGGCATCTAAATTAGAAGACCTGCGAGTAAAACTGAAGAAAGAAGGA 81 Y S N I S Y I V V N H Q G I S S R L K Y 241 TATTCTAATATTTCTTATATTGTTGTTAATCATCAAGGAATCTCTTCTCGATTAAAATAC 101 T H L K N K V S E H I P V Y Q Q E E N Q 301 ACACATCTTAAGAATAAGGTTTCAGAGCATATTCCTGTTTATCAACAAGAACAAAACCAA 121 T D V W T L L N G S K D D F L I Y D R C 361 ACAGATGTCTGGACTCTTTTAAATGGAAGCAAAGATGACTTCCTCATATATGATAGATGT 141 G R L V Y H L G L P F S F L T F P Y V E 421 GGCCGTCTTGTATATCATCTTGGTTTGCCTTTTCCTTCCTAACTTTCCCATATGTAGAA 161 E A I K I A Y C E K K C G N C S L T T L 481 GAAGCCATTAAGATTGCTTACTGTGAAAAGAAATGTGGAAACTGCTCTCTCACGACTCTC 181 K D E D F C K R V S L A T V D K T V E T 541 AAAGATGAAGACTTTTGTAAACGTGTATCTTTGGCTACTGTGGATAAAACAGTTGAAACT 201 P S P H Y H H E H H H N H G H Q H L G S 601 CCATCGCCTCATTACCATCATGAGCATCATCACAATCATGGACATCAGCACCTTGGCAGC 221 S E L S E N Q Q P G A P N T P T H P A P 661 AGTGAGCTTTCAGAGAATCAGCAACCAGGAGCACCAAATACTCCTACTCATCCTGCTCCT	SEQ ID NO:213

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		241 P G L H H H H K H K G Q H R Q G H P E N 721 CCAGGCCTTCATCACCACCATAAGCACAAGGGTCAGCATAGGCAGGGTCACCCAGAGAAC 261 R D M P A S E D L Q D L Q K K L C R K R 781 CGAGATATGCCAGCAAGTGAAGATTTACAAGATTTACAAAAGAAGCTCTGTCGAAAGAGA 281 C I N Q L L C K L P T D S E L A P R S U 841 TGTATAAATCAATTACTCTGTAAATTGCCCACAGATTCAGAGTTGGCTCCTAGGAGCTGA 301 C C H C R H L I F E K T G S A I T U Q C 901 TGCTGCCATTGTCGACATCTGATATTTGAAAAAACAGGGTCTGCAATCACCTGACAGTGT 321 K E N L P S L C S U Q G L R A E E N I T 961 AAAGAAAACCTCCCATCTTTATGTAGCTGACAGGGACTTCGGGCAGAGGAGAACATAACT 341 E S C Q U R L P P A A U Q I S Q Q L I P 1021 GAATCTTGTCAGTGACGTTTGCCTCCAGCTGCCTGACAAATAAGTCAGCAGCTTATACCC 361 T E A S A S U R U K N Q A K K U E U P S 1081 ACAGAAGCCAGTGCCAGTTGACGCTGAAAGAATCAGGCAAAAAAGTGAGAATGACCTTCA 381 N - 1141 AACTAA	
WBC043E03	Ribosomal protein S3A	1 cgcgactccc acttccgccc ttttggctct ctgaccagca ccatggcggt tggcaagaac 61 aagcgcctta cgaaaggcgg caaaaaggga gccaagaaga aagtggttga tccatttct 121 aagaaagatt ggtatgatgt gaaagcacct gctatgttca atataagaaa tattggaaag 181 acgctcgtca ccaggaccca aggaaccaaa attgcatctg atggtctcaa gggtcgtgtg 241 tttgaagtga gtcttgctga tttgcagaat gatgaagttg catttagaaa attcaagctg 301 attactgaag atgttcaggg taaaaactgc ctgactaact tccatggcat ggatcttacc 361 cgtgacaaaa tgtgttccat ggtcaaaaaa tggcagacaa tgattgaagc tcacgttgat 421 gtcaagacta ccgatggtta cttgcttcgt ctgttctgtg ttggttttac taaaaaacgc 481 aacaatcaga tacggaagac ctcttatgct cagcaccaac aggtccgcca aatccggaag 541 aagatgatgg aaatcatgac ccgagaggtg cagacaaatg acttgaaaga agtggtcaat 601 aaattgattc cagacagcat tggaaaagac atagaaaagg cttgccaatc tatttatcct 661 ctccatgatg tcttcgttag aaaagtaaaa atgctgaaga agcccaagtt tgaattggga 721 aagctcatgg agcttcatgg tgaaggcagt agttctggaa aagccactgg ggacgagaca 781 ggtgctaaag ttgaacgagc tgatggatat gaaccaccag tccaagaatc tgtttaaagt 841 tcagacttca aatagtggca aataaaaagt gctatttgta aaaaaaaaaa aaaaaaaaaa 901 aaaaaa 1 M A V G K N K R L T K G G K K G A K K K 1 ATGGCGGTTGGCAAGAACAAGCGCCTTACGAAAGGCGGCAAAAAGGGAGCCAAGAAGAAA 21 V V D P F S K K D W Y D V K A P A M F N	SEQ ID NO:214 SEQ ID NO:215

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		61 GTGGTTGATCCATTTTCTAAGAAAGATTGGTATGATGTGAAAGCACCTGCTATGTTCAAT 41 I R N I G K T L V T R T Q G T K I A S D 121 ATAAGAAATATTGGAAAGACGCTCGTCACCAGGACCCAAGGAACCAAAATTGCATCTGAT 61 G L K G R V F E V S L A D L Q N D E V A 181 GGTCTCAAGGGTCGTGTGTTTGAAGTGAGTCTTCCTGATTTGCAGAATGATGAAGTTGCA 81 F R K F K L I T E D V Q G K N C L T N F 241 TTTAGAAAATTCAAGCTGATTACTGAAGATGTTCAGGGTAAAAACTGCCTGACTAACTTC 101 H G M D L T R D K M C S M V K K W Q T M 301 CATGGCATGGATCTTACCCGTGACAAAATGTGTTCCATGGTCAAAAAATGGCAGACAATG 121 I E A H V D V K T T D G Y L L R L F C V 361 ATTGAAGCTCACGTTGATGTCAAGACTACCGATGGTTACTTGCTTCGTCTGTTCTGTGTT 141 G F T K K R N N Q I R K T S Y A Q H Q Q 421 GGTTTTACTAAAAAACGCAACAATCAGATACGGAAGACCTCTTATGCTCAGCACCAACAG 161 V R Q I R K K M M E I M T R E V Q T N D 481 GTCCGCCAAATCCGGAAGAAGATGATGGAAATCATGACCCGAGAGGTGCAGACAAATGAC 181 L K E V V N K L I P D S I G K D I E K A 541 TTGAAAGAAGTGGTCAATAAATTGATTCCAGACAGCATTGGAAAAGACATAGAAAAGGCT 201 C Q S I Y P L H D V F V R K V K M L K K 601 TGCCAATCTATTTATCCTCTCCATGATGTCTTCGTTAGAAAAGTAAAAATGCTGAAGAAG 221 P K F E L G K L M E L H G E G S S S G K 661 CCCAAGTTTGAATTGGGAAAGCTCATGGAGCTTCATGGTGAAGGCAGTAGTTCTGGAAAA 241 A T G D E T G A K V E R A D G Y E P P V 721 GCCACTGGGGACGAGACAGGTGCTAAAGTTGAACGAGCTGATGGATATGAACCACCAGTC 261 Q E S V - 781 CAAGAATCTGTTTAA	
Foe1019	Hemoglobin, beta (HBB)	1 ATGGTGCAACTGAGTGGTGAAGAGAAGGCAGCTGTCTTGGCCCTGTGGGACAAGGTGAAC 61 GAGGAAGAAGTTGGTGGTGAAGCCCTGGGCAGGCTGCTGGTTGTCTACCCATGGACTCAG 121 AGGTTCTTTGACTCCTTTGGGGATCTGTCCAATCCTGGTGCTGTGATGGGCAACCCCAAG 181 GTGAAGGCCCACGGCAAGAAAGTGCTACACTCCTTTGGTGAGGGCGTGCATCATCTTGAC 241 AACCTCAAGGGCACCTTTGCTGCGCTGAGTGAGCTGCACTGTGACAAGCTGCACGTGGAT 301 CCTGAGAACTTCAGGCTCCTGGGCAACGTGCTGGTTGTTGTGCTGGCTCGCCACTTTGGC 361 AAGGATTTCACCCCAGAGTTGCAGGCTTCCTATCAAAAGGTGGTGGCTGGTGTGGCCAAT 421 GCACTGGCCCACAAATACCACTGA	SEQ ID NO:216

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1 M V Q L S G E E K A A V L A L W D K V N 1 ATGGTGCAACTGAGTGGTGAAGAGAAGGCAGCTGTCTTGGCCCTGTGGGACAAGGTGAAC 21 E E E V G G E A L G R L L V V Y P W T Q 61 GAGGAAGAAGTTGGTGGTGAAGCCCTGGGCAGGCTGCTGGTTGTCTACCCATGGACTCAG 41 R F F D S F G D L S N P G A V M G N P K 121 AGGTTCTTTGACTCCTTTGGGGATCTGTCCAATCCTGGTGCTGTGATGGGCAACCCCAAG 61 V K A H G K K V L H S F G E G V H H L D 181 GTGAAGGCCCACGGCAAGAAAGTGCTACACTCCTTTGGTGAGGGCGTGCATCATCTTGAC 81 N L K G T F A A L S E L H C D K L H V D 241 AACCTCAAGGGCACCTTTGCTGCGCTGAGTGAGCTGCACTGTGACAAGCTGCACGTGGAT 101 P E N F R L L G N V L V V V L A R H F G 301 CCTGAGAACTTCAGGCTCCTGGGCAACGTGCTGGTTGTTGTGCTGGCTCGCCACTTTGGC 121 K D F T P E L Q A S Y Q K V V A G V A N 361 AAGGATTTCACCCCAGAGTTGCAGGCTTCCTATCAAAAGGTGGTGGCTGGTGTGGCCAAT 141 A L A H K Y H - 421 GCACTGGCCCACAAATACCACTGA	SEQ ID NO:217
Gi5441616	Equus caballus mRNA for interferon gamma inducing factor (IL-18)	1 ATGGCTGCTGGACCAGTAGAAGACAATTGCATTAGCTTGGTGGAAATGAAATTTATTGAC 61 AACACACTTTACTTTGTAGCTGAAAACGATGAAAACCTGGAATCAGATTACTTTGGCAGG 121 CTTGAACCTAAACTCTCAATCATACGAAATTTGAACGACCAAGTTCTCTTCATTAACCAG 181 GGAAATCAACCTGTGTTTGAGGATATGCCTGATTCTGATTGTACAGACAACGCACCCCAG 241 ACCGTATTTATCATATATATGTATAAAGATAGCCTCACTAGAGGTCTAGCGGTAACCATC 301 TCTGTGAAGTGTGAGAAAACGTCTACTCTCTCCTGTAAGAACAAAATTATTTCCTTTAAG 361 GAAATGAGTCCTCCTGAGAATATCAATGATGAAGGAAATGACATCATATTCTTTCAGAGA 421 AGTGTTCCAGGACATGATGATAAGATACAGTTTGAGTCTTCACTGTATAAAGGATACTTT 481 CTAGCTTGTGAAAAAGAGAATGATCTTTTCAAACTCATTTTGAAAGAAAAGGATGAAAAT 541 GGGGATAAATCTGTAATGTTCACTGTTCAAAACCAGAACTAG	SEQ ID NO:218
		1 M A A G P V E D N C I S L V E M K F I D 1 ATGGCTGCTGGACCAGTAGAAGACAATTGCATTAGCTTGGTGGAAATGAAATTTATTGAC 21 N T L Y F V A E N D E N L E S D Y F G R 61 AACACACTTTACTTTGTAGCTGAAAACGATGAAAACCTGGAATCAGATTACTTTGGCAGG 41 L E P K L S I I R N L N D Q V L F I N Q 121 CTTGAACCTAAACTCTCAATCATACGAAATTTGAACGACCAAGTTCTCTTCATTAACCAG	SEQ ID NO:219

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		61 G N Q P V F E D M P D S D C T D N A P Q 181 GGAAATCAACCTGTGTTTGAGGATATGCCTGATTCTGATTGTACAGACAACGCACCCCAG 81 T V F I I Y M Y K D S L T R G L A V T I 241 ACCGTATTTATCATATATATGTATAAAGATAGCCTCACTAGAGGTCTAGCGGTAACCATC 101 S V K C E K T S T L S C K N K I I S F K 301 TCTGTGAAGTGTGAGAAAACGTCTACTCTCTCCTGTAAGAACAAAATTATTTCCTTTAAG 121 E M S P P E N I N D E G N D I I F F Q R 361 GAAATGAGTCCTCCTGAGAATATCAATGATGAAGGAAATGACATCATATTCTTTCAGAGA 141 S V P G H D D K I Q F E S S L Y K G Y F 421 AGTGTTCCAGGACATGATGATAAGATACAGTTTGAGTCTTCACTGTATAAAGGATACTTT 161 L A C E K E N D L F K L I L K E K D E N 481 CTAGCTTGTGAAAAAGAGAATGATCTTTTCAAACTCATTTTGAAAGAAAAGGATGAAAAT 181 G D K S V M F T V Q N Q N - 541 GGGGATAAATCTGTAATGTTCACTGTTCAAAACCAGAACTAG	
B1961054	Interferon-gamma-inducible protein-10 (IP-10) (Ovis aries)	1 cactcctcaa ctcttcaggc agtctgagct actgcagaag taccttcagt tgcagcacca 61 tgaacaaaag tggttttctt attttctgcc ttatccttct gactctgagt caaggcatac 121 ctctctctag gaacacacgc tgcacctgca tcgagatcag taatggatct gttaatccaa 181 ggtccttaga aaaacttgaa ctgattcctg caagtcaatc ctgcccacgt gtcgagatta 241 ttgccacaat gaaaaggaat ggggagaaaa gatgtctgaa tccagaatct aagaccatca 301 agaatttact gaaagcaatt aacaagcaaa ggactaaaag atctcctcga acacagaaag 361 aggcataatc actgcactac tgataagatg gaccagagag aagctacctc tacaattgtt 421 tccctgtgta cagtatatgt caagccctaa ttgttcgtgg acttcagttc tcctaaaagg 481 tgaccaagcc agtcaccaaa tcagctgcta ctactcctgc agggggaggg tggctcatca 541 ccctgagctg ttcagtagtg actctgccct ggcactgtga ctgtaagcta taccggggcg 601 ctacgttctc agttaatgtg ctaagtccca gccttgctac tgacagcttc ttccccttc 661 caatctttct aggttattaa gggatctttc cagctctggg cttattagag accttaggat 721 ctcaaataac taagagacat tcaaaccaat aatgcaatct gctttttaaa gaaagatctt 781 tactccaggg gcttcactgc catccctcca aggggcccgt attctttcag gtgttatgta 841 catagttcca aatatacaga agcagccaga aatatctgga aatgtaggtc taaacagtat 901 tacttagtca aaaactatac aaagtagaat tcttgaagat atatgtttct tatatgattt 961 tcagtgttca tggaataact tgtatacaac tatcaactta tgtaattatt gcaatggaat 1021 aaatttttaa atttagatac atgttctgca ggctatgtaa gacaaatatg ctaaatgctt 1081 tccaaaataa aagtaatgtt ctctcccaga aatactaaga aagattatgt aattgtttta 1141 gaggccaaaa acataataaa taattataac t 1 M N K S G F L I F C L I L L T L S Q G I 1 ATGAACAAAAGTGGTTTTCTTATTTTCTGCCTTATCCTTCTGACTCTGAGTCAAGGCATA 21 P L S R N T R C T C I E I S N G S V N P	SEQ ID NO:220 SEQ ID NO:221

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		61 CCTCTCTCTAGGAACACACGCTGCACCTGCATCGAGATCAGTAATGGATCTGTTAATCCA 41 R S L E K L E L I P A S Q S C P R V E I 121 AGGTCCTTAGAAAAACTTGAACTGATTCCTGCAAGTCAATCCTGCCCACGTGTCGAGATT 61 I A T M K R N G E K R C L N P E S K T I 181 ATTGCCACAATGAAAAGGAATGGGGAGAAAAGATGTCTGAATCCAGAATCTAAGACCATC 81 K N L L K A I N K Q R T K R S P R T Q K 241 AAGAATTTACTGAAAGCAATTAACAAGCAAAGGACTAAAAGATCTCCTCGAACACAGAAA 101 E A - 301 GAGGCATAA	
B1961539	Calcium-binding protein in macrophages (MRP-14) macrophage migration inhibitory factor (MIF)-related protein	1 AAAACACTCTGTGTGGCTCCTCGGCTTTGACAGAGTGCAAGACGATGACTTGCAAAATGT 61 CCCAGATGGAGCGCGACATAGAGACCATCATCAATGTCTTCCACCAGTACTCTGTGCGAC 121 TGGGGCACCCGGACACCCTGAACCGGAAGGAATTCAAACAGCTGGTTCAAAAAGAGCTGG 181 CGAACTTCCTCAAGAGTAAGAAGAAGGATGAGAAAGCCATAAATCATATCATGGAGGACC 241 TGGATACCAATGAAGACAAGCAGCTGAGTTTCGAGGAGTTCATCATCCTGGTGGCCAGGC 301 TGACGCATGCCTCCCATGAGAAGATGCACGAGCATGACCAAGGCCACGGCCACTGCCATG 361 GGCCAGGCCTTGGGGAGGGCACCCCCTAAGACCACAGTGGCCAAGATCACAGTGGCCACG 421 GCCACGGCCACAGTCATGGTGGCCACGGCCACAGCCACCCAT 1 M T C K M S Q M E R D I E T I I N V F H 1 ATGACTTGCAAAATGTCCCAGATGGAGCGCGACATAGAGACCATCATCAATGTCTTCCAC 21 Q Y S V R L G H P D T L N R K E F K Q L 61 CAGTACTCTGTGCGACTGGGGCACCCGGACACCCTGAACCGGAAGGAATTCAAACAGCTG 41 V Q K E L A N F L K S K K K D E K A I N 121 GTTCAAAAAGAGCTGGCGAACTTCCTCAAGAGTAAGAAGAAGGATGAGAAAGCCATAAAT 61 H I M E D L D T N E D K Q L S F E E F I 181 CATATCATGGAGGACCTGGATACCAATGAAGACAAGCAGCTGAGTTTCGAGGAGTTCATC 81 I L V A R L T H A S H E K M H E H D Q G 241 ATCCTGGTGGCCAGGCTGACGCATGCCTCCCATGAGAAGATGCACGAGCATGACCAAGGC 101 H G H C H G P G L G E G T P - 301 CACGGCCACTGCCATGGGCCAGGCCTTGGGGAGGGCACCCCCTAA	SEQ ID NO:222 SEQ ID NO:223
BM735419	Villin 2 (ezrin)	1 cgcggcagga ggacgaggca gggcgggcgg gcgctctaag ggttctgctc tgactccagg 61 ttgggacagc gtcttcgctg ctgctggata gtcgtgtttt cggggatcga ggatactcac 121 cagaaaccga aaatgccgaa accaatcaat gtccgagtta ccaccatgga tgcagagctg	SEQ ID NO:224

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		181 gagtttgcaa tccagccaaa tacaactgga aaacagcttt ttgatcaggt ggtaaagact 241 atcggcctcc gggaagtgtg gtacttggc ctccactatg tggataataa aggatttcct 301 acctggctga agctggataa gaaggtgtct gcccaggagg tcaggaagga gaatcccctc 361 cagttcaagt tccgggccaa gttctaccct gaagatgtgg ctgaggagct catccaggac 421 atcacccaga aactttcttt cctccaagtg aaggaaggaa tccttagcga tgagatctac 481 tgccccctg agactgccgt gctcttgggg tcctacgctg tgcaggccaa gtttgtggac 541 tacaacaaag aagtgcacaa gtctggtac ctcagctctg agcggctgat ccctcaaaga 601 gtgatggacc agcacaaact taccagggac cagtgggagg accggatcca ggtgtggcat 661 gcggaacacc gtgggatgct caaagataat gctatgttgg aatacctgaa gattgctcag 721 gacctggaaa tgtatggaat caactatttc gagataaaaa acaagaaagg aacagacctt 781 tggcttggag ttgatgccct tggactgaat atttatgaga aagatgataa gttaacccca 841 aagattggct ttccttggag tgaaatcagg aacatctctt tcaatgacaa aaagtttgtc 901 attaaaccca tcgacaagaa ggcacctgac tttgtgtttt atgccccacg tctgagaatc 961 aacaagcgga tcctgcagct ctgcatgggc aaccatgagt tgtatatgcg ccgcaggaag 1021 cctgacacca tcgaggtgca gcagatgaag gcccaggccc gggaggagaa gcatcagaag 1081 cagctggagc ggcaacagct ggaaacagag aagaaaagga gagaaaccgt ggagagagag 1141 aagagcgaga tgatgcgcga gaaggaggag ttgatgctgc ggctgcagga ctatgaggag 1201 aagacaaaga aggcagagag agagctctcg gagcagattc agagggccct gcagctggag 1261 gaggagagga agcgggcaca ggaggaggcc gagcgcctag aggctgaccg tatggctgca 1321 ctgcgggcta aggaggagct ggagagacag gcggtggatc agataaagag ccaggagcag 1381 ctggctgcgg agcttgcaga atacactgcc aagattgccc tcctggaaga ggcgcggagg 1441 cgcaaggagg atgaagttga agagtggcag cacagggcca aagaagccca ggatgacctg 1501 gtgaagacca aggaggagct gcacctggtg atgacagcac cccgcccccc accacccccc 1561 gtgtacgagc cggtgagcta ccatgtccag gagagcttgc aggatgaggg cgcagagccc 1621 acgggctaca gcgcggagct gtctagtgag ggcatccggg atgaccgcaa tgaggagaag 1681 cgcatcactg aggcagagaa gaacgagcgt gtgcagcggc agctgctgac gctgagcagc 1741 gagctgtccc aggcccgaga tgagaataag aggacccaca atgacatcat ccacaacgag 1801 aacatgaggc aaggccggga caagtacaag acgctgcggc agatccggca gccaacacc 1861 aagcagcgca tcgacgagtt cgaggccctg taacagccag gccaggacca agggcagagg 1921 ggtgctcata gcgggcgctg ccagccccgc cacgcttgtg tctttagtgc tccaagtcta 1981 ggaactccct cagatcccag ttcctttaga aagcagttac ccaacagaaa cattctgggc 2041 tgggaaccag ggaggcgccc tggtttgttt tccccagttg taatagtgcc aagcaggcct 2101 gattctcgcg attattctcg aatcacctcc tgtgttgtgc tgggagcagg actgattgaa 2161 ttacggaaaa tgcctgtaaa gtctgagtaa gaaacttcat gctggcctgt gtgatacaag 2221 agtcagcatc attaaaggaa acgtggcagg acttccatct gtgccatact tgttctgtat 2281 tcgaaatgag ctcaaattga tttttaattt tctatgaagg atccatcttt gtatatttac 2341 atgcttagag gggtgaaaat tattttggaa attgagtctg aagcactctc gcacacacag 2401 tgattccctc ctcccgtcac tccacgcagc tggcagagag cacagtgatc accagcgtga 2461 gtggtggagg aggacacttg gattttttct tttgtttttt ttttttttgc ttaacagttt 2521 tagaatacat tgtacttata cacttatta atgatcagct atatactatt tatatacaag 2581 tgataataca gatttgtaac attagtttta aaaagggaaa gttttgttct gtatatttg 2641 ttacctttta cagaataaaa gaattacata tgaaaaaccc tctaaaccat ggcacttgat 2701 gtgatgtggc aggagggcag tggtggagct ggacctgcct gctgcagtca cgtgtaaaca 2761 ggattattat tagtgtttta tgcatgtaat ggactatgca cacttttaat tttgtcagat 2821 tcacacatgc cactatgagc tttcagactc cagctgtgaa gagactctgt ttgcttgtgt 2881 ttgtttgttt gcagtctctc tctgccatgg cctggcagg ctgctggaag gcagctttgtg 2941 gaggccgttg gttccgccca ctcattcctt ctcgtgcact gctttctcct tcacagctaa 3001 gatgccatgt gcaggtggat tccatgccgc agacatgaaa taaaagcttt gcaaaggcac

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		3061 gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3121 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1 M P K P I N V R V T T M D A E L E F A I 1 ATGCCGAAACCAATCAATGTCCGAGTTACCACCATGGATGCAGAGCTGGAGTTTGCAATC 21 Q P N T T G K Q L F D Q V V K T I G L R 61 CAGCCAAATACAACTGGAAAACAGCTTTTTGATCAGGTGGTAAAGACTATCGGCCTCCGG 41 E V W Y F G L H Y V D N K G F P T W L K 121 GAAGTGTGGTACTTTGGCCTCCACTATGTGGATAATAAAGGATTTCCTACCTGGCTGAAG 61 L D K K V S A Q E V R K E N P L Q F K F 181 CTGGATAAGAAGGTGTCTGCCCAGGAGGTCAGGAAGGAGAATCCCCTCCAGTTCAAGTTC 81 R A K F Y P E D V A E E L I Q D I T Q K 241 CGGGCCAAGTTCTACCCTGAAGATGTGGCTGAGGAGCTCATCCAGGACATCACCCAGAAA 101 L F F L Q V K E G I L S D E I Y C P P E 301 CTTTTCTTCCTCCAAGTGAAGGAAGGAATCCTTAGCGATGAGATCTACTGCCCCCCTGAG 121 T A V L L G S Y A V Q A K F G D Y N K E 361 ACTGCCGTGCTCTTGGGGTCCTACGCTGTGCAGGCCAAGTTTGGGGACTACAACAAAGAA 141 V H K S G Y L S S E R L I P Q R V M D Q 421 GTGCACAAGTCTGGGTACCTCAGCTCTGAGCGGCTGATCCCTCAAAGAGTGATGGACCAG 161 H K L T R D Q W E D R I Q V W H A E H R 481 CACAAACTTACCAGGGACCAGTGGGAGGACCGGATCCAGGTGTGGCATGCGGAACACCGT 181 G M L K D N A M L E Y L K I A Q D L E M 541 GGGATGCTCAAAGATAATGCTATGTTGGAATACCTGAAGATTGCTCAGGACCTGGAAATG 201 Y G I N Y F E I K N K K G T D L W L G V 601 TATGGAATCAACTATTTCGAGATAAAAAACAAGAAAGGAACAGACCTTTGGCTTGGAGTT 221 D A L G L N I Y E K D D K L T P K I G F 661 GATGCCCTTGGACTGAATATTTATGAGAAAGATGATAAGTTAACCCCAAAGATTGGCTTT 241 P W S E I R N I S F N D K K F V I K P I 721 CCTTGGAGTGAAATCAGGAACATCTCTTTCAATGACAAAAAGTTTGTCATTAAACCCATC 261 D K K A P D F V F Y A P R L R I N K R I 781 GACAAGAAGGCACCTGACTTTGTGTTTTATGCCCCACGTCTGAGAATCAACAAGCGGATC 281 L Q L C M G N H E L Y M R R R K P D T I 841 CTGCAGCTCTGCATGGGCAACCATGAGTTGTATATGCGCCGCAGGAAGCCTGACACCATC	SEQ ID NO:225

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		301 E V Q Q M K A Q A R E E K H Q K Q L E R 901 GAGGTGCAGCAGATGAAGGCCCAGGCCCGGGAGGAGAAGCATCAGAAGCAGCTGGAGCGG 321 Q Q L E T E K K R R E T V E R E K E Q M 961 CAACAGCTGGAAACAGAGAAGAAAAGGAGAGAAACCGTGGAGAGAGAGAAAGAGCAGATG 341 M R E K E E L M L R L Q D Y E E K T K K 1021 ATGCGCGAGAAGGAGGAGTTGATGCTGCGGCTGCAGGACTATGAGGAGAAGACAAAGAAG 361 A E R E L S E Q I Q R A L Q L E E E R K 1081 GCAGAGAGAGAGCTCTCGGAGCAGATTCAGAGGGCCCTGCAGCTGGAGGAGGAGAGGAAG 381 R A Q E E A E R L E A D R M A A L R A K 1141 CGGGCACAGGAGGAGGCCGAGCGCCTAGAGGCTGACCGTATGGCTGCACTGCGGGCTAAG 401 E E L E R Q A V D Q I K S Q E Q L A A E 1201 GAGGAGCTGGAGAGACAGGCGGTGGATCAGATAAAGAGCCAGGAGCAGCTGGCTGCGGAG 421 L A E Y T A K I A L L E E A R R R K E D 1261 CTTGCAGAATACACTGCCAAGATTGCCCTCCTGGAAGAGGCGCGGAGGCGCAAGGAGGAT 441 E V E E W Q H R A K E A Q D D L V K T K 1321 GAAGTTGAAGAGTGGCAGCACAGGGCCAAAGAAGCCCAGGATGACCTGGTGAAGACCAAG 461 E E L H L V M T A P P P P P P P V Y E P 1381 GAGGAGCTGCACCTGGTGATGACAGCACCCCCGCCCCCACCACCCCCCGTGTACGAGCCG 481 V S Y H V Q E S L Q D E G A E P T G Y S 1441 GTGAGCTACCATGTCCAGGAGAGCTTGCAGGATGAGGGCGCAGAGCCCACGGGCTACAGC 501 A E L S S E G I R D D R N E E K R I T E 1501 GCGGAGCTGTCTAGTGAGGGCATCCGGGATGACCGCAATGAGGAGAAGCGCATCACTGAG 521 A E K N E R V Q R Q L L T L S S E L S Q 1561 GCAGAGAAGAACGAGCGTGTGCAGCGGCAGCTGCTGACGCTGAGCAGCGAGCTGTCCCAG 541 A R D E N K R T H N D I I H N E N M R Q 1621 GCCCGAGATGAGAATAAGAGGACCCACAATGACATCATCCACAACGAGAACATGAGGCAA 561 G R D K Y K T L R Q I R Q G N T K Q R I 1681 GGCCGGGACAAGTACAAGACGCTGCGGCAGATCCGGCAGGGCAACACCAAGCAGCGCATC 581 D E F E A L - 1741 GACGAGTTCGAGGCCCTGTAA	
WBC013G08	cDNA FLJ16386 fis, clone	1 AGAACTCACATCGGATGATTCAGGCATGGCTCTGCTAACACTTTATTAAAAGCATGGATT	SEQ ID NO:226

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
	TRACH2000862, moderately similar to Mus musculus putative purine nucleotide binding protein mRNA	61 AATTTTACTTCCAAGTTTATTTTTACTGCACCGTCCCATTTGTGGAAACAACTAGCTTAC 121 TCAGCTTTTTTTTCCTTTTATAAAGGAAAGAACAGAAAAGTAAAAGGAGGAAGAAACA 181 AGAGGTGAGTGAGGCAACTGAAAACTGTTCTTGGACCTGCGGTGCTATAGAGCAGGCTCT 241 TCTAGGTTGGCAGTTGCCATGGAATCTGGACCCAAAATCTTGGCCCCGTTTGCCTGGTG 301 GAAAATAACAATGAGCAGCTATTGGTGAACCAGCAAGCTATACAGATTCTTGAAAGATT 361 TCTCAGCCAGTGGTGGTGGTGGCCATTGTAGGACTGTACCGTACAGGGAAATCCTACTTG 421 ATGAACCATCTGGCAGGACAGAATCATGGCTTCCCTCTGGGCTCCACGGTGCAGTCTGAA 481 ACCAAGGGCATCTGGATGTGGTGCGTGCCCCACCCATCCAAGCCAAACCACACCCTGGTC 541 CTTCTGGACACCGAAGGTCTGGGCGATGTGGAAAAGGGTGACCCTAAGAATGACTCCCTGG 601 ATCTTTGCCCTGGCTGTGCTCCTGTGCAGCACCTTTGTCTACAACAGCATGAGCACCATC 661 AACCACCAGGCCCTGGAGCAGCTGCATTATGTGACAGAGCTCACAGAGCTCATCAGGGCA 721 AAGTCTTCCCCAAGACCTGATGAAGTACACAAGATTCCACACAGAGTTTGTGAGTTCTTTCCA 781 GACTTTATCTGGACTGTACGGGATTTCACCCTGGAGCTGAAGTTAGACGGTCACCCTATC 841 ACAGAAGATGAGTACTTGGAGAATGCCTTGAAGCTGATTCCAGGCAAGAATCCCAAAGTC 901 CAAGCGTCCAATCTACCCAGAGAGTGCATCAGGCTATTCTTTCCAAAACGGAAATGTTTT 961 GTATTTGACCGGCCAATAAACGACAAAGCACTCCTAGCTGACATTGAGAATGTGTCTGAA 1021 AACGAACTGGATTCTAAATTCCAAGAACAAATAAACAAGTTCTGTTCTCACATCTTCACC 1081 CATGCAAGACCTAAGATCTTAGAGAGGGAATCATGGTCACTGGCAATCGGCTGAGGACT 1141 CTGGTGGTGACCTATGTGCGATACCATCAATACTGGAGCAGTGCCTTGTTTGGAGAATGCA 1201 GTGAGAACTCTGGCCCAACTTGAGAACTCAGTGGCCATGCAGAAGCCAGCGGACCATTAC 1261 AGTGAGCAGATGGCCGAGAAATTGAAGTTGCCCACAGACACACTCCAGGAGCTGCTGGAC 1321 GTGCACACAGCCTGTGAGAGAGAGGCCATTGCATTTTTCATGGAGCACTCCTTCAAGGAT 1381 GAAAATCAGGAATTCCAGAAGAAGTTCATGGAAACCACAATGAATAAGAAGGGGGATTTC 1441 TTGCTGCAGAATGAAGAGTCATCTGTTCAATACTGCCAGGCTAAACTCAATGAGCTCTCA 1501 AAGGGACTAATGGAAAGTATCTCAGCAGGAAGTTTCTCTGTTCCTGGAGGGCACAAGCTC 1561 TACATGGAAACAAAGGAAAGGATTGAACAGGACTATTGGCAAGTTCCCAGGAAAGGAGTA 1621 AAGGCAAAAGAGGTCTTCCAGAGGTTCCTGGAGTCACAGATGGTGATAGAGGAATCCATC 1681 TTGCAGTCAGATAAAGCCCTCACTGATAGAGAGAAGGCAGTAGCAGTGGATCGGGCCAAG 1741 AAGGAGGCAGCTGAGAAGGACAGAAACTTTAAAACAGAAATTACAGGAGCAGCAGCAA 1801 CAGATGGAGGCTCAAGATAAGAGTCGCAAGGAAAACATAGCCCAACTGAAGGAGAAGCTG 1861 CAGATGGAGAGAGAACACCTACTGAGAGAGCAGATTATGATGTTGGAGCACACGCAGAAG 1921 GTCCAAAATGATTGGCTTCATGAAGGATTTAAGAAGAAGTATGAGGAGATGAATGCAGAG 1981 ATAAGTCAATTTAAACGTATGATTGATTACTACAAAAAATGATGATACTCCCTGGATTGCA 2041 CGAACCTTGGACACACCTTGCCGATGAGCTAACTGCAATATTGTCTGCTCCTGCTAAATTA 2101 ATTGGTCATGGTGTCAAAGGTGTGAGCTCACTCTTTAAAAAGCATAAGCTCCCCTTTTAA 2161 GGATATTATAGATTGTACATATATATGCTTTGGACTATTTTTGATCTGTATGTTTTTCATTT 2221 TCATTCAGCAAGTTTTTTTTTTTTTCAGAGTCTTACTCTGTTGCCCAGGCTGGAGTACAG 2281 TGGTGCAATCTCAGCTCACTGCAACCTCTGCCTCCTGGGTTCAAGAGATTCACCTGCCTC 2341 AGCCCCCTAGTAGCTGGGATTATAGGTGTACACCACCACACCCAGCTAATTTTTGTATTT 2401 TTAGTAGAGATGGGGTTTCACTATGTTGGCCAGGCTGGTCTCGAACTCTTGACCTCAAAT 2461 GATCCACCCGCCTCGGCCTCCCAAAGTGCTGGGTTACAGGCATGAGCCACCATGCCCAG 2521 CCCTCATTTAGCAAACTTTTAAACATGAAAAGTGCTTATTAGAGGATATCAGTGCCTGGC 2581 CCACATGAGAGAACAGATCCATACACACTTTGAAAAACTTTGTTCACTTTAGGAAATAT 2641 AATTTTGAAAAATCATTTACATACAAGAGGTCCACTGAGGCATTGCTTTAATGGCAAAA 2701 TATTGCAATGTACTTGAATGTCCTTCACATTAGATTGGTAAGATAAATTTTAGTATGTGC 2761 ATGTACTGGAATATTATATAGCCACTAAACAAATTGACAATGAAGCTCTATTTGTACCAG 2821 TAAAGAATGGTCTTGAAGAGACATTGTAAAATGA	SEQUENCE IDENTIFIER:

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1 M E S G P K M L A P V C L V E N N N E Q 1 ATGGAATCTGGACCCAAAATGTTGGCCCCCGTTTGCCTGGTGGAAATAACAATGAGCAG 21 L L V N Q Q A I Q I L E K I S Q P V V V 61 CTATTGGTGAACCAGCAAGCTATACAGATTCTTGAAAAGATTTCTCAGCCAGTGGTGGTG 41 V A I V G L Y R T G K S Y L M N H L A G 121 GTGGCCATTGTAGGACTGTACCGTACAGGGAAATCCTACTTGATGAACCATCTGGCAGGA 61 Q N H G F P L G S T V Q S E T K G I W M 181 CAGAATCATGGCTTCCCTCTGGGCTCCACGGTGCAGTCTGAAACCAAGGGCATCTGGATG 81 W C V P H P S K P N H T L V L L D T E G 241 TGGTGCGTCCCCACCCATCCAAGCCAAACCACACCCTGGTCCTTCTGGACACCGAAGGT 101 L G D V E K G D P K N D S W I F A L A V 301 CTGGGCGATGTGGAAAAGGGTGACCCTAAGAATGACTCCTGGATCTTTGCCCTGGCTGTG 121 L L C S T F V Y N S M S T I N H Q A L E 361 CTCCTGTGCAGCACCTTTGTCTACAACAGCATGAGCACCATCAACCACCAGGCCCTGGAG 141 Q L H Y V T E L T E L I R A K S S P R P 421 CAGCTGCATTATGTGACAGAGCTCACAGAGCTCATCAGGGCAAAGTCTTCCCCAAGACCT 161 D E V Q D S T E F V S F F P D F I W T V 481 GATGAAGTACAAGATTCCACAGAGTTTGTGAGTTTCTTCCAGACTTTATCTGGACTGTA 181 R D F T L E L K L D G H P I T E D E Y L 541 CGGGATTTCACCCTGGAGCTGAAGTTAGACGGTCACCCTATCACAGAAGATGAGTACTTG 201 E N A L K L I P G K N P K V Q A S N L P 601 GAGAATGCCTTGAAGCTGATTCCAGGCAAGAATCCCAAAGTCCAAGCGTCCAATCTACCC 221 R E C I R L F F P K R K C F V F D R P I 661 AGAGAGTGCATCAGGCTATTCTTTCCAAAACGGAAATGTTTGTATTTGACCGGCCAATA 241 N D K A L L A D I E N V S E N E L D S K 721 AACGACAAAGCACTCCTAGCTGACATTGAGAATGTGTCTGAAACGAACTGGATTCTAAA 261 F Q E Q I N K F C S H I F T H A R P K T 781 TTCCAAGAACAAATAACAAGTTCTGTTCTCACATCTTCACCCATGCAAGACCTAAGACT 281 L R E G I M V T G N R L R T L V V T Y V 841 CTTAGAGAGGGAATCATGGTCACTGGAATCGGCTGAGGACTCTGGTGGTGACCTATGTG 301 D T I N T G A V P C L E N A V R T L A Q 901 GATACCATCAATACTGGAGCAGTGCCTTGTTTGGAGAATGCAGTGAGAACTCTGGCCCAA	SEQ ID NO:227

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		321 L E N S V A M Q K A A D H Y S E Q M A E 961 CTTGAGAACTCAGTGGCCATGCAGAAGGCAGCGGACCATTACAGTGAGCAGATGGCCGAG	
		341 K L K L P T D T L Q E L L D V H T A C E 1021 AAATTGAAGTTGCCCACAGACACACTCCAGGAGCTGCTGGACGTGCACACAGCCTGTGAG	
		361 R E A I A F F M E H S F K D E N Q E F Q 1081 AGAGAGGCCATTGCATTTTTCATGGAGCACTCCTTCAAGGATGAAAATCAGGAATTCCAG	
		381 K K F M E T T M N K K G D F L L Q N E E 1141 AAGAAGTTCATGGAAACCACAATGAATAAGAAGGGGATTTCTTGCTGCAGAATGAAGAG	
		401 S S V Q Y C Q A K L N E L S K G L M E S 1201 TCATCTGTTCAATACTGCCAGGCTAAACTCAATGAGCCTCAAAGGACTAATGGAAAGT	
		421 I S A G S F S V P G G H K L Y M E T K E 1261 ATCTCAGCAGGAAGTTTCTCTGTTCCTGGAGGGCACAAGCTCTACATGGAAACAAAGGAA	
		441 R I E Q D Y W Q V P P R K G V K A K E V F 1321 AGGATTGAACAGGACTATTGGCAAGTTCCCAGGAAAGGAGTAAAGGCAAAAGAGGTCTTC	
		461 Q R F L E S Q M V I E E S I L Q S D K A 1381 CAGAGGTTCCTGGAGTCACAGATGGTGATAGAGGAATCCATCTTGCAGTCAGATAAAGCC	
		481 L T D R E K A V A V D R A K K E A A E K 1441 CTCACTGATAGAGAGAAGGCAGTAGCAGTGGATCGGCCAAGAAGGCAGGCAGCTGAGAAG	
		501 E Q E L L K Q K L Q E Q Q Q M E A Q D 1501 GAACAGGAACTTTTAAAACAGAAATTACAGGAGCAGCAGCAACAGATGGAGGCTCAAGAT	
		521 K S R K E N I A Q L K E K L Q M E R E H 1561 AAGAGTCGCAAGGAAAACATAGCCCAACTGAAGGAGAAGCTGCAGATGGAGAGAGAACAC	
		541 L L R E Q I M M L E H T Q K V Q N D W L 1621 CTACTGAGAGAGCAGATTATGATGTTGGAGCACACGCAGAAGGTCCAAAATGATTGGCTT	
		561 H E G F K K K Y E E M N A E I S Q F K R 1681 CATGAAGGATTTAAGAAGAAGTATGAGGAGATGAATGCAGAGATAAGTCAATTTAAACGT	
		581 M I D T T K N D D T P W I A R T L D N L 1741 ATGATTGATACTACAAAAAATGATGATACTCCCTGGATTGCACGAACCTTGGACAACCTT	
		601 A D E L T A I L S A P A K L I G H G V K 1801 GCCGATGAGCTAACTGCAATATTGTCTGCTCCTGCTAAATTAATTGGTCATGGTGTCAAA	
		621 G V S S L F K K H K L P F - 1861 GGTGTGAGCTCACTCTTTAAAAAGCATAAGCTCCCCTTTTAA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
B1961648	Farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltrans transferase, geranyltranstransf erase)	1 ggaacaggat gcccctgtcc cgctggttga gatctgtggg ggtcttcctg ctgccagccc 61 cctactgggc accccgggag aggtggctgg gttccctacg gcggccctcc ctggtgcacg 121 ggtacccagt cctggcctgg cacagtgccc gctgctggtg ccaagcgtgg acagaggaac 181 ctcgagccct ttgctcctcc ctcagaatga acggagacca gaattcagat gtttatgccc 241 aagaaaagca ggatttcgtt cagcacttct cccagatcgt tagggtgctg actgaggatg 301 agatggggca cccagagata ggagatgcta ttgcccggct caaggaggtc ctggagtaca 361 atgccattgg aggcaagtat aaccggggtt tgacggtggt agtagcattc cgggagctgg 421 tggagccaag gaaacaggat gctgatagtc tccagcgggc ctggactgtg ggctggtgtg 481 tggaactgct gcaagctttc ttcctggtgg cagatgacat catggattca tcccttaccc 541 gccggggaca gatctgctgg tatcagaagc cgggcgtggg tttggatgcc atcaatgatg 601 ctaacctcct ggaagcatgt atctaccgcc tgctgaagct ctattgccgg gagcagccct 661 attacctgaa cctgatcgag ctcttcctgc agagttccta tcagactgag attgggcaga 721 ccctggacct cctcacagcc ccccagggca atgtggatct tgtcagattc actgaaaaga 781 ggtacaaatc tattgtcaag tacaagacag ctttctactc cttctacctt cctatagctg 841 cagccatgta catggcagga attgatggcg agaaggagca cgccaatgcc aagaagatcc 901 tgctggagat gggggagttc tttcagattc aggatgatta ccttgacctc tttggggacc 961 ccagtgtgac cggcaaaatt ggcactgaca tccaggacaa caaatgcagc tggctggtgg 1021 ttcagtgtct gcaacgggcc actccagaac agtaccagat cctgaaggaa aattacgggc 1081 agaaggaggc tgagaaagtg gcccgggtga aggcgctata tgaggagctg gatctgccag 1141 cagtgttctt gcaatatgag gaagacagtt acagccacat tatggctctc attgaacagt 1201 acgcagcacc cctgccccca gccgtctttc tggggcttgc gcgcaaaatc tacaagcgga 1261 gaaagtgacc tagagattgc aagggcgggg agaggaggct ctcaataaat aatcgtgtaa 1321 ccttaaaaaa aaaaaaaaaa aaaaa	SEQ ID NO:228
		1 M P L S R W L R S V G V F L L P A P Y W 1 ATGCCCCTGTCCCGCTGGTTGAGATCTGTGGGGGTCTTCCTGCTGCCAGCCCCCTACTGG 21 A P R E R W L G S L R R P S L V H G Y P 61 GCACCCCGGGAGAGGTGGCTGGGTTCCCTACGGCGGCCCTCCCTGGTGCACGGGTACCCA 41 V L A W H S A R C W C Q A W T E E P R A 121 GTCCTGGCCTGGCACAGTGCCCGCTGCTGGTGCCAAGCGTGGACAGAGGAACCTCGAGCC 61 L C S S L R M N G D Q N S D V Y A Q E K 181 CTTTGCTCCTCCCTCAGAATGAACGGAGACCAGAATTCAGATGTTTATGCCCAAGAAAAG 81 Q D F V Q H F S Q I V R V L T E D E M G 241 CAGGATTTCGTTCAGCACTTCTCCCAGATCGTTAGGGTGCTGACTGAGGATGAGATGGGG 101 H P E I G D A I A R L K E V L E Y N A I 301 CACCCAGAGATAGGAGATGCTATTGCCCGGCTCAAGGAGGTCCTGGAGTACAATGCCATT 121 G G K Y N R G L T V V V A F R E L V E P 361 GGAGGCAAGTATAACCGGGGTTTGACGGTGGTAGTAGCATTCCGGGAGCTGGTGGAGCCA 141 R K Q D A D S L Q R A W T V G W C V E L	SEQ ID NO:229

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		421 AGGAAACAGGATGCTGATAGTCTCCAGCGGGCCTGGACTGTGGGCTGGTGTGTGGAACTG 161 L Q A F F L V A D D I M D S S L T R R G 481 CTGCAAGCTTTCTTCCTGGTGGCAGATGACATCATGGATTCATCCCTTACCCGCCGGGGA 181 Q I C W Y Q K P G V G L D A I N D A N L 541 CAGATCTGCTGGTATCAGAAGCCGGGCGTGGGTTTGGATGCCATCAATGATGCTAACCTC 201 L E A C I Y R L L K L Y C R E Q P Y Y L 601 CTGGAAGCATGTATCTACCGCCTGCTGAAGCTCTATTGCCGGGAGCAGCCCTATTACCTG 221 N L I E L F L Q S S Y Q T E I G Q T L D 661 AACCTGATCGAGCTCTTCCTGCAGAGTTCCTATCAGACTGAGATTGGGCAGACCCTGGAC 241 L L T A P Q G N V D L V R F T E K R Y K 721 CTCCTCACAGCCCCCCAGGGCAATGTGGATCTTGTCAGATTCACTGAAAAGAGGTACAAA 261 S I V K Y K T A F Y S F Y L P I A A A M 781 TCTATTGTCAAGTACAAGACAGCTTTCTACTCCTTCTACCTTCCTATAGCTGCAGCCATG 281 Y M A G I D G E K E H A N A K K I L L E 841 TACATGGCAGGAATTGATGGCGAGAAGGAGCACGCCAATGCCAAGAAGATCCTGCTGGAG 301 M G E F F Q I Q D D Y L D L F G D P S V 901 ATGGGGGAGTTCTTTCAGATTCAGGATGATTACCTTGACCTCTTTGGGGACCCCAGTGTG 321 T G K I G T D I Q D N K C S W L V V Q C 961 ACCGGCAAAATTGGCACTGACATCCAGGACAACAAATGCAGCTGGCTGGTGGTTCAGTGT 341 L Q R A T P E Q Y Q I L K E N Y G Q K E 1021 CTGCAACGGGCCACTCCAGAACAGTACCAGATCCTGAAGGAAAATTACGGGCAGAAGGAG 361 A E K V A R V K A L Y E E L D L P A V F 1081 GCTGAGAAAGTGGCCCGGGTGAAGGCGCTATATGAGGAGCTGGATCTGCCAGCAGTGTTC 381 L Q Y E E D S Y S H I M A L I E Q Y A A 1141 TTGCAATATGAGGAAGACAGTTACAGCCACATTATGGCTCTCATTGAACAGTACGCAGCA 401 P L P P A V F L G L A R K I Y K R R K - 1201 CCCCTGCCCCCAGCCGTCTTTCTGGGGCTTGCGCGCAAAATCTACAAGCGGAGAAAGTGA	
WBC041B04	56-KDa protein induced by interferon	1 CCAGATCTCAGAGGAGCCTGGCTAAGCAAAACCCTGCAGAACGGCTGCCTAATTTACAGC 61 AACCATGAGTACAAATGGTGATGATCATCAGGTCAAGGATAGTCTGGAGCAATTGAGATG 121 TCACTTTACATGGGAGTTATCCATTGATGACGATGAAATGCCTGATTTAGAAAACAGAGT 181 CTTGGATCAGATTGAATTCCTAGACACCAAATACAGTGTGGGAATACACAACCTACTAGC	SEQ ID NO:230

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		241 CTATGTGAAACACCTGAAAGGCCAGAATGAGGAAGCCCTGAAGAGCTTAAAAGAAGCTGA 301 AAACTTAATGCAGGAAGAACATGACAACCAAGCAAATGTGAGGAGTCTGGTGACCTGGGG 361 CAACTTTGCCTGGATGTATTACCACATGGGCAGACTGGCAGAAGCTCAGACTTACCTGGA 421 CAAGGTGGAGAACACTTGCAAGAAGTTTGCAAATCCCTCCAGCTATAGAATCGACTGTCC 481 TCAGATGGACTGTGAGGAAGGATGGGCCTTGCTGAAATGTGGAGGAAAGAATTATAAACG 541 GGCCAGGCCTGCTTTGAAAAGGCTCTGGAAGTGGACCCAGAAAACCCTGAATTCAGCAC 601 TGGGTATGCAATCACCGCCTATCGCCTGGACGGCTTTAAATTAGCCACAAAAAATCACAA 661 GCCATTTCTTTGCTTCCCCTAAGGCAGGCTGTCCGCTTAAATCCAGACAATGGATATAT 721 TAAGGTTCTCCTTGCCCTGAAGCTTCAGGATGTAGACACAAGAAGCTGAAGGAGAAAAGTA 781 CATTGAAGAAGCGCTGACCAACACGTCCTCGCAGACCTATGTCCTTCGATATGCGCCAA 841 GTTTTACAGAAAAAAAGGCTCTCTGGATAAAGCTCTTCAGCTCTTTAAAAGGCCTTGAA 901 AGCAACACCCTCCTCTGCTTCGTGCATCACCAGATAGGGCTTTGCTACAGAGGACAAGT 961 GATTCAAATGAAGAAAGCTGCAAACTGGCAGCCTAGAGGACAGGATAGAAAAAAATGTTGA 1021 GAGAATTGCAAGATTAGCCCATATCTCATTTGGAATTTGCTCTGGAAGAAAACCCACACT 1081 TGATATTGCTTATGTAGACCTGGCAGAAATGTATATAGAAGCAGGTGACCACAGAAAAGC 1141 TGAAGACACTTATCAAAAAGTGTTAACCATGAAAGTACTCGAAGAAGAAAAGCTGCAAAG 1201 GGTACATTTCTCCTATGGCCGATTTTCAGGAATTTCCAAATATAAATCTGAAGACCATGCAAT 1261 TATCCATTATTTAAAAGCAGCACAAATAGCAAAACCCATCTTTCTAAGAGATAAAGTAT 1321 CAGGTCTTTGGAGAAATTGGCTTTAAAGAAACTTCAGAGAACCAGTGGTAGAAGAAACA 1381 ATGCAAGACATACATTCTACTATGGTCGGTTTCAGGAATTTCAAAAGAAATCTGACGTC 1441 AATGCAATTATCCATTATTTTAAAAGCTATATAAAAATAGAACAGGCATCATTAACAAGGGAT 1501 AAAAGTATCAATTCTTTGAAGAAATTGGTTTTAACGAAACTTCGGAGAAAGGCATTAGAT 1561 CTGGAAAGCTTGAGCCTCCTTGGGTTCGTCTACAAATTGGAAGGAAATATGAATGAAGCC 1621 CTGGAGTACTATGAGCGGCCCTGAGACTGGCTGCTGACTTTGAGAACTCTGTGAGACAA 1681 GGTCCTTAGGCACCCAGATATCAGCCACTTTCACATTTTATGTTAACACATACTAATCAT 1741 CTTACCTGCTTGCTGCTTTCAGAACATGTTATGTAATTTACTGTAATGATGCAATTTTTG 1801 AATAATAAATCTGACAAAATATT	SEQ ID NO:231
		1 M S T N G D D H Q V K D S L E Q L R C H 1 ATGAGTACAAATGGTGATGATCATCAGGTCAAGGATAGTCTGGAGCAATTGAGATGTCAC 21 F T W E L S I D D D E M P D L E N R V L 61 TTTACATGGGAGTTATCCATTGATGACGATGAAATGCCTGATTTAGAAAACAGAGTCTTG 41 D Q I E F L D T K Y S V G I H N L L A Y 121 GATCAGATTGAATTCCTAGACACCAAATACAGTGTGGGAATACACAACCTACTAGCCTAT 61 V K H L K G Q N E E A L K S L K E A E N 181 GTGAAACACCTGAAAGGCCAGAATGAGGAAGCCCTGAAGAGCTTAAAAGAAGCTGAAAAC 81 L M Q E E H D N Q A N V R S L V T W G N 241 TTAATGCAGGAAGAACATGACAACCAAGCAAATGTGAGGAGTCTGGTGACCTGGGGCAAC 101 F A W M Y Y H M G R L A E A Q T Y L D K 301 TTTGCCTGGATGTATTACCACATGGGCAGACTGGCAGAAGCTCAGACTTACCTGGACAAG 121 V E N T C K K F A N P S S Y R I D C P Q 361 GTGGAGAACACTTGCAAGAAGTTTGCAAATCCCTCCAGCTATAGAATCGACTGTCCTCAG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		141 M D C E E G W A L L K C G G K N Y K R A 421 ATGGACTGTGAGGAAGGATGGGCCTTGCTGAAATGTGGAGGAAAGAATTATAAACGGGCC 161 K A C F E K A L E V D P E N P E F S T G 481 AAGGCCTGCTTTGAAAAGGCTCTGGAAGTGGACCCAGAAAACCCTGAATTCAGCACTGGG 181 Y A I T A Y R L D G F K L A T K N H K P 541 TATGCAATCACCGCCTATCGCCTGGACGGCTTTAAATTAGCCACAAAAAATCACAAGCCA 201 F S L L P L R Q A V R L N P D N G Y I K 601 TTTTCTTTGCTTCCCCTAAGGCAGGCTGTCCGCTTAAATCCAGACAATGGATATATTAAG 221 V L L A L K L Q D V G Q E A E G E K Y I 661 GTTCTCCTTGCCCTGAAGCTTCAGGATGTAGGACAAGAAGCTGAAGGAGAAAAGTACATT 241 E E A L T N T S S Q T Y V L R Y A A K F 721 GAAGAAGCGCTGACCAACACGTCCTCGCAGACCTATGTCCTTCGATATGCGGCCAAGTTT 261 Y R K K G S L D K A L Q L F K K A L K A 781 TACAGAAAAAAAGGCTCTCTGGATAAAGCTCTTCAGCTCTTTAAAAAGGCCTTGAAAGCA 281 T P S S A F V H H Q I G L C Y R G Q V I 841 ACACCCTCCTCTGCCTTCGTGCATCACCAGATAGGGCTTTGCTACAGAGGACAAGTGATT 301 Q M K K A A N W Q P R G Q D R K N V E R 901 CAAATGAAGAAAGCTGCAAACTGGCAGCCTAGAGGACAGGATAGAAAAAATGTTGAGAGA 321 I A R L A I S H L E F A L E E K P T L D 961 ATTGCAAGATTAGCCATATCTCATTTGGAATTTGCTCTGGAAGAAAAACCCACACTTGAT 341 I A Y V D L A E M Y I E A G D H R K A E 1021 ATTGCTTATGTAGACCTGGCAGAAATGTATATAGAAGCAGGTGACCACAGAAAAGCTGAA 361 D T Y Q K V L T M K V L E E E K L Q R V 1081 GACACTTATCAAAAAGTGTTAACCATGAAAGTACTCGAAGAAGAAAAGCTGCAAAGGGTA 381 H F S Y G R F Q E F Q N K S E D H A I I 1141 CATTTCTCCTATGGCCGATTTCAGGAATTTCAAAATAAATCTGAAGACCATGCAATTATC 401 H Y L K A A E I E N A S F L R D K S I R 1201 CATTATTTAAAAGCAGCAGAAATAGAAAACGCATCTTTTCTAAGAGATAAAAGTATCAGG 421 S L E K L A L K K L Q R N Q W - 1261 TCTTTGGAGAAATTGGCTTTAAAGAAACTTCAGAGAAACCAGTGGTAG	
WBC001B11	No homology		

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1 TTTTCTTTCAGTCCTTTAAAGACGTCTTTCCATTGTCCTCTGTCATCCATTGTTTCTGTC 61 GAGTAGTCACCATAAGGCTTCTGGGTTTTTTGTTTTTTGAAGGTTATGACTGTTTTTCCC 121 TCTGGCTGTTTTTTAGGATTTTCCTCTATATTTTTGGTTTTCAGCAAGTGTGCTACAGTAT 181 GTCCAGGTGTGACTTCTTTTGTATTTTTCCCTTTGGGATTTGTACTACCGTCATGCATTA 241 CCCAACAATGGGGCTACATCCTGAGAAATGTGTTGTTAGGTGATTTCATCATTGTGTGAA 301 CATCATAGACTGTACTTATACAAACCTAGATGGCATAGTCTACTACACGCCTAGGCCATA 361 TGGTACCAATCTTATGGGACCACCATCACATATATGGTCCATTGTTGACTGAAACCTTGT 421 TACACAGTGCATGACTGCAATTATTAAATCTGTGGTTGGAAGGTAATTGGTCGCTGTCTC 481 TTCAAATATTGCTTCTGCCTCATTCTTTATCTTGTCTTTGTGGAACTTCAAACTAACCAT 541 ACTTTTGACCTTTTTATGTCAAAAATAAAATCTCCTATGGCTTTTATTTTTTTTAATATT 601 TTCCACCTTTTCTCTCTAAGTGCCTCATTCTGTTTATTTTCTTCTGACCTATCTTCTGGT 661 TCACTTATTATTTTTTTCTGGTGGTGTCTAATCTATTGGTAAACTCATCCATTGAGTTTT 721 TAATTATTTATTCTTCA	SEQ ID NO:232
		1 ATAGATAACCTCAGAAATTGTCTTGTTGAAACCTCTCGTTTTTCTAGATGTTCAAAGTGT 61 GGACCAGAGAGTTTGAGTGATGAGCTCAAGGAGACATGCTGTTAATGGCAAAGTCAGATC 121 TGGAACACAGCTGTCTCGATTTCTGGTGTATTTTGGTTCTCTTGGCAAAAATAGCACCTC 181 TGTGTCTTCTCTATCCAGTTTCATGCCTTCTTCATCTCTGTTCAAGTTTCATGTGGCCTG 241 GGTGTTGGTGACTGTGGGAAACTTGCCTTACAGAAGGAAGACCAATCTATCACCTTGAGT 301 TTCATTGACGAAAGCTAGAAAATCATGCCAAATGAGCGTCTTTTCTCAGTACTCAGTCCT 361 CTGACCCTCTGTGACTGTCATCCTAGCCTTTTAATCTCTGGAAATATAATTTATTTTTAG 421 CCTCAAACTAAATGATGAGTTTCTGGTGCTAGGCTCAATGTAGAATCCCACTTTTGCTTT 481 CTTTCACAGAAGTAAGGATGCATACTCAACCTCTGATCATCTTGAGAAATCTGTGTCAAA 541 TGCAGTGTTTTTCTTGTGTGTCCTGTGGCCAGACCACTGGTCATTCATTACCTGTTCAGT 601 TTGTGGGAGGTGGGGCCAGGCCATAAAGTCAAGTAAAAAAGAGGAAGAACCTTCATGTAA 661 AAGGGTTAGCTTTTCGTTGTGTATCATTGGGGATGTCCTAGCTATTTAAAAAA	SEQ ID NO:233
WBC032B11	Sphingosine-1-phosphate phosphatase 1	1 agactccgga gggtagagcg ctgtgccggt tccgctgccg ctggccagga gcgcggggac 61 agttcggggc tgcgccggag gccggcccgc cttcccgggg gttccgttat catgtcgctg 121 aggcagcgcc tggcccagct ggttggccgt ctgcaggacc cgcagaaagt ggcccgtttc 181 cagcggctgt gcggggtgga agcgccgccg cgccgctcag cagaccggag ggaggatgag 241 aaagcggagg cgcctctcgc cggagaccct cgactgcgag ggcggcagcc aggggcgcct 301 ggaggccccc agcctcccgg gagcgaccgc aatcagtgcc cggccaagcc ggacggcggc 361 ggcgccccca acggcgtgcg gaacgggctg gcggccgagc tgggcccggc ctcgccgcgg 421 cgcgcgggcg ctctgcgccg caactcgctg acgggcgagg agggccagct ggcccgcgtg 481 agcaactggc cgctctactg cctgttctgc ttcggcacgg agctgggcaa cgaactcttc 541 tacatcctgt tcttcccctt ctggatctgg aacctggacc ctctggtggg ccggaggctc 601 gtggtcatct gggtgctggt catgtacctg ggccagtgca ccaaggacat catccgctgg 661 ccgaggcccg cctcgccgcc cgtggtcaag ttggaggtct tctacaactc tgagtacagc 721 atgccctcca cccatgccat gtccggcacc gccatcccca tttctatggt cctcctcacc 781 tatggccgct ggcagtaccc tcttatatat ggactgattc ttattccctg ctggtgttct 841 ctagtttgcc taagtagaat ttacatggga atgcactcta ttctggatat tattgctgga 901 ttcctatata ccattttaat cttagctgtc ttctatccat ttgtggacct gattgacaac 961 ttcaaccaaa ctcacaaata tgctccattc atcatcatcg ggcttcattt agctttgggg 1021 atcttttctt tcactcttga cacctggagc acatcccgag gagacacagc cgagatacta 1081 ggaagtggtg ctggaattgc atgtggatct catgttactt ataacatggg tctagtatta	SEQ ID NO:234

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1141 gatccttctc tagatacatt accttagct gggccccca ttactgtgac tctgtttgga 1201 aaagccatat tgcggatcct cataggatg gtatttgtac taataatcag agatgtaatg 1261 aaaaagatca ccattccttt agcctgcaaa atcttcaata taccgtgtga tgatattcga 1321 aaagcaagac agcacatgga agttgaactt ccttatcgtt atattacctа tggaatggtt 1381 ggtttctcca tcacatttct tgttccttac atatttttct ttattggtat ctcttgatgg 1441 agaagtattg tttatgataa gaaaggaggg tatcagttac tgataccaa aaatatattc 1501 caggtaaagc caggtcagaa ttaggctttt gcaggaattt aacttaaata attatttaag 1561 taaattcata agagtcagtg cattttatca ttgcacatcc agatactgtt ttaggtgagc 1621 tgagctattt cgttactgag aaaatgataa gtatccattt agaatgttca tgtaatgttt 1681 ggagagtttt gtattatgga ttcaacttat atataatata tataagtac ataatatgca 1741 attgtgtatc tgatatatat tatatataaa ataatatacc taagtgtttt tttaaactat 1801 ggggtgtatt ataaaatcaa taataatatg caaacagttg tgcctgtgta tttgaactac 1861 atacaggtat gttgttatta acagatatat ttaacattta tttactatgg gagccatttc 1921 ctaattgaat tgcgtaatta ctagaccaga atgcatatgc tactatacat tgatttactg 1981 cctgttttta cactgccatt accttcatg ttatccatga tgttgaacat gggaggcatt 2041 tttaatggac caaattttta gaaaaattag tttttggatt ttttttaag ttctgtatac 2101 tgtttgaat gaacttatt tgcagctatt ctggatgtca gtttaataat tcagtactg 2161 atttttattg cttgctaatt gtgcctttcc gttgctaaat taagaaatgc tatgtgtact 2221 gtgatgtaaa aataagacat taactttatc ttaagttaca tataatcaag caaatatttt 2281 aaaaaatgta tgtcagggtg acaggcataa aagtaaatta cccttaactc tttagccttt 2341 atttagaaag aaatgtggaa tgggctaaac tttctcacca atttattaga aagctaaatg 2401 gataaatact tccctttttg tagatatttt tctgtgcatt gtaagttata ggagcaggac 2461 atatttttg tacattgtct tgattgttta tactgcaggt aggtatttcc agtgaatgga 2521 aacgttgaaa tttatagatg ggacaatgca catacttcat atgtaaacaa agcatttttc 2581 taaataattt ggaaaggatt ggatttagca ccgttaactt ttaataccca tttattggct 2641 atttaaggta aattataaaa cctaaaatta gtatcagtat tttagatcct attatttttt 2701 caacttccta ttatttcac agtggaaaat ttgcgtatag tattaaacta ttctttttc 2761 tgtctacctt tatattttga agtgtggttg tacttacgtt aatagtaagt gtatttgtag 2821 aaagtttttc ataaagaaga gattaacttt ccatataaat aaataccagg tatgaaatta 2881 ctgattttag tgcaatatct gtatgattat ccagaactat cacttcagat gtttctattt 2941 tgggcaccat aactatttga gctcatattt ttataattct gattgagaat ttagggcat 3001 ggtaatttt accaaaactg aagctggtaa ttttaagtaa agcaactaaa tttaccctt 3061 acttattagt taaaaggaaa ccaaggcatg taggaaaata ttggtacgtt ggaaaatgtg 3121 aaaagagctt tactttcaaa atgtatgttt aatgaattga attttaggga ccgtttccca 3181 taatttgggc ctatgctatc ctgttgattt ttatgtctag cttaaaggt atttgaaaat 3241 gttccatttg tgttttatta ttttctgtcc tatgacagtt ctatgctaaa tgtaatttaa 3301 aataaaagcc aaattgaaga ttaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3361 aaaaaagaaa aaaaaaaaaa a 1 M S L R Q R L A Q L V G R L Q D P Q K V 1 ATGTCGCTGAGGCAGCGCCTGGCCCAGCTGGTTGCCGTCTGCAGGACCCGCAGAAAGTG 21 A R F Q R L C G V E A P P R R S A D R R 61 GCCCGTTTCCAGCGGCTGTGCGGGGTGGAAGCGCCGCCGCCGCTCAGCAGACCGGAGG 41 E D E K A E A P L A G D P R L R G R Q P 121 GAGGATGAGAAAGCGGAGGCGCCTCTCGCCGGAGACCCTCGACTGCGAGGGCGGCAGCCA	SEQ ID NO:235

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		61 G A P G G P Q P P G S D R N Q C P A K P 181 GGGGCGCCTGGAGGCCCCCAGCCTCCGGGAGCGACCGCAATCAGTGCCCGGCCAAGCCG	
		81 D G G G A P N G G V R N G L A A E L G P A 241 GACGGCGGCGGCGCCCCCAACGGCGTGCGGAACGGCTGGCGGCCGAGCTGGGCCCGGCC	
		101 S P R R A G A L R R N S L T G E E G Q L 301 TCGCCGCGGCGCGGCGGCGCTCTGCGCCGCAACTCGCTGACGGGCGAGGAGGGCCAGCTG	
		121 A R V S N W P L Y C L F C F G T E L G N 361 GCCCGCGTGAGCAACTGGCCGCTCTACTGCCTGTTCTGCTTCGGCACCGAGCTGGGCAAC	
		141 E L F Y I L F F P F W I W N L D P L V G 421 GAACTCTTCTACATCCTGTTCTTCCCTTCTGGATCTGGAACCTGGACCCTCTGGTGGGC	
		161 R R L V V I W V L V M Y L G Q C T K D I 481 CGGAGGCTCGTGGTCATCTGGGTGCTGGTCATGTACCTGGGCCAGTGCACCAAGGACATC	
		181 I R W P R P A S P P V V K L E V F Y N S 541 ATCCGCTGGCCGAGGCCCGCCTCGCCGCCCGTGGTCAAGTTGGAGGTCTTCTACAACTCT	
		201 E Y S M P S T H A M S G T A I P I S M V 601 GAGTACAGCATGCCCTCCACCCATGCCATGTCCGGCACCGCCATCCCCATTTCTATGGTC	
		221 L L T Y G R W Q Y P L I Y G L I L I P C 661 CTCCTCACCTATGGCCGCTGGCAGTACCCTCTTATATATGGACTGATTCTTATTCCCTGC	
		241 W C S L V C L S R I Y M G M H S I L D I 721 TGGTGTTCTCTAGTTTGCCTAAGTAGAATTTACATGGGAATGCACTCTATTCTGGATATT	
		261 I A G F L Y T I L I L A V F Y P F V D L 781 ATTGCTGGATTCCTATATACCATTTTAATCTTAGCTGTCTTCTATCCATTTGTGGACCTG	
		281 I D N F N Q T H K Y A P F I I I G L H L 841 ATTGACAACTTCAACCAAACTCACAAATATGCTCCATTCATCATCGGGCTTCATTTA	
		301 A L G I F S F T L D T W S T S R G D T A 901 GCTTTGGGGATCTTTTCTTTCACTCTTGACACCTGGAGCACATCCCGAGGAGACACAGCC	
		321 E I L G S G A G I A C G S H V T Y N M G 961 GAGATACTAGGAAGTGCTGCTGGAATTGCATGTGGATCTCATGTTACTTATAACATGGGT	
		341 L V L D P S L D T L P L A G P P I T V T 1021 CTAGTATTAGATCCTTCTCTAGATACATTACCTTTAGCTGGGCCCCCCATTACTGTGACT	
		361 L F G K A I L R I L I G M V F V L I I R 1081 CTGTTTGGAAAAGCCATATTGCGGATCCTCATAGGGATGGTATTTGTACTAATAATCAGA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		381 D V M K K I T I P L A C K I F N I P C D 1141 GATGTAATGAAAAAGATCACCATTCCTTTAGCCTGCAAAATCTTCAATATACCGTGTGAT 401 D I R K A R Q H M E V E L P Y Y R Y I T Y 1201 GATATTCGAAAGCAAGACAGCACATGGAAGTTGAACTTCCTTATCGGTATATTACCTAT 421 G M V G F S I T F F V P Y I F F F I G I 1261 GGAATGGTTGGTTTCTCCATCACATTTTTTGTTCCTTACATATTTTTCTTTATTGGTATC 441 S - 1321 TCTTGA	
B1961185	Actin related protein 2/3 complex, subunit 1B, 41kDA	1 gcgcgtcgac tgcccagagt ccgcggccgg ggcgcgggag gagccaagcc gccatggcct 61 accacagctt cctggtggag cccatcagct gccacgcctg gaacaaggac cgcacccaga 121 ttgccatctg ccccaacaac catgaggtgc atatctatga aaagagcggt gccaaatgga 181 ccaaggtgca cgagctcaag ggcacaacg ggcagtgtgac aggcatcgac tgggcccccg 241 agagtaaccg tattgtgacc tgcggcacag accgcaacgc ctacgtgtgg acgctgaagg 301 gccgcacatg gaagcccacg ctggtcatcc tgcggatcaa ccgggctgcc cgctgcgtgc 361 gctgggcccc caacgagaac aagtttgctg tgggcaagcgg ctctcgtgtg atctccatct 421 gttatttcga gcaggagaat gactggtggg tttgcaagca catcaagaag cccatccgct 481 ccaccgtcct cagcctggac tggcacccca acaatgtgct gctggctgcc ggctcctgtg 541 acttcaagtg tcggatcttt tcagcctaca tcaaggaggt ggaggaacgg ccggcaccca 601 cccgtgggg ctccaagatg ccctttgggg aactgatgtt cgaatccagc agtagctgcg 661 gctgggtaca tggcgtctgt ttctcagcca gcgggagccg cgtggcctgg gtaagccacg 721 acagcaccgt ctgcctggct gatgccgaca agaagatggc cgtcgcgact ctggcctctg 781 aaacactacc actgctggcg ctgaccttca tcacagacaa cagcctggtg gcagcgggcc 841 acgactgctt cccgtgctg ttcacctatg acgccgccgc ggggatgctg agcttcggcg 901 ggcggctgga cgttcctaag cagagctcgc agcgtggctt gacggcccgc gagcgcttcc 961 agaacctgga caagaaggcg agctccgagg gtggcacggc tgcgggcgcg ggcctagact 1021 cgctgcacaa gaacagcgtc agccagatct cggtgctcag cggcggcaag gccaagtgct 1081 cgcagttctg caccactggc atggatggcg gcatgagtat ctgggatgtg aagagcttgg 1141 agtcagcctt gaaggacctc aagatcaaat gacctgtgag gaatatgttg ccttcatcct 1201 agctgctggg gaagcgggga gaggggtcag ggaggctaat ggttgctttg ctgaatgttt 1261 ctgggtacc aatacgagtt cccataggag gtgctcctc cttaaatgct ttcatttatt 1321 gggagctttt cttacctatt caaggaatac gtgccttttt cttaaatgct ttcatttatt 1381 gaaaaaaaaa aaaaatgccc ccaaagcact atgctggtca tgaactgctt caaaatgtgg 1441 aggtaataaa atgcaactgt gtaaaaaaaa aaaaaaaaaa aaaaa 1 M A Y H S F L V E P I S C H A W N N K D R 1 ATGGCCTACCACAGCTTCCTGGTGGAGCCCATCAGCTGCCACGCCTGGAACAAGGACCGC 21 T Q I A I C P N N H E V H I Y E K S G A 61 ACCCAGATTGCCATCTGCCCCAACAACCATGAGGTGCATATCTATGAAAAGAGCGGTGCC 41 K W T K V H E L K E H N G Q V T G I D W 121 AAATGGACCAAGGTGCACGAGCTCAAGGAGCACAACGGGCAGGTGACAGGCATCGACTGG	SEQ ID NO:236 SEQ ID NO:237

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		61 A P E S N R I V T C G T D R N A Y V W T 181 GCCCCCGAGAGTAACCGTATTGTGACCTGCGGCACAGACCGCAACGCCTACGTGTGGACG	
		81 L K G R T W K P T L V I L R I N R A A R 241 CTGAAGGGCCGCACATGGAAGCCCACGCTGGTCATCCTGCGGATCAACCGGGCTGCCCGC	
		101 C V R W A P N E N K F A V G S G S R V I 301 TGCGTGCGCTGGGCCCCCAACGAGAACAAGTTTGCTGTGGGCAGCGGCTCTCGTGTGATC	
		121 S I C Y F E Q E N D W W V C K H I K K P 361 TCCATCTGTTATTTCGAGCAGGAGAATGACTGGTGGTTTGCAAGCACATCAAGAAGCCC	
		141 I R S T V L S L D W H P N N V L L A A G 421 ATCCGCTCCACCGTCCTCAGCCTGGACTGGCACCCCAACAATGTGCTGCTGGCTGCCGGC	
		161 S C D F K C R I F S A Y I K E V E E R P 481 TCCTGTGACTTCAAGTGTCGGATCTTTTCAGCCTACATCAAGGAGGTGGAGGAACGGCCG	
		181 A P T P W G S K M P F G E L M F E S S S 541 GCACCCACCCCGTGGGGCTCCAAGATGCCCTTTGGGGAACTGATGTTCGAATCCAGCAGT	
		201 S C G W V H G V C F S A S G S R V A W V 601 AGCTGCGGCTGGGTACATGGCGTCTGTTTCTCAGCCAGCGGGAGCCGCGTGGCCTGGGTA	
		221 S H D S T V C L A D D K K M A V A T L 661 AGCCACGACAGCACCGTCTGCCTGGCTGATGCCGACAAGAAGATGGCCGTCGCGACTCTG	
		241 A S E T L P L L A L T F I T D N S L V A 721 GCCTCTGAAACACTACCACTGCTGGCGCTGACCTTCATCACAGACAACAGCCTGGTGGCA	
		261 A G H D C F P V L F T Y D A A A G M L S 781 GCGGGCCACGACTGCTTCCCGGTGCTGTTCACCTATGACGCCGCGCGGGGATGCTGAGC	
		281 F G G R L D V P K Q S S Q R G L T A R E 841 TTCGGCGGGCGGCTGGACGTTCCTAAGCAGAGCTCGCAGCGTGGCTTGACGGCCCGCGAG	
		301 R F Q N L D K K A S S E G G T A A G G 901 CGCTTCCAGAACCTGGACAAGAAGGCGAGCTCCGAGGGTGGCACGGCTGCGGGCGCGGGC	
		321 L D S L H K N S V S Q I S V L S G G K A 961 CTAGACTCGCTGCACAAGAACAGCGTCAGCCAGATCTCGGTGCTCAGCGGCGCCAAGGCC	
		341 K C S Q F C T T G M D G G M S I W D V K 1021 AAGTGCTCCAGTTCTCCACCACTGGCATGGATGCCGGCATGACTATCTGGGATGTGAAG	
		361 S L E S A L K D L K I K - 1081	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
B1961512	No homology	1 GCACGAGCGGCTGGGGAGGGAGGAGGAGCTGCTTAAGGAAACCGCAGATAAGTTGCGTTA 61 TTAGAAATAATAGAAGTTAGTACAATTCTTTAGGAGATGTAAATAGCGAGAATACTTAAG 121 TTAATGCTTAGCATTAAATTTTTAAAGTAGTTTCGATAATAAGATCTTGCCGAAGGGAAA 181 ATAATGAAGACTGACTTGAAAAGTAGTTTGAGAAAGGAGGAGAGAAGAAGAAAGATATTT 241 CTAGAATATGAGGGAGGTTAAGAGATGAAGCTTAGTAATGGAGTGAAATAATTTTAAATA 301 GCTGAAAGGACTGCGAAGTCCGAAATCAAAACGGCGTTAAATTGAAGAGCAGCGTTTTAG 361 ATTAACTTTAAAACGTAGATGACGTAAATAGAACCTAAACGTTTTAGAAAATGAGGTTTT 421 AGATGACGAAAATATTTTAAACGCCGTCTCTTAAAAAGATTAAAGGTGATTTAAGAGCGA 481 GACCTTCATGTTC	SEQ ID NO:238
		121 GTGAAATAATTTTAAATAGCTGAAAGGACTGCGAAGTCCGAAATCAAAACGGCGTTAAAT 181 TGAAGAGCAGCGTTTTAGATTAACTTTAAAACGTAGATGACGTAAATAGAACCTAAACGT 241 TTTAGAAAATGAGGTTTTAGATGACGAAAATATTTTAAACGCCGTCTCTTAAAAAGATTA 301 AAGGTGATTTAAGAGCGAGACCTTCATGTTCGTGGCGCAGGAAAGGTGATTTGAAGCCTA 361 GTTGGTCTTATGGCATTATTTGCTAAAAAGTGATAGTAATTGGGAGTGGCAGGATAAAAA 421 TTTGGAGAAAGAAGATTAGAAATTAGAAGTGGAAAACTCAGAAGACAGAAGTACAGGAAG 481 GTGAAGAAAAGACTTAGAAGATAGGAAAAATAGAAGATAAGACGCCTCTAGAAGACAGAA 541 ACTAATTTCAAACCCAAAAGGTAGGAAGCAGAAGAAAAAGTATTTAGACAAACTAGGAAA 601 CCAAAGCAGCTAAAGGACCAGATAG	SEQ ID NO:239
WBC008D05	No homology	1 GGACAATATCAAGCGTGCTAACATTCGGATTATAGGGGTCCCAGAAGGAGAAGAGAGAGA 61 CAAAGGGGCAGAAAATTTATTTGTCGAAATAATAGAGGAAAATTTTCCTCACCTGAGGAA 121 GGAAACAGACATCCAAGTTCAGGAAGCACAGAGAGCTCCAAACAAGAGAAGCCCAAAGAG 181 GCCCACACCAAGACATATTATAATCAAAATGTCTAAAATTAAAGAGAGAATCCTAAAAGC 241 AGCAAGAGAAAGGCCCCAAGTGGCATATAAAGGGAAGCCCATCAGGCTATCATCAGACTT 301 CTCAGCCGAGACCCTACAGGCGAGAAGAGAATGGCACGACATATTTAAAGTGCTAAAAGG 361 AAAAAACCTACAACCAAGAACACTCTATCCATCAAGGTTGTCATTCGGAATGGAAGGAGA 421 GATAAAGAGCTTCCCAGACAAGCAAAAATTAAAGGAGTTTATCACCAATAAACCAATTTT 481 GCAAGAAATGCTGAAGGGACTTCTTTAAGTGGGAAAGCAATGATCACAAATAGAAAAAAA 541 TTATCAAAAAACCCCAAAACAACAACAACAAAAAACAGGCAATAAAATCACTTGTAAGGT 601 AAAAGTATAATAAAGGCAGCAGATCAACTACCTGTGAAGATAATATGAAGGTTAAAAGAT 661 AAATGTACTAAAATCACCTATTTCAATGATAAGAGGGTAATGGATAGACACACACTAAAC 721 AAAAGACTATATATGATGTGAAAAACATAATATGGGAGGAGGGGAGTGAAAAAGTAGAGC 781 TTTTAGAAAGAAGTGAAGCTAAAGAGTCTATCTACTCAATTTAGACTGTTACATGCATAG 841 TGT	SEQ ID NO:240
		1 GGTAGCAATACTAATATCAGACAAAATAGACTTCAAATCAAAAACTGTGATAAGAGACAA 61 AGACGGGCACTACATAATGATAAAGGGAACAATCCAACAAGAAAATATAACACTTGCAAA 121 TATCTATGCACCCAACACAGGAGCACCTAAATATATAAAGCAATTATTAACAGACATAAG 181 AGGAGAAATAGACAGTAACACAATAATAGTAGGGGACTTTAACACTCCACTTACACCAAT 241 GGATAGATCATCCAAACAGAAGATCAATAAGGAAACACTCGCCTGAAAGGACACATTAAC 301 TAGATGGACTTAGTAGATAGATACAGAACATTCCATCCAAAAACCACAGAATACACATTC	SEQ ID NO:241

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		361 TTTTTACATGCCCATGGAACATTCTCTAGGATTGATCACATATTAGGCCACAAACAAGT 421 CTCAATAAATTTAAGAAGATCAAAATAATACCATGCAGCTTTTCTGACCACAAAGGTATG 481 AAACTGGAAATCAACTACAGAAAGAAAACCAGAAAGCCACANAAATGTGGAGATTGAAC 541 ANAATGCTACTGAACATGATTGGGTCAATGAAGAATTAAAAAAAAAAA	
WBC133	No homology	1 CCCCAGGCCGCCAAAGCGGTACTTGCGCACTTTGCTGCACCACCGCCGGCCCCTATATC 61 TTTAGTTTTTAATCTCTAATAAAATACATGTCCCCTCCATATGGCTCCTAAATTTTTAGT 121 CAAGCTATCGTTATATGCAACACGATCTTTATGCATGTCTAGTCTGGGGAGGAAATAGAGAA 181 GATTCAAGGAGAAAACGCTATGATGTAAAAGTAAGAAAATAATTAAAAATGCAAACTAGG 241 AATTAGTAAACACAGGAAATCTGAACCAGAGATGATCATTAAAATGCAGGTAACAGAGCA 301 CAGAGGATTTTTAGGGCAGTGAAACAATTCTGTCTGATACTTTAACAGTGGACACATGTC 361 ATTATACGTTTGTTTAAGCCCATAGAATGCACACAACCAGAGAAAACCCTAATGTTATC 421 TACAGACTTTGGGTGATAATGATGCGTCAATGTAGGTTCATCAATTGTAACAAATGTACC 481 ACTCTTGTGGAGAATTTTGATAATGGGGGAGGCTCTGCATGTTGAGGGCAGGGGATACG 541 GAAAATAGTTTTACCTTCTGCTCAATTTTGCTGTGAACCTAAAATTGTTCTAAATAAAAT 601 GTATTAAAAAAAGAAAGCAAAAGATCAGCTATTATGATCCTGAATGTATATAAAATATGAAT 661 TTTAGTATAAAAAAAAAGTAAGTTCNCCTGAAAATGCACACAAATGTATTGAGAAGAGTTTTC 721 AACAATAGTATTTCAAATAAATCTCTATGATTTCAAAAAAAAAAAAAAAAAAAA 1 AAAACGCTATGATGTAAAAGTAAGAAAATAATTAAAAATGCAAACTAGGAATTAGTAAAC 61 ACAGGAAATCTGAACCAGAGATGATCATTAAAATGCAGGTAACAGAGCACACAGAGGATTTT 121 TAGGGCAGTGAAACAATTCTGTCTGATACTTTAACAGTGGACACATGTCATTATACGTTT 181 GTTTAAGCCCATAGAATGCACACACCAAGAGAAAACCCTAATGTTATCTACAGACTTTG 241 GGTGATAATGATGCGTCAATGTAGGTTCATCAATTGTAACAAATGTACCACTCTTGTGGA 301 GAATTTTGATAATGGGGGAGGCTCTGCATGTTGAGGGCAGGGGATACGGAAAATAGTTT 361 TACCTTCTGCTCAATTTTGCTGTGAACCTAAAATTGTTCTAAATAAAATGTATTATAAAAA 421 AGAAAGCAAAAGATCACCTATTATGATCCTGAATGTATATAAAATATGAATTTTAGTATAAA 481 AAAAAGTAAGTCACCTGAAAATGCACAAATGTATTGAGAAGAGTTTTCAACAATAGTATT 541 TCAAATAAATCTCTATGATTTCAAAAAAAAAAAAAAAAAAAAA	SEQ ID NO:242 SEQ ID NO:243
BM781012	Equus caballus immunogobulin gamma 1 heavy chain constant region (IGHC1 gene)	1 GCCTCCACCACCGCCCCGAAGGTCTTCGCGCTGGCCCCCGGCTGTGGGACCACATCTGAC 61 TCCACGGTGGCCCTGGGCTGCCTTCTCTCCGGATACTTCCCCGAGCCAGTGAAGGTGTCC 121 TGGAACTCGGGCTCCCTGACCAGTGGCGTGCACACCTTCCCTCCGTCCTGCAGTCCTCA 181 GGGTTCTACTCCCTCAGCAGCATGGTGACCGTGCCTGCCAGCACCTGGACCAGCGAGACC 241 TACATCTGCAACGTAGTCCCACGCGCCAGCAACTTCAAGGTGGACAAGAGAATCGAGCCC 301 ATTCCCGACAACCACCAAAAAGTGTGCGACATGAGCAAGTGTCCCAAATGCCCAGCTCCT 361 GAGCTCCTGGGAGGGCCTTCGGTCTTCATCTTCCCCCCGAATCCCAAGGACACCCTCATG 421 ATCACCCGAACACCCGAGGTCACCTGCGTGGTGGTGGACGTGAGCCAGGAGGACCCTGAT 481 GTCAAGTTCAACTGGTACATGGACGGGGTGGAGGTGCGCACACCACGACGAGGCCGAAG 541 GAGGAGCAGTTCAACAGCACTTACCGCGTGGTCAGCGTCCTCCGCATCCAGCACCAGGAC 601 TGGCTGTCAGGAAAGGAGTTCAAGTGTAAGGTCAACAACCAAGCCCTCCCACAACCCATC 661 GAGAGGACCATCACCAAAGCCAAAGGGCGGTCCCAGGAGCCCGCAAGTGTACGTCCTGGCC 721 CCACACCCAGACGAGCTGTCCAAGAGCAAGGTCAGCGTGACCTGCCTGGTCAAGGACTTC 781 TACCCACCTGAAATCAACATCGAGTGGCAGAGTAATGGGCAGCCAGAGCTGGAGACCAAG	SEQ ID NO:244

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		841 TACAGCACCACCCAAGCCCAGCAGGACAGCGACGGGTCCTACTTCCTGTACAGCAAGCTC 901 TCCGTGGACAGGAACAGGTGGCAGCAGGGCACGACATTCACGTGTGGGGTGATGCACGAG 961 GCTCTCCACAATCACTACACACAGAAGAACGTCTCCAAGAACCCGGGTAAATGAGCCATG 1021 GGCCCGGCACCCAGCAAGCCATCCCTCCTTCCCCGTGGGCTCTCAGAGTCCAGCGAGGAC 1081 ACCTGAGCCCCCACCCCTGTGTACATACCTTCCCGGGCACCCAGCATGAAATAAAGCACC 1141 CAGCATGCTCGTGCC 1 A S T T A P K V F A L A P G C G T T S D 1 GCCTCCACCACCGCCCCGAAGGTCTTCGCGCTGGCCCCCGGCTGTGGGACCACATCTGAC 21 S T V A L G C L V S G Y F P E P V K V S 61 TCCACGGTGGCCCTGGGCTGCCTTGTCTCCGGATACTTCCCCGAGCCAGTGAAGGTGTCC 41 W N S G S L T S G V H T F P S V L Q S S 121 TGGAACTCGGGCTCCCTGACCAGTGGCGTGCACACCTTCCCTCCGTCCTGCAGTCCTCA 61 G F Y S L S S M V T V P A S T W T S E T 181 GGGTTCTACTCCCTCAGCAGCATGGTGACCGTGCCTGCCAGCACCTGGACCAGCGAGACC 81 Y I C N V V H A A S N F K V D K R I E P 241 TACATCTGCAACGTAGTCCACGCGGCCAGCAACTTCAAGGTGGACAAGAGAATCGAGCCC 101 I P D N H Q K V C D M S K C P K C P A P 301 ATTCCCGACAACCACCAAAAAGTGTGCGACATGAGCAAGTGTCCCAAATGCCCAGCTCCT 121 E L L G G P S V F I F P P N P K D T L M 361 GAGCTCCTGGGAGGGCCTTCGGTCTTCATCTTCCCCCCGAATCCCAAGGACACCCTCATG 141 I T R T P E V T C V V V D V S Q E N P D 421 ATCACCCGAACACCCGAGGTCACCTGCGTGGTGGTGGACGTGAGCCAGGAGAACCCTGAT 161 V K F N W Y M D G V E V R T A T T R P K 481 GTCAAGTTCAACTGGTACATGGACGGGTGGAGGTGCGCACAGCCACGACGAGGCCGAAG 181 E E Q F N S T Y R V V S V L R I Q H Q D 541 GAGGAGCAGTTCAACAGCACTTACCGCGTGGTCAGCGTCCTCCGCATCCAGCACCAGGAC 201 W L S G K E F K C K V N N Q A L P Q P I 601 TGGCTGTCAGGAAAGGAGTTCAAGTGTAAGGTCAACAACCAAGCCCTCCCACAACCCATC 221 E R T I T K T K G R S Q E P Q V Y V L A 661 GAGAGGACCATCACCAAGACCAAAGGGCGGTCCCAGGAGCCGCAAGTGTACGTCCTGGCC 241 P H P D E L S K S K V S V T C L V K D F 721 CCACACCCAGACGAGCTGTCCAAGAGCAAGGTCAGCGTGACCTGCCTGGTCAAGGACTTC 261 Y P P E I N I E W Q S N G Q P E L E T K	SEQ ID NO:245

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		781 TACCCACCTGAAATCAACATCGAGTGGCAGAGTAATGGGCAGCCAGAGCTGGAGACCAAG 281 Y S T T Q A Q Q D S D G S Y F L Y S K L 841 TACAGCACCACCCAAGCCCAGCAGGACAGCGACGGGTCCTACTTCCTGTACAGCAAGCTC 301 S V D R N R W Q Q G T T F T C G V M H E 901 TCCGTGGACAGGAACAGGTGGCAGCAGGGCACGACATTCACGTGTGGGGTGATGCACGAG 321 A L H N H Y T Q K N V S K N P G K - 961 GCTCTCCACAATCACTACACACAGAAGAACGTCTCCAAGAACCCGGGTAAATGA	
WBC005B09	CDC-like kinase 1	1 gacgcagtca gctgcgtgat tcccgtgatt gcgttacaag ctttgtctcc ttcgacttgg 61 agtctttgtc caggacgatg agacactcaa agagaactta ctgtcctgat tgggatgaca 121 aggattggga ttatggaaaa tggaggagca gcagcagtca taaaagaagg aagagatcac 181 atagcagtgc ccaggagaac aagcgctgca aatacaatca ctctaaaatg tgtgatagcc 241 attatttgga aagcaggtct ataaatgaga aagattatca tagtcgacgc tacattgatg 301 agtacagaaa tgactacact caaggatgtg aacctggaca tcgccaaaga gaccatgaaa 361 gccggtatca gaaccatagt agcaagtctt ctggtagaag tggaagaagt agttataaaa 421 gcaaacacag gattcaccac agtacttcac atcgtcgttc acatgggaag agtcaccgaa 481 ggaaaagaac caggagtgta gaggatgatg aggagggtca cctgatctgt cagagtggag 541 acgtactaag tgcaagatat gaaattgttg atactttagg tgaaggagct tttggaaaag 601 ttgtggagtg catcgatcat aaagcgggag gtagacatgt agcagtaaaa atagttaaaa 661 atgtggatag atactgtgaa gctgctcgct cagaaataca agttctggaa catctgaata 721 caacagaccc caacagtact ttccgctgtg tccagatgtt ggaatggttt gagcatcatg 781 gtcacatttg cattgttttt gaactattgg gacttagtac ttacgacttc attaaagaaa 841 atggttttct accatttcga ctggatcata tcagaaagat ggcatatcag atatgcaagt 901 ctgtgaattt tttgcacagt aataagttga ctcacacaga cttaaagcct gaaaacatct 961 tatttgtgca gtctgactac acagaggcgt ataatcccaa aataaaacgt gatgaacgca 1021 ccttaataaa tccagatatt aaagttgtag actttggtag tgcaacatat gatgacgaac 1081 atcacagtac attggtatct acaagacatt atagagcacc tgaagttatt ttagccctag 1141 ggtggtccca accatgtgat gtctggagca taggatgcat tcttattgaa tactatcttg 1201 ggtttaccgt atttccaaca cacgatagta aggagcattt agcaatgatg gaaaggattc 1261 ttggacctct accaaaacat atgatacaga aaaccaggaa acgtaaatat tttcaccacg 1321 atcgattaga ctgggatgaa cacagttctg ccggcagata tgtttcaaga cgctgtaaac 1381 ctctgaagga atttatgctt tctcaagatg ttgaacatga gcgtctcttt gacctcattc 1441 agaaaatgtt ggagtatgat ccagccaaaa gaattactct cagagaagcc ttaaagcatc 1501 ctttctttga ccttctgaag aaaagtatat agatctgtaa ttggacagct ctctcgaaga 1561 gatcttacag actgtatcag tctaattttt aaattttaag ttattttgta cagctttgta 1621 aattcttaac atttttatat tgccatgttt attttgtttg ggtaatttgg ttctttaagt 1681 acatagctaa ggtaatgaac atctttttca gtaattgtaa agtgatttat tcagaataaa 1741 ttttttgtgc ttatgaaaaa aaaaaaaaaa aaa	SEQ ID NO:246
		1 M R H S K R T Y C P D W D D K D W D Y G 1 ATGAGACACTCAAAGAGAACTTACTGTCCTGATTGGGATGACAAGGATTGGGATTATGGA 21 K W R S S S S H K R R K R S H S S A Q E	SEQ ID NO:247

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		61 AAATGGAGGAGCAGCAGCAGTCATAAAAGAAGGAAGAGATCACATAGCAGTGCCCAGGAG	
		41 N K R C K Y N H S K M C D S H Y L E S R	
		121 AACAAGCGCTGCAAATACAATCACTCTAAAATGTGTGATAGCCATTATTTGGAAAGCAGG	
		61 S I N E K D Y H S R R Y I D E Y R N D Y	
		181 TCTATAAATGAGAAAGATTATCATAGTCGACGCTACATTGATGAGTACAGAAATGACTAC	
		81 T Q G C E P G H R Q R D H E S R Y Q N H	
		241 ACTCAAGGATGTGAACCTGGACATCGCCAAAGAGACCATGAAAGCCGGTATCAGAACCAT	
		101 S S K S S G R S G R S S Y K S K H R I H	
		301 AGTAGCAAGTCTTCTGGTAGAAGTGGAAGAAGTAGTTATAAAAGCAAACACAGGATTCAC	
		121 H S T S H R R S H G G K S H R R K R T R S	
		361 CACAGTACTTCACATCGTCGTTCACATGGGAAGAGTCACCGAAGGAAAAGAACCAGGAGT	
		141 V E D D E E G H L I C Q S G D V L S A R	
		421 GTAGAGGATGATGAGGAGGGTCACCTGATCTGTCAGAGTGGAGACGTACTAAGTGCAAGA	
		161 Y E I V D T L G E G A F G K V V E C I D	
		481 TATGAAATTGTTGATACTTTAGGTGAAGGAGCTTTTGGAAAAGTTGTGGAGTGCATCGAT	
		181 H K A G G R H V A V K I V K N V D R Y C	
		541 CATAAAGCGGGAGGTAGACATGTAGCAGTAAAAATAGTTAAAAATGTGGATAGATACTGT	
		201 E A A R S E I Q V L E H L N T T D P N S	
		601 GAAGCTGCTCGCTCAGAAATACAAGTTCTGGAACATCTGAATACAACAGACCCCAACAGT	
		221 T F R C V Q M L E W F E H H G H I C I V	
		661 ACTTTCCGCTGTGTCCAGATGTTGGAATGGTTTGAGCATCATGGTCACATTTGCATTGTT	
		241 F E L L G L S T Y D F I K E N G F L P F	
		721 TTTGAACTATTGGGACTTAGTACTTACGACTTCATTAAAGAAAATGGTTTCTACCATTT	
		261 R L D H I R K M A Y Q I C K S V N F L H	
		781 CGACTGGATCATATATCAGAAAGATGGCATATCAGATATGCAAGTCTGTGAATTTTTTGCAC	
		281 S N K L T H T D L K P E N I L F V Q S D	
		841 AGTAATAAGTTGACTCACACAGACTTAAAGCCTGAAAACATCTTATTTGTGCAGTCTGAC	
		301 Y T E A Y N P K I K R D E R T L I N P D	
		901 TACACAGAGGCGTATAATCCCAAAATAAAACGTGATGAACGCACCTTATAAATCCAGAT	
		321 I K V V D F G S A T Y D D E H H S T L V	
		961 ATTAAAGTTGTAGACTTTGGTAGTGCAACATATGATGACGAACATCACAGTACATTGGTA	
		341 S T R H Y R A P E V I L A L G W S Q P C	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1021 TCTACAAGACATTATAGAGCACCTGAAGTTATTTTAGCCCTAGGGTGGTCCCAACCATGT 361 D V W S I G C I L I E Y Y L G F T V F P 1081 GATGTCTGGAGCATAGGATGCATTCTTATTGAATACTATCTTGGGTTTACCGTATTTCCA 381 T H D S K E H L A M M E R I L G P L P K 1141 ACACACGATAGTAAGGAGCATTTAGCAATGATGGAAAGGATTCTTGGACCTCTACCAAAA 401 H M I Q K T R K R K Y F H H D R L D W D 1201 CATATGATACAGAAAACCAGGAAACGTAAATATTTTCACCACGATCGATTAGACTGGGAT 421 E H S S A G R Y V S R R C K P L K E F M 1261 GAACACAGTTCTGCCGGCAGATATGTTTCAAGACGCTGTAAACCTCTGAAGGAATTTATG 441 L S Q D V E H E R L F D L I Q K M L E Y 1321 CTTTCTCAAGATGTTGAACATGAGCGTCTCTTTGACCTCATTCAGAAAATGTTGGAGTAT 461 D P A K R I T L R E A L K H P F F D L L 1381 GATCCAGCCAAAAGAATTACTCTCAGAGAAGCCTTAAAGCATCCTTTCTTTGACCTTCTG 481 K K S I - 1441 AAGAAAAGTATATAG	
WBC040E12	Arachidonate 5-lipoxygenase-activating protein (ALOX5AP).	1 ACTTCCCCTTCCTGTACAGGGCAGGTTGTGCAGCTGGAGGCAGAGCAGTCCTCACTGCGG 61 GGAGCCTGGAGCGAACATGGATCAAGAAACCGTGGGCAATGTTGTCCTGCTGGCCATCGT 121 CACCCTCATTAGCGTGATCCAGAATGGGTTCTTCGCCCACAAGGTGGAACACGAAAGCAA 181 GACTCAGAATGGGCGGAGCTTCCAGAGGACGGGAACACTTGCCTTTGAGCGGGTCTACAC 241 TGCCAACCAAAACTGTGTAGACGCGTACCCCACTTTCCTTGTCATGCTCTGGAGCGCCGG 301 GCTACTCTGCAGCCAAGTTCCTGCCGCCTTTGCTGGGCTGATGTACCTGTTCGTGAGGCA 361 GAAGTACTTCGTGGGCTATCTGGGAGAGAGAAGGCAGAGCACACCCGGCTACATATTTGG 421 GAAACGCATCATACTGTTCCTGTTCCTCATGTCCCTTGCTGGAATATTCAACTATTATCT 481 CATCCTCTTTTTCGGAAGTGACTTTGAAAACTACATAAAGACGATAACCACCACCATCTC 541 CCCTCTACTTCTCATTCCCTAACTCTCTGCTGAATACAGGGTTGGTGCTCTCATCTAATC 601 AATACCTACAAGTCATCATAATTCAGCTCTTGAGAGCATTCTGCTCTTCTTTAGATTGCT 661 GTAAATCTAATGACCATCTGGGCTTCGCGTCTTGAGTTAACCTTGCTTTTCCTGGAACAA 721 AATGATGTCATGTCAGCTCCGCCCCTTGAACATGACCGTGGCCTCAGATTTGTTATTCAG 781 ATCCATTCTGTGTGTTTCTTGACTTACCCTGCTTTCTGAAGATATTTTGTGACCCAGATT 841 TATGTTTTCCTAAAATAAAATGCAGAGACATGTTTT 1 M D Q E T V G N V V L L A I V T L I S V 1 ATGGATCAAGAAACCGTGGGCAATGTTGTCCTGCTGGCCATCGTCACCCTCATTAGCGTG 21 I Q N G F F A H K V E H E S K T Q N G R 61 ATCCAGAATGGGTTCTTCGCCCACAAGGTGGAACACGAAAGCAAGACTCAGAATGGGCGG 41 S F Q R T G T L A F E R V Y T A N Q N C	SEQ ID NO:248 SEQ ID NO:249

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		121 AGCTTCCAGAGGACGGGAACACTTGCCTTTGAGCGGGTCTACACTGCCAACCAAAACTGT	
		61 V D A Y Y P T F L V M L W S A G L L C S Q	
		181 GTAGACGCGTACCCCACTTTCCTTGTCATGCTCTGGAGCGCCGGGCTACTCTGCAGCCAA	
		81 V P A A F A G L M Y L F V R Q K Y F V G	
		241 GTTCCTGCCGCCTTTGCTGGGCTGATGTACCTGTTCGTGAGGCAGAAGTACTTCGTGGGC	
		101 Y L G E R R Q S T P G Y I F G K R I I L	
		301 TATCTGGGAGAGAAGGCAGAGCACACCCGGCTACATATTTGGGAAACGCATCATACTG	
		121 F L F L M S L L A G I F N Y Y L I L F F G	
		361 TTCCTGTTCCTCATGTCCCTTGCTGGAATATTCAACTATTATCTCATCCTCTTTTTCGGA	
		141 S D F E N Y L K T I T T T I S P L L L I	
		421 AGTGACTTTGAAAACTACATAAAGACGATAACCACCACCATCTCCCCTCTACTTCTCATT	
		161 P -	
		481 CCCTAA	

TABLE 2

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
Pleckstrin		
B1960933.V1.3_at	ACTTGAGAGGCTGCGTGGTGACTTC	SEQ ID NO:250
B1960933.V1.3_at	GCCCCTGGGAGCGATTCACTTGAGA	SEQ ID NO:251
B1960933.V1.3_at	GAATTTTCATCTGGCAGGGTTCCGA	SEQ ID NO:252
B1960933.V1.3_at	GAACCTCTTTGAGATCATCACGGCG	SEQ ID NO:253
B1960933.V1.3_at	GAATTCCAGCGATGATGACGTGATT	SEQ ID NO:254
B1960933.V1.3_at	GAAGACCCTGCATATGTGCACTACA	SEQ ID NO:255
B1960933.V1.3_at	GTTCATTATTTCTTGCAAGCGGCCA	SEQ ID NO:256
B1960933.V1.3_at	GGATAAACTCGGTCCAGGGCCTGTC	SEQ ID NO:257
B1960933.V1.3_at	GTGACTTCAGTGGAGGGCAACCCAG	SEQ ID NO:258
B1960933.V1.3_at	GGGCCTGTCCACTTCTGGTGACAAG	SEQ ID NO:259
B1960933.V1.3_at	GGAAGTGAGGGCACACCTGCAGCTC	SEQ ID NO:260
G protein-coupled receptor HM74a		
B1961009.V1.3_at	AGACAGGTATTTCCGGGTGGTCCAT	SEQ ID NO:261
B1961009.V1.3_at	AGCATCATCTTCCTCACGGTGGTGG	SEQ ID NO:262
B1961009.V1.3_at	AATCCAGCCGGATTTTCCTGTTCAA	SEQ ID NO:263
B1961009.V1.3_at	AATGGCCTTGCCCTTTGGATTTTCT	SEQ ID NO:264
B1961009.V1.3_at	GAAAAACTGCTGTGTGTTCCGGGAT	SEQ ID NO:265
B1961009.V1.3_at	GTTCCGGGATGACTTCATTGCCAAT	SEQ ID NO:266
B1961009.V1.3_at	GGATCATGCTCTTCATGCTGGCCAT	SEQ ID NO:267
B1961009.V1.3_at	TGGATTTTCTGTTTCCACCTCAAAT	SEQ ID NO:268
B1961009.V1.3_at	TGACTTTCTCTTGATCATCTGCCTA	SEQ ID NO:269
B1961009.V1.3_at	TCCTGTTCAACTTAGCCGTGGCTGA	SEQ ID NO:270
B1961009.V1.3_at	TAGGTGAGGAGCTCCCTAGGACCAG	SEQ ID NO:271
B1961185.V1.3_at	ATCTCCATCTGCTACTTCGAGCAGG	SEQ ID NO:272
B1961185.V1.3_at	AGTGGGTCAAGGTGCACGAGCTCAA	SEQ ID NO:273
B1961185.V1.3_at	CGAGAGTAACCGCATTGTGACCTGC	SEQ ID NO:274
B1961185.V1.3_at	ACAGCTTCCTGGTGGAGCCCATCAG	SEQ ID NO:275
B1961185.V1.3_at	ACAAGTTCGCTGTGGGCAGCGGCTC	SEQ ID NO:276
B1961185.V1.3_at	AACCACGAGGTGCACATCTATGAGA	SEQ ID NO:277
B1961185.V1.3_at	AACGGGCAGGTGACAGGCATCGACT	SEQ ID NO:278
B1961185.V1.3_at	AAGGACCGCACACAGATTGCCATCT	SEQ ID NO:279
B1961185.V1.3_at	GCAACGCCTACGTGTGGACGCTGAA	SEQ ID NO:280
B1961185.V1.3_at	GTGCAAACACATCAAGAAGCCCATT	SEQ ID NO:281
B1961185.V1.3_at	GGACGCTGAAGGGTCACACATGGAA	SEQ ID NO:282
PREDICTED: Homo sapiens steroid receptor RNA activator 1 (SRA1)		
B1961443.V1.3_at	TGGGAGGCCTTCTCTAATTTGGCTC	SEQ ID NO:283
B1961443.V1.3_at	AGGCTCCATAATCCTGTGGGTTCCC	SEQ ID NO:284
B1961443.V1.3_at	ATGTGATGACATCAGCCGACGCCTG	SEQ ID NO:285
B1961443.V1.3_at	ATGGCTCTGCTGGTGCAAGAGCTTT	SEQ ID NO:286
B1961443.V1.3_at	AGGAGCACCAGACCGTACCAGGCAT	SEQ ID NO:287

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
B1961443.V1.3_at	AAGAGCTTTCAAGCCACCGTTGGGA	SEQ ID NO:288
B1961443.V1.3_at	AAGAGGAGCCTGTCTTCAGAGGAGA	SEQ ID NO:289
B1961443.V1.3_at	GCATTGGACGATTGCCGTGGCCACA	SEQ ID NO:290
B1961443.V1.3_at	GAAGAGAAATCTACAGCCACAGCTG	SEQ ID NO:291
B1961443.V1.3_at	GGGAAGCTGTCAACGCCTGTAAAGA	SEQ ID NO:292
B1961443.V1.3_at	TTACCACTTTGGAGACTGTCTGCCC	SEQ ID NO:293
HREV107-3		
B1961494.V1.3_at	AGTGCCCCGCAGCGACCAGGTCAGA	SEQ ID NO:294
B1961494.V1.3_at	CAGCGACCAGGTCAGAGACGCCATC	SEQ ID NO:295
B1961494.V1.3_at	GCCCCGCAGCGACCAGGTCAGAGAC	SEQ ID NO:296
B1961494.V1.3_at	GCAGCGACCAGGTCAGAGACGCCAT	SEQ ID NO:297
B1961494.V1.3_at	GAGTGCCCCGCAGCGACCAGGTCAG	SEQ ID NO:298
B1961494.V1.3_at	GTGCCCCGCAGCGACCAGGTCAGAG	SEQ ID NO:299
B1961494.V1.3_at	TGCCCCGCAGCGACCAGGTCAGAGA	SEQ ID NO:300
B1961512.V1.3_at	AACTCAGAAGACAGAAGTACAGGAA	SEQ ID NO:301
B1961512.V1.3_at	GCGCAGGAAAGGTGATTTGAAGCCT	SEQ ID NO:302
B1961512.V1.3_at	ATAGTAATTGGGAGTGGCAGGATAA	SEQ ID NO:303
B1961512.V1.3_at	ACCTTCATGTTCGTGGCGCAGGAAA	SEQ ID NO:304
B1961512.V1.3_at	AAGATAAGACGCCTCTAGAAGACAG	SEQ ID NO:305
B1961512.V1.3_at	CCTAGTTGGTCTTATGGCATTATTT	SEQ ID NO:306
B1961512.V1.3_at	GACGCCTCTAGAAGACAGAAACTAA	SEQ ID NO:307
B1961512.V1.3_at	GAGACCTTCATGTTCGTGGCGCAGG	SEQ ID NO:308
B1961512.V1.3_at	GTGATTTGAAGCCTAGTTGGTCTTA	SEQ ID NO:309
B1961512.V1.3_at	GGTCTTATGGCATTATTTGCTAAAA	SEQ ID NO:310
B1961512.V1.3_at	TTCAAACCCAAAAGGTAGGAAGCAG	SEQ ID NO:311
B1961539.V1.3_at	ATATCATGGAGGACCTGGATACCAA	SEQ ID NO:312
B1961539.V1.3_at	ATCATCAATGTCTTCCACCAGTACT	SEQ ID NO:313
B1961539.V1.3_at	ACGGCCACAGCCACTAATCTGGAGG	SEQ ID NO:314
B1961539.V1.3_at	CAAGCAGCTGAGTTTCGAGGAGTTC	SEQ ID NO:315
B1961539.V1.3_at	GAGCTGGCGAACTTCCTCAAGAGTA	SEQ ID NO:316
B1961539.V1.3_at	GATGCACGAGCATGACCAAGGCCAC	SEQ ID NO:317
B1961539.V1.3_at	GAGGAGTTCATCATCCTGGTGGCCA	SEQ ID NO:318
B1961539.V1.3_at	GGAACTGTCCCAGATGGAGCGCGAC	SEQ ID NO:319
B1961539.V1.3_at	GGAGAGTGGCCATGGTCACAGCCAT	SEQ ID NO:320
B1961539.V1.3_at	GGAGCGCGACATAGAGACCATCATC	SEQ ID NO:321
B1961539.V1.3_at	TGACGCATGCCTCCCATGAGAAGAT	SEQ ID NO:322
ILT11A mRNA for immunoglobulin-like transcript 11 protein		
B1961620.V1.3_at	AGGACGTGACCTACGCCCAGGTGAA	SEQ ID NO:323
B1961620.V1.3_at	AGGGACCCCAGAAGACATAGGAGCT	SEQ ID NO:324
B1961620.V1.3_at	AGGTGAACCACTTGACCCTCAGAGG	SEQ ID NO:325
B1961620.V1.3_at	AGTGGTACGCTGCTATGGCCATCCA	SEQ ID NO:326
B1961620.V1.3_at	AGCAGAGCCCAGTGGTACGCTGCTA	SEQ ID NO:327
B1961620.V1.3_at	CATAGGAGCTGCCTCCAGAGGACAC	SEQ ID NO:328
B1961620.V1.3_at	GAGACTGCAGGGACCCCAGAAGACA	SEQ ID NO:329

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
B1961620.V1.3_at	GATGCCACCCTCCATGGAGGGAGAC	SEQ ID NO:330
B1961620.V1.3_at	GTATGCACAGGCTGCTATATCTGAA	SEQ ID NO:331
B1961620.V1.3_at	TGGCCATCCACTAGCCCAGGAAGGA	SEQ ID NO:332
B1961620.V1.3_at	TAGCCCAGGAAGGACCCGGATGCCA	SEQ ID NO:333
Mn-SOD mRNA for manganese superoxide dismutase		
B1961637.V1.3_at	AGATTGTTGCCTGTCCTAACCAGGA	SEQ ID NO:334
B1961637.V1.3_at	GCATTATCGTTACACCGAGTGCATT	SEQ ID NO:335
B1961637.V1.3_at	CGTGACTTTGGTTCCTTCGACAAAT	SEQ ID NO:336
B1961637.V1.3_at	GCAGCCTGCACTCAAGTTCAATGGT	SEQ ID NO:337
B1961637.V1.3_at	GAAGTTGACTGCTGTATCGGCTGGT	SEQ ID NO:338
B1961637.V1.3_at	TAAGGACCAGGGACGCCTCCAGATT	SEQ ID NO:339
B1961637.V1.3_at	GGAGGCCATATCAATCATACCATTT	SEQ ID NO:340
B1961637.V1.3_at	GGAACAACAGGTCTTATTCCCCTGC	SEQ ID NO:341
B1961637.V1.3_at	GGAGCACGCTTATTACCTTCAGTAT	SEQ ID NO:342
B1961637.V1.3_at	TTGCTGGACGCCATCAAACGTGACT	SEQ ID NO:343
B1961637.V1.3_at	TTTTCTGGACAAACCTGAGCCCCAA	SEQ ID NO:344
B1961648.V1.3_at	ATATGAGGAGCTGAACCTGCCGGCT	SEQ ID NO:345
B1961648.V1.3_at	GGGCTCATCGAGCAGTACGCTACGC	SEQ ID NO:346
B1961648.V1.3_at	AGGAAGACAGTTACAGCCGCCTTAT	SEQ ID NO:347
B1961648.V1.3_at	AACAGCGCCAGATCCTGCAGGAGAA	SEQ ID NO:348
B1961648.V1.3_at	CAAGACAGCTTTCTATTCCTTCTAC	SEQ ID NO:349
B1961648.V1.3_at	CTGGCTGGTGGTTCAGTGTCTGCAA	SEQ ID NO:350
B1961648.V1.3_at	GACGGGCAAGATTGGCACTGACATC	SEQ ID NO:351
B1961648.V1.3_at	GGGCGAGTTCTTTCAGATTCAGGAC	SEQ ID NO:352
B1961648.V1.3_at	GGACGATTACCTTGATCTCTTTGGG	SEQ ID NO:353
B1961648.V1.3_at	TGCCGGCTGTGTTCCTGCAGTATGA	SEQ ID NO:354
B1961648.V1.3_at	TTCCTGTAGCTGCTGCCATGTACAT	SEQ ID NO:355
NAD synthetase 1		
B1961671.V1.3_at	AGAGCTGGAGCCCTTGACCAACGGA	SEQ ID NO:356
B1961671.V1.3_at	AGAAAACCAGGTTCTCCAGCTCGAG	SEQ ID NO:357
B1961671.V1.3_at	ACGGCGTGGTCAGCAAGTCTTGTTT	SEQ ID NO:358
B1961671.V1.3_at	AAGACCGGGCCCTATAGCATGTTCT	SEQ ID NO:359
B1961671.V1.3_at	GAAGTACTCCGCGAACAGACACAAG	SEQ ID NO:360
B1961671.V1.3_at	GACAACAGGTTCGATCTGCGGCCAT	SEQ ID NO:361
B1961671.V1.3_at	GACCAACGGACAGGTGTCGCAGACT	SEQ ID NO:362
B1961671.V1.3_at	TGAAGCGGTTTTTCTCGAAGTACTC	SEQ ID NO:363
B1961671.V1.3_at	GTGGCAGTTCCGGTGCATAGAAAAC	SEQ ID NO:364
B1961671.V1.3_at	GGATGACGTACGCAGAGCTCTCCGT	SEQ ID NO:365
B1961671.V1.3_at	TATAGCATGTTCTGCAGACTCCTCA	SEQ ID NO:366
Formin homology 2 domain containing 1		
B1961682.V1.3_at	ATATGGGCCCCGGTATGCAGTGCAA	SEQ ID NO:367
B1961682.V1.3_at	CGTGGCAACCGCAAGTCTTTGAGGC	SEQ ID NO:368
B1961682.V1.3_at	AGAGGCATGGTCCAGAACAGCTCCC	SEQ ID NO:369

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
B1961682.V1.3_at	AGAAGAATCCCCAGGCTCCAGTTTA	SEQ ID NO:370
B1961682.V1.3_at	AAGCCTGAGGACACCACACATGGTC	SEQ ID NO:371
B1961682.V1.3_at	TCCAGTTTACCCAGTGACACTTCAG	SEQ ID NO:372
B1961682.V1.3_at	GCTGCCTCCAGGACATCTATATGGG	SEQ ID NO:373
B1961682.V1.3_at	GCATGAAGATTCTGCTCACCAGCAA	SEQ ID NO:374
B1961682.V1.3_at	GACTGAGCAAGGGTTCTGACCTGGA	SEQ ID NO:375
B1961682.V1.3_at	GAGATCATGGACCTGCTAGTGCAGT	SEQ ID NO:376
B1961682.V1.3_at	TTAGCTGCTCGAGAACGCAAGCGTT	SEQ ID NO:377
No Homology		
B1961711.V1.3_at	CCGTTCGCGTGCACCCAGGGAGGAC	SEQ ID NO:378
B1961711.V1.3_at	GTCGCCGTGGTCACCCACAGGAAGG	SEQ ID NO:379
B1961711.V1.3_at	CAGCCTGGGTTTTCTCGGGCGGCTC	SEQ ID NO:380
B1961711.V1.3_at	CATTTTCTTCTGGTCGCCGTGGTCA	SEQ ID NO:381
B1961711.V1.3_at	CAGGTCTCAGCCTGTGAGGACTGCG	SEQ ID NO:382
B1961711.V1.3_at	GACTGCGGCGAGTCTGGAGACCCCA	SEQ ID NO:383
B1961711.V1.3_at	GAGGGCCATCTGCTGACAGAGCAAC	SEQ ID NO:384
B1961711.V1.3_at	GTGTGGACCCACGAGGGCCATCTGC	SEQ ID NO:385
B1961711.V1.3_at	GTGGGCTCTGTCTGGTTCACAGAGC	SEQ ID NO:386
B1961711.V1.3_at	TGCACCCAGGGAGGACTCGGAGTCC	SEQ ID NO:387
B1961711.V1.3_at	TCTTCGGGACTGTGTGGACCCACGA	SEQ ID NO:388
Tumor necrosis factor-inducible (TSG-6) mRNA fragment, adhesion receptor CD44 putative CDS		
B1961885.V1.3_at	AGGTTGCTTGGCTGACTATGTTGAA	SEQ ID NO:389
B1961885.V1.3_at	ACTCAAGTATGGTCAGCGTATTCAC	SEQ ID NO:390
B1961885.V1.3_at	AATGCGGTGGCATCTTTACAGATAC	SEQ ID NO:391
B1961885.V1.3_at	CTAAGCGATGCTTCGGTGACCGCAG	SEQ ID NO:392
B1961885.V1.3_at	GCGTATTCACCTGAGTTTTCTGGAC	SEQ ID NO:393
B1961885.V1.3_at	GAACCCCTTTGATCTCAGTTTTGTA	SEQ ID NO:394
B1961885.V1.3_at	GTGACCGCAGGAGGTTTCCAAATCA	SEQ ID NO:395
B1961885.V1.3_at	TTTTAAATCTCCAGGCTTCCCAAAT	SEQ ID NO:396
B1961885.V1.3_at	TAACCAAGTCTGCTACTGGCACATC	SEQ ID NO:397
B1961885.V1.3_at	TACAAGCACTACTTCTACGGGAAAT	SEQ ID NO:398
B1961885.V1.3_at	TATGGTTGTCTCTTTTGGAACCCCT	SEQ ID NO:399
Fibroblast mRNA for aldolase A		
B1961941.V1.3_at	AGGGCTTTAGGCTGTTCTTTCCCAT	SEQ ID NO:400
B1961941.V1.3_at	AGGAGGAGGCATCCATCAACCTCAA	SEQ ID NO:401
B1961941.V1.3_at	AGTGGAGGTATTCTAAGGCTGCCCC	SEQ ID NO:402
B1961941.V1.3_at	AAATACACCCCAAGTGGTCACGCTG	SEQ ID NO:403
B1961941.V1.3_at	TGAAGCCCAATATGGTAACCCCAGG	SEQ ID NO:404
B1961941.V1.3_at	GATTGCCATGGCAACTGTCACGGCA	SEQ ID NO:405
B1961941.V1.3_at	GTCTGTGGTATTGTCTGTGTATGCT	SEQ ID NO:406
B1961941.V1.3_at	GGAATATGTCAAGCGAGCCCTGGCC	SEQ ID NO:407
B1961941.V1.3_at	TGGGATCACCTTCCTATCTGGAGGC	SEQ ID NO:408

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
B1961941.V1.3_at	TTGCCTCCCTGGTGACATTGGTCTG	SEQ ID NO:409
B1961941.V1.3_at	TTCATCTCTAACCATGCCTACTAAG	SEQ ID NO:410
High-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 beta mRNA		
BM734457.V1.3_at	ATGATGACTGCACCCCACGGAGGAG	SEQ ID NO:411
BM734457.V1.3_at	AGGCCCTACGGCTATGCCTGGCAGG	SEQ ID NO:412
BM734457.V1.3_at	AGGAGTTGCTCTGAAACCTACCGCA	SEQ ID NO:413
BM734457.V1.3_at	AGATCTGCAAGGTGGCAGTGGCCAC	SEQ ID NO:414
BM734457.V1.3_at	ACCCCACGGAGGAGTTGCTCTGAAA	SEQ ID NO:415
BM734457.V1.3_at	CACGGTGAAGGTGGTCATTATCCCC	SEQ ID NO:416
BM734457.V1.3_at	AACCTACCGCATGCCAGTGATGGAA	SEQ ID NO:417
BM734457.V1.3_at	CTGCTGAGAACATCCGTCACGGTGA	SEQ ID NO:418
BM734457.V1.3_at	GATTGATCTGCTGAGAACATCCGTC	SEQ ID NO:419
BM734457.V1.3_at	GGCAGTGGCCACTCTGAGCCATGAG	SEQ ID NO:420
BM734457.V1.3_at	TGAGCCATGAGCAGATGATTGATCT	SEQ ID NO:421
No homology		
BM734531.V1.3_at	ACCACTTCATGTTCTCTACAGAGCT	SEQ ID NO:422
BM734531.V1.3_at	ACAGAGCTGTCCAGAGCCGAGGCTG	SEQ ID NO:423
BM734531.V1.3_at	AAACGAGTCCGAGGGCACAGCCAGG	SEQ ID NO:424
BM734531.V1.3_at	CGTTGCCCGCTGTTGGTCATGACAA	SEQ ID NO:425
BM734531.V1.3_at	GAGTCTCTGTCAGGATCCTTTTGAA	SEQ ID NO:426
BM734531.V1.3_at	GAGTCACCCAAGGAACTTATGCAGA	SEQ ID NO:427
BM734531.V1.3_at	GTCCTGTGGCTTTTGTGTGTCTCTC	SEQ ID NO:428
BM734531.V1.3_at	GGCCTTGCTTGAGAGAGGTCCATCC	SEQ ID NO:429
BM734531.V1.3_at	GGTCACTTAGCAGCGACTTCTTGGA	SEQ ID NO:430
BM734531.V1.3_at	GGAGCCAGGTGTCTGCATTTGAACA	SEQ ID NO:431
BM734531.V1.3_at	TTATGCAGATGCCATGTCCTCACTC	SEQ ID NO:432
No homology		
BM734654.V1.3_at	ACCTAGACGACCTCTCGGGATTGAC	SEQ ID NO:433
BM734654.V1.3_at	CGATTCCGTTATGCGGTCCAAGCAA	SEQ ID NO:434
BM734654.V1.3_at	TGAACGGGACCAGCCAAACGACGGG	SEQ ID NO:435
BM734654.V1.3_at	AGAACTTCTCATGCTTCATCTACAT	SEQ ID NO:436
BM734654.V1.3_at	GACCGTGATGGTCAACACCAGCCAA	SEQ ID NO:437
BM734654.V1.3_at	GACGACGTCCAGTATTTCCTGTATA	SEQ ID NO:438
BM734654.V1.3_at	GGGATCCAGTTCTTCGATTCCGTTA	SEQ ID NO:439
BM734654.V1.3_at	GGAATGTCCCCGTTACATGAGCGAC	SEQ ID NO:440
BM734654.V1.3_at	TCTACATCGTGCACTTCATGATCTG	SEQ ID NO:441
BM734654.V1.3_at	TTTCGGAGAAGCTCGTCTACACCAA	SEQ ID NO:442
BM734654.V1.3_at	TTGACCTCTTACAATTACTTCGTGG	SEQ ID NO:443
No homology		
BM734719.V1.3_at	ACGCCAATGGGTCAAACTAACTCTG	SEQ ID NO:444
BM734719.V1.3_at	AGAAGTCCTCTCTGAGACTCAAGGG	SEQ ID NO:445
BM734719.V1.3_at	AAAGCCCATGAGCTGCTTCTTTGTT	SEQ ID NO:446
BM734719.V1.3_at	AAAAATCTCTCATCCTATTCTGCTT	SEQ ID NO:447

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
BM734719.V1.3_at	AAGCCTTCCTAAAAGCACACTTGCC	SEQ ID NO:448
BM734719.V1.3_at	AAGGGCTAAGGCAAGGTCTTCCAGA	SEQ ID NO:449
BM734719.V1.3_at	CAAGAAATGACAGCCTCCAAGCCTT	SEQ ID NO:450
BM734719.V1.3_at	GAAGCTTCTTCCCACCTAGAAAGAA	SEQ ID NO:451
BM734719.V1.3_at	GGTGACAACGCTGGCTGCTGAAAGC	SEQ ID NO:452
BM734719.V1.3_at	TTTCCACTGTCGTCAGAGCCAACAA	SEQ ID NO:453
BM734719.V1.3_at	TTCTTTGTTCTCTGTCACGGGACAA	SEQ ID NO:454
No homology		
BM734722.V1.3_at	CGGGCGACTCGCAGAATCAATACAT	SEQ ID NO:455
BM734722.V1.3_at	ACAGAGCCCCGGTCAGCGGGTGAAA	SEQ ID NO:456
BM734722.V1.3_at	AACTGAACGATAACCATCCGACCGA	SEQ ID NO:457
BM734722.V1.3_at	AATCAATACATTTTCCCGAGTCTGG	SEQ ID NO:458
BM734722.V1.3_at	TCGGCTGCCTGGTGAAGAGGTTCCT	SEQ ID NO:459
BM734722.V1.3_at	GCGTTTCTGCAGCTATTTTTCTACT	SEQ ID NO:460
BM734722.V1.3_at	GGTCCCGCGCATCAAAGACAAACTG	SEQ ID NO:461
BM734722.V1.3_at	GCGACTTCCAGTACGAGCTGGTCAT	SEQ ID NO:462
BM734722.V1.3_at	GAAGAGGTTCCTCCGGAGACACAGT	SEQ ID NO:463
BM734722.V1.3_at	GGAGACACAGTCTGTTCCAGCCGGT	SEQ ID NO:464
BM734722.V1.3_at	TGAAGTTTGGCCAAGAGGCTTCCCG	SEQ ID NO:465
Triggering receptor expressed on myeloid cells 1, transcript variant 2		
BM734862.V1.3_at	ATCTACATCCATCTGGCAGTTGTGC	SEQ ID NO:466
BM734862.V1.3_at	ATGAGGATGACCTCTGATCTCCATC	SEQ ID NO:467
BM734862.V1.3_at	AGCATTGTCATTCCTGTGGCGTGCG	SEQ ID NO:468
BM734862.V1.3_at	ACAAAGGTTATTTCTGAGGCTCAGG	SEQ ID NO:469
BM734862.V1.3_at	CTCGTGACTAAGAGCCTGGTCCTTA	SEQ ID NO:470
BM734862.V1.3_at	CCCTCATTTCACTGATGACCGTGGG	SEQ ID NO:471
BM734862.V1.3_at	GAAGTCATTTGGATCCTAGGCCCAT	SEQ ID NO:472
BM734862.V1.3_at	TGGCGTGCGCACTCGTGACTAAGAG	SEQ ID NO:473
BM734862.V1.3_at	GGCAGCGACATGAGTTGGATCCGTT	SEQ ID NO:474
BM734862.V1.3_at	TAAAAGAGCAGACACGGCCCCAAAC	SEQ ID NO:475
BM734862.V1.3_at	TTACTGTCCTGTTTGCTGTCACACA	SEQ ID NO:476
Nuclear receptor binding factor 1		
BM734865.V1.3_at	ACCACAGTCCAGAGCAGTTCCAGGG	SEQ ID NO:477
BM734865.V1.3_at	AGGACTACCAGCGTGCCTTGGAAAC	SEQ ID NO:478
BM734865.V1.3_at	AAGGCCAGAGGAGCCAGAGCCAAGT	SEQ ID NO:479
BM734865.V1.3_at	CAAGCAGATTCTCACCATGGGATAA	SEQ ID NO:480
BM734865.V1.3_at	GATCAGCAGGACTGGTTTCGGGCCC	SEQ ID NO:481
BM734865.V1.3_at	GAAACTGCGATGCAGCCCTTCGTGT	SEQ ID NO:482
BM734865.V1.3_at	GAAGCCAGCCAAGGCTTTTCCCAGG	SEQ ID NO:483
BM734865.V1.3_at	GGCTTTTGGTTGTCCCAGTGGAAGA	SEQ ID NO:484
BM734865.V1.3_at	TGATCCTCACGCTGTGCGATCTCAT	SEQ ID NO:485
BM734865.V1.3_at	TCACTGTCACTTCCAACCAGAAGAA	SEQ ID NO:486
BM734865.V1.3_at	TTCGTGTCTTCCAAGCAGATTCTCA	SEQ ID NO:487

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
Equus caballus lipopolysaccharide receptor (CD14) mRNA, member 6 variant		
BM734889.V1.3_at	AGGAATCCCTATCTGGACCCTGAAG	SEQ ID NO:488
BM734889.V1.3_at	AGCAAGACCAGAACTCCGGCGTGGT	SEQ ID NO:489
BM734889.V1.3_at	AGCGCACTGAGTTCTCTCAACTTGT	SEQ ID NO:490
BM734889.V1.3_at	AACAGGCTCAACAAGGCGCCGCGAG	SEQ ID NO:491
BM734889.V1.3_at	CAACTTGTCCTTCGCTGGGCTGGAG	SEQ ID NO:492
BM734889.V1.3_at	GCCTAAAGGACTACCGGGCAAGCTT	SEQ ID NO:493
BM734889.V1.3_at	GCCTCATTAGGACGTCTTAACCAAC	SEQ ID NO:494
BM734889.V1.3_at	GCTGCCCGTGGTGAGTAATCTGATA	SEQ ID NO:495
BM734889.V1.3_at	GAATTGACTCAGATTGCCCTGGCTC	SEQ ID NO:496
BM734889.V1.3_at	GACCCTGAAGCGTCCAAGCAGCAAG	SEQ ID NO:497
BM734889.V1.3_at	TTAGCGTGCTTGATCTCAGCTGCAA	SEQ ID NO:498
COP9 constitutive photomorphogenic homolog subunit 7A		
BM735102.V1.3_at	AGGAACAGGTGAGCCGTGCCAACCA	SEQ ID NO:499
BM735102.V1.3_at	AACTGAAGGGACTGTCGTCTCTTTC	SEQ ID NO:500
BM735102.V1.3_at	AATCAGCGGCTGGAGGTTGACTACA	SEQ ID NO:501
BM735102.V1.3_at	GCATAGATCACACCTTCTCTAGGGA	SEQ ID NO:502
BM735102.V1.3_at	GACTACAGCATTGGGCGGGACATCC	SEQ ID NO:503
BM735102.V1.3_at	GTTACAACAGCAGCAGCAGCCGCAG	SEQ ID NO:504
BM735102.V1.3_at	GGACCCTGAGCAACACCTGACTGAG	SEQ ID NO:505
BM735102.V1.3_at	TAATCCTAGGTTCATGACCCTTCAC	SEQ ID NO:506
BM735102.V1.3_at	TGAGGGAACCAGCTCCTGGCACTAA	SEQ ID NO:507
BM735102.V1.3_at	TGCCCGAACCCTGCAAGAGTGGTGT	SEQ ID NO:508
BM735102.V1.3_at	TTTAGGAGTCCTCAGAGAGCCTTCC	SEQ ID NO:509
No homology		
BM735166.V1.3_at	ATGGTCGCCAACTGGAACGTCTGGT	SEQ ID NO:510
BM735166.V1.3_at	AGGCAGGATGCCCAGTGGCCAATAC	SEQ ID NO:511
BM735166.V1.3_at	AGGGCACCCAGCATGGTTGAGTCTG	SEQ ID NO:512
BM735166.V1.3_at	AGTGCAGGTTGCCTGTGGCATCCAT	SEQ ID NO:513
BM735166.V1.3_at	AGCTCAGGGCCTTGTAGTGCAGGTT	SEQ ID NO:514
BM735166.V1.3_at	CATGTTTATTATTACCCCGTGGCGG	SEQ ID NO:515
BM735166.V1.3_at	CTGTGGGTTCAGGTTCATGTTTATT	SEQ ID NO:516
BM735166.V1.3_at	GAAGGCCTTCCTTGAAGGAGCCCAT	SEQ ID NO:517
BM735166.V1.3_at	GGAGGAACCCACAGGCAGATGCTCA	SEQ ID NO:518
BM735166.V1.3_at	TGTGCGGACAAGCAGCCACTGATCA	SEQ ID NO:519
BM735166.V1.3_at	TCAACCTCTGCTGACCACTGAGTGA	SEQ ID NO:520
TAP2E		SEQ ID NO:521
BM735167.V1.3_at	AGGCTCTGCAGGACTGGATATCCCG	SEQ ID NO:522
BM735167.V1.3_at	ATGGCTGTCTTCATGACCTGGAGTA	SEQ ID NO:523
BM735167.V1.3_at	GCTCACAGGCTGCAGACGGTTCAGA	
BM735167.V1.3_at	GAACGGTGCTGGTGATCGCTCACAG	SEQ ID NO:524
BM735167.V1.3_at	GATTTGGACCTTGTGTGCTTTCATT	SEQ ID NO:525

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
BM735167.V1.3_at	GTGTCCATGAACCTTATTTCCTTGA	SEQ ID NO:526
BM735167.V1.3_at	GGAGTAGCTCCTGCTTTGAGTTTCC	SEQ ID NO:527
BM735167.V1.3_at	TGGACGTCCAGTGTGAGCAGGCTCT	SEQ ID NO:528
BM735167.V1.3_at	TGGATCATGCCCAGCTCATGGAGGG	SEQ ID NO:529
BM735167.V1.3_at	TGGATGAAGCCACCAGTGCCCTGGA	SEQ ID NO:530
BM735167.V1.3_at	TTCAGAACGCTGACCAGATCCTGGT	SEQ ID NO:531
Ferritin light chain		
BM735286.V1.3_at	AGGAGCCTCCGGAGTCCAGCGGCCT	SEQ ID NO:532
BM735286.V1.3_at	AGCTTTTTAACTAGCCTGGAGCCTT	SEQ ID NO:533
BM735286.V1.3_at	CGTCAGAGCTTCTGCCTGAGCCTCT	SEQ ID NO:534
BM735286.V1.3_at	CTGCAGCCACTAGAGATAGCTTTTT	SEQ ID NO:535
BM735286.V1.3_at	CTCCGGAGTCCAGCGGCCTTTGAGG	SEQ ID NO:536
BM735286.V1.3_at	CTGGCGTCAGAGCTTCTGCCTGAGC	SEQ ID NO:537
BM735286.V1.3_at	GAGATAGCTTTTTAACTAGCCTGGA	SEQ ID NO:538
BM735286.V1.3_at	TTTGGTATCCCCCTGGCGTCAGAGC	SEQ ID NO:539
BM735286.V1.3_at	TCCCTGCAGCCACTAGAGATAGCTT	SEQ ID NO:540
BM735286.V1.3_at	TTTTAACTAGCCTGGAGCCTTCTGC	SEQ ID NO:541
BM735286.V1.3_at	TAACTAGCCTGGAGCCTTCTGCCCA	SEQ ID NO:542
BM735286.V1.3_s_at	ATGAAAGCCGCCATTGTCCTGGAGA	SEQ ID NO:543
BM735286.V1.3_s_at	ATTGTCCTGGAGAAGAGCCTGAACC	SEQ ID NO:544
BM735286.V1.3_s_at	ATCCAGAGGCTCGTTGGCTCCCAAG	SEQ ID NO:545
BM735286.V1.3_s_at	ATCTCTGTGACTTCTTGGAGAGCCA	SEQ ID NO:546
BM735286.V1.3_s_at	GATGGGCGACCATCTGACCAACATC	SEQ ID NO:547
BM735286.V1.3_s_at	GGGCTGGGCGAGTATCTCTTTGAAA	SEQ ID NO:548
BM735286.V1.3_s_at	GGGTACAACCCTGGATGCCATGAAA	SEQ ID NO:549
BM735286.V1.3_s_at	TGGAGAGCCACTTCCTAGACGAGGA	SEQ ID NO:550
BM735286.V1.3_s_at	TCTTTGAAAGGCTCACCCTCAAGCA	SEQ ID NO:551
BM735286.V1.3_s_at	TGAACCAGGCCCTTTTGGATCTGCA	SEQ ID NO:552
BM735286.V1.3_s_at	TTGGATCTGCATGCCCTGGGTTCTG	SEQ ID NO:553
No homology		
BM735352.V1.3_at	ATCAGACTGCACTGCCTGCGGGAGG	SEQ ID NO:554
BM735352.V1.3_at	AGCAGTCAAACCAAAGCATTCCATT	SEQ ID NO:555
BM735352.V1.3_at	GTTATGGCCTAATGCCCACTTTTGT	SEQ ID NO:556
BM735352.V1.3_at	GACGGAGCAAGCTCTTGCCATCAGA	SEQ ID NO:557
BM735352.V1.3_at	GACCCAGGGAGAGAACGTCGCTGCT	SEQ ID NO:558
BM735352.V1.3_at	GTCTGTGTTCAAGTACCTCACGGGA	SEQ ID NO:559
BM735352.V1.3_at	GTCGCTGCTGTATACTGTAACGTCT	SEQ ID NO:560
BM735352.V1.3_at	GGGACGCTCCAGATATTTGAATCTC	SEQ ID NO:561
BM735352.V1.3_at	TGATCCTCCTCCTGCGCAGAATAGA	SEQ ID NO:562
BM735352.V1.3_at	TGCTCACACGTAACAGTCTGGTGGG	SEQ ID NO:563
BM735352.V1.3_at	TCTCTATTAACTTACTGCTCACACG	SEQ ID NO:564
No homology		
BM735409.V1.3_at	ATCTTGCACCTTCTTCAGGATTTTA	SEQ ID NO:565
BM735409.V1.3_at	ACCTGCCTGGGCTTCTGGGCCTGTG	SEQ ID NO:566
BM735409.V1.3_at	ACAGAGGGAGCCAGCAGCTGTCCCC	SEQ ID NO:567
BM735409.V1.3_at	ACACACTTTGCGTATCTGAGCGCGC	SEQ ID NO:568

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
BM735409.V1.3_at	AAAGCAGTACCTGGTGGCCGTGTGC	SEQ ID NO:569
BM735409.V1.3_at	GAAGTCAGAAGCCAAGCTTTCTCCC	SEQ ID NO:570
BM735409.V1.3_at	GTACCTCCTCCTCTGGAGGTGCTGG	SEQ ID NO:571
BM735409.V1.3_at	GGAAGCGCTGGAGCCACCCCGTGAA	SEQ ID NO:572
BM735409.V1.3_at	TGGCCTGGGCTCTGTCTACAGCCAC	SEQ ID NO:573
BM735409.V1.3_at	TCGCACTGGGTCTTATCTTGCACCT	SEQ ID NO:574
BM735409.V1.3_at	TCTGTGGGCCGCACGTACACACACA	SEQ ID NO:575
JKTBP1 (alternative splicing).		
BM735419.V1.3_at	ACCGAATCCAGGTGTGGCACGCGGA	SEQ ID NO:576
BM735419.V1.3_at	AGAAGGCGCCTGACTTCGTGTTCTA	SEQ ID NO:577
BM735419.V1.3_at	ACGAGCTGTACATGCGCCGCAGGAA	SEQ ID NO:578
BM735419.V1.3_at	AAAGATTGGCTTCCCGTGGAGTGAA	SEQ ID NO:579
BM735419.V1.3_at	ACAAGTCTGGGTACCTAGGCTCTGA	SEQ ID NO:580
BM735419.V1.3_at	AACAAGCGGATCCTGCAGCTGTGCA	SEQ ID NO:581
BM735419.V1.3_at	CTACGCTGTGCAGGCCAAGTTTGGA	SEQ ID NO:582
BM735419.V1.3_at	GAACAGACCTTTGGCTTGGAGTCGA	SEQ ID NO:583
BM735419.V1.3_at	GATGCCCTTGGACTGAATATTTATG	SEQ ID NO:584
BM735419.V1.3_at	GTATCTGAAGATTGCCCAGGACCTG	SEQ ID NO:585
BM735419.V1.3_at	TGTGCATGGGCAACCACGAGCTGTA	SEQ ID NO:586
WD repeat domain 1		
BM735441.V1.3_at	ATGATGGTGTACGTCTGGACCCTCA	SEQ ID NO:587
BM735441.V1.3_at	ATGGTCACCATGCAAAGATCGTCTG	SEQ ID NO:588
BM735441.V1.3_at	AGTGGTCACAGTCTTAAGCGTTGCT	SEQ ID NO:589
BM735441.V1.3_at	AGATCTGTACACGTCCTTCTGAAAG	SEQ ID NO:590
BM735441.V1.3_at	AGAACGCGGCGTTTCTCTAAATCCT	SEQ ID NO:591
BM735441.V1.3_at	ACGGGCCGCATCAGGGACGAGATTC	SEQ ID NO:592
BM735441.V1.3_at	GACAACGAGCATTTTGCCTCTGGCG	SEQ ID NO:593
BM735441.V1.3_at	GTTGCTGACGGCTACTCGGAGAACA	SEQ ID NO:594
BM735441.V1.3_at	GTCAAGATCCAAGATGCACACCGCT	SEQ ID NO:595
BM735441.V1.3_at	TGGACGAGCACACGTTGGTCACGAC	SEQ ID NO:596
BM735441.V1.3_at	TCGTCTCTCTACAGGGTGTTCAGAT	SEQ ID NO:597
Lymphocyte surface antigen precursor CD44		
BM735450.V1.3_at	ATTCTCGCAGTTTGCATTGCTGTCA	SEQ ID NO:598
BM735450.V1.3_at	AGAGAAGACTCCCACTACCAAAGAC	SEQ ID NO:599
BM735450.V1.3_at	AGAGCAGTCCCTGGGTGTCTGACAG	SEQ ID NO:600
BM735450.V1.3_at	AGAATGGCTGATCATCTTGGCGTCC	SEQ ID NO:601
BM735450.V1.3_at	ACCTGCACCTTGACCTTGGGAAGAA	SEQ ID NO:602
BM735450.V1.3_at	CGACGAGACACGGAACCTGCAGAAT	SEQ ID NO:603
BM735450.V1.3_at	GACCAGTTTATGACAGCCGACGAGA	SEQ ID NO:604
BM735450.V1.3_at	GACCACCCACGGATCTGAAACAAGT	SEQ ID NO:605
BM735450.V1.3_at	GAGTCGTCAGAGACCCAAGACCAGT	SEQ ID NO:606
BM735450.V1.3_at	GGGTCCCATACGGAGACCTCAAATT	SEQ ID NO:607
BM735450.V1.3_at	TGTGATGTGCTACTGACTGCTTCAT	SEQ ID NO:608
No homology		
BM735457.V1.3_at	AGGAACCTAACCTGATGCTCTTTCG	SEQ ID NO:609

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
BM735457.V1.3_at	AGGACCCAACTCTGAATACATTTTT	SEQ ID NO:610
BM735457.V1.3_at	AGGGCAGTTTTCTTTGCCCAAGCCT	SEQ ID NO:611
BM735457.V1.3_at	AGCCTGCACATCTTCTCAGCAAAAA	SEQ ID NO:612
BM735457.V1.3_at	AAGCCTTCGGTGCTAGTTAGCTCTC	SEQ ID NO:613
BM735457.V1.3_at	AACTCCCTTAATCTTTCACACATGC	SEQ ID NO:614
BM735457.V1.3_at	GCAATAATCCCCACCTGTCTAAAAA	SEQ ID NO:615
BM735457.V1.3_at	GAAGATTTCTCTCTGTGACTGCAAC	SEQ ID NO:616
BM735457.V1.3_at	GAGAGGTTGCCCTACGAACAGACAG	SEQ ID NO:617
BM735457.V1.3_at	GAAATGTTAACTCCCTTTTGCAGAA	SEQ ID NO:618
BM735457.V1.3_at	GATTGAGATTCAACCTGGCCTTACC	SEQ ID NO:619
No Homology		
BM735487.V1.3_at	GAGTTCGAAGTCACCCTAATCACGT	SEQ ID NO:620
BM735487.V1.3_at	CACCAGGACTCTAGCCCCAGAGTGG	SEQ ID NO:621
BM735487.V1.3_at	AAATGGAACTCTCCTTTTCGAGCAT	SEQ ID NO:622
BM735487.V1.3_at	CGGCCCGGACACAAGGAGGAAGCTC	SEQ ID NO:623
BM735487.V1.3_at	GCGTCTGACCCCAGCGAAGGGCCAG	SEQ ID NO:624
BM735487.V1.3_at	GAAGGGCCAGCCTTGCTTGGTTCAG	SEQ ID NO:625
BM735487.V1.3_at	GACTGTGGAGGGACAGGCTTCCCCT	SEQ ID NO:626
BM735487.V1.3_at	GTTAGCTTCCCCAAAAGAATTGTGT	SEQ ID NO:627
BM735487.V1.3_at	GTCACCCTAATCACGTAAATGGAAC	SEQ ID NO:628
BM735487.V1.3_at	GTGCTTGCTTGGGAGTTCGAAGTCA	SEQ ID NO:629
BM735487.V1.3_at	TAGCCCCAGAGTGGCTCCAGAAGGT	SEQ ID NO:630
Ring finger protein 10, clone ERLTF2001835		
BM735519.V1.3_at	CAGGCTACCTTCTCCATTTGGTTTT	SEQ ID NO:631
BM735519.V1.3_at	AGATGTGTGGCCCAAAACTGCTCCA	SEQ ID NO:632
BM735519.V1.3_at	AGCCTTCATGAAGCTGGACACGCCA	SEQ ID NO:633
BM735519.V1.3_at	AGAAGCTCCTGTTCAGCACCTCAGT	SEQ ID NO:634
BM735519.V1.3_at	AATACAGTGTATTTTCCAGCTTCCT	SEQ ID NO:635
BM735519.V1.3_at	CAAGTGACACTACTGGCCCAGGCTA	SEQ ID NO:636
BM735519.V1.3_at	CCGTGCTTTTGTTTTGCTGCTGTAA	SEQ ID NO:637
BM735519.V1.3_at	TGAAAACAGCTTAATTCCTCCTGCC	SEQ ID NO:638
BM735519.V1.3_at	TGATAACTCGGACCGTGTTCCTGTG	SEQ ID NO:639
BM735519.V1.3_at	TTCCAGAATTCCTTCAGCCAAGCTA	SEQ ID NO:640
BM735519.V1.3_at	TTCGGATCCCCTCTCTGAAGAGAAA	SEQ ID NO:641
PREDICTED: Bos taurus similar to hypothetical protein (LOC515494)		
BM735534.V1.3_at	ATTAGAGGGCAGCTCAGCCTCCCTT	SEQ ID NO:642
BM735534.V1.3_at	AGGATCATAGGCCTGGACACTCCAT	SEQ ID NO:643
BM735534.V1.3_at	AGTCACAGTGACAACAACCCATTAG	SEQ ID NO:644
BM735534.V1.3_at	AGAGGATGAGCCACTGCTTGCCTGA	SEQ ID NO:645
BM735534.V1.3_at	ACTGCTTGCCTGAGGTGACCTGGCT	SEQ ID NO:646
BM735534.V1.3_at	AATGCCAATTGGCTGGAGACTTCCA	SEQ ID NO:647
BM735534.V1.3_at	AATGCCATAGGTTAGATGTCCCTCA	SEQ ID NO:648

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
BM735534.V1.3_at	CACCATTCAGGTGGCTGTTTTTAAA	SEQ ID NO:649
BM735534.V1.3_at	GCATTTGGGCAGAGCCTGAACTCAA	SEQ ID NO:650
BM735534.V1.3_at	GAGAGAGGGCTCACACAGAGCTCCC	SEQ ID NO:651
BM735534.V1.3_at	TATCCCATAGCTAGGTTATTGCCCA	SEQ ID NO:652
Transglutaminase E3 (TGASE3) (6-sialyltransferase), transcript variant 2		
BM735536.V1.3_at	GTCCCGGGTACGTTTTGAGATCCTG	SEQ ID NO:653
BM735536.V1.3_at	ACAAGTTCCCTGCAATCAAGGCCAT	SEQ ID NO:654
BM735536.V1.3_at	ATGCTGTCCATCGACGTGGCTGAGT	SEQ ID NO:655
BM735536.V1.3_at	AGTCGGTCTGGACTGTTTGCTGATC	SEQ ID NO:656
BM735536.V1.3_at	AGCGACCCTCCGAATGGATGCTCAG	SEQ ID NO:657
BM735536.V1.3_at	ACGCCCATCAATGCTGCAGGACAGA	SEQ ID NO:658
BM735536.V1.3_at	GACAGAGTGGCACCTGACCCAGCGA	SEQ ID NO:659
BM735536.V1.3_at	GACTTGATCACTTTTGCACATTCCC	SEQ ID NO:660
BM735536.V1.3_at	GGTTAACCATCTGTCATGGCACTCG	SEQ ID NO:661
BM735536.V1.3_at	TGCAGTTGGGACATTCGTGCTACTC	SEQ ID NO:662
BM735536.V1.3_at	TTGCTGACTTCTCCTGCGACAAGTT	SEQ ID NO:663
CD68 protein		
BM735545.V1.3_at	ACAGGAGCCTTTGGGCCAAGTTTCT	SEQ ID NO:664
BM735545.V1.3_at	ATTACCTTCTGTGTCATCCGGAGAC	SEQ ID NO:665
BM735545.V1.3_at	AGAGACCAAATTATCTTCCTTCCCT	SEQ ID NO:666
BM735545.V1.3_at	AGAAACGCAAGCATCGCTCTTTCAC	SEQ ID NO:667
BM735545.V1.3_at	AAATCTTTGTCCCTGATTTCCCTTG	SEQ ID NO:668
BM735545.V1.3_at	AAGTTTCTCTTGTCCCAGTGACCAG	SEQ ID NO:669
BM735545.V1.3_at	CTGAAGCTACAAGCTGCTCAGCTGA	SEQ ID NO:670
BM735545.V1.3_at	CCTAGGCCAGAGATTCAGTTGCAGA	SEQ ID NO:671
BM735545.V1.3_at	TACTCGGCCGACTCAGAGACCAAAT	SEQ ID NO:672
BM735545.V1.3_at	TACCAGCCACTCTGAGCGTTTATCC	SEQ ID NO:673
BM735545.V1.3_at	TTCCCTCTCTGTCCTGAAGAACAAA	SEQ ID NO:674
No Homology		
BM735573.V1.3_at	ACTAGTGTGGGAGAAACCAGCTTTT	SEQ ID NO:675
BM735573.V1.3_at	ATCACTGCTTTACTCTGTTAATTTA	SEQ ID NO:676
BM735573.V1.3_at	AAAAATCACTGCTTTACTCTGTTAA	SEQ ID NO:677
BM735573.V1.3_at	AAATCACTGCTTTACTCTGTTAATT	SEQ ID NO:678
BM735573.V1.3_at	CACTGCTTTACTCTGTTAATTTACA	SEQ ID NO:679
BM735573.V1.3_at	GCTTTTACTGTTTAAAAATCACTGC	SEQ ID NO:680
BM735573.V1.3_at	GCTTTACTCTGTTAATTTACAAGGA	SEQ ID NO:681
BM735573.V1.3_at	GAATTCGGCACGAGGAAATTCCTAA	SEQ ID NO:682
BM735573.V1.3_at	GATACTACAGTGAAACTAGTGTGGG	SEQ ID NO:683
BM735573.V1.3_at	TGGGAGAAACCAGCTTTTACTGTTT	SEQ ID NO:684
BM735573.V1.3_at	TCGGCACGAGGAAATTCCTAACAAG	SEQ ID NO:685
Minor histocompatibility antigen H13 isoform 1 (H13), desmosome associated protein		

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
(PNN)		
BM735576.V1.3_at	ATCTTCATCATGCACATCTTCAAGC	SEQ ID NO:686
BM735576.V1.3_at	AGGGATGGACCAGCACAGGCCTGCA	SEQ ID NO:687
BM735576.V1.3_at	CATCCTGGTGGCACTGGCCAAAGGA	SEQ ID NO:688
BM735576.V1.3_at	GCATGTGGCAGGATCCCTCCAGCAG	SEQ ID NO:689
BM735576.V1.3_at	GAAATGATGCGGCTGCTGCCTGACC	SEQ ID NO:690
BM735576.V1.3_at	GAGTCAAGCCCTAAGGATCCAGCGG	SEQ ID NO:691
BM735576.V1.3_at	GATCCAGCGGCAGTGACAGAATCCA	SEQ ID NO:692
BM735576.V1.3_at	GGGAACAGAGGCCTCAGCATCAAAG	SEQ ID NO:693
BM735576.V1.3_at	TGCGGTTTGACATCAGCTTGAAGAA	SEQ ID NO:694
BM735576.V1.3_at	TGGGTCTTACCATCTTCATCATGCA	SEQ ID NO:695
BM735576.V1.3_at	TTGAAGAAGAACACCCACACCTACT	SEQ ID NO:696
Fc-epsilon-receptor gamma-chain		
BM735585.V1.3_at	ATGATTCCAGCAGTGGTCTTGCTCT	SEQ ID NO:697
BM735585.V1.3_at	ACCCTACCCCTGTAATGATGCTATG	SEQ ID NO:698
BM735585.V1.3_at	CTGCCATTAATGCTAGCTGACCCTA	SEQ ID NO:699
BM735585.V1.3_at	GTACCCGGACCCAGGAGACTTATGA	SEQ ID NO:700
BM735585.V1.3_at	GAGAGCCTCAGCTTTGCTATATTCT	SEQ ID NO:701
BM735585.V1.3_at	GATGCCATCCTGTTCTTGTATGGTA	SEQ ID NO:702
BM735585.V1.3_at	TGTTTATATTCTAGTCTCACCCCTA	SEQ ID NO:703
BM735585.V1.3_at	TTTCAAACAGATGCCCTTGGTCACA	SEQ ID NO:704
BM735585.V1.3_at	TAACGGACATCAGTGGTTCCTCTTC	SEQ ID NO:705
BM735585.V1.3_at	TTGGTTGAACAAGCAGCGGCCCTGG	SEQ ID NO:706
BM735585.V1.3_at	TTGCTCTTACTCCTTTTGGTTGAAC	SEQ ID NO:707
BM781012.V1.3_at	CAGAAGAACGTCTCCAAGAACCCGG	SEQ ID NO:708
BM781012.V1.3_at	CACCAAGACCAAAGGGCGGTCCCAG	SEQ ID NO:709
BM781012.V1.3_at	AGGAGCCGCAAGTGTACGTCCTGGC	SEQ ID NO:710
BM781012.V1.3_at	AGTTCAACAGCACTTACCGCGTGGT	SEQ ID NO:711
BM781012.V1.3_at	AATCAACATCGAGTGGCAGAGTAAT	SEQ ID NO:712
BM781012.V1.3_at	ACCCAGACGAGCTGTCCAAGAGCAA	SEQ ID NO:713
BM781012.V1.3_at	ACGAGCTGTCCAAGAGCAAGGTCAG	SEQ ID NO:714
BM781012.V1.3_at	AAGCTCTCCGTGGACAGGAACAGGT	SEQ ID NO:715
BM781012.V1.3_at	GCACTTACCGCGTGGTCAGCGTCCT	SEQ ID NO:716
BM781012.V1.3_at	TCGAGAGGACCATCACCAAGACCAA	SEQ ID NO:717
BM781012.V1.3_at	TACCCACCTGAAATCAACATCGAGT	SEQ ID NO:718
GM2 ganglioside activator		
BM781174.V1.3_at	AGCTGGCTCAGCAACGGGAACTACC	SEQ ID NO:719
BM781174.V1.3_at	AACGCTGTCACAGACCTAGCAGTTA	SEQ ID NO:720
BM781174.V1.3_at	AAGTGGCTGGCGTATGGGTCAAAAT	SEQ ID NO:721
BM781174.V1.3_at	GCGGACCCACCATTTGCAATGAGAC	SEQ ID NO:722
BM781174.V1.3_at	GCTGTACTTTTGACAATGCCTGTGA	SEQ ID NO:723
BM781174.V1.3_at	TAGCAGTTAACCAGGCGCGGACCCA	SEQ ID NO:724
BM781174.V1.3_at	GAACTACCGTGTCCAGAGCATCCTG	SEQ ID NO:725
BM781174.V1.3_at	GGGAAGGACCCTATGGTGCTCAAAA	SEQ ID NO:726

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
BM781174.V1.3_at	GGCTCCGTAGCTTTTCCTGGGATAA	SEQ ID NO:727
BM781174.V1.3_at	TGGTGCTCAAAAGCCTGACTCTGGA	SEQ ID NO:728
BM781174.V1.3_at	TGATATACTAGACGCTTTGACTCCC	SEQ ID NO:729
No homology		
BM781178_unkn.V1.3_at	ATAGCCTCCATTTCCTTCAATAGAT	SEQ ID NO:730
BM781178_unkn.V1.3_at	ATCGTTTAAGGCAGATGTCCCCGGA	SEQ ID NO:731
BM781178_unkn.V1.3_at	ATCACCAGTTCTTATGTCACCTTAG	SEQ ID NO:732
BM781178_unkn.V1.3_at	AGTGGGATGCCTTAAACACCCGCAC	SEQ ID NO:733
BM781178_unkn.V1.3_at	CAAACTGGTATCTGTCATCTGGTAA	SEQ ID NO:734
BM781178_unkn.V1.3_at	GCAGACCGATGTGGTACCGGCTGAA	SEQ ID NO:735
BM781178_unkn.V1.3_at	GATGTCCCCGGAAGAGCAGTTTTTT	SEQ ID NO:736
BM781178_unkn.V1.3_at	GGGATGCCTCAAAATGCAGACCGAT	SEQ ID NO:737
BM781178_unkn.V1.3_at	GGATCCGATCTATTGTTACAGGCAC	SEQ ID NO:738
BM781178_unkn.V1.3_at	TGGTTCGTTATCTTCTCTTTGGCAA	SEQ ID NO:739
BM781178_unkn.V1.3_at	TGGGTTGCTACTGCCATGGTTTGAA	SEQ ID NO:740
BM781178.V1.3_at	ATTTTGAGGCATCCCTTCTAGGTGC	SEQ ID NO:741
BM781178.V1.3_at	AAATGGAGGCTATCGTCATGGCAGG	SEQ ID NO:742
BM781178.V1.3_at	CAGTTCCTTCAAACCATGGCAGTAG	SEQ ID NO:743
BM781178.V1.3_at	GATCCCCTCTGGTTATAGTTCGTGA	SEQ ID NO:744
BM781178.V1.3_at	GTAGCAACCCAGTGCCTGTAACAAT	SEQ ID NO:745
BM781178.V1.3_at	GGGAATATTCTTTCAGCCGGTACCA	SEQ ID NO:746
BM781178.V1.3_at	TTTAAGGCATCCCACTGTAGACTCT	SEQ ID NO:747
BM781178.V1.3_at	TGTAGACTCTTCTCTCGGGAATATT	SEQ ID NO:748
BM781178.V1.3_at	TCTGTCCCCACCATTGATTCTAAGG	SEQ ID NO:749
BM781178.V1.3_at	TACCACATCGGTCTGCATTTTGAGG	SEQ ID NO:750
BM781178.V1.3_at	TAGGTGCTCAATGCCATTACCAGAT	SEQ ID NO:751
Membrane-spanning 4-domains, subfamily A, member 6A, transcript variant 1		
BM781186.V1.3_at	ATAGGAGCCTTGTGTTTTGTCATCT	SEQ ID NO:752
BM781186.V1.3_at	AAGCCTTTGGTTCAGAGCAGCCTAG	SEQ ID NO:753
BM781186.V1.3_at	AAGTTCTCGGGACTATCCAGATCCT	SEQ ID NO:754
BM781186.V1.3_at	CAGCATTTTACCCAAGCGTTTTCTA	SEQ ID NO:755
BM781186.V1.3_at	CTGCAAACATTCTGAGCTCTCTATC	SEQ ID NO:756
BM781186.V1.3_at	GAAGGCTGCTTACCCATTCATAGGA	SEQ ID NO:757
BM781186.V1.3_at	GAATTATTTTGGCATCGGCTTCCTT	SEQ ID NO:758
BM781186.V1.3_at	GTCATACTGGCTTCTTTGGGTCCTG	SEQ ID NO:759
BM781186.V1.3_at	GTCATCTCTGGATCTCTATCAATCA	SEQ ID NO:760
BM781186.V1.3_at	TAGCTGGAACCAACGGGCTGATCCT	SEQ ID NO:761
BM781186.V1.3_at	TATCAGCTCTGGTGGGTTTCATCCT	SEQ ID NO:762
No homology		
BM781334.V1.3_at	GTCAAGTCTGACTGAATGAGGCCAC	SEQ ID NO:763
BM781334.V1.3_at	AGAGGGACCTCGTCAGGCACTTCTA	SEQ ID NO:764
BM781334.V1.3_at	ACTGCAGTAGTGACCCTTCAAGAGG	SEQ ID NO:765
BM781334.V1.3_at	AAGAGACGTCATGGCCCCGTACGTG	SEQ ID NO:766
BM781334.V1.3_at	CAGCCACTGGCTGATTTCAAGTCAT	SEQ ID NO:767

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
BM781334.V1.3_at	CTGGTGGAAGAGATCCCGCGGAACC	SEQ ID NO:768
BM781334.V1.3_at	GCCCTCGGAGCTTCTGCTGGTGGAA	SEQ ID NO:769
BM781334.V1.3_at	GAAGCCCCTAGCTCAGGCAGAACAG	SEQ ID NO:770
BM781334.V1.3_at	TGGAAAGTCCAGAGGTGTCACCAGG	SEQ ID NO:771
BM781334.V1.3_at	TGGCTGTGATTGGAGTTCCGGACAT	SEQ ID NO:772
BM781334.V1.3_at	TGTCCCACAGGGAGCTCAAAGAGTG	SEQ ID NO:773
No homology		
BM781417.V1.3_at	ATTTAGCTACTTTATTGCCTTTACA	SEQ ID NO:774
BM781417.V1.3_at	AATTGTTATTATTACGCTCTTTGCG	SEQ ID NO:775
BM781417.V1.3_at	GCCTTTACATTGCTTATTCTTATTG	SEQ ID NO:776
BM781417.V1.3_at	GCACTTTCTTTGATTACACTTCCAT	SEQ ID NO:777
BM781417.V1.3_at	GAATTCTGTCCTTCATTTACTTTGT	SEQ ID NO:778
BM781417.V1.3_at	GAAAAGTCGTCTCCTAGTAACCAGT	SEQ ID NO:779
BM781417.V1.3_at	GACAAACAGCTTTAAGTGCACTTTC	SEQ ID NO:780
BM781417.V1.3_at	GATCTAGCTGGGAAACTGTCATGAG	SEQ ID NO:781
BM781417.V1.3_at	GTTGCTTTTTCCTTCTTTGATCTAA	SEQ ID NO:782
BM781417.V1.3_at	TAACTTCAATCCTCAGATCTAGCTG	SEQ ID NO:783
BM781417.V1.3_at	TTCTGAAGCCTTTTATGTACCACTA	SEQ ID NO:784
Homo sapiens 15 kDa selenoprotein, transcript variant 1		
Foe1060.V1.3_at	ATTTCCATTCTCCTACATTTGTTGA	SEQ ID NO:785
Foe1060.V1.3_at	AGATATTCTAGCCTCCACAGATTGC	SEQ ID NO:786
Foe1060.V1.3_at	AGATGATTGCTATGCTTCCTGTGCT	SEQ ID NO:787
Foe1060.V1.3_at	ACCTTTCTGAGGATTTGTGTGGATC	SEQ ID NO:788
Foe1060.V1.3_at	CCTCCAATCCGCTCATATTTTTGTA	SEQ ID NO:789
Foe1060.V1.3_at	GAAACATTCACAAAGATTCGCGTTA	SEQ ID NO:790
Foe1060.V1.3_at	GTTGGCAAGCTTAACAAACCTGTTT	SEQ ID NO:791
Foe1060.V1.3_at	GTGTGGATCTGATATCCGGCAAATT	SEQ ID NO:792
Foe1060.V1.3_at	GGCAAATTTTTGTGCTTTACATTCT	SEQ ID NO:793
Foe1060.V1.3_at	TGTATTACCCAGCTTTCCTTTAAAT	SEQ ID NO:794
Foe1060.V1.3_at	TGTGCTGTGTGCTCCTTGAAAGTAA	SEQ ID NO:795
Transducin (beta)-like 1X-linked receptor 1		
Foe1072.V1.3_at	ATAGATGTTCTATGCTGTCCTGGAC	SEQ ID NO:796
Foe1072.V1.3_at	ACATCACAATGATTTGTCCCCAGCG	SEQ ID NO:797
Foe1072.V1.3_at	AACCAGCCCATGACAGTTTTTTGTA	SEQ ID NO:798
Foe1072.V1.3_at	GCAGTTTCCCTTTGCATTGTATTGC	SEQ ID NO:799
Foe1072.V1.3_at	GACCCTTTTATCCTTTCTAGGCACA	SEQ ID NO:800
Foe1072.V1.3_at	GACTGCATTTTGTAGCTCTGTAATC	SEQ ID NO:801
Foe1072.V1.3_at	GTAATTTTCTTCTTTCCTGACTTTG	SEQ ID NO:802
Foe1072.V1.3_at	GTGAGCCTACCTATAGCACTGGATT	SEQ ID NO:803
Foe1072.V1.3_at	TGTCTGCATCATTTCTTTAGTTATC	SEQ ID NO:804
Foe1072.V1.3_at	TTTGGGTCTAATTCTGTGAGCCTAC	SEQ ID NO:805
Foe1072.V1.3_at	TTCTGCATGTTGTATCTAGTCTGAT	SEQ ID NO:806
Homo sapiens mRNA; cDNA DKFZp666I186		

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
(from clone DKFZp666I186)		
Foe545.V1.3_at	ATGTGATAACAGCACCTCTTCATCT	SEQ ID NO:807
Foe545.V1.3_at	ACTTCAAGTCTTGCAATGGTGCTTT	SEQ ID NO:808
Foe545.V1.3_at	AAACGCAACCAGTTCATCGGGATTT	SEQ ID NO:809
Foe545.V1.3_at	CTTCCAAATTGGCTTTTACAGATCC	SEQ ID NO:810
Foe545.V1.3_at	CAGCACCTCTTCATCTTTAACTTGA	SEQ ID NO:811
Foe545.V1.3_at	CTTGGTTAGGAGTGGTTTGCTGCCC	SEQ ID NO:812
Foe545.V1.3_at	GAAATTTCCTTTTCTGAGTGTTGAA	SEQ ID NO:813
Foe545.V1.3_at	GTTAGCAGACTAGAAGACTTCCAAA	SEQ ID NO:814
Foe545.V1.3_at	GGAACATTTTACACACTTCAAGTCT	SEQ ID NO:815
Foe545.V1.3_at	TTTGCTGCCCTCCTCTAAAGGCAGT	SEQ ID NO:816
Foe545.V1.3_at	TTCCTGTCAGTTTCATCCAATCTTA	SEQ ID NO:817
Foe1019.V1.3_at	AAAGTGCTACACTCCTTTGGTGAGG	SEQ ID NO:818
Foe1019.V1.3_at	AACGTGCTGGTTGTTGTGCTGGCTC	SEQ ID NO:819
Foe1019.V1.3_at	AAGAGAAGGCAGCTGTCTTGGCCCT	SEQ ID NO:820
Foe1019.V1.3_at	TGGCAAGGATTTCACCCCAGAGTTG	SEQ ID NO:821
Foe1019.V1.3_at	CAGAGTTGCAGGCTTCCTATCAAAA	SEQ ID NO:822
Foe1019.V1.3_at	GACAAGCTGCACGTGGATCCTGAGA	SEQ ID NO:823
Foe1019.V1.3_at	GAGAAAGGCCTCTTTGTGCCCAAAG	SEQ ID NO:824
Foe1019.V1.3_at	GAGATCCTGGCTTCTGCCTAATAAA	SEQ ID NO:825
Foe1019.V1.3_at	GATCTGTCCAATCCTGGTGCTGTGA	SEQ ID NO:826
Foe1019.V1.3_at	TGGTTGTCTACCCATGGACTCAGAG	SEQ ID NO:827
Foe1019.V1.3_at	TGAGGGCGTGCATCATCTTGACAAC	SEQ ID NO:828
Equus caballus gelsolin mRNA		
GI1592834.V1.3_at	ATCACCGTCGTGAAGCAAGGCTTTG	SEQ ID NO:829
GI1592834.V1.3_at	AAAGACGGAAGCCTTGACCTCTGCT	SEQ ID NO:830
GI1592834.V1.3_at	AACGATGCCTTTGTCCTGAAAACTC	SEQ ID NO:831
GI1592834.V1.3_at	AAGGCAGCGAGCCAGACAGCTTCTG	SEQ ID NO:832
GI1592834.V1.3_at	GAAGACCTGGCCACTGATGACGTCA	SEQ ID NO:833
GI1592834.V1.3_at	GAAGAGGTCCCTGGCGAGTTCATGC	SEQ ID NO:834
GI1592834.V1.3_at	GACCAGGTCTTTGTCTGGGTCGGAA	SEQ ID NO:835
GI1592834.V1.3_at	GACAGCTACTGGTCTGTGGATCCCT	SEQ ID NO:836
GI1592834.V1.3_at	GTATATCGACACAGACCCAGCTCAT	SEQ ID NO:837
GI1592834.V1.3_at	GGAGCCACCCGAGCCGTTGAGATAA	SEQ ID NO:838
GI1592834.V1.3_at	TCTTTGCCTGCTCCAACAAGATTGG	SEQ ID NO:839
gi5441616.V1.3_at	ATAGCCTCACTAGAGGTCTAGCGGT	SEQ ID NO:840
gi5441616.V1.3_at	AAACGTCTACTCTCTCCTGTAAGAA	SEQ ID NO:841
gi5441616.V1.3_at	GCACCCCAGACCGTATTTATCATAT	SEQ ID NO:842
gi5441616.V1.3_at	GAATCAGATTACTTTGGCAGGCTTG	SEQ ID NO:843
gi5441616.V1.3_at	GACAACACACTTTACTTTGTAGCTG	SEQ ID NO:844
gi5441616.V1.3_at	GACCAAGTTCTCTTCATTAACCAGG	SEQ ID NO:845
gi5441616.V1.3_at	GGCAGGCTTGAACCTAAACTCTCAA	SEQ ID NO:846
gi5441616.V1.3_at	GGATATGCCTGATTCTGATTGTACA	SEQ ID NO:847

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
gi5441616.V1.3_at	GGAAATGAGTCCTCCTGAGAATATC	SEQ ID NO:848
gi5441616.V1.3_at	TGATTGTACAGACAACGCACCCCAG	SEQ ID NO:849
gi5441616.V1.3_at	TAGCGGTAACCATCTCTGTGAAGTG	SEQ ID NO:850
Equus caballus Ig epsilon heavy chain (partial)		
gi576646.V1.3_s_at	TTAAGCCTGAACTGGTCCCGGGAGA	SEQ ID NO:851
gi576646.V1.3_s_at	AGAGCTCCAAGGACAAGGTCACCCT	SEQ ID NO:852
gi576646.V1.3_s_at	AGACCCTGGTAAATGATGCCCTCTG	SEQ ID NO:853
gi576646.V1.3_s_at	AATTTGCCTGCAAGGTGGTCCACGA	SEQ ID NO:854
gi576646.V1.3_s_at	GAGACTTACAAGTGCACCGTGTCCC	SEQ ID NO:855
gi576646.V1.3_s_at	GAAAGAGGTGTCCAAAGACCCTGGT	SEQ ID NO:856
gi576646.V1.3_s_at	TGTCCCAAAGGACCCTCCAGAAAGA	SEQ ID NO:857
gi576646.V1.3_s_at	GTGGACACCACCGACTGGATCGAGG	SEQ ID NO:858
gi576646.V1.3_s_at	GGGAGCCCCTGCAGAAGCACACACT	SEQ ID NO:859
gi576646.V1.3_s_at	TGCCCAGGGAAGTCGTGCGCTCCAT	SEQ ID NO:860
gi576646.V1.3_s_at	TAATCCAGACAGACCAGCAAGCCAC	SEQ ID NO:861
Equus caballus Toll-like receptor 4 mRNA		
GI9717252-3_at	ATCTTTGACATCTTAGCCATCCTAA	SEQ ID NO:862
GI9717252-3_at	AGAAGGCTCCTGATTCAGATCCTCC	SEQ ID NO:863
GI9717252-3_at	ACATCGTCTCCCAAGTCTTTTGAAT	SEQ ID NO:864
GI9717252-3_at	ACAGGACTGCTAATCCCTTTGAGTT	SEQ ID NO:865
GI9717252-3_at	AAACATCCTGGTCATTCTTTAGCGT	SEQ ID NO:866
GI9717252-3_at	AAGTCAGCTAAGGAGTCCGTGCCAG	SEQ ID NO:867
GI9717252-3_at	GCTGCAACATACCAGGCATTGTGCT	SEQ ID NO:868
GI9717252-3_at	GAATGGAAACCATCTCATCTTTGAC	SEQ ID NO:869
GI9717252-3_at	GACTGGGCCCCAGTGAGTTCAGAAA	SEQ ID NO:870
GI9717252-3_at	GGCAGGTGATTCTGTCGTGCACAAG	SEQ ID NO:871
GI9717252-3_at	TCTCTGTTCAATTTTCCCTTTTCTA	SEQ ID NO:872
GI9717252-3M_at	ATAAGTTCTATTTCCACCTGATGCT	SEQ ID NO:873
GI9717252-3M_at	AGAGACTTCATTCCTGGTGTGGCCA	SEQ ID NO:874
GI9717252-3M_at	AAAGTTATTGTCGTGGTGTCCCAGC	SEQ ID NO:875
GI9717252-3M_at	CAGCACTTCATTCAGAGCCGATGGT	SEQ ID NO:876
GI9717252-3M_at	GCGGGTCGGTTTTCAGTATACTCAT	SEQ ID NO:877
GI9717252-3M_at	CTGATGCTTCTTGCTGGCTGCAAAA	SEQ ID NO:878
GI9717252-3M_at	GCATGCCCGTGCTGGGTTTTAACAA	SEQ ID NO:879
GI9717252-3M_at	GATGCCTTTGTTATCTACTCAAGCC	SEQ ID NO:880
GI9717252-3M_at	GGTGTGTGCAATACCCTTACAGATG	SEQ ID NO:881
GI9717252-3M_at	TGAGTATGAGATTGCCCAGACCTGG	SEQ ID NO:882
GI9717252-3M_at	TTAACAATGCCACCTGTCAGATTAG	SEQ ID NO:883
GI9717252-5_at	AGTTAGGCAGCCATAGCTTCTCCAA	SEQ ID NO:884
GI9717252-5_at	AGAAGTTCCCCATTGGACATCTCAA	SEQ ID NO:885
GI9717252-5_at	CATCTCTCCACCTTGATATTGACAG	SEQ ID NO:886
GI9717252-5_at	GAAAATGCCAGGATGATGCCGCCCA	SEQ ID NO:887
GI9717252-5_at	GACCTGAATCTCTACAAAATCCCTG	SEQ ID NO:888
GI9717252-5_at	GTGCAGGTGGTTCCTAACACTACTT	SEQ ID NO:889

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
GI9717252-5_at	GTGGCCGTGGAGACAAAGCTTTCAT	SEQ ID NO:890
GI9717252-5_at	TGGACTCTCCAGTTTACAGACGCTG	SEQ ID NO:891
GI9717252-5_at	TGGACCTGAGCTTTAACCCCTTGAA	SEQ ID NO:892
GI9717252-5_at	TGATGCATATCAGGGCCTCAACCAT	SEQ ID NO:893
GI9717252-5_at	TTACGGTGCGTCATGCTTTCACAGG	SEQ ID NO:894
GI9717252-5M_at	AAACAGGCCAGTGATTTTCCAGTAT	SEQ ID NO:895
GI9717252-5M_at	AAAGATTTGACACATCTGCCCTGCG	SEQ ID NO:896
GI9717252-5M_at	GATATTTCTTACACTAACACCCGAG	SEQ ID NO:897
GI9717252-5M_at	GCGCGGACTGCACAATTTGACGATT	SEQ ID NO:898
GI9717252-5M_at	GAATTCCGGTTAGCATACATTGATA	SEQ ID NO:899
GI9717252-5M_at	GAAGGATTTCCCACATTGGAGCTCA	SEQ ID NO:900
GI9717252-5M_at	GATTTTCCAGTATTCTTATCCCTCA	SEQ ID NO:901
GI9717252-5M_at	GGATTTCCAGCATTCCACTTTGAAA	SEQ ID NO:902
GI9717252-5M_at	GGAGCTCACCTCTCTCAAAAGGTTG	SEQ ID NO:903
GI9717252-5M_at	TGAGTTTCAAGTCCTGCTGTTCTGA	SEQ ID NO:904
GI9717252-5M_at	TACCAAGCCTTGAGTTTCTAGATCT	SEQ ID NO:905
No Homology		
WBC001A07_V1.3_at	ATGGTGCCATGGCTGGTAGCTTTTA	SEQ ID NO:906
WBC001A07_V1.3_at	AGGCAGACACTGCTGTATTTAGAAA	SEQ ID NO:907
WBC001A07_V1.3_at	AAAACAGAACTCACAGCCTTTCTCC	SEQ ID NO:908
WBC001A07_V1.3_at	GCTAATGAAGCTTCTCATCTTCTAT	SEQ ID NO:909
WBC001A07_V1.3_at	GAATATCTTGGCACACTTTAATGTC	SEQ ID NO:910
WBC001A07_V1.3_at	GATATTTGTTGCACAGGCAGACACT	SEQ ID NO:911
WBC001A07_V1.3_at	GTAGCTTTTAGTGAGTGCTGCAAGA	SEQ ID NO:912
WBC001A07_V1.3_at	GATTTTTCATCTGATTTGTTCACGC	SEQ ID NO:913
WBC001A07_V1.3_at	GTTCACGCAAATGTAGTTCTTATCA	SEQ ID NO:914
WBC001A07_V1.3_at	TATACAAAATTTCCATTCCTCCCAA	SEQ ID NO:915
WBC001A07_V1.3_at	TTCTCCCTGTGTCTTTGGCAATGTA	SEQ ID NO:916
WBC001B11_V1.3_at	ATGAGCGTCTTTTCTCAGTACTCAG	SEQ ID NO:917
WBC001B11_V1.3_at	AAAATAGCACCTCTGTGTCTTCTCT	SEQ ID NO:918
WBC001B11_V1.3_at	AACACAGCTGTCTCGATTTCTGGTG	SEQ ID NO:919
WBC001B11_V1.3_at	AAGGATGCATACTCAACCTCTGATC	SEQ ID NO:920
WBC001B11_V1.3_at	AATGCAGTGTTTTTCTTGTGTGTCC	SEQ ID NO:921
WBC001B11_V1.3_at	GAGACCACTGGTCATTCATTACCTG	SEQ ID NO:922
WBC001B11_V1.3_at	GTAGAATCCCACTTTTGCTTTCTTT	SEQ ID NO:923
WBC001B11_V1.3_at	GGAAGACCAATCTATCACCTTGAGT	SEQ ID NO:924
WBC001B11_V1.3_at	TGTGACTGTCATCCTAGCCTTTTAA	SEQ ID NO:925
WBC001B11_V1.3_at	TCTGGTGTATTTTGGTTCTCTTGGC	SEQ ID NO:926
WBC001B11_V1.3_at	TCAAGTTTCATGTGGCCTGGGTGTT	SEQ ID NO:927
WBC001C11_V1.3_at	ATCTATTTTCTTCAAACTTCTGCAA	SEQ ID NO:928
WBC001C11_V1.3_at	AGCTGACTTTTTTATGTGCTCTAAA	SEQ ID NO:929
WBC001C11_V1.3_at	AGCTCTTTAATCTCTTTATAAGTTA	SEQ ID NO:930
WBC001C11_V1.3_at	ACAACAGTTGGTTAGCAAGCTGACT	SEQ ID NO:931
WBC001C11_V1.3_at	AACTGGATCTCCAATTGATATTTTC	SEQ ID NO:932

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
WBC001C11_V1.3_at	GCCAGTCCCTGACATATCATGGAAA	SEQ ID NO:933
WBC001C11_V1.3_at	GACTTGTTTCAAGCTCTTTAATCTC	SEQ ID NO:934
WBC001C11_V1.3_at	GAGTGCTTTCATTTTGATAACTGGA	SEQ ID NO:935
WBC001C11_V1.3_at	GTATAACTCATTTGCAGTCTGGAAA	SEQ ID NO:936
WBC001C11_V1.3_at	GGCACAAATTTCTTTTTAAGACTTG	SEQ ID NO:937
WBC001C11_V1.3_at	TTTTTTAGTGCCAGTCCCTGACATA	SEQ ID NO:938
WBC001C11_V1.3_s_at	ATGCCTGCTTAGTGCTTTCTGATTA	SEQ ID NO:939
WBC001C11_V1.3_s_at	ACTCGCATTCTGTTTCTTGCTTTAA	SEQ ID NO:940
WBC001C11_V1.3_s_at	ACACACACTCATGGGATTCCAGTTA	SEQ ID NO:941
WBC001C11_V1.3_s_at	TCTTTGCAAGTGCTTTTGGAACTAA	SEQ ID NO:942
WBC001C11_V1.3_s_at	CCCCACAATGATTTTCTTTGCAAGT	SEQ ID NO:943
WBC001C11_V1.3_s_at	GCTTTCTGATTACTCGCATTCTGTT	SEQ ID NO:944
WBC001C11_V1.3_s_at	GCAGTTCTGTAGTGTCATTTCTTAT	SEQ ID NO:945
WBC001C11_V1.3_s_at	GATTCCAGTTATTACGAGTTGCTTT	SEQ ID NO:946
WBC001C11_V1.3_s_at	GTTGGATCAGTATTGCAGTTCTGTA	SEQ ID NO:947
WBC001C11_V1.3_s_at	GTTTAAAGCCTAACACCATTCTAAT	SEQ ID NO:948
WBC001C11_V1.3_s_at	TCTTGGATTAACTGATGCCTGCTTA	SEQ ID NO:949
No Homology		
WBC001C12_V1.3_at	ATTACTCACTTTTCACTTCTATCTA	SEQ ID NO:950
WBC001C12_V1.3_at	AGTCAACTCCAAATTCTCATTCTTC	SEQ ID NO:951
WBC001C12_V1.3_at	AGAATGACTGTTGGAGGCCGGCCCA	SEQ ID NO:952
WBC001C12_V1.3_at	ACATGCTGTGCTTTGGTGGCCTAGG	SEQ ID NO:953
WBC001C12_V1.3_at	AATGACCCAACCCTGTATTTATGCA	SEQ ID NO:954
WBC001C12_V1.3_at	AATAATCAACAGTCTTCCCTTTCCT	SEQ ID NO:955
WBC001C12_V1.3_at	GGGCTATAACCCCAACATATCGTGA	SEQ ID NO:956
WBC001C12_V1.3_at	GGGTGTAGACCGACACAGCACGCAT	SEQ ID NO:957
WBC001C12_V1.3_at	GGAAGCTCTTATTGGGCATATCTGC	SEQ ID NO:958
WBC001C12_V1.3_at	TGTGGGCTCAGCATGAAGTCAACTC	SEQ ID NO:959
WBC001C12_V1.3_at	TGCTGTGGCGGCATTCCATGTAGAA	SEQ ID NO:960
RAB10, member RAS oncogene family (RAB10),		
WBC001F08_V1.3_at	AAGTCTCTTGGGATCCTGTGTAGAA	SEQ ID NO:961
WBC001F08_V1.3_at	AATTTTACTGTCTTGTTGCTTTCCT	SEQ ID NO:962
WBC001F08_V1.3_at	GTTAAGTCCATTCTCTGGTACTAGC	SEQ ID NO:963
WBC001F08_V1.3_at	GCAGCATTGCCAAATAATCCCTAAT	SEQ ID NO:964
WBC001F08_V1.3_at	GTTGCTTTCCTTCATCTGGAATGTG	SEQ ID NO:965
WBC001F08_V1.3_at	GGTACTAGCTACAATTCGGTTTCAT	SEQ ID NO:966
WBC001F08_V1.3_at	GGCTACCTTTTGTTAAATCTGCACT	SEQ ID NO:967
WBC001F08_V1.3_at	TTGCCCCTTTTTCTGTAAGTCTCTT	SEQ ID NO:968
WBC001F08_V1.3_at	TATGCCTCACTGGTGGTTGTTCTTA	SEQ ID NO:969 .
WBC001F08_V1.3_at	TTTGCTTAATATTAGGGCCTTGCCC	SEQ ID NO:970
WBC001F08_V1.3_at	TTTCCCTCACTTGACTTTATCATTG	SEQ ID NO:971
Retinoblastoma-like 2 (p130)		
WBC001F11_V1.3_at	ATTAAGAGGGATCAGCTGGCTAAGT	SEQ ID NO:972
WBC001F11_V1.3_at	ATATCTTTGAGTGTGTTCCTGGCAG	SEQ ID NO:973

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
WBC001F11_V1.3_at	ATCTTCTTTGATGCTTTTGTACTTT	SEQ ID NO:974
WBC001F11_V1.3_at	TTGTTAAAGCCCCAGTAGCCACCTT	SEQ ID NO:975
WBC001F11_V1.3_at	AAATTATGACCTCTTCCTTTAGGAG	SEQ ID NO:976
WBC001F11_V1.3_at	AAACCTCTCAGATACTGCTACTGTA	SEQ ID NO:977
WBC001F11_V1.3_at	GCTATTGTTCCAGCAGTTTTAACGT	SEQ ID NO:978
WBC001F11_V1.3_at	GAAATTCTCCAGTTTTTGATTATTA	SEQ ID NO:979
WBC001F11_V1.3_at	GTAGCCACCTTTTGGGCATATTTGA	SEQ ID NO:980
WBC001F11_V1.3_at	TACTAGGTAACTTCACATTGCTCTG	SEQ ID NO:981
WBC001F11_V1.3_at	TATACACCTTTATTAATCGCTATTG	SEQ ID NO:982
Activated RNA polymerase II transcription cofactor 4 variant protein (incomplete)		
WBC001H09_V1.3_at	ATTTCCCGTACTCTTGGCATTTTAT	SEQ ID NO:983
WBC001H09_V1.3_at	GAATACTCCTACCTCATTAGCTAGT	SEQ ID NO:984
WBC001H09_V1.3_at	AAGAGTGTGTACATCCTGGCTTGGC	SEQ ID NO:985
WBC001H09_V1.3_at	AATTGTGGAATACCTGTCTGCTTTG	SEQ ID NO:986
WBC001H09_V1.3_at	GGAGTAAACATTCACGTAGTCACAA	SEQ ID NO:987
WBC001H09_V1.3_at	GAAATTCTTTGCAACTCTCTTTTTA	SEQ ID NO:988
WBC001H09_V1.3_at	GATTAACCTATTCTACATAACGTGT	SEQ ID NO:989
WBC001H09_V1.3_at	GATTATTCTCTTTTGTTTTGCTTCA	SEQ ID NO:990
WBC001H09_V1.3_at	GTCTGCTTTGTTTGGTACATCTTCC	SEQ ID NO:991
WBC001H09_V1.3_at	TGTTTTGCTTCATCAATGCCTAAGA	SEQ ID NO:992
WBC001H09_V1.3_at	TACAAGCAGCATTTGACCCATTTCC	SEQ ID NO:993
No homology		
WBC003D11_V1.3_at	ATCTTCATTTCCTCTTAGCTGTCAG	SEQ ID NO:994
WBC003D11_V1.3_at	AGACAGAGTGTGCATTCCTTCTTGC	SEQ ID NO:995
WBC003D11_V1.3_at	CATCGGACCAACTTGTAGCTGACTA	SEQ ID NO:996
WBC003D11_V1.3_at	AATGTGCCCAGGCTGAACTGCTGGA	SEQ ID NO:997
WBC003D11_V1.3_at	CGATAAGTCTCGCTTGTTCTTGCAC	SEQ ID NO:998
WBC003D11_V1.3_at	GAGGTTGTCCTTAATCAGCCATCGG	SEQ ID NO:999
WBC003D11_V1.3_at	GAGGGTGATTCGCATCTTCATTTCC	SEQ ID NO:1000
WBC003D11_V1.3_at	GTCACATCCATGAGCCCAGTCAAGA	SEQ ID NO:1001
WBC003D11_V1.3_at	GTCATTCCATTATACCAGCTGAGGT	SEQ ID NO:1002
WBC003D11_V1.3_at	TATGGCTTGGCCTTGAGACTTGCTT	SEQ ID NO:1003
WBC003D11_V1.3_at	TTCTTGCCCGTTACACGATAAGTCT	SEQ ID NO:1004
IBR domain containing 3 (IBRDC3)		
WBC003F02_V1.3_at	ATGTGCCAGACATCACCTCAGATGA	SEQ ID NO:1005
WBC003F02_V1.3_at	AGCAAGCCTTGGGACATCAGCCTGG	SEQ ID NO:1006
WBC003F02_V1.3_at	CCTGGCCTGTGCTTTACTACAATGA	SEQ ID NO:1007
WBC003F02_V1.3_at	GCCCTAGAGGGTGTCCTTGTGTGAA	SEQ ID NO:1008
WBC003F02_V1.3_at	GAAGCACACTTGTTATGCACCTGCT	SEQ ID NO:1009
WBC003F02_V1.3_at	GAAAGACTGTTTGGCCAGCAAGCCT	SEQ ID NO:1010
WBC003F02_V1.3_at	GAGAGCATCCGCAGTGACCTGGAGA	SEQ ID NO:1011
WBC003F02_V1.3_at	GATTCTTATCTCATGGGCACTGTAG	SEQ ID NO:1012

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
WBC003F02_V1.3_at	GGATTGAATGCTCCTGTTCTGAGAA	SEQ ID NO:1013
WBC003F02_V1.3_at	GGCACTGTAGCCAGACTTAGCACAT	SEQ ID NO:1014
WBC003F02_V1.3_at	TGGAGAGCTCCGATACGCAGTCAGA	SEQ ID NO:1015
CGI-54 protein		
WBC003H01_V1.3_at	ATATCAACATGACCCACTACATTCG	SEQ ID NO:1016
WBC003H01_V1.3_at	ATGACTTGCAGAGCTTCGGCCTCGA	SEQ ID NO:1017
WBC003H01_V1.3_at	ATGACCCACTACATTCGGCACCTGT	SEQ ID NO:1018
WBC003H01_V1.3_at	AGAGCTTCGGCCTCGACAATATCAA	SEQ ID NO:1019
WBC003H01_V1.3_at	GGGCATTGTGAACCCCCTGGACCGC	SEQ ID NO:1020
WBC003H01_V1.3_at	ACGTCCATGACTTGCAGAGCTTCGG	SEQ ID NO:1021
WBC003H01_V1.3_at	CTTCGGCCTCGACAATATCAACATG	SEQ ID NO:1022
WBC003H01_V1.3_at	CTACATTCGGCACCTGTCATTCGGG	SEQ ID NO:1023
WBC003H01_V1.3_at	GCACGTCCATGACTTGCAGAGCTTC	SEQ ID NO:1024
WBC003H01_V1.3_at	GGAGGACTACCCGGGCATTGTGAAC	SEQ ID NO:1025
WBC003H01_V1.3_at	GGCCTCGACAATATCAACATGACCC	SEQ ID NO:1026
Heterogeneous nuclear ribonucleoprotein F		
WBC004B05_V1.3_at	ACTGTGATTTCTTTTTGGGTGTATT	SEQ ID NO:1027
WBC004B05_V1.3_at	ACATTTCTCATGTTTGTTCATTCTA	SEQ ID NO:1028
WBC004B05_V1.3_at	AAACTTTCTTTGTACTGTGATTTCT	SEQ ID NO:1029
WBC004B05_V1.3_at	GAAAACTCAAGGTGCTAGATCCCTA	SEQ ID NO:1030
WBC004B05_V1.3_at	GAGACGTGCTTTTTTGGAAAACTCA	SEQ ID NO:1031
WBC004B05_V1.3_at	GAGACACATTACTAATACTGTAGGA	SEQ ID NO:1032
WBC004B05_V1.3_at	GGGTGTATTTTGCTAAGTGAAACTT	SEQ ID NO:1033
WBC004B05_V1.3_at	GTTCATTCTAGTTTATTTTCATTTA	SEQ ID NO:1034
WBC004B05_V1.3_at	GTGAGGCCTTGACTTAAAACTTTCT	SEQ ID NO:1035
WBC004B05_V1.3_at	GGTGCTAGATCCCTAATTCGAAGAG	SEQ ID NO:1036
WBC004B05_V1.3_at	TTACACCACATCACCGTGAACACAT	SEQ ID NO:1037
WBC004B05_V1.3_s_at	ATTACCTCTTCAGTGTTTTCTCATG	SEQ ID NO:1038
WBC004B05_V1.3_s_at	AAAGCAGTTAACTCTAGAGGGAGCT	SEQ ID NO:1039
WBC004B05_V1.3_s_at	AACATTTTGGTAGTGTACTTCAGAG	SEQ ID NO:1040
WBC004B05_V1.3_s_at	GCAAACTTTCTTCTAGCATGTGATA	SEQ ID NO:1041
WBC004B05_V1.3_s_at	GGACCCATTTTGCACCATGAGTTTG	SEQ ID NO:1042
WBC004B05_V1.3_s_at	GGAGCATTTGAGTTGTTTCAATCAA	SEQ ID NO:1043
WBC004B05_V1.3_s_at	TGTGGATCTTTTACACCACATCACC	SEQ ID NO:1044
WBC004B05_V1.3_s_at	TAGAGGGAGCTGTGGGACCCATTTT	SEQ ID NO:1045
WBC004B05_V1.3_s_at	TTCAGCTTTTCTCAATTAACATTTT	SEQ ID NO:1046
WBC004B05_V1.3_s_at	TTTTCTCATGCAAACTTTCTTCTAG	SEQ ID NO:1047
WBC004B05_V1.3_s_at	TTCAATCAAATTTTCACAGGCAGCC	SEQ ID NO:1048
Dendritic cell protein variant, clone: CAE03638		
WBC004C03_V1.3_at	ATATCTTGGCTTTTCCTTGTGTGAG	SEQ ID NO:1049
WBC004C03_V1.3_at	ATGTTTCCGCTCATGCTTCAGAGTA	SEQ ID NO:1050
WBC004C03_V1.3_at	AGGCACTGCATTGGGTCATACTTAA	SEQ ID NO:1051
WBC004C03_V1.3_at	AAATCTGTTTTGTCTTCTACTCCCT	SEQ ID NO:1052
WBC004C03_V1.3_at	CTACCTTTTACTTCATGTTTCCGCT	SEQ ID NO:1053

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
WBC004C03_V1.3_at	GAGAGACCTGTCAACATTTTGTTAT	SEQ ID NO:1054
WBC004C03_V1.3_at	GTTATTGTTTGCTGCTAGTCGCTTT	SEQ ID NO:1055
WBC004C03_V1.3_at	GTAATCCACTATCCAGAGAGACCTG	SEQ ID NO:1056
WBC004C03_V1.3_at	GTGGCATGTTTCCAAGGCACTGCAT	SEQ ID NO:1057
WBC004C03_V1.3_at	TGTTTTGTATCTTCTGTCAGAGCCA	SEQ ID NO:1058
WBC004C03_V1.3_at	TTCCCTTCCCAAACATGTCTATGTT	SEQ ID NO:1059
No Homology		
WBC004D07_V1.3_at	ATCCATCCCACAGTCAACTGGTTGA	SEQ ID NO:1060
WBC004D07_V1.3_at	AGTTTGCTGGCCAATTGCACCTGCT	SEQ ID NO:1061
WBC004D07_V1.3_at	ACCTGCTGTGTTGTTTTCCATCCAT	SEQ ID NO:1062
WBC004D07_V1.3_at	AAACGGTCTGTGATTTTGGAACTGG	SEQ ID NO:1063
WBC004D07_V1.3_at	CATACCTTCTCATGTGCATTTCAGT	SEQ ID NO:1064
WBC004D07_V1.3_at	GAAAGACTTCTTAGCGTTCCAGTTT	SEQ ID NO:1065
WBC004D07_V1.3_at	GACTGTGGCACACTGATGCACTGAA	SEQ ID NO:1066
WBC004D07_V1.3_at	GAGTCATGGATTTCTTTGCTTACAA	SEQ ID NO:1067
WBC004D07_V1.3_at	GTAACACCATTTTTCTTTGAGACTA	SEQ ID NO:1068
WBC004D07_V1.3_at	GTGGCTGCAGGAATTCTTTTCTAAA	SEQ ID NO:1069
WBC004D07_V1.3_at	TTATTTCTCCCCATGACTTCAAACA	SEQ ID NO:1070
TRAF-interacting protein with a forkhead-associated domain		
WBC004E04_V1.3_at	ACGAAGTGGTGTGCCGGTACTGATC	SEQ ID NO:1071
WBC004E04_V1.3_at	CAACGGTCATTTGTTTTCAAGGTCA	SEQ ID NO:1072
WBC004E04_V1.3_at	ACTAGTGTTGTAGCCTGTTGGTACT	SEQ ID NO:1073
WBC004E04_V1.3_at	AAGGAACTCTCTCTTGGTTTGGTCA	SEQ ID NO:1074
WBC004E04_V1.3_at	GTTAGTCATCGATTTGGTCTCCTGT	SEQ ID NO:1075
WBC004E04_V1.3_at	GTACTTATAGTACCAGTGTCCTGGA	SEQ ID NO:1076
WBC004E04_V1.3_at	GGTCATATTATTTCACAACGGTCAT	SEQ ID NO:1077
WBC004E04_V1.3_at	TGTTATTGTTATCTGCTGTGCTGGC	SEQ ID NO:1078
WBC004E04_V1.3_at	TCTCCTGTTGCATTCCTGGATGTAT	SEQ ID NO:1079
WBC004E04_V1.3_at	TCCCCTTCGTTACTGTGGTATGTTA	SEQ ID NO:1080
WBC004E04_V1.3_at	TAGACGCTCCGCTTACGAAGTGGTG	SEQ ID NO:1081
WBC005B09_V1.3_at	GCGCTGTAAGCCTCTGAAGGAATTT	SEQ ID NO:1082
WBC005B09_V1.3_at	GAATTTATGCTTTCTCAAGATGCTG	SEQ ID NO:1083
WBC005B09_V1.3_at	GACCGATTGGACTGGGATGAACATA	SEQ ID NO:1084
WBC005B09_V1.3_at	GATGCTGAACATGAGCTGCTCTTTG	SEQ ID NO:1085
WBC005B09_V1.3_at	GTATTGCCGTGTTTATTTTGCTTAA	SEQ ID NO:1086
WBC005B09_V1.3_at	GTAAATATTTCCATCATGACCGATT	SEQ ID NO:1087
WBC005B09_V1.3_at	GGGTTTACAGTATTTCCAACACATG	SEQ ID NO:1088
WBC005B09_V1.3_at	GGAGATATGTTTCAAGGCGCTGTAA	SEQ ID NO:1089
WBC005B09_V1.3_at	TGAGCTGCTCTTTGACCTCATTGAG	SEQ ID NO:1090
WBC005B09_V1.3_at	TCCCAACCATGTGATGTCTGGAGTA	SEQ ID NO:1091
WBC005B09_V1.3_at	TAAAGCATCCTTTCTTTTACCCTCT	SEQ ID NO:1092
Homo sapiens hypothetical protein		

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
FLJ22662, mRNA		
WBC005D02_V1.3_at	ATCTTCCGGCGCGACCAAGGGAAAG	SEQ ID NO:1093
WBC005D02_V1.3_at	ATCTGCTGCCGTGAGGACCTGAACT	SEQ ID NO:1094
WBC005D02_V1.3_at	ATGCCAGAGGCCTACAACTTTGATT	SEQ ID NO:1095
WBC005D02_V1.3_at	AGTCCTGGAGGCTGCTACGATACGA	SEQ ID NO:1096
WBC005D02_V1.3_at	ACAGCCTATGCCATTAGTGGTCCCA	SEQ ID NO:1097
WBC005D02_V1.3_at	AGCTGGGTTTGGACTTCTCTTATGA	SEQ ID NO:1098
WBC005D02_V1.3_at	ACCGGTTCAACAAAACTCTCCATGA	SEQ ID NO:1099
WBC005D02_V1.3_at	AAATCTACAACTGGAGTGGCTACCC	SEQ ID NO:1100
WBC005D02_V1.3_at	GTGGCTACCCAATGCTGGTTCAGAA	SEQ ID NO:1101
WBC005D02_V1.3_at	GTGGTCTCCCTGTTTTTCACTGGAA	SEQ ID NO:1102
WBC005D02_V1.3_at	TTCTCTTATGATCTGGCTCCACGAG	SEQ ID NO:1103
Polymeric immunoglobulin receptor 3 precursor (PIGR3)		
WBC005F10_V1.3_at	TTTCGACTGGCGCAACGTTTGGTAA	SEQ ID NO:1104
WBC005F10_V1.3_at	ATAACTTTTGTACCGTGCCCTCTAT	SEQ ID NO:1105
WBC005F10_V1.3_at	AGTGGTTAAGGCTTCCTATCCAGAA	SEQ ID NO:1106
WBC005F10_V1.3_at	AGCCCAGCTTCCTGAGTACCAATAA	SEQ ID NO:1107
WBC005F10_V1.3_at	CAGTGACTGACCCATATGTAGCAAA	SEQ ID NO:1108
WBC005F10_V1.3_at	GCCTGCAGCGTGAGAAGACTTCCCA	SEQ ID NO:1109
WBC005F10_V1.3_at	GCTGCTCACTCACTGTGGGATGTTA	SEQ ID NO:1110
WBC005F10_V1.3_at	GATAATACCCACTTTCTAGGATTGT	SEQ ID NO:1111
WBC005F10_V1.3_at	GATGTTATGAAAGCGACCCTTCCAA	SEQ ID NO:1112
WBC005F10_V1.3_at	TAACGTTTGACCCTGAGGCCCAGAG	SEQ ID NO:1113
WBC005F10_V1.3_at	TTCCTTCTGGATCGTTTCTCCAAGA	SEQ ID NO:1114
Homo sapiens methionine adenosyltransferase II, beta (MAT2B)		
WBC006E03_V1.3_at	ATAAAACTGTCCTTTTCACTCCATG	SEQ ID NO:1115
WBC006E03_V1.3_at	AGGTTTTTATGCTCGAGATCTTTCG	SEQ ID NO:1116
WBC006E03_V1.3_at	ACAGATCTGCTGTAGACTTGTTTTT	SEQ ID NO:1117
WBC006E03_V1.3_at	GTATATTGGAACTCCTGCAGCTTCG	SEQ ID NO:1118
WBC006E03_V1.3_at	TGGCTTAACTCGCTGTTTGCGTATA	SEQ ID NO:1119
WBC006E03_V1.3_at	GGCCTTGTAAGTCTTTTGACCATTC	SEQ ID NO:1120
WBC006E03_V1.3_at	TGCTCTTGCGCTAGTGAAATGGTCT	SEQ ID NO:1121
WBC006E03_V1.3_at	TTTGCAACTGTTGACCCTTTTATGT	SEQ ID NO:1122
WBC006E03_V1.3_at	TGCATCGTTCATTCCTATAAGCTCT	SEQ ID NO:1123
WBC006E03_V1.3_at	TATTTGCTTTGCCTGAGCTCAGATC	SEQ ID NO:1124
WBC006E03_V1.3_at	TATCATTTTGTTTGTTCTGGCTTAA	SEQ ID NO:1125
Ubiquitin-conjugating enzyme E2B (RAD6 homolog) (UBE2B)		
WBC006H06_V1.3_at	ATTCACAATTTGCACCTCTATCATG	SEQ ID NO:1126
WBC006H06_V1.3_at	AGGCTACTTGTTACTGTTTCTTCAT	SEQ ID NO:1127
WBC006H06_V1.3_at	ACAAGCTATCCTATGCCTTCAAATA	SEQ ID NO:1128

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
WBC006H06_V1.3_at	AATGTTTTAATACTAGGGCCTGCTG	SEQ ID NO:1129
WBC006H06_V1.3_at	AATCCATGCCCCACTATTAACAATG	SEQ ID NO:1130
WBC006H06_V1.3_at	AATTGGCACCTCTACCTTGAGCAGA	SEQ ID NO:1131
WBC006H06_V1.3_at	GCTGAGTTGCTTTCTCTTGTGGAGA	SEQ ID NO:1132
WBC006H06_V1.3_at	GCAATTGCCTATCTGTTTATTCTGG	SEQ ID NO:1133
WBC006H06_V1.3_at	GTTAAACTGTACCTTTTGCGATTCA	SEQ ID NO:1134
WBC006H06_V1.3_at	GTTTCTTCATGCACTACTTACTGTT	SEQ ID NO:1135
WBC006H06_V1.3_at	GTCTGTCCAACTCTGTATTTAGGCT	SEQ ID NO:1136
No homology		
WBC007A09_V1.3_at	ATCAATCCAGCAATCTGAGCGCTTC	SEQ ID NO:1137
WBC007A09_V1.3_at	AGGGCTTATGCTATTTCCTGTTTCT	SEQ ID NO:1138
WBC007A09_V1.3_at	AGCATCATGTCTCACTTGGGTTACT	SEQ ID NO:1139
WBC007A09_V1.3_at	GAATTCTACTTCTGCCTAGGGCTTA	SEQ ID NO:1140
WBC007A09_V1.3_at	GAGGTCTCCTTGATCCTTTAGTATA	SEQ ID NO:1141
WBC007A09_V1.3_at	GGAACGTTCTACTAGGCGCTACATG	SEQ ID NO:1142
WBC007A09_V1.3_at	TGAGCGCTTCTCAGGACTGTACTAC	SEQ ID NO:1143
WBC007A09_V1.3_at	TAAGATGTGTGTTGTCTCTTTCCCT	SEQ ID NO:1144
WBC007A09_V1.3_at	TATGATCTTTCCTCAAGTGTCACCT	SEQ ID NO:1145
WBC007A09_V1.3_at	TTCCTTGCTTCCTTTAACACACGAA	SEQ ID NO:1146
WBC007A09_V1.3_at	TTGGGTTACTGCAGTAGCTCCCTGA	SEQ ID NO:1147
Transmembrane protein 23		
WBC007G03_V1.3_at	ATTAGTTATCCATACTCTCATGACA	SEQ ID NO:1148
WBC007G03_V1.3_at	ATATCCATTCTGTATTTTACGTGCA	SEQ ID NO:1149
WBC007G03_V1.3_at	CATACTCTCATGACAATTTTGTTGG	SEQ ID NO:1150
WBC007G03_V1.3_at	CTGATATCTTAACAGCTTACCTAGA	SEQ ID NO:1151
WBC007G03_V1.3_at	GCAGAATTATCTTCCGTAGGGTTTT	SEQ ID NO:1152
WBC007G03_V1.3_at	GTGCAGAAACTGCATGTAATTCTAA	SEQ ID NO:1153
WBC007G03_V1.3_at	TTACGTGCAGCAGAATTATCTTCCG	SEQ ID NO:1154
WBC007G03_V1.3_at	GTGTTCACATTCGTCACAAAGTTGT	SEQ ID NO:1155
WBC007G03_V1.3_at	GGCTCTTATTTCTAATGTGTTCACA	SEQ ID NO:1156
WBC007G03_V1.3_at	TTCTAAGTTTTACTCCTAACATAAG	SEQ ID NO:1157
WBC007G03_V1.3_at	TTCTATTCTATACTTGCCAATGTGG	SEQ ID NO:1158
No Homology		
WBC007G12_V1.3_at	ATGTGTGTACTGTATCTGCCTTTCC	SEQ ID NO:1159
WBC007G12_V1.3_at	AGTTGTGCAGTTTTTCTTTTCAGAA	SEQ ID NO:1160
WBC007G12_V1.3_at	ACTGCCTGCTTTTTTGACCTTTGTT	SEQ ID NO:1161
WBC007G12_V1.3_at	ACTGATTACTGTGTCTTGCTCTTCG	SEQ ID NO:1162
WBC007G12_V1.3_at	AACAGTGATCCTAGGGCTGACCGCA	SEQ ID NO:1163
WBC007G12_V1.3_at	GCAGCCTCTTTTGCATAGTCATGTA	SEQ ID NO:1164
WBC007G12_V1.3_at	GGATTCAGTCTTGTCTTTTGTCTAG	SEQ ID NO:1165
WBC007G12_V1.3_at	TGTTCATACAATGTGGCAGCCTCTT	SEQ ID NO:1166
WBC007G12_V1.3_at	TGCCTTTCCACCACATTTTTATGAC	SEQ ID NO:1167
WBC007G12_V1.3_at	TTATGACACTGTATTCCACTGCCTG	SEQ ID NO:1168
WBC007G12_V1.3_at	TTGTTCCCTCGGATTTGTCCTATAA	SEQ ID NO:1169
WBC008D05_V1.3_at	ATGCCCATGGAACATTCTCTAGGAT	SEQ ID NO:1170

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
WBC008D05_V1.3_at	AGGATTGATCACATATTAGGCCACA	SEQ ID NO:1171
WBC008D05_V1.3_at	AGAACATTCCATCCAAAAACCACAG	SEQ ID NO:1172
WBC008D05_V1.3_at	ACACATTCTTTTTACATGCCCATGG	SEQ ID NO:1173
WBC008D05_V1.3_at	AATACCATGCAGCTTTTCTGACCAC	SEQ ID NO:1174
WBC008D05_V1.3_at	AATATCTATGCACCCAACACAGGAG	SEQ ID NO:1175
WBC008D05_V1.3_at	GCAGCTTTTCTGACCACAAAGGTAT	SEQ ID NO:1176
WBC008D05_V1.3_at	TAAGAGACAAAGACGGGCACTACAT	SEQ ID NO:1177
WBC008D05_V1.3_at	GAAACACTCGCCTGAAAGGACACAT	SEQ ID NO:1178
WBC008D05_V1.3_at	TTTAACACTCCACTTACACCAATGG	SEQ ID NO:1179
WBC008D05_V1.3_at	TTAGGCCACAAAACAAGTCTCAATA	SEQ ID NO:1180
No Homology		
WBC008F06_V1.3_at	ATATTTCTGATTGGTGCCTTTCCAC	SEQ ID NO:1181
WBC008F06_V1.3_at	AGTTGGTTATAGTCTTCTGTTCTGA	SEQ ID NO:1182
WBC008F06_V1.3_at	CAACCAGCTCGGACATTTGTGTTTT	SEQ ID NO:1183
WBC008F06_V1.3_at	CATAAGCCGTTTTTCTGTTTAATGG	SEQ ID NO:1184
WBC008F06_V1.3_at	GCCTTTCCACTTTTTAGCAGCAATG	SEQ ID NO:1185
WBC008F06_V1.3_at	GATGTTTTCGTTCCCAAATGTGACT	SEQ ID NO:1186
WBC008F06_V1.3_at	GTTATCTGCTTTCCTTCATTTTTGA	SEQ ID NO:1187
WBC008F06_V1.3_at	TGTCATAAACCCCATCATAAGCCGT	SEQ ID NO:1188
WBC008F06_V1.3_at	TGAAATTCTTTCATGTCCTTTCCCT	SEQ ID NO:1189
WBC008F06_V1.3_at	TTTCACTCATGCCAAAACAACCAGC	SEQ ID NO:1190
WBC008F06_V1.3_at	TTTGAGCCTGTTATTCGACACCATC	SEQ ID NO:1191
v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein		
WBC008F12_V1.3_at	AGGGCCTCTTCTCTGTTTGTTTCAG	SEQ ID NO:1192
WBC008F12_V1.3_at	AGTGTGACATGGGTTCTTCTGAAGA	SEQ ID NO:1193
WBC008F12_V1.3_at	AGACATCTGCTACCTCTCGTAGGAT	SEQ ID NO:1194
WBC008F12_V1.3_at	AAAACCCAGTATTCAGCACATGTCC	SEQ ID NO:1195
WBC008F12_V1.3_at	CTCCGAGAATTGGTTGCTGTTTAGA	SEQ ID NO:1196
WBC008F12_V1.3_at	GAAGGATGCGATAAGCCGTTGCCCC	SEQ ID NO:1197
WBC008F12_V1.3_at	TGCACCTGGAGCTTGAGAGGGCCTC	SEQ ID NO:1198
WBC008F12_V1.3_at	GATTGCCCCGTAATTCTAAATTTAG	SEQ ID NO:1199
WBC008F12_V1.3_at	GTTGTGTTCCAAAGTCCTGAAGCCA	SEQ ID NO:1200
WBC008F12_V1.3_at	TGGAAAGCATCTTGTATCTCCTCCC	SEQ ID NO:1201
WBC008F12_V1.3_at	TGAAGCCAGAGCCTGCGCCAGACAT	SEQ ID NO:1202
Human mRNA for complement receptor type 1 (CR1, C3b/C4b receptor, CD35)		
WBC009B10_V1.3_at	ACTGTGTTCAGCCTCAAAGTCTGCA	SEQ ID NO:1203
WBC009B10_V1.3_at	CTCATAGTCGGCATATTCTTCGGTA	SEQ ID NO:1204
WBC009B10_V1.3_at	CTTCGTTCTCTGGATTTGTCTGTAT	SEQ ID NO:1205
WBC009B10_V1.3_at	CTGGTTTCCTCCAATGAACTGCTTA	SEQ ID NO:1206
WBC009B10_V1.3_at	GCTTACAGCCCCAGCAAGAGAGGAA	SEQ ID NO:1207
WBC009B10_V1.3_at	GCAATTCCTCTGTTATTTCCTAATA	SEQ ID NO:1208
WBC009B10_V1.3_at	GTATGATCTTCTTTATTGTACCCAT	SEQ ID NO:1209

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
WBC009B10_V1.3_at	GTGATTATCCATTTACATCCCCAAC	SEQ ID NO:1210
WBC009B10_V1.3_at	TACATCCCCAACAAGGCAACTGTGT	SEQ ID NO:1211
WBC009B10_V1.3_at	TAGTTTCCACGTCCCAAATTGCAAT	SEQ ID NO:1212
WBC009B10_V1.3_at	TTGTACCCATCATTATTTCCTGTTG	SEQ ID NO:1213
Down-regulator of transcription 1, TBP-binding (negative cofactor 2)		
WBC009E12_V1.3_at	ATTAAATACATTTCTCCCATGCCAC	SEQ ID NO:1214
WBC009E12_V1.3_at	AGGATAGATTTCAGCTCCCAGGATC	SEQ ID NO:1215
WBC009E12_V1.3_at	AGTGTTGGACTTCTTAATGATCATA	SEQ ID NO:1216
WBC009E12_V1.3_at	AGCTCCCAGGATCCCAATTTTAATT	SEQ ID NO:1217
WBC009E12_V1.3_at	AATTTCTGTATTCACCAAGCCCAAG	SEQ ID NO:1218
WBC009E12_V1.3_at	GACATTCTTGTGATTTCATATGCTG	SEQ ID NO:1219
WBC009E12_V1.3_at	GTTCGAAGCCTGGTGACTTTTCATT	SEQ ID NO:1220
WBC009E12_V1.3_at	GTAATCTAAATTCCTGTGTCAGTTG	SEQ ID NO:1221
WBC009E12_V1.3_at	GTACTGTAACATCCTTATACTTTAT	SEQ ID NO:1222
WBC009E12_V1.3_at	GTGTTGGCTTTTCTAATTTGTACTG	SEQ ID NO:1223
WBC009E12_V1.3_at	GTGTCAGTTGCCAAATCACTTAAAT	SEQ ID NO:1224
3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)		
WBC010F04_V1.3_at	ATGACATGAGCCTTATAGACTGTAA	SEQ ID NO:1225
WBC010F04_V1.3_at	AGTCCATTGCCAGCAGTGGGCAGGC	SEQ ID NO:1226
WBC010F04_V1.3_at	AATTACTTCATTTTAACATCCACTG	SEQ ID NO:1227
WBC010F04_V1.3_at	CACCTTATTAACTGTGAGGTCATAA	SEQ ID NO:1228
WBC010F04_V1.3_at	GCAGGCCTGGCATTATTGGCACAGA	SEQ ID NO:1229
WBC010F04_V1.3_at	GAGCATTAACTGTGCACCTTATTAA	SEQ ID NO:1230
WBC010F04_V1.3_at	GATCTCTTTGGTGCTGAACTATGAC	SEQ ID NO:1231
WBC010F04_V1.3_at	GGGTGTCAGGAAATGGGTATTCTCA	SEQ ID NO:1232
WBC010F04_V1.3_at	GGTATTCTCAAAGTCCATTGCCAGC	SEQ ID NO:1233
WBC010F04_V1.3_at	TAAAGCATTTTCTCCGACTTTCACC	SEQ ID NO:1234
WBC010F04_V1.3_at	TAGACAGTTTTGTAGATCTCTTTGG	SEQ ID NO:1235
Pinin, desmosome associated protein (PNN)		
WBC012E07_V1.3_at	AATCAGATCTTTGCAGCTTTGAGGG	SEQ ID NO:1236
WBC012E07_V1.3_at	AATTTGGTTGGCATTTTCTTCATGA	SEQ ID NO:1237
WBC012E07_V1.3_at	CTTTTGTGTTGGCTCTAACTCTGAA	SEQ ID NO:1238
WBC012E07_V1.3_at	CCTCCTCATCTTTAAACCACGTATT	SEQ ID NO:1239
WBC012E07_V1.3_at	GAGCATCATTCTTTTGTCTCCATGG	SEQ ID NO:1240
WBC012E07_V1.3_at	GTTTCCTCACTTTTATTTGCCTTAG	SEQ ID NO:1241
WBC012E07_V1.3_at	GTCTCCATGGTTACTTGTGTGATAC	SEQ ID NO:1242
WBC012E07_V1.3_at	GTGGTCTTGTCTTAACTTTTGTGTT	SEQ ID NO:1243
WBC012E07_V1.3_at	GGAGTATCTGTTGCCCATTACTATA	SEQ ID NO:1244
WBC012E07_V1.3_at	TACTGTTTTTTCTAATCTCCCTTGT	SEQ ID NO:1245
WBC012E07_V1.3_at	TTTAATCTAAGCATTTTCCCCTCCT	SEQ ID NO:1246

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
Complement component 5 receptor 1 (C5a ligand)		
WBC012F07_V1.3_at	GAAACAACCAGGAGCCCGTACGGAG	SEQ ID NO:1247
WBC012F07_V1.3_at	ATATCAGCTGCCTAGAATCCGGACG	SEQ ID NO:1248
WBC012F07_V1.3_at	ACATCGACACTTCCTTCTAGAGAGA	SEQ ID NO:1249
WBC012F07_V1.3_at	GACGCGGTCTAACCCTGTTGAGAAA	SEQ ID NO:1250
WBC012F07_V1.3_at	GGGAAAATCTGACTTACTCCTTTGT	SEQ ID NO:1251
WBC012F07_V1.3_at	GGAAGCTACACTGAAGACCGAGGTT	SEQ ID NO:1252
WBC012F07_V1.3_at	GGACCTACCCAAGCTTTTGTAAGTG	SEQ ID NO:1253
WBC012F07_V1.3_at	GGCAATATTGGTTGGGTCCCTGCAG	SEQ ID NO:1254
WBC012F07_V1.3_at	TCCACCCACGGACTTTGAGAAACAA	SEQ ID NO:1255
WBC012F07_V1.3_at	TGCGCGAGCAGAGCCCACGAATAGA	SEQ ID NO:1256
WBC012F07_V1.3_at	TAGAGAGACCCAACCATTCTTTCCA	SEQ ID NO:1257
Soc-2 suppressor of clear homolog (C. elegans)		
WBC012G02_V1.3_at	CTTGACGCTCAAATTCAGGACTGAA	SEQ ID NO:1258
WBC012G02_V1.3_at	ATATCCTTTCTTCTTTTTTCCATCT	SEQ ID NO:1259
WBC012G02_V1.3_at	CAGTATTGTAAATGTGTGCCCCTTA	SEQ ID NO:1260
WBC012G02_V1.3_at	CGTATTGCTGCTTGGTTTTCTTTTT	SEQ ID NO:1261
WBC012G02_V1.3_at	GCGGGTGCATTCTAGATATCATTCT	SEQ ID NO:1262
WBC012G02_V1.3_at	GAGACTCACAGAGCGGGTGCATTCT	SEQ ID NO:1263
WBC012G02_V1.3_at	GATAGATTTTCTTTTGCTTTACTGC	SEQ ID NO:1264
WBC012G02_V1.3_at	GTTATTTTGCTTTTCTTGACGCTCA	SEQ ID NO:1265
WBC012G02_V1.3_at	GTACTCTTACTTTTGGTAGTGTCAG	SEQ ID NO:1266
WBC012G02_V1.3_at	GTGTGCCCCTTATACAGTACTCTTA	SEQ ID NO:1267
WBC012G02_V1.3_at	TTTTCCATCTACTGTGGCTTTTCAG	SEQ ID NO:1268
Sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase), transcript variant 2		
WBC013A09_V1.3_at	AGCTCAGGCCCGATCTGCTTGGGAA	SEQ ID NO:1269
WBC013A09_V1.3_at	AGCCCATCTCTCTGAAGGGATTTAT	SEQ ID NO:1270
WBC013A09_V1.3_at	AATTCCTGGCTCTCTTTATGTTCTG	SEQ ID NO:1271
WBC013A09_V1.3_at	GCCGCTTACTGCTGCGTGAACTAAT	SEQ ID NO:1272
WBC013A09_V1.3_at	GAATTGCAGGAAAGCCCATCTCTCT	SEQ ID NO:1273
WBC013A09_V1.3_at	GAAGGTGGCATTCCATCAGCAGAAG	SEQ ID NO:1274
WBC013A09_V1.3_at	GTAGCCATCTATTCAGCCTATATCA	SEQ ID NO:1275
WBC013A09_V1.3_at	GTGAACTAATCTTTTCCACCTCTCT	SEQ ID NO:1276
WBC013A09_V1.3_at	TGGTGTGGGACCCTGAGACTACACT	SEQ ID NO:1277
WBC013A09_V1.3_at	TCATGATATCCTCTAATCCTTCCAA	SEQ ID NO:1278
WBC013A09_V1.3_at	TTAATTCTGTGCTCTCTCTATATGG	SEQ ID NO:1279
Ras GTPase-activating-like protein (IQGAP1)		
WBC013C03_V1.3_at	AGCCTCCACTTTCTCTGATGTGTTG	SEQ ID NO:1280
WBC013C03_V1.3_at	AGCCGACGCTGTTACACTTGATATT	SEQ ID NO:1281
WBC013C03_V1.3_at	ACTAGGATTTATCTGCAGGGTTGCA	SEQ ID NO:1282

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
WBC013C03_V1.3_at	AATCTGTTTTCCCTCATTTCTTTCT	SEQ ID NO:1283
WBC013C03_V1.3_at	GAATCCTGCCTGAAATAGACTCAAA	SEQ ID NO:1284
WBC013C03_V1.3_at	GAGCTCCAGTTTTATGGGTTTAGTC	SEQ ID NO:1285
WBC013C03_V1.3_at	GATGTGTTGGTTCAGTTTTCTTTTA	SEQ ID NO:1286
WBC013C03_V1.3_at	GTGCCTTTATTTTTATGAGCTCCAG	SEQ ID NO:1287
WBC013C03_V1.3_at	GGGCTTATCTGTATATCTGAACTCT	SEQ ID NO:1288
WBC013C03_V1.3_at	TTGAAATCATGCTGCTGAGCCTCCA	SEQ ID NO:1289
WBC013C03_V1.3_at	TTGCTGCCCACATGGTGCCTTTATT	SEQ ID NO:1290
Homo sapiens cDNA FLJ45679 fis, clone ERLTF2001835		
WBC013E10_V1.3_at	AGAGGATCTCTCTTTTGAAAAGCTA	SEQ ID NO:1291
WBC013E10_V1.3_at	AAGAACACTTACAGCTCATATACAG	SEQ ID NO:1292
WBC013E10_V1.3_at	AAGGAGTTTCCTGTGGTTTCTGCCG	SEQ ID NO:1293
WBC013E10_V1.3_at	CGACTATTACTTTCTCTCAAGTGCC	SEQ ID NO:1294
WBC013E10_V1.3_at	GAATATGTTCTCCTTTGTAGCCTCT	SEQ ID NO:1295
WBC013E10_V1.3_at	GAAAAACACAGCTTAGCCCCTTCCT	SEQ ID NO:1296
WBC013E10_V1.3_at	GTAGAATGACACCAAAGCTGCAACT	SEQ ID NO:1297
WBC013E10_V1.3_at	GGAAATCAGTCAGTACCATCGTTAA	SEQ ID NO:1298
WBC013E10_V1.3_at	TTGTAGCCTCTTGACAAAGCAGGAA	SEQ ID NO:1299
WBC013E10_V1.3_at	TTGTCCACTGAAACTTTGCTAACGT	SEQ ID NO:1300
WBC013E10_V1.3_at	TTCCTCTAGCCTTCAGTCAATTTTT	SEQ ID NO:1301
WBC013G08_V1.3_at	AGTAAATTGACAGTGGAGCTCCATT	SEQ ID NO:1302
WBC013G08_V1.3_at	AGGCATGTACACTTTGATATAGCAG	SEQ ID NO:1303
WBC013G08_V1.3_at	AATGCCTGGCCCATGTTACATAGAA	SEQ ID NO:1304
WBC013G08_V1.3_at	CAGTGGAGCTCCATTTTACAAATGT	SEQ ID NO:1305
WBC013G08_V1.3_at	GTTCAGGCATTGCTTTAAACGATGA	SEQ ID NO:1306
WBC013G08_V1.3_at	GAATACGTCTGGAATGATCCATTAG	SEQ ID NO:1307
WBC013G08_V1.3_at	GATATAGCAGGTTCACCTTAGGAAA	SEQ ID NO:1308
WBC013G08_V1.3_at	GTGCAGTCTTACATGTGTACACATA	SEQ ID NO:1309
WBC013G08_V1.3_at	GGAAGACTATGTAGCCAGCAAGTAA	SEQ ID NO:1310
WBC013G08_V1.3_at	TGAATTTAACACATCCATATACTGG	SEQ ID NO:1311
WBC013G08_V1.3_at	TAGAGGGTATCAATGCCTGGCCCAT	SEQ ID NO:1312
RAB6 interacting protein 1 (RAB6IP1)		
WBC013H03_V1.3_at	TTCCCAAAGGGACTTCAGCGAGTTG	SEQ ID NO:1313
WBC013H03_V1.3_at	ACTGAGCCTGCGGTTGCACAGAAGT	SEQ ID NO:1314
WBC013H03_V1.3_at	GAAACCAGCTACAGTATGGCCCACT	SEQ ID NO:1315
WBC013H03_V1.3_at	GCTTATTTTGAAGCTGGCGCCCTCC	SEQ ID NO:1316
WBC013H03_V1.3_at	CCCTCCATTGTGTGTTTTAAGTCTT	SEQ ID NO:1317
WBC013H03_V1.3_at	GAAAAGCTTGTCACAGTCTAACTGG	SEQ ID NO:1318
WBC013H03_V1.3_at	GAGACGAGGTTGGTGCCGCTTATTT	SEQ ID NO:1319
WBC013H03_V1.3_at	GAGAGGAAATGTACACTCACTGTAA	SEQ ID NO:1320
WBC013H03_V1.3_at	GATTTGCTTTTTACACACTTTCATG	SEQ ID NO:1321
WBC013H03_V1.3_at	GTATTATTTATTTAACCCTCCATTG	SEQ ID NO:1322
WBC013H03_V1.3_at	GGACCGAGAGAGACTCACCCTGCAG	SEQ ID NO:1323

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
RTN4-C (RTN4)		
WBC014G08_V1.3_at	ATAGAACTCTTCACGTCGACTGCAT	SEQ ID NO:1324
WBC014G08_V1.3_at	AGGTGCACTACCATCTGTTTTCAAC	SEQ ID NO:1325
WBC014G08_V1.3_at	AACTTGCCTTTCTGGTATGTTCTAG	SEQ ID NO:1326
WBC014G08_V1.3_at	AACCCTTTTCACAGTTTGTGCACTG	SEQ ID NO:1327
WBC014G08_V1.3_at	AAGCTTAGAGACCTTTACCTTCCAG	SEQ ID NO:1328
WBC014G08_V1.3_at	CAAACTCTGACTCTGTGGACTGAAT	SEQ ID NO:1329
WBC014G08_V1.3_at	CCCACAGTGCTTGATCTTTCAGAGA	SEQ ID NO:1330
WBC014G08_V1.3_at	GACTGCATCGCACAGACTTGCTATA	SEQ ID NO:1331
WBC014G08_V1.3_at	GACGCCATGCACATAGAACTCTTCA	SEQ ID NO:1332
WBC014G08_V1.3_at	GAGAGTCTTTGGTTGTACGTGTGTA	SEQ ID NO:1333
WBC014G08_V1.3_at	GTTTTCAACGTGAACCGACGCCATG	SEQ ID NO:1334
Homo sapiens mRNA; cDNA DKFZp564C012		
WBC014H06_V1.3_at	CTAACATTTGTATGGACCCCTTCAT	SEQ ID NO:1335
WBC014H06_V1.3_at	CAGCAGGACTGATTGCCGGGTGCAA	SEQ ID NO:1336
WBC014H06_V1.3_at	ACCGTTTTTGTCCTAATGCTTCTGT	SEQ ID NO:1337
WBC014H06_V1.3_at	ACCTCTCTGCCAAACGTGATCTTAA	SEQ ID NO:1338
WBC014H06_V1.3_at	AAATCACACCATCCAGACTGACAAT	SEQ ID NO:1339
WBC014H06_V1.3_at	AACAACTCTCTTTTTGGCAGCAACT	SEQ ID NO:1340
WBC014H06_V1.3_at	AAGCCACACCGTCGTCTGTGAGAAA	SEQ ID NO:1341
WBC014H06_V1.3_at	CTTTGCTCCATTTCATTTTGCCAGA	SEQ ID NO:1342
WBC014H06_V1.3_at	GAGAAAGTGCGCCTCCTTAAAGGGT	SEQ ID NO:1343
WBC014H06_V1.3_at	GCTTCTGTTTTATGTGGTGATCGCA	SEQ ID NO:1344
WBC014H06_V1.3_at	TAAAGTGTTCGTTGTGGTGGCCGTC	SEQ ID NO:1345
No homology		
WBC016A12_V1.3_at	ATGCAGATCAGATGGCGTTTCTCCC	SEQ ID NO:1346
WBC016A12_V1.3_at	ACGTGTTCAGACTTGTGTTTTCATA	SEQ ID NO:1347
WBC016A12_V1.3_at	AAGTATGGGCTGTTTCACGTGTTCA	SEQ ID NO:1348
WBC016A12_V1.3_at	GACTATGTACTGTCCACCTGCATTA	SEQ ID NO:1349
WBC016A12_V1.3_at	GATTGATTTCCTACTAGTCTTTGAC	SEQ ID NO:1350
WBC016A12_V1.3_at	GTTTCTCCCAGCTCAGTGGATTTTC	SEQ ID NO:1351
WBC016A12_V1.3_at	GGAGCCTGGCTTATTTGATTGATTT	SEQ ID NO:1352
WBC016A12_V1.3_at	GGAAGTCCCTGTTCTGACTATGTAC	SEQ ID NO:1353
WBC016A12_V1.3_at	TCCCTTCATTCTGGTTTCCATGTGA	SEQ ID NO:1354
WBC016A12_V1.3_at	TCACCAACTCCCTTTTGGATTTCAT	SEQ ID NO:1355
WBC016A12_V1.3_at	TAAACAACCATGTCTGCATCTAGGG	SEQ ID NO:1356
Homo sapiens gene for JKTBP2, JKTBP1 (alternative splicing).		
WBC018B01_V1.3_s_at	ATAGCTGCCAATTAGTTTTCTTTGT	SEQ ID NO:1357
WBC018B01_V1.3_s_at	AGGCACAACTGTGTCCAACTGTATA	SEQ ID NO:1358
WBC018B01_V1.3_s_at	AACCCATCTTGCAGGACGACATTGA	SEQ ID NO:1359
WBC018B01_V1.3_s_at	GAAGATTGGTCTTCTGTTGATCTAA	SEQ ID NO:1360
WBC018B01_V1.3_s_at	GACTTTCTAGTGTACAAGGCACAAC	SEQ ID NO:1361
WBC018B01_V1.3_s_at	GACTCAATGTGGATTTGTGTTTATA	SEQ ID NO:1362

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
WBC018B01_V1.3_s_at	GTTTTTACTTTGTCCTTTGCTATCT	SEQ ID NO:1363
WBC018B01_V1.3_s_at	GTGTCCAACTGTATATAGCTGCCAA	SEQ ID NO:1364
WBC018B01_V1.3_s_at	GGAGATTGCTAAAGTAACCCATCTT	SEQ ID NO:1365
WBC018B01_V1.3_s_at	TGCTATCTGTGTTATGACTCAATGT	SEQ ID NO:1366
WBC018B01_V1.3_s_at	TTTGTCCTTTGCTATCTGTGTTATG	SEQ ID NO:1367
Predicted: Mitogen-activated protein kinase kinase kinase 1 (MAP3K1)		
WBC018D05_V1.3_at	GACTTCCAGGGCTTAAGGGCTAACT	SEQ ID NO:1368
WBC018D05_V1.3_at	ATTTGCTGTGTGACTATGATTCCTA	SEQ ID NO:1369
WBC018D05_V1.3_at	CAAACTGCCTCTAGATGTCCAAATC	SEQ ID NO:1370
WBC018D05_V1.3_at	CTCAGCTCGCTGGTAATTGTGGTGT	SEQ ID NO:1371
WBC018D05_V1.3_at	GAGGAACCTCAGCTAATCAGTATTA	SEQ ID NO:1372
WBC018D05_V1.3_at	GTATTACTTGTAGATCCCCATGCCA	SEQ ID NO:1373
WBC018D05_V1.3_at	GTTTGAGTTTGTTTGCAGTTCCCTC	SEQ ID NO:1374
WBC018D05_V1.3_at	TCAGGTGTCCTATAGATTTTTCTTC	SEQ ID NO:1375
WBC018D05_V1.3_at	TAACGTCTACTGCTGTTTATTCCAG	SEQ ID NO:1376
WBC018D05_V1.3_at	TTTACCCCATCGAACCATTTTATAG	SEQ ID NO:1377
WBC018D05_V1.3_at	TTTATTCCAGTTTCTACTACCTCAG	SEQ ID NO:1378
Homo sapiens mRNA; cDNA DKFZp686M2414		
WBC019B05_V1.3_at	ATATATGCTGTCTGTTTTGTGTACA	SEQ ID NO:1379
WBC019B05_V1.3_at	AACTCACTCTTACAGTAGTCTGCTT	SEQ ID NO:1380
WBC019B05_V1.3_at	AATGTTGTCTTTTAAATACTCCGAT	SEQ ID NO:1381
WBC019B05_V1.3_at	CAAGCCATTTGTGGGAATCCTAAAA	SEQ ID NO:1382
WBC019B05_V1.3_at	CCAGCTGTTTATTTTATTGAGTCCT	SEQ ID NO:1383
WBC019B05_V1.3_at	GAGTAACAAACTCAGCCTTCTGTAA	SEQ ID NO:1384
WBC019B05_V1.3_at	GAGGATCATCTGACTTTTCACTTAC	SEQ ID NO:1385
WBC019B05_V1.3_at	GTAGTCTGCTTATTTCCAGCTGTTT	SEQ ID NO:1386
WBC019B05_V1.3_at	GTGCTTTATGTACTGTTATCCTATA	SEQ ID NO:1387
WBC019B05_V1.3_at	TGTAAAAACTCCTTTTCTGCCACAC	SEQ ID NO:1388
WBC019B05_V1.3_at	TTGGGTTTTCTTTTCAACTCACTCT	SEQ ID NO:1389
No homology		
WBC020B04_V1.3_at	ATATTGGGCTTTGTCAGTCTTCTGA	SEQ ID NO:1390
WBC020B04_V1.3_at	ATGACAGCTTTTTCTAACGGACAAA	SEQ ID NO:1391
WBC020B04_V1.3_at	AGGATACTCCGTTCTGTAGACACAG	SEQ ID NO:1392
WBC020B04_V1.3_at	ACTCAATTCTGCTGTTGTCGCACAA	SEQ ID NO:1393
WBC020B04_V1.3_at	CAAATTTCCCTTCTTCTGGCTAATT	SEQ ID NO:1394
WBC020B04_V1.3_at	CTGCCGTCACTGTCATGTTCTAAAT	SEQ ID NO:1395
WBC020B04_V1.3_at	GTCAGATCAGACTCCTGTTACAGCT	SEQ ID NO:1396
WBC020B04_V1.3_at	GGATGTTTTATCTGAACGCCTGCTC	SEQ ID NO:1397
WBC020B04_V1.3_at	TGGCTAATTCCTACACTTTTTCTCA	SEQ ID NO:1398
WBC020B04_V1.3_at	TAAGGTCCACCACTTGTTCTTTGTT	SEQ ID NO:1399
WBC020B04_V1.3_at	TAAGAGCTCTCTAACACTGGCTGCT	SEQ ID NO:1400
Hypothetical protein FLJ20481		

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
WBC021B08_V1.3_at	ATAGCTCAGGGCGATTCTGTGTCGT	SEQ ID NO:1401
WBC021B08_V1.3_at	AACATACTTAGACCTCCAGACGAGC	SEQ ID NO:1402
WBC021B08_V1.3_at	AGCATTATCAACACCTAGAGCTTAA	SEQ ID NO:1403
WBC021B08_V1.3_at	AACGCGTGGCTCTTTCTTGAAATTG	SEQ ID NO:1404
WBC021B08_V1.3_at	AAAGTTTTGCCCTGAAGCATCCAGA	SEQ ID NO:1405
WBC021B08_V1.3_at	AATCGTGAAGAGAGCGCCTCAGACA	SEQ ID NO:1406
WBC021B08_V1.3_at	GCAACTCCCTCATTCACAAGTAATA	SEQ ID NO:1407
WBC021B08_V1.3_at	GACAGTACATTTTCCCAGCAAAGTG	SEQ ID NO:1408
WBC021B08_V1.3_at	GAGCCATGTGTTTTCACTGCCAAAA	SEQ ID NO:1409
WBC021B08_V1.3_at	GGTCTCACTTAGTTATTGATCAGCA	SEQ ID NO:1410
WBC021B08_V1.3_at	TATTGTGCTGTCCTGATTGGTTTAC	SEQ ID NO:1411
No homology		
WBC021D01_V1.3_at	CGTTCTCCGGTCTGTAGCGATTTGA	SEQ ID NO:1412
WBC021D01_V1.3_at	AAGAAGTAAGCAGCACCCGTTCTCC	SEQ ID NO:1413
WBC021D01_V1.3_at	AGGCGCCTGTGCCAGATTATAATCA	SEQ ID NO:1414
WBC021D01_V1.3_at	AGTGACACACTTAGCTTTCTTTCTG	SEQ ID NO:1415
WBC021D01_V1.3_at	AAGCTCACTCTTTCATGTTGGATGG	SEQ ID NO:1416
WBC021D01_V1.3_at	CTGCCCTCCATCTTAACTTTTATTA	SEQ ID NO:1417
WBC021D01_V1.3_at	GAAACTTGTCCTTATTCATTGTTGT	SEQ ID NO:1418
WBC021D01_V1.3_at	GGATCACAAATCGTTCATAGACCAT	SEQ ID NO:1419
WBC021D01_V1.3_at	TAATCAACACATCGCTTCCTTTATC	SEQ ID NO:1420
WBC021D01_V1.3_at	TTTCACACAAGTTACAACTGCCCTC	SEQ ID NO:1421
WBC021D01_V1.3_at	TTTCTTTCTGGCACAAGCTCACTCT	SEQ ID NO:1422
Toll-like receptor 8 (TLR8)		
WBC022B05_V1.3_at	TCCCAAACTTTCTACGATGCTTACG	SEQ ID NO:1423
WBC022B05_V1.3_at	AAAGACGCCTCTGTTACGGACTGGG	SEQ ID NO:1424
WBC022B05_V1.3_at	ATTCCCAGTATTTGCGGCTGCGGCA	SEQ ID NO:1425
WBC022B05_V1.3_at	ATTGGGACCCGGGATTAGCCATCAT	SEQ ID NO:1426
WBC022B05_V1.3_at	AAAAGGCTACAGGTCTCTTTCCACA	SEQ ID NO:1427
WBC022B05_V1.3_at	AAACAGCATTCTACTTGGCCTTGCA	SEQ ID NO:1428
WBC022B05_V1.3_at	GAGCCAGTGTTACAGCATTCCCAGT	SEQ ID NO:1429
WBC022B05_V1.3_at	GATGCTTACGTTTCTTATGACACCA	SEQ ID NO:1430
WBC022B05_V1.3_at	GATTGTATTTATTCTGCTGGAGCCA	SEQ ID NO:1431
WBC022B05_V1.3_at	TGATAAATGAGCTGCGCTTCCACCT	SEQ ID NO:1432
WBC022B05_V1.3_at	TTAGCCATCATCGATAACCTCATGC	SEQ ID NO:1433
Immunoglobulin superfamily, member 6 variant		
WBC022B06_V1.3_at	AATAAGCCACAACCGACTCTAGATG	SEQ ID NO:1434
WBC022B06_V1.3_at	AAAATCACTTACATCATGCCGCCAA	SEQ ID NO:1435
WBC022B06_V1.3_at	AAGTGCCCACATTTGAGTCAGCGAA	SEQ ID NO:1436
WBC022B06_V1.3_at	AAGGCGCCTCTGCAATACTGATTTT	SEQ ID NO:1437
WBC022B06_V1.3_at	AATCATCTTGAAAACTACCTTGGAG	SEQ ID NO:1438
WBC022B06_V1.3_at	CAAACGATTCCTCTGGTATTGCCAT	SEQ ID NO:1439
WBC022B06_V1.3_at	CTCTAGATGTCAGTGTTGTGCCAAA	SEQ ID NO:1440
WBC022B06_V1.3_at	GTGATGGGCCAGTCAGACTAAGCTG	SEQ ID NO:1441

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
WBC022B06_V1.3_at	GGTATAGTGCACATTTTCCTGCCAG	SEQ ID NO:1442
WBC022B06_V1.3_at	TTTCCTGCCAGGGTATACAAAATCA	SEQ ID NO:1443
WBC022B06_V1.3_at	TAGGAGTGGGCAAGGCACCGTCCTT	SEQ ID NO:1444
Phosphogluconate dehydrogenase		
WBC022F08_V1.3_at	ATGCCTAATCAGACTCCTTGTGTTA	SEQ ID NO:1445
WBC022F08_V1.3_at	ATGCAGGTGAATTCCCTTTTTCCTC	SEQ ID NO:1446
WBC022F08_V1.3_at	AGGCAGCAGCTCCTATCACATAGAT	SEQ ID NO:1447
WBC022F08_V1.3_at	AGTGTGTCATCCTCTTCGTACAATG	SEQ ID NO:1448
WBC022F08_V1.3_at	ACCCGGACAGTTTATCCACACTAAT	SEQ ID NO:1449
WBC022F08_V1.3_at	ACTGCTCTTTCCTTCTATGATGGAT	SEQ ID NO:1450
WBC022F08_V1.3_at	CTTGTCTCTTGGGACTGACCAGGAA	SEQ ID NO:1451
WBC022F08_V1.3_at	CTATTTTCTGCTCACATCTCTTAAA	SEQ ID NO:1452
WBC022F08_V1.3_at	GATGGCGCAAACCAGCTGCCTGAAG	SEQ ID NO:1453
WBC022F08_V1.3_at	GTATGAACTCTTAGCCAAACCCGGA	SEQ ID NO:1454
WBC022F08_V1.3_at	TAGACCAGGACATTCCATTTGCCAC	SEQ ID NO:1455
Adducin 3 (gamma) (ADD3), transcript variant 2		
WBC024B05_V1.3_at	ATGAACCTCTGTGTCCTGTGGAAAA	SEQ ID NO:1456
WBC024B05_V1.3_at	ATGAGCCAATGAACCTCTGTGTCCT	SEQ ID NO:1457
WBC024B05_V1.3_at	AGTGAACTATTTGCACCTTTTGCTA	SEQ ID NO:1458
WBC024B05_V1.3_at	CACCTTTTGCTAATGCCTCTATTTA	SEQ ID NO:1459
WBC024B05_V1.3_at	CAGTGTTTTAATCTCTTAGTGGAAA	SEQ ID NO:1460
WBC024B05_V1.3_at	CTGGTTCTGTTTGGCGTATGTGTAT	SEQ ID NO:1461
WBC024B05_V1.3_at	GCCTCTATTTACTTGCTTTGGCATA	SEQ ID NO:1462
WBC024B05_V1.3_at	GATCTCACTAACTACTGGAATCAGT	SEQ ID NO:1463
WBC024B05_V1.3_at	GTAACCTGTGAACTATGCTTTTCCA	SEQ ID NO:1464
WBC024B05_V1.3_at	GGAAACTCTCAGTTGCTTAATTCTG	SEQ ID NO:1465
WBC024B05_V1.3_at	GGAAATTTCATTTTAGATCTCACTA	SEQ ID NO:1466
No homology		
WBC024C11_V1.3_at	ATGTCTATTTCATGCCTACGCTTAA	SEQ ID NO:1467
WBC024C11_V1.3_at	AGACCATACAGTTTTATCCCACAAG	SEQ ID NO:1468
WBC024C11_V1.3_at	CCTGCCTCGTGGTTTCTCTAGAAAA	SEQ ID NO:1469
WBC024C11_V1.3_at	GTTTACCTGGGCTTGGAATTCTAGA	SEQ ID NO:1470
WBC024C11_V1.3_at	GATCTGACTCTGAAATTTCCTTTAG	SEQ ID NO:1471
WBC024C11_V1.3_at	GTTTTTCACTCTAATCTGCATTCCC	SEQ ID NO:1472
WBC024C11_V1.3_at	TTTTCCCCAGGCTGCTTGTAAGATC	SEQ ID NO:1473
WBC024C11_V1.3_at	TAGTCCTTTCTTCTGGTTAACTAAT	SEQ ID NO:1474
WBC024C11_V1.3_at	TCACATCATATATTGCCTCTTTCCT	SEQ ID NO:1475
WBC024C11_V1.3_at	TAGTTATCCTGTCTTTTTTCCCCAG	SEQ ID NO:1476
WBC024C11_V1.3_at	TATAAGTGGTAGACACCTCCTGCCT	SEQ ID NO:1477
No homology		
WBC024C12_V1.3_at	AGGCCACATATCTCCGTCTTTTTAA	SEQ ID NO:1478
WBC024C12_V1.3_at	ATATGCTTTCATTTCTCTTGTGTAA	SEQ ID NO:1479
WBC024C12_V1.3_at	AAATACGCCACAATTTGTCCACTCA	SEQ ID NO:1480
WBC024C12_V1.3_at	AAAACTCCTTGGGTGTGATCACGCA	SEQ ID NO:1481

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
WBC024C12_V1.3_at	AATGTTTTCTCATATCCCTGTTATA	SEQ ID NO:1482
WBC024C12_V1.3_at	GCATTTATTTGTGCTAACCTCTGAA	SEQ ID NO:1483
WBC024C12_V1.3_at	GTATGTACTCTTTTGGGTCTGGTTC	SEQ ID NO:1484
WBC024C12_V1.3_at	GTCTGGTTCATCCATGTTGTAGCAT	SEQ ID NO:1485
WBC024C12_V1.3_at	GTGAACCTACTTAACAATCCTCGTC	SEQ ID NO:1486
WBC024C12_V1.3_at	TATTCACTGTTGTCTGTTCTTCTAG	SEQ ID NO:1487
WBC024C12_V1.3_at	TTAGATACCAACCTCCAAGATGCCA	SEQ ID NO:1488
No homology		
WBC024F08_V1.3_at	ATGTGTGTCTCTATGTACCCAAGCC	SEQ ID NO:1489
WBC024F08_V1.3_at	AGCTCTGCAAGTCACTTACCTGAAG	SEQ ID NO:1490
WBC024F08_V1.3_at	AGACTCAGGGATGCTGTTTCCAGCT	SEQ ID NO:1491
WBC024F08_V1.3_at	AGCGTGTGTCTACATGTGTGTCTCT	SEQ ID NO:1492
WBC024F08_V1.3_at	AAGCACAGTGTCTCTCGAATTTCGG	SEQ ID NO:1493
WBC024F08_V1.3_at	GAGAGGCGAGCATCTGGCTGTACTT	SEQ ID NO:1494
WBC024F08_V1.3_at	GTACCCTCCTCACATTTTTGCATAT	SEQ ID NO:1495
WBC024F08_V1.3_at	GGTGGCCACCTGCATGAGTGTATTA	SEQ ID NO:1496
WBC024F08_V1.3_at	GGATGCATTCTCTTGTTTTGCTTGA	SEQ ID NO:1497
WBC024F08_V1.3_at	TGAGTCCTGTGAGATGCCCTTGTTA	SEQ ID NO:1498
WBC024F08_V1.3_at	TCTGGTTCTCTCTCTCAGGAATAAG	SEQ ID NO:1499
Migration-inducing gene 10 protein		
WBC026E02_V1.3_at	AGGTGGTGCCAGTTTAGAGCTCCTG	SEQ ID NO:1500
WBC026E02_V1.3_at	ACTGCCACTTGCTGTGCCAAATGGA	SEQ ID NO:1501
WBC026E02_V1.3_at	AAACAGTTGCACAGCATCTCAGCTC	SEQ ID NO:1502
WBC026E02_V1.3_at	CAATGTTTAGTACTTTCCTGCCTTT	SEQ ID NO:1503
WBC026E02_V1.3_at	GCTTTGTCATTGTTTCACTACTCAG	SEQ ID NO:1504
WBC026E02_V1.3_at	GAGCTGTTAGCCTAGTTCTCTTTTT	SEQ ID NO:1505
WBC026E02_V1.3_at	GAGATGCAGCACCAGGAACCCTTAA	SEQ ID NO:1506
WBC026E02_V1.3_at	TGTGCGCAGCCCTTAAGTCAACTTA	SEQ ID NO:1507
WBC026E02_V1.3_at	TAAGTCAACTTAGCGCTTTCCACAT	SEQ ID NO:1508
WBC026E02_V1.3_at	TCAGGATCCCATTTGCATTTCTTAG	SEQ ID NO:1509
WBC026E02_V1.3_at	TACTGCACTCTGGATTTGCCTACAT	SEQ ID NO:1510
No homology		
WBC027D07_V1.3_at	ATTTTTGTCTTTCACTCTTTTCCTG	SEQ ID NO:1511
WBC027D07_V1.3_at	ATCCCTGATAATTTTCCTCACTTGG	SEQ ID NO:1512
WBC027D07_V1.3_at	CACTTGGTTGTTTGCTCTGTCTGAA	SEQ ID NO:1513
WBC027D07_V1.3_at	GATTAACTCTGTCTTTTAGCTGGTA	SEQ ID NO:1514
WBC027D07_V1.3_at	GTAAGCCTCTTTATCATTCTCTAAT	SEQ ID NO:1515
WBC027D07_V1.3_at	GTGGGTTTCCTCTAGATAGCATATA	SEQ ID NO:1516
WBC027D07_V1.3_at	GGCTCTTGTTTTTTGATTCACTCTG	SEQ ID NO:1517
WBC027D07_V1.3_at	TCCAGCTTTCTTTTGCCTAGTGTTA	SEQ ID NO:1518
WBC027D07_V1.3_at	TATACTGTTTTCTACTGGTTGCCCT	SEQ ID NO:1519
WBC027D07_V1.3_at	TAATGCCCTTCTTTATCCCTGATAA	SEQ ID NO:1520
WBC027D07_V1.3_at	TATATTTTTCTCCATCCCTTTACTT	SEQ ID NO:1521
No homology		
WBC027E07_V1.3_at	ATAGGGTGGTGGACCTTATGGCCCA	SEQ ID NO:1522

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
WBC027E07_V1.3_at	ATATTGAGAGTCTCCTGACCTCCAC	SEQ ID NO:1523
WBC027E07_V1.3_at	AGAAAGGCCCTCAGCTGCTGGGAAT	SEQ ID NO:1524
WBC027E07_V1.3_at	ACTTTGTCAAGCTCATTTCCTGGTA	SEQ ID NO:1525
WBC027E07_V1.3_at	GCTGGGAATGCTTGTCCCAACTTGA	SEQ ID NO:1526
WBC027E07_V1.3_at	GAGACTAGTTCTCTCGTGACACCCA	SEQ ID NO:1527
WBC027E07_V1.3_at	GGCCCACATGGCCTCCAAGGAGTAA	SEQ ID NO:1528
WBC027E07_V1.3_at	GGAGCCCTACCTTGTCATGTACCAT	SEQ ID NO:1529
WBC027E07_V1.3_at	GGACCACCAATCACCCAGCAAGAGA	SEQ ID NO:1530
WBC027E07_V1.3_at	TGACCTCCACAGTTTCCATCTCAGA	SEQ ID NO:1531
WBC027E07_V1.3_at	TTGCCCTCAACGACCACTTTGTCAA	SEQ ID NO:1532
Ras homolog gene family, member A		
WBC028C01_V1.3_at	AGTGGGCATCCAGTTTTTTGAAAAT	SEQ ID NO:1533
WBC028C01_V1.3_at	AGTGTATGATTACTGGCCTTTTCCA	SEQ ID NO:1534
WBC028C01_V1.3_at	AGATTTCATCGCATAGCTCTGGAGT	SEQ ID NO:1535
WBC028C01_V1.3_at	ACACCAGGCGCTAATTCAAGGAATT	SEQ ID NO:1536
WBC028C01_V1.3_at	AAAGGCCCAAGTCCGTGAGCAGCTA	SEQ ID NO:1537
WBC028C01_V1.3_at	AACATGTCCTGACTGTCATCTGTCA	SEQ ID NO:1538
WBC028C01_V1.3_at	GAAGTCATCTTGCTACGAGTATTTA	SEQ ID NO:1539
WBC028C01_V1.3_at	GAGCTTTACTCCTTAACAGATTTCA	SEQ ID NO:1540
WBC028C01_V1.3_at	GTGAGTCACCACTTCAGAGCTTTAC	SEQ ID NO:1541
WBC028C01_V1.3_at	TCATCTGTCAGCTGCAAGGTACTCT	SEQ ID NO:1542
WBC028C01_V1.3_at	TATTAATGATGTCCAACCCACCTGA	SEQ ID NO:1543
No homology		
WBC028D09_V1.3_at	AGGAGTCGGCGCACTGGGTCACCCA	SEQ ID NO:1544
WBC028D09_V1.3_at	ATGAAAAGGTCCATCGCCGACAGCG	SEQ ID NO:1545
WBC028D09_V1.3_at	AGAAGAAGACCAACTCTGCTCCCAA	SEQ ID NO:1546
WBC028D09_V1.3_at	AAGCCGGCCTTGATTCTAGAGAGAA	SEQ ID NO:1547
WBC028D09_V1.3_at	GAAGCCTCCGTGTGGAGCCATGAAA	SEQ ID NO:1548
WBC028D09_V1.3_at	GAAGCTCTTCTGGAAAAGTCGGGAA	SEQ ID NO:1549
WBC028D09_V1.3_at	GAAAGCTCTGTTGGCTGCACTTTTT	SEQ ID NO:1550
WBC028D09_V1.3_at	GAGTCGGTCTCAAAGCCAGATGTCA	SEQ ID NO:1551
WBC028D09_V1.3_at	GGGCCTCTGTTTGACGGCATTAGAA	SEQ ID NO:1552
WBC028D09_V1.3_at	TAAGTCTCTGTTCACAACTCACAGC	SEQ ID NO:1553
WBC028D09_V1.3_at	TTAGAAAGTTGTCCGCCGAGCTGGC	SEQ ID NO:1554
Homo sapiens cDNA FLJ13038 fis, clone NT2RP3001272, weakly similar to Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein		
WBC028E07_V1.3_at	ATACTTGGGTCTTCCTTTTGACACT	SEQ ID NO:1555
WBC028E07_V1.3_at	AGTGGCAGCTTCTTGTTATGACAGA	SEQ ID NO:1556
WBC028E07_V1.3_at	AAATATTTTCCTGACCTGCTCTGTG	SEQ ID NO:1557
WBC028E07_V1.3_at	CAGCACTGGCACTTATTTGGTATGT	SEQ ID NO:1558
WBC028E07_V1.3_at	GAAGATTGATTATTCCCTCCTTTTA	SEQ ID NO:1559

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
WBC028E07_V1.3_at	GTGTTAATCTTACCCTTTCTCAAAT	SEQ ID NO:1560
WBC028E07_V1.3_at	GGAGACCGTGTACTTTTTGTGCAAC	SEQ ID NO:1561
WBC028E07_V1.3_at	TGCTCTGTGCATAGCTTACCCAGAA	SEQ ID NO:1562
WBC028E07_V1.3_at	TTTATTGTTGGCACTTCCTCAGGGA	SEQ ID NO:1563
WBC028E07_V1.3_at	TTTCTCCCTATTGGTCAGTGTGATT	SEQ ID NO:1564
WBC028E07_V1.3_at	TTGACTTCCCCAAACTGAACAGGCT	SEQ ID NO:1565
No homology		
WBC028F05_V1.3_at	AGATGTCTTCCTTCTCAATTTTGAG	SEQ ID NO:1566
WBC028F05_V1.3_at	AAAGATCTTTTGGTTTCTCTGTCAA	SEQ ID NO:1567
WBC028F05_V1.3_at	AAACTGTCCTTTCCATTAGCATTCT	SEQ ID NO:1568
WBC028F05_V1.3_at	AAGAATTTGTCCTAGGGCTGCTTTC	SEQ ID NO:1569
WBC028F05_V1.3_at	CAGCCTTTACAGACCTTGTTTTCAG	SEQ ID NO:1570
WBC028F05_V1.3_at	GTTTTTTCCCCTCATACATTCTAGA	SEQ ID NO:1571
WBC028F05_V1.3_at	GTTCAGTTCGTTTCCATAGTAGCCA	SEQ ID NO:1572
WBC028F05_V1.3_at	GTAGCTTTAATCACATCTCTTCCTT	SEQ ID NO:1573
WBC028F05_V1.3_at	TCTTCCTTAGAAGTCTCAGCCTTTA	SEQ ID NO:1574
WBC028F05_V1.3_at	TAGGACCCATTTATCTTTCTTACCA	SEQ ID NO:1575
WBC028F05_V1.3_at	TTGCCTGAGAACATTCATCCTGCTT	SEQ ID NO:1576
No homology		
WBC030C04_V1.3_at	ATGCGCACATTTACTAGCACCTACT	SEQ ID NO:1577
WBC030C04_V1.3_at	ATGGACTTCCCTGCATTGTATGAGA	SEQ ID NO:1578
WBC030C04_V1.3_at	ATGTGCTGTGTGCTCTGTGTACCCT	SEQ ID NO:1579
WBC030C04_V1.3_at	AGTTGTCTGGCCCAAAGCATCAGCA	SEQ ID NO:1580
WBC030C04_V1.3_at	GAGTTCGATTCCCATCTGAAACGAC	SEQ ID NO:1581
WBC030C04_V1.3_at	GAGACATTTTCCGTTGTCACAACTT	SEQ ID NO:1582
WBC030C04_V1.3_at	GAGAGGTCACCGATGCTGCTAAACA	SEQ ID NO:1583
WBC030C04_V1.3_at	GTGTGGCCTTAGTGACCAATCAGTC	SEQ ID NO:1584
WBC030C04_V1.3_at	TGTGTACCCTCAGATCACGTGAACT	SEQ ID NO:1585
WBC030C04_V1.3_at	TACTGAGGGCTTACCATGTGCTGTG	SEQ ID NO:1586
WBC030C04_V1.3_at	TTCACCCCTCGGAACATCGATGATG	SEQ ID NO:1587
Putative membrane protein (GENX-3745 gene)		
WBC030D02_V1.3_at	AAGAAAGTTCCACCATAATGACCCT	SEQ ID NO:1588
WBC030D02_V1.3_at	CTATGGTCTTTATTTCTTGTGGTGA	SEQ ID NO:1589
WBC030D02_V1.3_at	CCTAATTCCCTTCCTGATGTGTATT	SEQ ID NO:1590
WBC030D02_V1.3_at	GTTGTTTAACGTCTTCTGATTCAGT	SEQ ID NO:1591
WBC030D02_V1.3_at	GTCAGTAGGATTTTTGGTACCACCA	SEQ ID NO:1592
WBC030D02_V1.3_at	GTAAAATTCTCCAACTGCTATCTAT	SEQ ID NO:1593
WBC030D02_V1.3_at	GGTGAAACGATGTGCCTTTCCTTGC	SEQ ID NO:1594
WBC030D02_V1.3_at	TGGCTGGTCATTAACTTCCAACTAT	SEQ ID NO:1595
WBC030D02_V1.3_at	TCCTTCACACATCAGGCTCATTAAG	SEQ ID NO:1596
WBC030D02_V1.3_at	TAATGACCCTCCCAAGCTAGGAAAA	SEQ ID NO:1597
WBC030D02_V1.3_at	TTTGGATTTTGCTTCTTCCTTCACA	SEQ ID NO:1598
DDHD domain containing 1		
WBC032B05_V1.3_at	ATGTCTCTGCATGTTATCACGGAAT	SEQ ID NO:1599

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
WBC032B05_V1.3_at	GCAACATTCAAAACCGCCTTTTCAA	SEQ ID NO:1600
WBC032B05_V1.3_at	AAATATGTCTGCTTCCCTTTTTTCA	SEQ ID NO:1601
WBC032B05_V1.3_at	GCTTTCAGTTCATTATTTCATCCAT	SEQ ID NO:1602
WBC032B05_V1.3_at	GCAGCTTTATTTCAGCAAGTACTAA	SEQ ID NO:1603
WBC032B05_V1.3_at	GAAGAGTCCTTTTCACCTAAGAGTG	SEQ ID NO:1604
WBC032B05_V1.3_at	GATATTCTGCATTACTGGACGGATA	SEQ ID NO:1605
WBC032B05_V1.3_at	GGTGGTATGACACTCAAATGCCTAC	SEQ ID NO:1606
WBC032B05_V1.3_at	GGATTCATTCTTAACCACTACGGTG	SEQ ID NO:1607
WBC032B05_V1.3_at	GGACGGATATTTTGCTTTCAGTTCA	SEQ ID NO:1608
WBC032B05_V1.3_at	TACAGTACTCTTGTTTCCATGTCTC	SEQ ID NO:1609
WBC032B11_V1.3_at	ATTTGGGTCTATGCTATGTTATTAA	SEQ ID NO:1610
WBC032B11_V1.3_at	ATCGGTACGTTGGAAACTGTGCAAA	SEQ ID NO:1611
WBC032B11_V1.3_at	ACTTTTGTGCAATATCTGTCTGATT	SEQ ID NO:1612
WBC032B11_V1.3_at	AACTATTCTTGATTCTGTCTGTGCC	SEQ ID NO:1613
WBC032B11_V1.3_at	AAGATGTTTCTATTTTGGGCAGCAT	SEQ ID NO:1614
WBC032B11_V1.3_at	CTTTGTGTTTTATTTTCTGTCCTAT	SEQ ID NO:1615
WBC032B11_V1.3_at	GAAGATATTCCATTTCTTTGTGTTT	SEQ ID NO:1616
WBC032B11_V1.3_at	GATTCTGTCTGTGCCTTTATATTTT	SEQ ID NO:1617
WBC032B11_V1.3_at	GTATGGAATTACTGACTTTTGTGCA	SEQ ID NO:1618
WBC032B11_V1.3_at	GGCACTTAGGAACATATCGGTACGT	SEQ ID NO:1619
WBC032B11_V1.3_at	TTAGAGTCTATTTCCCATAATTTGG	SEQ ID NO:1620
Glycerol kinase (GK)		
WBC032G05_V1.3_at	ATGAACCGCGACTGTGGGATTCCAC	SEQ ID NO:1621
WBC032G05_V1.3_at	AAACAACGGCTCTGGGAGCTGCCAT	SEQ ID NO:1622
WBC032G05_V1.3_at	GCTGACATTCTGTACATCCCAGTAG	SEQ ID NO:1623
WBC032G05_V1.3_at	GAATCCAGTGGTTGTCTCTAAATGT	SEQ ID NO:1624
WBC032G05_V1.3_at	GAACCCGAGGATTTGTCAGCTGTCA	SEQ ID NO:1625
WBC032G05_V1.3_at	GTAGTGAAGCCCTCGATGCCTGAAA	SEQ ID NO:1626
WBC032G05_V1.3_at	GATTCCACTCAGTCATTTGCAGGTA	SEQ ID NO:1627
WBC032G05_V1.3_at	GTTGGGTTACAACTCAGTCTTCGGA	SEQ ID NO:1628
WBC032G05_V1.3_at	GTGGGCTCACACAGTTCACCAATAA	SEQ ID NO:1629
WBC032G05_V1.3_at	TGCCATATTGCTTTTGCCGCATTAG	SEQ ID NO:1630
WBC032G05_V1.3_at	TAGAAGCTGTCTGTTTCCAAACCCG	SEQ ID NO:1631
Selenoprotein P		
WBC037F12_V1.3_at	ATCTTGATTTTTACTACCACATATG	SEQ ID NO:1632
WBC037F12_V1.3_at	ATCTTGTTTTCTTTATCTAGCATCG	SEQ ID NO:1633
WBC037F12_V1.3_at	AATATCCACTTATACGTACATCTAA	SEQ ID NO:1634
WBC037F12_V1.3_at	CCTGAACTCCTTTATGGTTAATACT	SEQ ID NO:1635
WBC037F12_V1.3_at	GCTATCTTTGTCTTTTTCATCTTAT	SEQ ID NO:1636
WBC037F12_V1.3_at	GAATGCAATACACAGTTGGCCAAGT	SEQ ID NO:1637
WBC037F12_V1.3_at	GAATATTTTGCTATGACTACAGTTT	SEQ ID NO:1638
WBC037F12_V1.3_at	GAATGTTGTCTATCTCTTGATTGCT	SEQ ID NO:1639
WBC037F12_V1.3_at	GAAATGTGAGAGTGCCCCTTGAAAG	SEQ ID NO:1640
WBC037F12_V1.3_at	TCTAGCATCGTATCGCACTTTGAAA	SEQ ID NO:1641
WBC037F12_V1.3_at	TAAGTCCTATAAACCTGAACTCCTT	SEQ ID NO:1642

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
No Homology		
WBC038G11_V1.3_at	ATCTGTGGCGGATGTTTCTTCTCTG	SEQ ID NO:1643
WBC038G11_V1.3_at	AGGAGTTCTCCTGAGCTCAGCCGAG	SEQ ID NO:1644
WBC038G11_V1.3_at	AGCAGTTCTTCCTGAACGGCTTTGA	SEQ ID NO:1645
WBC038G11_V1.3_at	AGACTGACAGCTGACTCCCAGGAGT	SEQ ID NO:1646
WBC038G11_V1.3_at	ACGTGCATGTGTCTTCCAGGAGCAT	SEQ ID NO:1647
WBC038G11_V1.3_at	AAACAAGCGACATCAGCACCTGGGA	SEQ ID NO:1648
WBC038G11_V1.3_at	AAGGAAGGGCTCTGCCTGAGCAGTT	SEQ ID NO:1649
WBC038G11_V1.3_at	GAACTTGGTCGCATTTGGTCTGAAA	SEQ ID NO:1650
WBC038G11_V1.3_at	GAAGGAGTTCCCTGATCGGCTACAG	SEQ ID NO:1651
WBC038G11_V1.3_at	GTGAACTGCCTGTTGAACTTGGTCG	SEQ ID NO:1652
WBC038G11_V1.3_at	GGAGCATTGCACGTTGCCTGTAGAA	SEQ ID NO:1653
Leu-8 pan leukocyte antigen		
WBC039F12_V1.3_at	ACATGCACCTTCAACTGCTCAGAAG	SEQ ID NO:1654
WBC039F12_V1.3_at	AAACATTTGGCTGATTTTTGCTTTT	SEQ ID NO:1655
WBC039F12_V1.3_at	GCAGGATACCAAGCTCTATGTTTTA	SEQ ID NO:1656
WBC039F12_V1.3_at	GATCATCAGGAATCTGGTCCAGCAC	SEQ ID NO:1657
WBC039F12_V1.3_at	GTTGGCATTTATCATTTGGCTGGCA	SEQ ID NO:1658
WBC039F12_V1.3_at	GTTTTATAGACATCAGTCCCTGGAG	SEQ ID NO:1659
WBC039F12_V1.3_at	GTGAAGCAGCCCAGTACATACTTTC	SEQ ID NO:1660
WBC039F12_V1.3_at	GTCATGGTTACTGCATTATCTGGGT	SEQ ID NO:1661
WBC039F12_V1.3_at	GGTCCAGCACTAGTCCAATGTGTCA	SEQ ID NO:1662
WBC039F12_V1.3_at	TGGACAGGAGTTTCACGGCGATCAA	SEQ ID NO:1663
WBC039F12_V1.3_at	TCATCCCTGTGGCAGTCATGGTTAC	SEQ ID NO:1664
WBC040E12_V1.3_at	AAATCATCATAACTCAACTCCTACG	SEQ ID NO:1665
WBC040E12_V1.3_at	AACTTTGTGTCAGCGATACCCTTTA	SEQ ID NO:1666
WBC040E12_V1.3_at	AACTATTATCTCATCCTCTTTTTCG	SEQ ID NO:1667
WBC040E12_V1.3_at	AATACAGGGTTGGTGCTCTCATCTA	SEQ ID NO:1668
WBC040E12_V1.3_at	GAAGTACTTCGTGGGCTATCTGGGA	SEQ ID NO:1669
WBC040E12_V1.3_at	GAAACGCATCATACTGTTCCTGTTC	SEQ ID NO:1670
WBC040E12_V1.3_at	GAGTTAACCTTGCTTTTCCTGGAAG	SEQ ID NO:1671
WBC040E12_V1.3_at	GATCCATTCTGTGTGTTTCTTGACT	SEQ ID NO:1672
WBC040E12_V1.3_at	TGGGCTTCGCGTCTTGAGTTAACCT	SEQ ID NO:1673
WBC040E12_V1.3_at	TACGGTCCTCTTTAGATTGCTGTAA	SEQ ID NO:1674
WBC040E12_V1.3_at	TTGACTTACCCTGCTTTCTGAAGAT	SEQ ID NO:1675
WBC041B04_V1.3_at	ATAAAGCCCTGGAGGGCCCTGAGGC	SEQ ID NO:1676
WBC041B04_V1.3_at	AGAATGGGACCATTTCTCTGTGAAT	SEQ ID NO:1677
WBC041B04_V1.3_at	ACCACTTTCCTATTTCACCTGATTT	SEQ ID NO:1678
WBC041B04_V1.3_at	AAGGGTACATTTCTCCTATGGCCGA	SEQ ID NO:1679
WBC041B04_V1.3_at	CTATGGCCGATTTCAGGAATTTCAA	SEQ ID NO:1680
WBC041B04_V1.3_at	CCTGAGGCTCACTGCTGACTGAGAA	SEQ ID NO:1681
WBC041B04_V1.3_at	GACTGAGAACTCTGTGGAACATGAT	SEQ ID NO:1682
WBC041B04_V1.3_at	GAGAATCCTTCAGTTCATTCACAAA	SEQ ID NO:1683

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
WBC041B04_V1.3_at	GTGTTAACCATGAAAGTACTCGAAG	SEQ ID NO:1684
WBC041B04_V1.3_at	GGAACATGATCCTAGGCACTGAAGT	SEQ ID NO:1685
WBC041B04_V1.3_at	GGCACTGAAGTATCGACCACTTTCC	SEQ ID NO:1686
ARP3 actin-related protein 3 homolog (yeast)		
WBC041B05_V1.3_at	ATTTATCGGTATGTAGATAGCTCTA	SEQ ID NO:1687
WBC041B05_V1.3_at	ACACTTCTAAGTGGGCAATGCAAGA	SEQ ID NO:1688
WBC041B05_V1.3_at	AATGCTTGAATTGTACACTTCTAAG	SEQ ID NO:1689
WBC041B05_V1.3_at	AATATTTGAATCTTATGTGTAACCA	SEQ ID NO:1690
WBC041B05_V1.3_at	CCAAGATTTGATGGGATTTATCGGT	SEQ ID NO:1691
WBC041B05_V1.3_at	GCAAGAGCTTGTTTATATTTCATAC	SEQ ID NO:1692
WBC041B05_V1.3_at	GTAGATAGCTCTATAATGCTTGAAT	SEQ ID NO:1693
WBC041B05_V1.3_at	TGGGTTTTAGTTCTTTCTGTGCCCT	SEQ ID NO:1694
WBC041B05_V1.3_at	TCATACTTTTTATACTTTGAGGAAA	SEQ ID NO:1695
WBC041B05_V1.3_at	TTTAGTTCTTTCTGTGCCCTGATAT	SEQ ID NO:1696
WBC041B05_V1.3_at	TTCTGTGCCCTGATATTTTGTATAT	SEQ ID NO:1697
WBC041B05_V1.3_s_at	ATGCCTGCTTAGTGCTTTCTGATTA	SEQ ID NO:1698
WBC041B05_V1.3_s_at	AGCCTCATGAGACTTGGCATACACA	SEQ ID NO:1699
WBC041B05_V1.3_s_at	ACTCGCATTCTGTTTCTTGCTTTAA	SEQ ID NO:1700
WBC041B05_V1.3_s_at	TCTTTGCAAGTGCTTTTGGAACTAA	SEQ ID NO:1701
WBC041B05_V1.3_s_at	CCCCACAATGATTTTCTTTGCAAGT	SEQ ID NO:1702
WBC041B05_V1.3_s_at	GCTTTCTGATTACTCGCATTCTGTT	SEQ ID NO:1703
WBC041B05_V1.3_s_at	GCAGTTCTGTAGTGTCATTTCTTAT	SEQ ID NO:1704
WBC041B05_V1.3_s_at	GTTTAAAGCCTAACACCATTCTAAT	SEQ ID NO:1705
WBC041B05_V1.3_s_at	GGGATTCCAGTTATTACGAGTTGCT	SEQ ID NO:1706
WBC041B05_V1.3_s_at	TCTTGGATTAACTGATGCCTGCTTA	SEQ ID NO:1707
WBC041B05_V1.3_s_at	TACACACACACTCATGGGATTCCAG	SEQ ID NO:1708
WBC043E03_V1.3_at	ATGACCCGAGAGGTGCAGACCAATG	SEQ ID NO:1709
WBC043E03_V1.3_at	ATCCACTCCATGATGTCTTTGTTAG	SEQ ID NO:1710
WBC043E03_V1.3_at	ATGGGATGGATCTTACTCGTGACAA	SEQ ID NO:1711
WBC043E03_V1.3_at	ATGGTTATTTGCTTCGTCTGTTCTG	SEQ ID NO:1712
WBC043E03_V1.3_at	AACTGCCTAACTAACTTCCATGGGA	SEQ ID NO:1713
WBC043E03_V1.3_at	AAGGCTTGCCAGTCTATTTATCCAC	SEQ ID NO:1714
WBC043E03_V1.3_at	GATTCGGAAGACCTCTTATGCTCAG	SEQ ID NO:1715
WBC043E03_V1.3_at	GTCTGTTCTGTGTTGGTTTTACTAA	SEQ ID NO:1716
WBC043E03_V1.3_at	TGACGGATACGAGCCACCAGTGCAA	SEQ ID NO:1717
WBC043E03_V1.3_at	TTATGCTCAGCACCAACAGGTCCGT	SEQ ID NO:1718
WBC043E03_V1.3_at	TGACGTCAAGACTACCGATGGTTAT	SEQ ID NO:1719
Homo sapiens high mobility group nucleosomal binding domain 4, mRNA		
WBC043G11_V1.3_at	CAGTTTTGCTTGTCATACGTCTTTA	SEQ ID NO:1720
WBC043G11_V1.3_at	CAGTGTTGAATCTTCCAATCCATGA	SEQ ID NO:1721
WBC043G11_V1.3_at	GACCTGTAACACTGTCTCTTTCATA	SEQ ID NO:1722

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
WBC043G11_V1.3_at	GATGGTTTCTGTTCTGACTCACTGG	SEQ ID NO:1723
WBC043G11_V1.3_at	GTCAATTTGTCTAACCTGTGGCAGT	SEQ ID NO:1724
WBC043G11_V1.3_at	GTGGCAGTACTATACAATCCTGAGT	SEQ ID NO:1725
WBC043G11_V1.3_at	GGTTGTTGCAGCACCATTTTCTGAA	SEQ ID NO:1726
WBC043G11_V1.3_at	TGAAAAGTTCATCCTTTCCTCACTG	SEQ ID NO:1727
WBC043G11_V1.3_at	TTTGTGTGGGTCTCTTGATGGTTTC	SEQ ID NO:1728
WBC043G11_V1.3_at	TTAGCCATTTGCTTTTCCATACAAT	SEQ ID NO:1729
WBC043G11_V1.3_at	TTCTTCCTTGAGAGTATCTTGGCTA	SEQ ID NO:1730
WBC133.V1.3_at	ATGTTATCTACAGACTTTGGGTGAT	SEQ ID NO:1731
WBC133.V1.3_at	AGCCCATAGAATGCACAACACCAAG	SEQ ID NO:1732
WBC133.V1.3_at	CAGAGGATTTTTAGGGCAGTGAAAC	SEQ ID NO:1733
WBC133.V1.3_at	CAGCTATTATGATCCTGAATGTATA	SEQ ID NO:1734
WBC133.V1.3_at	GCAGGTAACAGAGCACAGAGGATTT	SEQ ID NO:1735
WBC133.V1.3_at	GAGAAAACCCTAATGTTATCTACAG	SEQ ID NO:1736
WBC133.V1.3_at	GTAAACACAGGAAATCTGAACCAGA	SEQ ID NO:1737
WBC133.V1.3_at	GTCTGATACTTTAACAGTGGACACA	SEQ ID NO:1738
WBC133.V1.3_at	GTGGACACATGTCATTATACGTTTG	SEQ ID NO:1739
WBC133.V1.3_at	GGCAGTGAAACAATTCTGTCTGATA	SEQ ID NO:1740
WBC133.V1.3_at	TATACGTTTGTTTAAGCCCATAGAA	SEQ ID NO:1741
Mst3 and SOK1-related kinase (MASK)		
WBC166.gRSP.V1.3_at	TTTAGTCAAAGTGCCCATTACCTCC	SEQ ID NO:1742
WBC166.gRSP.V1.3_at	AAAATTTTCACCTGCTGTCTAACTG	SEQ ID NO:1743
WBC166.gRSP.V1.3_at	CATTACCTCCTCTGTTTTTGTAATA	SEQ ID NO:1744
WBC166.gRSP.V1.3_at	CTGCTGTCTAACTGAAATTCCATTA	SEQ ID NO:1745
WBC166.gRSP.V1.3_at	GAAATTCTTTTCATTGGTGCCTGTA	SEQ ID NO:1746
WBC166.gRSP.V1.3_at	GTTTGGATCTGCACAATTGGGTTTT	SEQ ID NO:1747
WBC166.gRSP.V1.3_at	GTTAGTAGTCCTGTAAAGTGTTTCT	SEQ ID NO:1748
WBC166.gRSP.V1.3_at	GGTGCCTGTACTGTAACAATTACTT	SEQ ID NO:1749
WBC166.gRSP.V1.3_at	GGGTTTTTGCACAGAAGTCATTTTT	SEQ ID NO:1750
WBC166.gRSP.V1.3_at	TCTAGGTGAAGCATACTCCAGTGTT	SEQ ID NO:1751
WBC166.gRSP.V1.3_at	TTGACGACACAACTGTATCATGGAT	SEQ ID NO:1752
CGG triplet repeat binding protein 1 (CGGBP1),		
WBC434.gRSP.V1.3_at	ATGGAGGCTCCATACCTAAGTCAGA	SEQ ID NO:1753
WBC434.gRSP.V1.3_at	AACTGCATCGCTTCAGTGCAACAGT	SEQ ID NO:1754
WBC434.gRSP.V1.3_at	AAGACTGCTTTGTATGTGACTCCCC	SEQ ID NO:1755
WBC434.gRSP.V1.3_at	AAGGAGGCTACCACCATTGTGATCA	SEQ ID NO:1756
WBC434.gRSP.V1.3_at	AAGTCTGCCATTAGTGACCACCTCA	SEQ ID NO:1757
WBC434.gRSP.V1.3_at	CTGAATCATGTTCGCAAGTCTGCCA	SEQ ID NO:1758
WBC434.gRSP.V1.3_at	CAGCTCCTCAACTCACAAGATTGTT	SEQ ID NO:1759
WBC434.gRSP.V1.3_at	GCACTTCTTGCAATGTGGTTCTGAA	SEQ ID NO:1760
WBC434.gRSP.V1.3_at	GGAGGAAAACTCTTCTGCACTTCTT	SEQ ID NO:1761
WBC434.gRSP.V1.3_at	GGAGGCCAACATCCCACTTGAGAAG	SEQ ID NO:1762
WBC434.gRSP.V1.3_at	TTCCTGTCTCGCCACGTGAAGAATG	SEQ ID NO:1763

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
Homo sapiens mRNA; cDNA DKFZp667N084		
WBC493.V1.3_at	AGTGTCACAGTACATTTTCAAGTTT	SEQ ID NO:1764
WBC493.V1.3_at	ACAGTGCCTCTGTATGCTTTTTGTA	SEQ ID NO:1765
WBC493.V1.3_at	AACGCTTCTTTATTTTTGATACACA	SEQ ID NO:1766
WBC493.V1.3_at	CAGACTGCAGTCGTACTTGATTTTT	SEQ ID NO:1767
WBC493.V1.3_at	CCAGTTCATCTTTAGCTTTCGTTGT	SEQ ID NO:1768
WBC493.V1.3_at	GAACTGCACAGTCCTAATAATCAAA	SEQ ID NO:1769
WBC493.V1.3_at	GATACCTCTTAAACTTATGTCTTTT	SEQ ID NO:1770
WBC493.V1.3_at	GATATATCCCTTTAGCATTACCTTA	SEQ ID NO:1771
WBC493.V1.3_at	GTTTAGACTTGAATCCCAGTTCATC	SEQ ID NO:1772
WBC493.V1.3_at	TGTTTCCTATTTTTTGATACCTCTT	SEQ ID NO:1773
WBC493.V1.3_at	TCGTTGTGCTTTTTTAACGCTTCTT	SEQ ID NO:1774
Zinc Finger Protein 198		
WBC590.V1.3_at	ATGTTTTCGCTTTTATTGTTATGTG	SEQ ID NO:1775
WBC590.V1.3_at	AGAGTGTATGCCTATTTTTATGTTG	SEQ ID NO:1776
WBC590.V1.3_at	ACTTGTGATTTCTTTCTTTTGAGGA	SEQ ID NO:1777
WBC590.V1.3_at	AAGCAGCATCTTTGTTACGTTAAAT	SEQ ID NO:1778
WBC590.V1.3_at	AAGTTTGGTTGATTTTCTGTTCTGA	SEQ ID NO:1779
WBC590.V1.3_at	GAACAAGCGTTATCATCATTATTAT	SEQ ID NO:1780
WBC590.V1.3_at	GATGTGAAACTGCACCTTTTTGCTA	SEQ ID NO:1781
WBC590.V1.3_at	GGCTTAAATTTATCCATACCAGTTT	SEQ ID NO:1782
WBC590.V1.3_at	GGTATTTGAGGACTGACATTTGACA	SEQ ID NO:1783
WBC590.V1.3_at	GGCACTTGTTAATTTTTTCAGTCTG	SEQ ID NO:1784
WBC590.V1.3_at	TTCAGTCTGTCAATTCACACCTTTT	SEQ ID NO:1785
No Homology		
BM780906.V1.3_at	AGCTGAAACACATCTCTTGGGTCCT	SEQ ID NO:1786
BM780906.V1.3_at	GCTTCCCATCATAGTTTTGCCGTTA	SEQ ID NO:1787
BM780906.V1.3_at	GATTCCCAGAATGCCATCGATGACC	SEQ ID NO:1788
BM780906.V1.3_at	GTTCCGTTTTCAAGGACCAGTCAGC	SEQ ID NO:1789
BM780906.V1.3_at	GTAACAGTGACTCCTGATTCCCAGA	SEQ ID NO:1790
BM780906.V1.3_at	GTGTGAGCAGCTCCTCCTGTATAGT	SEQ ID NO:1791
BM780906.V1.3_at	TGGAGCTTTTGCCTGTAGCTTGAGA	SEQ ID NO:1792
BM780906.V1.3_at	TGTATAGTCCTCTTCTTCACTGAAT	SEQ ID NO:1793
BM780906.V1.3_at	TCAGTACGTCAGTGGTGGAGCTTTT	SEQ ID NO:1794
BM780906.V1.3_at	TTCACTGAATGCTGGAACCTCCAAC	SEQ ID NO:1795
BM780906.V1.3_at	TTTACCCGCAGTATCAAGCACAAGA	SEQ ID NO:1796
B1961054.V1.3_at	TCAGTAGTAACTCTGCCTTGGCACT	SEQ ID NO:1797
B1961054.V1.3_at	ATATGTCAAGCCCTAATTGTCCCCG	SEQ ID NO:1798
B1961054.V1.3_at	ATGGTTCATCATCCTGAGCTGTTCA	SEQ ID NO:1799
B1961054.V1.3_at	AATTAGCTGCTACTACTCCTGCAGG	SEQ ID NO:1800
B1961054.V1.3_at	CAACGTGTTGAGATCATTGCCACAA	SEQ ID NO:1801
B1961054.V1.3_at	GCCATCATTTCCCTGCATACAGTAT	SEQ ID NO:1802
B1961054.V1.3_at	GAATCCAGAGTCCAAGACCGTCAAG	SEQ ID NO:1803
B1961054.V1.3_at	GGTACTACTGATACGGATGGCCCAA	SEQ ID NO:1804

Probe Set Name	PROBE SEQUENCE	Sequence Identifier
B1961054.V1.3_at	GTTCTCCTAAGATGACCAACCAGTC	SEQ ID NO:1805
B1961054.V1.3_at	GGTCTAAAAGATCTCCTCGAACACT	SEQ ID NO:1806
B1961054.V1.3_at	TAATTGTCCCCGGATTGCAGTTCTC	SEQ ID NO:1807

TABLE 3

AMINO ACID SUB-CLASSIFICATION

Sub-classes	Amino acids
Acidic	Aspartic acid, Glutamic acid
Basic	Noncyclic: Arginine, Lysine; Cyclic: Histidine
Charged	Aspartic acid, Glutamic acid, Arginine, Lysine, Histidine
Small	Glycine, Serine, Alanine, Threonine, Proline
Polar/neutral	Asparagine, Histidine, Glutamine, Cysteine, Serine, Threonine
Polar/large	Asparagine, Glutamine
Hydrophobic	Tyrosine, Valine, Isoleucine, Leucine, Methionine, Phenylalanine, Tryptophan
Aromatic	Tryptophan, Tyrosine, Phenylalanine
Residues that influence chain orientation	Glycine and Proline

TABLE 4

EXEMPLARY AND PREFERRED AMINO ACID SUBSTITUTIONS

Original Residue	Exemplary Substitutions	Preferred Substitutions
Ala	Val, Leu, Ile	Val
Arg	Lys, Gln, Asn	Lys
Asn	Gln, His, Lys, Arg	Gln
Asp	Glu	Glu
Cys	Ser	Ser
Gln	Asn, His, Lys,	Asn
Glu	Asp, Lys	Asp
Gly	Pro	Pro
His	Asn, Gln, Lys, Arg	Arg
Ile	Leu, Val, Met, Ala, Phe, Norleu	Leu
Leu	Norleu, Ile, Val, Met, Ala, Phe	Ile
Lys	Arg, Gln, Asn	Arg
Met	Leu, Ile, Phe	Leu
Phe	Leu, Val, Ile, Ala	Leu
Pro	Gly	Gly
Ser	Thr	Thr
Thr	Ser	Ser
Trp	Tyr	Tyr
Tyr	Trp, Phe, Thr, Ser	Phe
Val	Ile, Leu, Met, Phe, Ala, Norleu	Leu

TABLE 5

PRIORITY RANKING OF GENES BASED ON P VALUES

Gene Name	Day	P.Value	Day	P.Value	Day	P.Value	Day	P.Value	Day	P.Value	Day	P.Value	Day	P.Value
BM734889	0	5.62E-020	2	1.14E-09	4	7.81E-07	7	6.7E-09						
WBC005D02	0	8.19E-020	2	1.32E-12	4	1.59E-06	7	5.94E-05						
BM734862	0	1.13E-13	2	4.21E-06	4	0.047483	7	8.48E-06						
B1961941	0	1.45E-13	2	1.75E-12	4	7.44E-05	7	4.09E-08						
WBC001C12	9	3.77E-12	11	1.84E-05	14	0.000645								
BM735487	0	4E-12	2	1.07E-10	4	3.07E-05	7	1.27E-14						
BM734722	0	4.27E-11	2	5.64E-10	4	3.22E-07	7	4.34E-11	9	0.005597	11	0.007828		
WBC008F06	9	8.8E-10	11	6.43E-07	14	0.037099								
B1961620	0	3.23E-09	2	1.46E-05	4	0.002125	7	6.48E-09	9	0.000103	11	0.012906	14	0.00011
BM735585	0	5.47E-09	2	6.71E-10	4	0.000125	7	2.85E-10						
WBC022F08	0	5.61E-09	2	5.81E-12	7	0.000304								
BM735573	0	7.07E-09	2	2.72E-07	4	0.001579								
B1961682	0	7.71E-09	2	0.024969	7	0.000375	14	0.005519						
WBC021B08	2	9.14E-09	7	1.24E-07	9	2.61E-09	11	1.81E-06						
WBC032G05	0	1.38E-08	2	3.35E-05	7	0.000114	11	0.008059						
BM781178	0	1.38E-08	2	1.35E-05	4	0.012404								
gi576646	0	1.87E-08	2	9.73E-06	4	0.000899	7	1.12E-06	9	9.62E-07	14	5.64E-05		
GI1592834	0	2.53E-08	2	7.16E-08	7	0.000149								
B1961443	0	3.82E-08	7	0.000109	9	0.021125	14	0.021335						
WBC030C04	0	4.93E-08	2	3.01E-10	4	1.22E-09	7	7.54E-12	9	3.84E-05	14	0.035821		
BM781334	0	6.32E-08	7	0.000608	9	0.027236	14	0.033821						
B1961885	0	6.83E-08	2	4.67E-06	7	0.000802								

Gene Name	Day	P.Value	Day	P.Value	Day	P.Value	Day	P.Value	Day	P.Value	Day	P.Value	Day	P.Value
BM781174	0	8.96E-08	2	0.000313	4	0.003936	7	0.033205						
WBC434	2	1.08E-07	4	0.005926	7	2.94E-11	9	3.71E-08	11	0.001727				
B1961671	0	1.14E-07	2	1.51E-05	4	0.000753	7	7.49E-08	9	4.37E-05	11	0.02579	14	3.46E-05
WBC024F08	2	1.78E-07	7	3.09E-08	9	0.000111	11	0.00276	17	0.021939				
WBC007G12	0	2.09E-07	2	0.022205	7	0.003859								
WBC001F11	9	2.15E-07	11	6.5E-05	14	0.001586								
WBC003D11	2	2.81E-07	7	0.000171	9	0.009387								
WBC022B05	2	5.27E-07	7	1.65E-07	9	0.001287								
BM780906	0	6.11E-07	2	2.93E-06	7	0.000897								
WBC012F07	0	8.91E-07	2	3.32E-07	7	1.59E-06								
BM734865	0	9.12E-07	2	1.05E-05	7	7.76E-06	9	2.22E-05	11	0.00057	14	0.046599		
WBC014G08	9	1.04E-06	11	0.006248	14	0.001349								
WBC028C01	0	1.15E-06	2	0.002318	7	0.008866								
WBC013E10	2	1.24E-06	4	0.03163	7	0.000149	9	0.014568						
WBC009B10	2	1.55E-06	7	0.008422	9	0.000196								
BM734654	0	1.57E-06	2	4.23E-05	4	0.002656	7	1.42E-05						
BM735536	0	1.97E-06	2	2.54E-12	4	6.46E-09	7	7.41E-14	9	2.01E-11	11	0.000125		
WBC003F02	7	2.42E-06	9	5.83E-06	11	2.53E-06								
WBC012E07	0	3.05E-06	4	0.018001	7	4.76E-07	9	4.2E-06	14	0.000272				
WBC014H06	2	3.33E-06	7	1.81E-08	9	5.88E-09	11	0.002383						
BM735576	0	3.53E-06	2	0.021658	7	2.73E-05	9	0.00685						
BM735352	2	4.38E-06	7	4.37E-06	9	0.005436	11	0.039799						
WBC007A09	0	6.08E-06	2	1.2E-06	7	9.74E-06	9	0.000112	11	0.000195				
BM735457	2	6.8E-06	7	6.34E-05	9	1.91E-08								
WBC005F10	0	8.6E-06	2	2.42E-09	7	1.08E-05								

Gene Name	Day	P.Value	Day	P.Value	Day	P.Value	Day	P.Value	Day	P.Value	Day	P.Value	Day	P.Value
WBC020B04	0	8.98E-06	2	0.00137	7	0.022142								
WBC028E07	2	1.14E-05	7	0.000466	9	0.001507	11	9.31E-06						
BM735534	0	1.21E-05	2	4.54E-08	4	0.03855	7	3.37E-10	9	0.045945				
WBC038G11	0	1.45E-05	2	5.1E-05	7	0.000481								
B1961711	0	1.62E-05	2	0.044085	7	1.69E-05								
B1961637	2	1.66E-05	7	6.29E-08	9	0.00037	11	0.007214						
WBC024C12	0	1.85E-05	2	0.008355	7	9.02E-06								
BM735450	0	1.92E-05	2	0.009622	4	0.003305	7	3.46E-05						
WBC006H06	7	1.97E-05	9	1.55E-05	14	0.005638								
WBC013H03	0	2.2E-05	2	3.3E-05	7	0.000509								
WBC030D02	7	2.28E-05	9	3.74E-08	11	4.8E-05	14	0.000181						
WBC006E03	9	2.92E-05	11	0.004223	14	6.36E-05								
WBC022B06	2	3.06E-05	7	6.19E-06	11	0.026743								
WBC028F05	0	3.15E-05	2	7.49E-07	4	0.003321	7	1.68E-09	9	7.18E-07	11	7.49E-05		
WBC009E12	9	3.25E-05	11	0.004629	14	0.0005								
WBC003H01	0	3.31E-05	7	0.000992	14	0.014301								
WBC026E02	0	3.43E-05	2	1.29E-07	7	0.021843								
WBC018D05	7	3.47E-05	9	0.027649	14	0.008898								
BM735166	0	3.88E-05	4	0.00401	7	0.000304	14	0.000601						
WBC028D09	0	4.84E-05	4	0.001241	7	6.41E-08	9	0.000202						
BM734531	0	4.96E-05	2	5.36E-08	7	0.000196								
WBC013A09	9	5.04E-05	11	6.13E-05	14	0.006365								
WBC010F04	4	5.04E-05	7	4.2E-05	9	1.68E-08	14	0.035866						
B1961109	0	5.05E-05	2	1.51E-05	4	0.03924	7	1.31E-05	9	0.000187	11	8.7E-05	14	0.046035
WBC001F08	7	5.49E-05	9	2.05E-05	11	0.006456	14	2.88E-06						

Gene Name	Day	P.Value	Day	P.Value	Day	P.Value	Day	P.Value	Day	P.Value	Day	P.Value	Day	P.Value
BM734457	7	5.65E-05	9	2.45E-06	14	0.004615								
WBC166	9	6.43E-05	11	0.000632	14	0.000648								
WBC024B05	7	8.41E-05	9	3.42E-09	11	2.11E-07	14	0.000172						
WBC004D07	9	8.87E-05	11	0.000708	14	0.002727								
WBC032B05	7	9.38E-05	9	1.47E-05	11	1.22E-05	14	1.97E-06						
WBC021D01	7	0.000118	9	0.000841	14	0.001455								
WBC008F12	0	0.000119	2	2.32E-08	4	0.002886	7	1.85E-08						
WBC027E07	0	0.000152	2	0.009696	7	0.003137								
BM735102	0	0.000152	7	0.000595	9	0.034995								
WBC041B05	9	0.000158	11	0.025083	14	0.022571								
WBC039F12	0	0.00019	2	3.68E-05	7	5.79E-09								
BM735286	0	0.000203	2	2.5E-05	4	0.015183	7	9.79E-05	11	0.018883				
WBC493	7	0.000215	9	0.000323	11	0.002796	14	6.25E-05						
WBC001C11	9	0.000252	11	0.002114	14	0.027481								
WBC019B05	0	0.000256	2	5.5E-05	4	0.000479	7	1.87E-12	9	8.09E-08	11	0.000637	14	1.43E-05
GI9717252	2	0.000267	7	0.001244	11	0.005664								
WBC043G11	7	0.000268	9	0.003323	14	0.003005								
Foe545	9	0.00027	11	0.008383	14	0.000604								
BM735519	0	0.000272	2	9.28E-07	7	0.001646								
BM735409	0	0.0003	4	0.005135	7	3.7E-09								
WBC004C03	0	0.0003	2	0.000373	7	1.14E-06	9	0.015975	14	0.008483				
WBC001A07	9	0.000309	11	0.031959	14	0.011618								
BM734719	2	0.000313	4	1.5E-05	7	2.69E-06	9	0.00355	11	0.012181				
WBC018B01	7	0.000344	9	0.048555	14	0.015517								
Foe1072	7	0.000351	9	1.38E-05	14	0.028866								

Gene Name	Day	P.Value	Day	P.Value	Day	P.Value	Day	P.Value	Day	P.Value	Day	P.Value	Day	P.Value
B1961494	7	0.000382	11	1.52E-06	14	9.11E-06								
WBC007G03	9	0.000385	11	0.026939	14	0.013456								
WBC004E04	7	0.000412	9	2.33E-09	11	7.14E-07	14	2.53E-05						
BM735545	0	0.000476	2	1.02E-06	4	1.1E-05	7	0.001412	11	0.007853	14	0.036358		
BM735167	2	0.000484	7	9.77E-05	9	6.49E-13	11	1.52E-05						
B1960933	7	0.000506	9	0.007447	11	0.048364								
BM735441	0	0.000541	2	0.00586	7	0.000179								
Foe1060	9	0.000551	11	0.010201	14	0.02297								
WBC590	9	0.000596	11	0.02401	14	0.001841								
WBC001H09	7	0.00061	9	0.021894	14	0.022122								
WBC027D07	0	0.000667	2	1.12E-06	4	3E-05	7	8.55E-015	9	2.94E-06	11	0.001128	14	2.75E-07
WBC013C03	9	0.000778	11	0.000615	14	0.002414								
WBC024C11	2	0.000799	4	4.91E-06	7	4E-10	9	1.81E-06	14	8.89E-06				
WBC016A12	0	0.000806	2	0.005596	4	0.026774	7	0.000604	9	0.002168				
BM781186	0	0.000863	2	0.000524	4	0.002977	7	0.016418						
WBC012G02	7	0.000863	9	0.000161	14	0.000843								
BM781417	0	0.000961	7	0.0002	9	0.002666	11	0.012894	14	0.004028				

TABLE 6

GENE PRIORITY ORDER BASED ON T VALUE

Gene Name	Day	M	t	P.Value	B
WBC008F06_V1.3_at	9	-0.53075	-7.92738	8.8E-10	21.27623
WBC007G12_V1.3_at	0	-0.34772	-6.96751	2.09E-07	16.05095
WBC001F11_V1.3_at	9	-0.53926	-6.96303	2.15E-07	16.03718
WBC014G08_V1.3_at	9	-0.50112	-6.67446	1.04E-06	14.53887
WBC013E10_V1.3_at	2	-0.44979	-6.64137	1.24E-06	14.37086
WBC012E07_V1.3_at	0	-0.46294	-6.47256	3.05E-06	13.50699
WBC024C12_V1.3_at	0	-0.44376	-6.12738	1.85E-05	11.79847
WBC006H06_V1.3_at	7	-0.42431	-6.11448	1.97E-05	11.73829
WBC030D02_V1.3_at	7	-0.47564	-6.08505	2.28E-05	11.59508
WBC006E03_V1.3_at	9	-0.48246	-6.03644	2.92E-05	11.35935
WBC028F05_V1.3_at	0	-0.48118	-6.02243	3.15E-05	11.29056
WBC009E12_V1.3_at	9	-0.7531	-6.01545	3.25E-05	11.25809
WBC018D05_V1.3_at	7	-0.51854	-6.00257	3.47E-05	11.19618
WBC010F04_V1.3_at	4	-0.76635	-5.9324	5.04E-05	10.76647
WBC013A09_V1.3_at	9	-0.32137	-5.92857	5.04E-05	10.84143
WBC001F08_V1.3_at	7	-0.31702	-5.91162	5.49E-05	10.76031
WBC166.gRSP.V1.3_at	9	-0.70207	-5.87988	6.43E-05	10.60961
WBC024B05_V1.3_at	7	-0.4822	-5.82594	8.41E-05	10.35363
WBC004D07_V1.3_at	9	-0.38487	-5.81519	8.87E-05	10.30359
WBC032B05_V1.3_at	7	-0.42227	-5.80372	9.38E-05	10.24879
WBC021D01_V1.3_at	7	-0.37385	-5.75613	0.000118	10.02519
WBC041B05_V1.3_at	9	-0.60661	-5.69821	0.000158	9.755808
WBC493.V1.3_at	7	-0.75113	-5.63393	0.000215	9.456588
WBC001C11_V1.3_s_at	9	-0.459	-5.60169	0.000252	9.309492
WBC019B05_V1.3_at	0	-0.57447	-5.60118	0.000256	9.309371
Foe545.V1.3_at	9	-0.40775	-5.58788	0.00027	9.246056
WBC043G11_V1.3_at	7	-0.3362	-5.58774	0.000268	9.243826
WBC004C03_V1.3_at	0	-0.41087	-5.56794	0.0003	9.157128
WBC001A07_V1.3_at	9	-0.53398	-5.55969	0.000309	9.116868
BM734719.V1.3_at	2	-0.41143	-5.55799	0.000313	9.108264
WBC018B01_V1.3_at	7	-0.67086	-5.53604	0.000344	9.00706
Foe1072.V1.3_at	7	-0.49276	-5.5316	0.000351	8.986814
WBC007G03_V1.3_at	9	-0.77183	-5.51378	0.000385	8.90749
WBC004E04_V1.3_at	7	-0.3488	-5.4981	0.000412	8.834262
Foe1060.V1.3_at	9	-0.4171	-5.43881	0.000551	8.568091
WBC590.V1.3_at	9	-0.46943	-5.42207	0.000596	8.492765

Gene Name	Day	M	t	P.Value	B
WBC001H09_V1.3_at	7	-0.55531	-5.41491	0.00061	8.458322
WBC027D07_V1.3_at	0	-0.39411	-5.40118	0.000667	8.402682
WBC013C03_V1.3_at	9	-0.29677	-5.36572	0.000778	8.240336
WBC024C11_V1.3_at	2	-0.29424	-5.36158	0.000799	8.220603
WBC016A12_V1.3_at	0	-0.48188	-5.36119	0.000806	8.224168
WBC012G02_V1.3_at	7	-0.53236	-5.34123	0.000863	8.128662
BM781417.V1.3_at	0	-0.54661	-5.32386	0.000961	8.05831
BM781186.V1.3_at	0	0.607083	5.346723	0.000863	8.159792
BM735441.V1.3_at	0	0.253862	5.44514	0.000541	8.600034
B1960933.V1.3_at	7	0.716823	5.454949	0.000506	8.638769
BM735167.V1.3_at	2	0.414248	5.46725	0.000484	8.695428
BM735545.V1.3_at	0	0.589494	5.471981	0.000476	8.721067
B1961494.V1.3_at	7	0.354654	5.513986	0.000382	8.906528
BM735409.V1.3_at	0	0.269757	5.568459	0.0003	9.159479
BM735519.V1.3_at	0	0.323515	5.588238	0.000272	9.250006
GI9717252-3M_at	2	0.63348	5.591229	0.000267	9.260645
BM735286.V1.3_at	0	0.247435	5.648946	0.000203	9.529213
WBC039F12_V1.3_at	0	0.351171	5.66273	0.00019	9.592888
BM735102.V1.3_at	0	0.356539	5.707416	0.000152	9.800038
WBC027E07_V1.3_at	0	0.290616	5.708292	0.000152	9.804113
WBC008F12_V1.3_at	0	0.269626	5.75662	0.000119	10.02939
BM734457.V1.3_at	7	0.430304	5.905849	5.65E-05	10.73278
B1961109.V1.3_at	0	0.72204	5.929105	5.05E-05	10.84356
BM734531.V1.3_at	0	0.633646	5.932699	4.96E-05	10.86069
WBC028D09_V1.3_at	0	0.291809	5.937444	4.84E-05	10.88332
BM735166.V1.3_at	0	0.357974	5.981577	3.88E-05	11.09433
WBC026E02_V1.3_at	0	0.339222	6.005673	3.43E-05	11.20996
WBC003H01_V1.3_at	0	0.398243	6.012941	3.31E-05	11.24489
WBC022B06_V1.3_at	2	0.431945	6.027528	3.06E-05	11.31647
WBC013H03_V1.3_at	0	0.472666	6.093231	2.2E-05	11.6326
BM735450.V1.3_at	0	0.292831	6.119368	1.92E-05	11.75951
B1961637.V1.3_at	2	0.525483	6.147262	1.66E-05	11.89799
B1961711.V1.3_at	0	0.364045	6.152405	1.62E-05	11.92041
WBC038G11_V1.3_at	0	0.409732	6.174059	1.45E-05	12.02617
BM735534.V1.3_at	0	0.372736	6.209232	1.21E-05	12.19843
WBC028E07_V1.3_at	2	0.582508	6.220488	1.14E-05	12.25714
WBC020B04_V1.3_at	0	0.418213	6.266942	8.98E-06	12.48239
WBC005F10_V1.3_at	0	0.472342	6.27517	8.6E-06	12.523
BM735457.V1.3_at	2	0.410421	6.319517	6.8E-06	12.74701

Gene Name	Day	M	t	P.Value	B
WBC007A09_V1.3_at	0	0.568251	6.341687	6.08E-06	12.85253
BM735352.V1.3_at	2	0.628248	6.403566	4.38E-06	13.16644
BM735576.V1.3_at	0	0.472577	6.445128	3.53E-06	13.36913
WBC014H06_V1.3_at	2	0.785821	6.455537	3.33E-06	13.42745
WBC003F02_V1.3_at	7	0.367974	6.516236	2.42E-06	13.73495
BM735536.V1.3_at	0	1.024189	6.55447	1.97E-06	13.92057
BM734654.V1.3_at	0	0.802667	6.597475	1.57E-06	14.13893
WBC009B10_V1.3_at	2	0.664414	6.599032	1.55E-06	14.15456
WBC028C01_V1.3_at	0	0.290434	6.655002	1.15E-06	14.43232
BM734865.V1.3_at	0	0.656049	6.698282	9.12E-07	14.65401
WBC012F07_V1.3_at	0	0.584337	6.702508	8.91E-07	14.6757
BM780906.V1.3_at	0	0.416052	6.772214	6.11E-07	15.03457
WBC022B05_V1.3_at	2	0.646312	6.799413	5.27E-07	15.18522
WBC003D11_V1.3_at	2	1.337346	6.914252	2.81E-07	15.78363
WBC024F08_V1.3_at	2	0.518276	6.997403	1.78E-07	16.22033
B1961671.V1.3_at	0	0.453662	7.077614	1.14E-07	16.63083
WBC434.gRSP.V1.3_at	2	0.448914	7.087078	1.08E-07	16.69443
BM781174.V1.3_at	0	0.618002	7.120547	8.96E-08	16.85824
B1961885.V1.3_at	0	0.983887	7.169149	6.83E-08	17.11655
BM781334.V1.3_at	0	0.475758	7.183024	6.32E-08	17.19046
WBC030C04_V1.3_at	0	0.602389	7.22709	4.93E-08	17.42568
B1961443.V1.3_at	0	0.505935	7.272533	3.82E-08	17.66902
GI1592834.V1.3_at	0	0.611795	7.345617	2.53E-08	18.06199
gi576646.V1.3_s_at	0	1.280838	7.399041	1.87E-08	18.35048
BM781178_unkn.V1.3_at	0	0.386001	7.452231	1.38E-08	18.63874
WBC032G05_V1.3_at	0	0.596733	7.452338	1.38E-08	18.63932
WBC021B08_V1.3_at	2	0.792947	7.524122	9.14E-09	19.04904
B1961682.V1.3_at	0	0.545432	7.553677	7.71E-09	19.19129
BM735573.V1.3_s_at	0	0.483434	7.568776	7.07E-09	19.27384
WBC022F08_V1.3_at	0	0.553469	7.608824	5.61E-09	19.49316
BM735585.V1.3_at	0	0.402875	7.613483	5.47E-09	19.51871
B1961620.V1.3_at	0	0.584057	7.704254	3.23E-09	20.01797
BM734722.V1.3_at	0	0.736865	8.435653	4.27E-11	24.13395
BM735487.V1.3_at	0	0.445341	8.825278	4E-12	26.38603
WBC001C12_V1.3_at	9	0.76454	8.834995	3.77E-12	26.47277
B1961941.V1.3_at	0	0.478102	9.36128	1.45E-13	29.53961
BM734862.V1.3_at	0	0.727226	9.401378	1.13E-13	29.77781
WBC005D02_V1.3_at	0	0.680964	11.60693	8.19E-020	43.19762
BM734889.V1.3_at	0	1.083673	11.66465	5.62E-020	43.55399

The priority ranking of genes is based on increasing value of t value for the first day each gene is significant ($p<0.001$) following stress induction, and for genes that were significant for at least three sampling times.

TABLE 7

TWO GENES SELECTED

Genes		Sensitivity	Specificity	Success
WBC001F11	B1961443	0.926829268	0.802816901	0.881443299
WBC030D02	BM735536	0.918699187	0.802816901	0.87628866
WBC030D02	BM735536	0.918699187	0.802816901	0.87628866
B1961443	WBC027D07	0.910569106	0.816901408	0.87628866
B1961443	WBC030D02	0.910569106	0.816901408	0.87628866
BM735536	BM734865	0.886178862	0.816901408	0.860824742
BM735536	B1961494	0.894308943	0.802816901	0.860824742
BM735409	B1961443	0.926829268	0.746478873	0.860824742
WBC010F04	WBC003H01	0.918699187	0.76056338	0.860824742
BM734865	BM735536	0.886178862	0.816901408	0.860824742
WBC001C11	B1961443	0.918699187	0.746478873	0.855670103
BM735576	BM735536	0.902439024	0.774647887	0.855670103
B1961443	WBC030C04	0.886178862	0.802816901	0.855670103
WBC004D07	B1961443	0.894308943	0.774647887	0.850515464
B1961443	WBC003D11	0.869918699	0.816901408	0.850515464
B1961443	WBC004D07	0.894308943	0.774647887	0.850515464
WBC012G02	WBC028D09	0.894308943	0.774647887	0.850515464
BM735536	WBC019B05	0.886178862	0.788732394	0.850515464
B1961443	BM734719	0.886178862	0.788732394	0.850515464
B1961443	WBC021B08	0.886178862	0.788732394	0.850515464

TABLE 8

THREE GENES SELECTED

Genes			Sensitivity	Specificity	Success
B1961443	WBC004E04	B1961620	0.910569106	0.873239437	0.896907216
B1961443	BM735441	BM735536	0.943089431	0.802816901	0.891752577
WBC003H01	WBC004E04	BM735536	0.93495935	0.802816901	0.886597938
B1961443	B1961494	Foe545	0.910569106	0.845070423	0.886597938
WBC028D09	B1961443	BM735487	0.918699187	0.830985915	0.886597938
Foe545	WBC013E10	B1961443	0.93495935	0.802816901	0.886597938
WBC027E07	WBC010F04	B1961443	0.910569106	0.830985915	0.881443299
B1961109	WBC013C03	BM735536	0.910569106	0.816901408	0.87628866
BM735487	WBC028D09	WBC021D01	0.894308943	0.845070423	0.87628866
WBC041B05	WBC028D09	WBC019B05	0.910569106	0.816901408	0.87628866
WBC030D02	BM735536	WBC018D05	0.902439024	0.816901408	0.871134021
B1961443	WBC030D02	WBC012F07	0.910569106	0.802816901	0.871134021
WBC003D11	B1961620	B1961443	0.894308943	0.830985915	0.871134021
Foe545	WBC007G03	B1961443	0.918699187	0.788732394	0.871134021
WBC003D11	B1961443	WBC590	0.894308943	0.830985915	0.871134021
WBC003D11	WBC001C12	B1961443	0.894308943	0.816901408	0.865979381
B1961443	BM735585	WBC001F11	0.894308943	0.816901408	0.865979381
WBC009E12	BM735536	BM735167	0.894308943	0.816901408	0.865979381
WBC028E07	BM735536	WBC493	0.902439024	0.802816901	0.865979381
B1961682	B1961443	WBC493	0.910569106	0.788732394	0.865979381

TABLE 9

FOUR GENES SELECTED

Genes				Sensitivity	Specificity	Success
B1961443	WBC019B05	WBC024C12	BM735585	0.93495935	0.85915493	0.907216495
WBC006E03	WBC030C04	WBC003D11	B1961443	0.926829268	0.85915493	0.902061856
WBC021D01	BM735536	B1961443	WBC020B04	0.93495935	0.845070423	0.902061856
B1961443	BM734862	BM735536	WBC007G03	0.93495935	0.845070423	0.902061856
BM735536	B1961671	WBC038G11	WBC003H01	0.93495935	0.830985915	0.896907216
WBC027D07	B1961711	B1961443	BM735487	0.926829268	0.830985915	0.891752577
BM734722	B1961443	WBC028E07	WBC030D02	0.886178862	0.901408451	0.891752577
B1961885	B1961443	B1961620	WBC041B05	0.910569106	0.85915493	0.891752577
BM735536	B1961109	Foe545	WBC001F11	0.910569106	0.845070423	0.886597938
B1960933	B1961885	B1961443	WBC012G02	0.902439024	0.85915493	0.886597938
WBC007A09	WBC166	WBC028D09	WBC005F10	0.910569106	0.845070423	0.886597938
B1961443	BM735457	WBC030C04	WBC008F06	0.886178862	0.873239437	0.881443299
WBC024F08	BM735536	WBC022B05	B1961109	0.902439024	0.845070423	0.881443299
WBC019B05	BM735167	WBC008F12	BM735102	0.894308943	0.85915493	0.881443299
WBC028F05	WBC003H01	B1961443	BM735536	0.918699187	0.816901408	0.881443299
WBC005D02	BM781174	WBC028D09	WBC166	0.910569106	0.830985915	0.881443299
GI1592834	BM735534	B1961443	WBC004E04	0.902439024	0.845070423	0.881443299
WBC001F08	BM734457	B1961443	WBC039F12	0.902439024	0.830985915	0.87628866
WBC010F04	WBC007G03	BM735102	B1961443	0.918699187	0.802816901	0.87628866
BM735536	WBC038G11	BM781334	BM734865	0.894308943	0.845070423	0.87628866

TABLE 10

FIVE GENES SELECTED

Genes					Sensitivity	Specificity	Success
Foe1072	BM735441	B1961885	B1961443	WBC009B10	0.926829268	0.887323944	0.912371134
B1961885	WBC041B05	BM735534	B1961443	WBC024F08	0.93495935	0.85915493	0.907216495
BM735409	WBC010F04	B1961443	B1960933	BM734719	0.93495935	0.85915493	0.907216495
WBC019B05	B1961443	WBC012E07	BM735585	WBC027D07	0.93495935	0.85915493	0.907216495
B1961885	B1961443	WBC003D11	WBC041B05	WBC006E03	0.926829268	0.85915493	0.902061856
WBC003F02	B1961443	BM735167	WBC032G05	WBC493	0.918699187	0.873239437	0.902061856
BM734719	WBC024C11	WBC010F04	B1961443	B1961941	0.943089431	0.830985915	0.902061856
WBC013C03	BM735536	WBC032G05	WBC019B05	WBC166	0.93495935	0.845070423	0.902061856
BM735487	WBC027D07	WBC016A12	WBC001F11	B1961443	0.926829268	0.845070423	0.896907216
BM781334	B1961443	WBC019B05	WBC026E02	WBC032G05	0.918699187	0.85915493	0.896907216
WBC030C04	BM734889	WBC001F08	B1961443	Foe1060	0.918699187	0.85915493	0.896907216
WBC493	B1961443	WBC009E12	BM735534	BM734889	0.926829268	0.845070423	0.896907216
BM734719	WBC003H01	WBC014G08	B1961443	BM735534	0.894308943	0.901408451	0.896907216
BM781334	BM734889	BM735536	BM735534	WBC013C03	0.918699187	0.845070423	0.891752577
WBC001A07	BM735487	WBC030D02	WBC013A09	B1961443	0.910569106	0.85915493	0.891752577
WBC016A12	WBC038G11	B1961443	WBC010F04	WBC004E04	0.926829268	0.830985915	0.891752577
WBC004C03	B1961443	WBC027E07	WBC001F11	WBC010F04	0.910569106	0.845070423	0.886597938
WBC032G05	BM735573	WBC003H01	WBC004C03	Foe545	0.926829268	0.816901408	0.886597938
BM735536	B1961682	B1961494	WBC009E12	WBC021B08	0.918699187	0.830985915	0.886597938
B1961443	WBC013C03	WBC030D02	BM735457	BM735534	0.902439024	0.85915493	0.886597938

TABLE 11

SIX GENES SELECTED

Genes						Sensitivity	Specificity	Success
WBC006H06	B1961443	BM735536	WBC019B05	WBC007G03	WBC009E12	0.951219512	0.873239437	0.922680412
WBC013C03	BM781334	WBC032G05	BM735536	WBC043G11	WBC010F04	0.951219512	0.845070423	0.912371134
B1961443	WBC166	WBC006H06	WBC012E07	BM735536	BM735167	0.951219512	0.830985915	0.907216495
WBC001H09	BM735536	WBC027D07	WBC009B10	WBC028D09	B1961443	0.918699187	0.887323944	0.907216495
WBC028D09	WBC434	Foe545	WBC001F11	B1961443	BM735573	0.93495935	0.85915493	0.907216495
BM781178	B1961671	WBC028D09	WBC005F10	BM781417	BM735536	0.93495935	0.845070423	0.902061856
WBC013E10	WBC166	BM781417	BM735450	B1961494	B1961443	0.93495935	0.845070423	0.902061856
WBC028F05	BM735102	BM735534	B1961443	WBC019B05	B1961885	0.918699187	0.873239437	0.902061856
WBC003H01	BM734531	B1961109	gi576646	WBC019B05	BM735536	0.926829268	0.85915493	0.902061856
BM735409	BM735352	BM735536	WBC028D09	WBC014H06	BM734865	0.910569106	0.873239437	0.896907216
WBC019B05	B1961443	WBC028F05	WBC021D01	WBC003D11	WBC012E07	0.902439024	0.887323944	0.896907216
WBC028D09	BM781417	WBC019B05	BM735536	WBC039F12	WBC004D07	0.918699187	0.85915493	0.896907216
WBC026E02	Foe1072	WBC008F06	B1961885	B1961443	WBC028F05	0.910569106	0.873239437	0.896907216
BM735536	BM734457	WBC028D09	BM780906	BM735487	B1961671	0.910569106	0.873239437	0.896907216
WBC028C01	BM734722	B1961620	WBC013C03	BM735534	BM735536	0.918699187	0.85915493	0.896907216
WBC493	B1961682	WBC001C11	WBC012E07	WBC003D11	B1961443	0.918699187	0.85915493	0.896907216
WBC005D02	BM735536	BM734457	WBC003F02	BM781334	Foe545	0.93495935	0.830985915	0.896907216
B1961443	WBC021D01	BM781417	B1961494	BM735585	BM735457	0.910569106	0.85915493	0.891752577
WBC434	BM734457	B1961443	B1961941	BM735534	WBC030C04	0.93495935	0.816901408	0.891752577
BM780906	WBC030D02	WBC001C12	Foe545	B1961443	B1961109	0.918699187	0.845070423	0.891752577

TABLE 12

SEVEN GENES SELECTED

Genes							Sensitivity	Specificity	Success
BM735536	WBC016A12	B1961637	B1961941	B1961443	BM734722	WBC030D02	0.93495935	0.873239437	0.91237113
B1961682	Foe545	WBC001F11	BM734862	WBC003D11	B1961443	WBC028F05	0.93495935	0.873239437	0.91237113
BM734889	B1961443	WBC434	Foe1072	WBC004C03	B1961885	WBC007G03	0.93495935	0.873239437	0.91237113
WBC006E03	BM735573	B1961443	WBC001H09	B1961682	WBC019B05	WBC022B06	0.943089431	0.85915493	0.91237113
BM734862	WBC013C03	WBC032G05	WBC004D07	WBC028D09	WBC008F06	BM735536	0.93495935	0.85915493	0.90721649
WBC004D07	WBC003H01	WBC001A07	BM735487	BM735536	BM734865	BM780906	0.926829268	0.873239437	0.90721649
B1961443	WBC012F07	gi576646	BM734862	WBC019B05	WBC022B06	WBC001F08	0.943089431	0.845070423	0.90721649
WBC003F02	BM735536	WBC003H01	Foe545	WBC003D11	WBC004E04	BM735573	0.943089431	0.830985915	0.90206186
WBC005D02	WBC028D09	B1961637	B1961443	WBC030D02	BM735576	BM735457	0.894308943	0.915492958	0.90206186
WBC014G08	WBC007G12	BM735102	WBC001F08	WBC006E03	gi576646	BM735536	0.951219512	0.816901408	0.90206186
B1961494	BM781334	BM735585	BM735536	WBC009B10	B1961620	WBC041B05	0.926829268	0.85915493	0.90206186
BM735585	BM735102	B1961443	WBC001F11	WBC008F06	WBC003D11	WBC027D07	0.910569106	0.887323944	0.90206186
BM735536	WBC001F08	WBC004C03	WBC007G12	B1961494	B1961682	BM735286	0.93495935	0.845070423	0.90206186
WBC038G11	BM781334	GI1592834	WBC019B05	WBC027E07	WBC007A09	B1961671	0.926829268	0.85915493	0.90206186
B1961671	B1961443	WBC004C03	WBC004D07	BM735536	WBC012E07	WBC021D01	0.910569106	0.873239437	0.89690722
WBC009B10	WBC038G11	B1961682	B1961443	WBC001C11	WBC006E03	WBC030C04	0.926829268	0.845070423	0.89690722
BM735573	WBC019B05	WBC028E07	WBC003H01	WBC006H06	BM735441	BM734654	0.943089431	0.816901408	0.89690722
WBC003H01	WBC041B05	B1961443	BM735457	BM735585	WBC007G12	BM735441	0.918699187	0.85915493	0.89690722
Foe1072	BM734865	WBC026E02	WBC010F04	B1961443	WBC022B06	WBC001F11	0.910569106	0.873239437	0.89690722
WBC027E07	BM735536	WBC008F06	BM735450	WBC013A09	WBC032G05	WBC007G03	0.918699187	0.85915493	0.89690722

TABLE 13

EIGHT GENES SELECTED

Genes								Sensitivity	Specificity	Success
B1961443	B1961941	WBC009E12	BM735545	BM735585	BM735536	BM734457	WBC043G11	0.93495935	0.90140845	0.92268
BM734865	BM735536	B1960933	B1961443	WBC027E07	WBC007G12	WBC019B05	GI1592834	0.943089431	0.88732394	0.92268
BM735536	B1961443	BM734862	WBC013C03	WBC028C01	BM734719	BM735286	BM735585	0.943089431	0.88732394	0.92268
B1961109	B1961443	BM734654	BM735576	WBC032G05	WBC003D11	WBC019B05	WBC013C03	0.943089431	0.87323944	0.917526
WBC001C11	B1961711	BM734862	BM735536	WBC039F12	WBC004C03	B1961443	BM735166	0.93495935	0.87323944	0.912371
BM734531	WBC041B05	Foe545	B1961620	WBC027D07	B1961637	WBC021B08	B1961443	0.926829268	0.88732394	0.912371
WBC021D01	WBC006H06	B1961109	WBC001F11	WBC019B05	BM735536	B1961443	WBC005D02	0.93495935	0.85915493	0.907216
B1961443	BM735573	B1961885	BM734457	WBC041B05	WBC009B10	B1961620	WBC005F10	0.926829268	0.87323944	0.907216
WBC019B05	B1961620	WBC041B05	WBC032B05	WBC013C03	WBC013H03	B1961443	BM734531	0.926829268	0.87323944	0.907216
B1961885	BM735573	WBC028E07	WBC026E02	WBC003H01	BM735536	WBC013C03	B1961682	0.910569106	0.90140845	0.907216
BM735536	WBC007G03	BM734457	WBC003H01	WBC041B05	WBC016A12	WBC022B06	BM735573	0.93495935	0.85915493	0.907216
WBC010F04	WBC493	BM734719	B1961682	WBC019B05	WBC006H06	B1961443	WBC032G05	0.918699187	0.88732394	0.907216
WBC030C04	B1961443	WBC016A12	BM735166	WBC019B05	WBC005F10	GI1592834	B1961885	0.910569106	0.88732394	0.902062
BM735441	WBC009B10	WBC003H01	WBC003D11	BM735536	B1961671	WBC010F04	WBC027E07	0.93495935	0.84507042	0.902062
WBC019B05	WBC022B05	B1961682	WBC024C12	WBC028E07	B1961443	GI9717252-3M	WBC001F08	0.93495935	0.84507042	0.902062
WBC001C11	WBC007G12	BM781334	WBC030C04	BM781174	BM735409	BM735536	WBC004D07	0.910569106	0.88732394	0.902062
WBC013H03	WBC028D09	B1961885	WBC009E12	B1961941	WBC005F10	WBC001F11	B1961671	0.926829268	0.85915493	0.902062
WBC005D02	BM734865	GI9717252-3M	WBC012E07	BM735536	WBC043G11	BM735441	WBC004D07	0.93495935	0.84507042	0.902062
WBC013C03	BM735536	BM781178	WBC003H01	gi576646	WBC028F05	WBC003F02	Foe545	0.943089431	0.83098592	0.902062
B1961620	GI1592834	BM735585	WBC009B10	WBC007G03	B1961443	BM781417	gi576646	0.902439024	0.90140845	0.902062

TABLE 14

NINE GENES SELECTED

Genes									Sensitivity	Specificity	Success
WBC019B05	WBC003F02	BM781334	WBC004D07	WBC013E10	WBC434	B1961443	WBC010F04	WBC007G03	0.95121951	0.901408	0.93299
WBC028C01	WBC001F08	BM735536	WBC013H03	BM735573	WBC012F07	WBC013A09	WBC005F10	BM735409	0.95121951	0.859155	0.917526
B1961443	WBC007G03	B1961109	B1961637	BM735585	WBC001F08	BM735450	BM735536	BM734457	0.92682927	0.887324	0.912371
WBC001H09	WBC020B04	BM735536	BM735102	BM734531	WBC003H01	BM735457	WBC001A07	WBC019B05	0.92682927	0.887324	0.912371
BM781186	WBC001A07	B1961443	WBC019B05	BM735167	WBC022B05	WBC013C03	WBC018B01	B1961941	0.91056911	0.915493	0.912371
WBC024C12	BM735536	WBC016A12	BM735102	B1961443	Foe545	WBC006H06	WBC028C01	WBC004E04	0.93495935	0.873239	0.912371
WBC018D05	WBC010F04	BM734722	GI9717252-3M	WBC039F12	BM735519	BM781174	WBC019B05	B1961443	0.92682927	0.873239	0.907216
WBC003H01	WBC006H06	WBC012G02	WBC014H06	WBC004C03	WBC019B05	WBC007A09	WBC020B04	BM735536	0.93495935	0.859155	0.907216
WBC001A07	BM735573	WBC012G02	B1961443	WBC043G11	gi576646	BM735536	BM734719	WBC024B05	0.93495935	0.859155	0.907216
WBC004C03	WBC005D02	BM734865	WBC024B05	BM735536	WBC014H06	WBC013C03	WBC012E07	BM734719	0.93495935	0.859155	0.907216
BM735534	BM735457	WBC019B05	BM735166	WBC434	B1961443	WBC038G11	WBC005D02	BM735585	0.92682927	0.873239	0.907216
WBC024B05	BM735536	WBC038G11	WBC010F04	BM735457	Foe1072	WBC003H01	B1961443	WBC006E03	0.93495935	0.84507	0.902062
WBC004D07	B1961941	WBC022B05	WBC022B06	BM735534	B1961443	WBC010F04	BM735167	WBC004E04	0.92682927	0.859155	0.902062
WBC032G05	BM735409	WBC004C03	WBC012F07	B1961620	B1961443	WBC019B05	WBC021D01	WBC016A12	0.91056911	0.887324	0.902062
B1961682	BM735450	WBC028F05	BM735102	B1961443	WBC001F08	WBC021D01	BM735487	WBC030C04	0.91056911	0.887324	0.902062
WBC041B05	BM735585	B1961443	WBC028E07	WBC020B04	B1961637	WBC013E10	WBC010F04	BM781178	0.92682927	0.859155	0.902062
Foe545	Foe1060	BM735536	BM735167	BM735585	WBC009E12	GI1592834	WBC024C12	WBC006H06	0.92682927	0.859155	0.902062
BM735536	WBC038G11	BM735534	WBC004C03	WBC003H01	BM735457	WBC007G12	B1961620	WBC004D07	0.91869919	0.873239	0.902062
BM735166	WBC003H01	WBC043G11	BM734722	WBC022B05	BM734531	BM735536	WBC008F06	WBC434	0.92682927	0.859155	0.902062
WBC012E07	BM735167	WBC004D07	WBC013H03	WBC019B05	WBC021B08	B1961443	WBC022F08	BM735450	0.94308943	0.830986	0.902062

TABLE 15

TEN GENES SELECTED

Genes	Sensitivity	Specificity	Success
BM735536; WBC030C04; WBC019B05; BM734531; WBC018B01; BM735166; WBC006E03; WBC007A09; WBC018D05; B1961885	0.95122	0.859155	0.917526
BM734719; BM735534; B1961443; B1960933; WBC026E02; BM735536; BM735573; WBC022B05; WBC019B05; WBC001F11	0.926829	0.901408	0.917526
WBC004D07; BM735450; WBC004C03; B1961711; Foe1072; WBC039F12; B1961443; WBC013H03; WBC032G05; WBC001F08	0.934959	0.873239	0.912371
BM734531; WBC028C01; BM735536; BM734722; WBC019B05; WBC041B05; BM735166; WBC013H03; BM735487; WBC032G05	0.943089	0.859155	0.912371
BM735102; WBC434; BM734531; WBC005D02; WBC007G03; WBC010F04; BM781417; BM735441; BM734719; B1961443	0.934959	0.873239	0.912371
WBC032B05; WBC005F10; WBC028D09; B1961443; Foe1072; WBC027E07; WBC434; B1960933; BM734654; B1961885	0.943089	0.859155	0.912371
WBC019B05; WBC043G11; B1961941; BM781186; B1961682; WBC018D05; WBC024C12; WBC012F07; WBC001F08; WBC003D11	0.934959	0.859155	0.907216
WBC010F04; B1961443; BM735585; WBC434; WBC493; WBC022B06; WBC013H03; BM735352; WBC027D07; WBC001A07	0.926829	0.873239	0.907216
BM734865; WBC021B08; BM735573; BM735536; WBC001F08; WBC007G03; B1961637; BM735519; WBC032G05; WBC001H09	0.934959	0.859155	0.907216
WBC008F06; WBC434; B1961443; BM735487; WBC166; WBC012F07; BM735536; Foe1072; WBC007G12; WBC004D07	0.934959	0.859155	0.907216
BM734862; BM734654; WBC001C12; Foe1072; BM734889; B1961443; BM735487; WBC039F12; BM735519; WBC001F08	0.934959	0.859155	0.907216
WBC008F12; WBC001C12; WBC043G11; BM734862; Foe1060; WBC013C03; WBC022B05; WBC007G12; WBC009E12; BM735536	0.943089	0.84507	0.907216
WBC021D01; BM781174; B1961443; Foe1060; BM781334; WBC024B05; Foe545; WBC028E07; WBC026E02; WBC005D02	0.910569	0.901408	0.907216
WBC590; WBC010F04; BM735576; WBC021B08; BM735573; WBC003D11; WBC027D07; WBC008F12; Foe545; B1961443	0.918699	0.887324	0.907216
WBC007G03; BM735585; B1961443; WBC009B10; GI1592834; BM734722; BM735536; BM735519; BM735409; WBC022B06	0.910569	0.887324	0.902062
WBC043G11; BM781417; B1961443; WBC005F10; BM780906; BM735166; WBC028F05; BM735573; WBC019B05; WBC003D11	0.910569	0.887324	0.902062
WBC493; BM735286; WBC004C03; BM735167; BM735536; BM734722; WBC003H01; BM735487; B1961711; BM735576	0.934959	0.84507	0.902062
WBC006E03; WBC043G11; WBC024C11; BM735576; WBC004E04; WBC021B08; BM735536; WBC010F04; B1961443; WBC166	0.926829	0.859155	0.902062
WBC020B04; BM781186; WBC003H01; BM781174; BM735573; BM735536; WBC028D09; B1961682; BM735519; WBC012E07	0.918699	0.873239	0.902062
BM735536; WBC022B05; WBC590; BM735519; BM781174; B1961443; B1961494; WBC039F12; WBC005F10; WBC021B08	0.926829	0.859155	0.902062

TABLE 16

TWENTY GENES SELECTED

Genes	Sensitivity	Specificity	Success
WBC013C03; WBC019B05; WBC041B05; B1961637; BM780906; WBC004C03; WBC030D02; WBC434; BM781178; WBC032G05; BM781186; WBC018B01; BM781334; B1961885; BM734722; WBC010F04; WBC030C04; WBC038G11; WBC012E07; WBC008F06	0.95935	0.887324	0.93299
B1960933; WBC019B05; B1961443; WBC007A09; WBC010F04; WBC024C11; WBC434; WBC018D05; WBC013E10; WBC009E12; BM781186; WBC018B01; BM781334; B1961885; BM734722; WBC010F04; WBC030C04; WBC038G11; WBC012E07; WBC008F06	0.95935	0.887324	0.93299
WBC013A09; BM735441; WBC028E07; WBC003D11; BM734531; BM735573; WBC028D09; WBC005F10; WBC030C04; WBC021B08; BM735487; BM781417; B1961494; B1961109; BM734531; WBC005D02; B1961637; WBC028E07; BM735352; BM735167	0.95122	0.901408	0.93299
BM735536; WBC006H06; WBC018B01; WBC019B05; WBC003D11; BM735166; WBC009E12; BM735167; WBC493; BM735352; WBC028C01; WBC009B10; WBC014G08; WBC019B05; BM735585; BM735450; BM781334; BM735536; Foe545; WBC001C11	0.943089	0.901408	0.927835
WBC019B05; BM734719; WBC434; WBC028F05; B1961443; BM735573; Foe1072; WBC001F08; BM735519; WBC013A09; BM781174; WBC043G11; WBC032G05; WBC041B05; WBC006E03; WBC001H09; WBC007G12; WBC004D07; B1961637; WBC004C03	0.934959	0.915493	0.927835
BM734722; WBC030D02; BM735166; WBC022B06; BM735167; BM735441; WBC006E03; BM734531; WBC032G05; WBC012G02; WBC166; WBC021B08; WBC024F08; WBC013E10; BM734654; BM735409; BM734531; BM735536; WBC043G11; B1960933	0.943089	0.887324	0.92268
WBC004E04; BM735536; WBC001F11; WBC018B01; WBC024F08; WBC009E12; WBC001F08; gi576646; BM735576; BM735457; BM735457; WBC024F08; WBC013C03; WBC018B01; WBC166; WBC001F08; BM735536; BM735409; Foe1060; WBC028F05	0.943089	0.887324	0.92268
WBC008F12; WBC032G05; WBC010F04; WBC001F11; WBC018B01; B1960933; WBC012E07; BM735450; WBC022B06; BM735441; WBC019B05; WBC009B10; B1961109; BM734457; BM734531; BM735545; WBC001C12; WBC024C12; WBC006E03; BM781334	0.95122	0.873239	0.92268
B1961443; WBC001A07; WBC013E10; B1960933; WBC005F10; Foe545; WBC012F07; WBC010F04; WBC004D07; BM735487; Foe545; WBC434; WBC019B05; BM735167; WBC028C01; BM735576; BM734862; WBC009B10; Foe1072; WBC012F07	0.943089	0.887324	0.92268
WBC003H01; BM735457; WBC004C03; BM734457; WBC006H06; WBC020B04; B1961443; WBC019B05; BM735536; WBC038G11; BM734531; WBC027D07; WBC032G05; WBC004C03; WBC007G03; WBC032B05; WBC001F11; WBC003F02; BM735536; WBC003H01	0.926829	0.915493	0.92268
WBC019B05; WBC018B01; BM734722; WBC030D02; B1961109; BM735536; GI1592834; WBC003D11; BM735573; WBC026E02; BM735573; BM734719; BM781417; WBC005D02; WBC012F07; WBC024C11; WBC004D07; BM735487; BM734865; WBC024B05	0.934959	0.901408	0.92268
BM734865; BM735102; WBC001F08; B1961443; BM780906; Foe1072; WBC038G11; B1961637; WBC019B05; WBC024B05; WBC018D05; BM781178; WBC001F08; B1961443; WBC028F05; WBC013A09; WBC014G08; BM735487; Foe545; WBC012E07	0.926829	0.915493	0.92268
B1961494; BM735536; WBC038G11; WBC004E04; WBC039F12; BM735167; WBC001F08; WBC004C03; BM734722; WBC019B05; WBC003H01; BM735457; BM735536; WBC043G11; WBC001C11; GI9717252-3M; WBC004D07; WBC032G05; WBC016A12; WBC026E02	0.943089	0.887324	0.92268
WBC003D11; BM734457; B1961443; BM735450; BM734531; WBC004C03; WBC012G02; BM734889; BM735585; WBC018B01; WBC007A09; GI1592834; BM781186; B1961682; BM734531; BM735352; WBC001H09; WBC493; WBC024B05; WBC005D02	0.918699	0.915493	0.917526

Genes	Sensitivity	Specificity	Success
WBC024C11; WBC001A07; WBC434; WBC032G05; WBC028E07; WBC004C03; WBC027D07; BM734531; gi576646; BM734654; WBC019B05; BM735409; BM735487; WBC005F10; WBC005D02; WBC014G08; WBC012F07; WBC007G12; WBC010F04; B1961671	0.943089	0.873239	0.917526
WBC009B10; Foe545; Foe1060; WBC027E07; WBC012G02; BM735457; WBC019B05; BM735409; GI1592834; WBC030C04; BM734457; WBC030C04; WBC010F04; WBC003H01; BM735102; BM735545; BM781417; BM781174; WBC014G08; WBC007A09	0.943089	0.873239	0.917526
BM735441; WBC010F04; WBC008F12; BM735573; B1961443; WBC012F07; B1960933; WBC004D07; WBC043G11; WBC014H06; BM780906; WBC016A12; WBC041B05; BM781178; WBC010F04; WBC434; WBC005D02; WBC014H06; BM734865; WBC028D09	0.934959	0.887324	0.917526
BM735573; WBC007G03; GI1592834; BM734722; B1961711; WBC021B08; BM735536; WBC493; WBC019B05; B1961443; WBC024C11; WBC006E06; WBC493; WBC013C03; BM734719; BM735487; WBC019B05; WBC024F08; WBC016A12; WBC004E04	0.926829	0.901408	0.917526
WBC590; WBC028F05; BM735166; B1961885; BM735519; WBC018B01; WBC019B05; B1961637; WBC021B08; B1961941; WBC001F08; WBC026E02; BM735534; BM735585; WBC006E03; WBC004E04; WBC009B10; WBC008F12; Foe1072; WBC018B01	0.943089	0.873239	0.917526
WBC027D07; BM735534; BM735487; BM781334; WBC013A09; WBC028D09; WBC590; WBC024F08; WBC024C12; B1961941; WBC006E03; WBC005D02; B1961711; WBC009E12; WBC003H01; WBC026E02; WBC166; WBC001F11; BM735536; BM735167	0.926829	0.901408	0.917526

TABLE 17

STRESS MARKER GENE ONTOLOGY

Gene	Genbank Homology	UNIPROT	CELLULAR COMPONENT	MOLECULAR FUNCTION	BIOLOGICAL PROCESS
WBC590	Zinc Finger Protein 198	Q5W0T3	nucleus	zinc ion binding	-
WBC493	Homo sapiens mRNA; cDNA DKFZp667N084	NA			
WBC434	CGG triplet repeat binding protein 1 (CGGBP1),	O15183	nucleus	double-stranded DNA binding	-
WBC166	Mst3 and SOK1-related kinase (MASK)	Q9P289	-	ATP binding, protein serine/threonine kinase activity, protein-tyrosine kinase activity	protein amino acid phosphorylation
WBC043G11.bFSP_20021401.esd	Homo sapiens high mobility group nucleosomal binding domain 4, mRNA	Q53XL9	-	-	-
WBC041B05	ARP3 actin-related protein 3 homolog (yeast)	Q59FV6	-	-	-
WBC039F12	Leu-8 pan leukocyte antigen	NA			
WBC038G11_V1.3_at	No Homology	NA			
WBC032G05	Glycerol kinase (GK)	NA			
WBC032B05	DDHD domain containing 1	NA			
WBC030D02	Putative membrane protein (GENX-3745 gene)	Q9NY35	-	-	-
WBC030C04	No homology	NA			
WBC028F05	No homology	NA			
WBC028E07	Homo sapiens cDNA FLJ13038 fis, clone NT2RP3001272, weakly similar to Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein	NA			
WBC028D09	No homology	NA			
WBC028C01_V1.3_at	Ras homolog gene family, member A	Q5U024	-	-	-

Gene	Genbank Homology	UNIPROT	CELLULAR COMPONENT	MOLECULAR FUNCTION	BIOLOGICAL PROCESS
WBC027E07	No homology	NA			
WBC027D07	No homology	NA			
WBC026E02	Migration-inducing gene 10 protein	Q5J7W1	-	-	-
WBC024F08	No homology	NA			
WBC024C12	No homology	NA			
WBC024C11	No homology	NA			
WBC024B05	Adducin 3 (gamma) (ADD3), transcript variant 2	Q5VU08	-	-	-
WBC022F08	Phosphogluconate dehydrogenase	P52209	-	electron transporter activity	pentose-phosphate shunt, oxidative branch
WBC022B06	Immunoglobulin superfamily, member 6 variant	NA			
WBC022B05	Toll-like receptor 8 (TLR8)	Q9NR97	integral to membrane	receptor activity, Toll binding	detection of virus, I-kappaB kinase/NF-kappaB cascade, innate immune response
WBC021D01	No homology	NA			
WBC021B08	Hypothetical protein FLJ20481	Q7L5N7	-	acyltransferase activity, calcium ion binding	metabolism
WBC020B04	No homology	NA			
WBC019B05	Homo sapiens mRNA; cDNA DKFZp686M2414	NA			
WBC018D05	Predicted: Mitogen-activated protein kinase kinase kinase 1 (MAP3K1)	NA			
WBC018B01_V1.3_s_at	Homo sapiens gene for JKTBP2, JKTBP1 (alternative splicing).	NA			
WBC016A12	No homology	NA			
WBC014H06	Homo sapiens mRNA; cDNA DKFZp564C012	Q9H0V1	-	-	-

Gene	Genbank Homology	UNIPROT	CELLULAR COMPONENT	MOLECULAR FUNCTION	BIOLOGICAL PROCESS
WBC014G08_V1.3_at	RTN4-C (RTN4)	Q6IPN0	endoplasmic reticulum	unknown	-
WBC013H03_V1.3_at	RAB6 interacting protein 1 (RAB6IP1)	Q6IQ26	-	-	-
WBC013E10	Homo sapiens cDNA FLJ45679 fis, clone ERLTF2001835	NA			
WBC013C03_V1.3_at	Ras GTPase-activating-like protein (IQGAP1)	P46940	actin filament	calmodulin binding	GTPase activator activity, GTPase inhibitor activity, signal transduction
WBC013A09	Sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase), transcript variant 2	P15907	integral to membrane	beta-galactoside alpha-2,6-sialyltransferase activity	growth, humoral immune response, oligosaccharide metabolism, protein modification
WBC012G02	Soc-2 suppressor of clear homolog (C. elegans)	Q5VZS9			
WBC012F07	Complement component 5 receptor 1 (C5a ligand)	NA			
WBC012E07	Pinin, desmosome associated protein (PNN)	Q99738	intercellular junction, intermediate filament, plasma membrane	structural molecule activity	cell adhesion
WBC010F04	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	Q01581	cytoplasm, soluble fraction	hydroxymethylglut aryl-CoA synthase activity	lipid metabolism
WBC009E12	Down-regulator of transcription 1, TBP-binding (negative cofactor 2)	Q01658	-	DNA binding, transcription corepressor activity, transcription factor binding	Negative regulation of transcription from RNA polymerase II promoter

Gene	Genbank Homology	UNIPROT	CELLULAR COMPONENT	MOLECULAR FUNCTION	BIOLOGICAL PROCESS
WBC009B10_V1.3_at	Human mRNA for complement receptor type 1 (CR1, C3b/C4b receptor, CD35)	P17927	integral to plasma membrane	complement receptor activity	complement activation
WBC008F12	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein	Q7T383	-	GTP binding	Small GTPase mediated signal transduction
WBC008F06_V1.3_at	No Homology	NA			
WBC007G12_V1.3_at	No Homology	NA			
WBC007G03	Transmembrane protein 23 cDNA clone MGC:17342 IMAGE:4342258 also called Phosphatidylcholine:ceramide cholinephosphotransferase 1 (Sphingomyelin synthase 1) (Mob protein	Q86VZ5	Cellular component, integral to golgi	ceramide cholinephosphotransferase activity	Sphingomyelin biosynthesis
WBC007A09	No homology	NA			
WBC006H06	Ubiquitin-conjugating enzyme E2B (RAD6 homolog) (UBE2B)				
WBC006E03_V1.3_at	Homo sapiens methionine adenosyltransferase II, beta (MAT2B)		Intracellular	Protein binding	S-adenosylmethionine biosynthesis
WBC005F10	Polymeric immunoglobulin receptor 3 precursor (PIGR3)	Q8NHL4	-	receptor activity	-
WBC005D02_V1.3_at	Homo sapiens hypothetical protein FLJ22662, mRNA	Q6P4A8	-	-	-
WBC004E04	TRAF-interacting protein with a forkhead-associated domain	Q96CG3	nucleus	-	-
WBC004D07_V1.3_at	No Homology	NA			
WBC004B05	Heterogeneous nuclear ribonucleoprotein F	P52597	heterogeneous nuclear ribonucleoprotein complex	RNA binding	RNA processing

Gene	Genbank Homology	UNIPROT	CELLULAR COMPONENT	MOLECULAR FUNCTION	BIOLOGICAL PROCESS
WBC004C03	Dendritic cell protein variant, clone: CAE03638	Q53HL6 ?clone CAE0363 8	-	-	-
WBC003H01	CGI-54 protein	Q9Y282	-	-	-
WBC003F02	IBR domain containing 3 (IBRDC3)	NA			
WBC003D11	No homology	NA			
WBC001H09	Activated RNA polymerase II transcription cofactor 4 variant protein (incomplete)	Q59G24	-	-	-
WBC001F11	Retinoblastoma-like 2 (p130)	Q08999	-	protein binding	-
WBC001F08	RAB10, member RAS oncogene family (RAB10),	P61026	-	-	-
WBC001C12_V1.3_at	No Homology	NA			
WBC001C11 (Same as WBC041B05)	ARP3 actin-related protein 3 homolog (yeast)	Q59FV6	-	-	-
WBC001A07_V1.3_at	No Homology	NA			
GI9717252	Equus caballus Toll-like receptor 4 mRNA	Q5XWB9	membrane	transmembrane receptor activity	inflammatory response
GI1592834	Equus caballus gelsolin mRNA	Q6X9X6	-	actin binding	-
Gi576646	Equus caballus Ig epsilon heavy chain (partial)	NA			
Foe 545	Homo sapiens mRNA; cDNA DKFZp666I186 (from clone DKFZp666I186)	Q658M2	-	-	-
Foe 1072	Transducin (beta)-like 1X-linked receptor 1	NA			
Foe 1060	Homo sapiens 15 kDa selenoprotein, transcript variant 1		Endoplasmic reticulum lumen	Protein binding, Se binding	Post-translational protein folding.
BM781417	No homology	NA			

Gene	Genbank Homology	UNIPROT	CELLULAR COMPONENT	MOLECULAR FUNCTION	BIOLOGICAL PROCESS
BM781334	No homology	NA			
BM781186	Membrane-spanning 4-domains, subfamily A, member 6A, transcript variant 1		Integral to membrane	Receptor activity	Signal transduction
BM781178	No homology	NA			
BM781174	GM2 ganglioside activator		Lysosome	Sphingolipid activator protein activity	Lipid metabolism
BM780906.V1.3_at	No Homology	NA			
BM735585	Fc-epsilon-receptor gamma-chain		Integral to plasma membrane	Receptor activity	Humoral response.
BM735576	Minor histocompatibility antigen H13 isoform 1 (H13)		Integral to membrane	Peptidase activity	D-alanyl-D-alanine endopeptidase activity
BM735573	No Homology	NA			
BM735545	CD68 protein		Lysosome, membrane	NA	NA
BM735536	Transglutaminase E3 (TGASE3)		NA	NA	NA
BM735534	PREDICTED: Bos taurus similar to hypothetical protein (LOC515494),		NA	NA	NA
BM735519	Ring finger protein 10	NA			
BM735487.V1.3_at	No Homology	NA			
BM735457	No homology	NA			
BM735450	Lymphocyte surface antigen precursor CD44		Type I membrane protein	Cell surface receptor	Lymphocyte homing
BM735441	WD repeat domain 1, transcript variant 2		Cytoskeleton	Protein binding	Actin binding
BM735409	No homology	NA			
BM735352	No homology	NA			
BM735286	Ferritin light chain		Ferritin complex	Iron ion binding	Iron homeostasis
BM735167	TAP2E`		NA	NA	NA
BM735166	No homology	NA			
BM735102	COP9 constitutive photomorphogenic homolog subunit 7A		Signalasome complex	Unknown	Unknown

Gene	Genbank Homology	UNIPROT	CELLULAR COMPONENT	MOLECULAR FUNCTION	BIOLOGICAL PROCESS
BM734889.V1.3_at	Equus caballus lipopolysaccharide receptor (CD14) mRNA		Plasma membrane	Peptidoglycan receptor activity	Apoptosis, signal transduction, phagocytosis.
BM734865	Nuclear receptor binding factor 1		NA	NA	NA
BM734862.V1.3_at	Triggering receptor expressed on myeloid cells 1		Receptor activity	Humoral immune response.	Intracelluar signalling cascade
BM734722	No homology	NA			
BM734719	No homology	NA			
BM734654	No homology	NA			
BM734531	No homology	NA			
BM734457	High-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 beta mRNA		NA	NA	NA
B1961941	Fibroblast mRNA for aldolase A		NA	Fructose-bisphosphate aldolase activity	Glycolysis
B1961885	Tumor necrosis factor-inducible (TSG-6) mRNA fragment, adhesion receptor CD44 putative CDS		Extracellular region	Protein binding	Inflammtory response, cell adhesion, protein binding.
B1961711.V1.3_at	No Homology	NA			
B1961682.V1.3_at	Formin homology 2 domain containing 1		Nucleus, cytoplasm	Actin binding	Cell organisation and biogenesis.
B1961671	NAD synthetase 1			ATP binding	NAD biosynthesis
B1961637	Mn-SOD mRNA for manganese superoxide dismutase		Mitochondrian	Superoxide dismutase activity	Response to oxidative stress
B1961620	ILT11A mRNA for immunoglobulin-like transcript 11 protein		NA	NA	NA
B1961494	HREV107-3		NA	Tumor suppressor, associated with cell death.	NA
B1961443	PREDICTED: Homo sapiens steroid receptor RNA activator 1 (SRA1)		NA	NA	NA

Gene	Genbank Homology	UNIPROT	CELLULAR COMPONENT	MOLECULAR FUNCTION	BIOLOGICAL PROCESS
B1961009	G protein-coupled receptor HM74a		Integral to membrane	Receptor activity	G-protein coupled receptor protein signaling pathway
B1960933	Pleckstrin		NA	Calcium ioni binding	NA
WBC037F12	Selenoprotein P		Extracellular region	Selenium binding	Response to oxidative stress
WBC043E03	Ribosomal protein S3A		Ribosome	Constitutive component of ribosome	Protein biosynthesis
Foe1019	Hemoglobin, beta (HBB)				Oxygen transport
Gi5441616	Equus caballus mRNA for interferon gamma inducing factor (IL-18)		Extracellular region	Cytokine activity	Interferon gamma induction
B1961054	Interferon-gamma-inducible protein-10 (IP-10) (Ovis aries)		Extracellular regioin	Chemokine activity	Immune response.
B1961539	Calcium-binding protein in macrophages (MRP-14) macrophage migration inhibitory factor (MIF)-related protein		NA	Signal transducer activity	Cell-cell signalling, inflammatory response.
BM735419	Villin 2 (ezrin)		Membrane bound, (extracellular)	Connection of cytoskeleton to plasma membrane	NA
WBC013G08	cDNA FLJ16386 fis, clone TRACH2000862, moderately similar to Mus musculus putative purine nucleotide binding protein mRNA		NA	NA	NA
B1961648	Farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase)		Cyotplasmic	Catalytic	Cholesterol biosynthesis
WBC041B04	56-KDa protein induced by interferon	NA	NA	NA	NA
WBC001B11	No homology	NA	NA	NA	NA
WBC032B11	Sphingosine-1-phosphate phosphatase 1		Endoplasmic reticulum	Enzymatic activity	Regulates S1P levels
B1961185	Actin related protein 2/3 complex, subunit 1B, 41kDA		ARP2/3 protein complex	Cytoskeleton	Cell motility

Gene	Genbank Homology	UNIPROT	CELLULAR COMPONENT	MOLECULAR FUNCTION	BIOLOGICAL PROCESS
B1961512	No homology	NA			
WBC008D05	No homology	NA			
WBC133	No homology	NA			
BM781012	Equus caballus immunogobulin gamma 1 heavy chain constant region (IGHC1 gene)	NA	NA	NA	NA
WBC005B09	CDC-like kinase 1			Non-membrane spanning protein tyrosine kinase activity	Regulation of cell cycle
WBC040E12	Arachidonate 5-lipoxygenase-activating protein (ALOX5AP).		Integral to membrane	Enzyme activator activity	Inflammatory response.

WHAT IS CLAIMED IS:

1. A method for determining the presence or degree of a physiological response to stress or a related condition in a test subject, comprising detecting in the test subject aberrant expression of at least one stress marker gene selected from the group consisting of: (a) a gene having a polynucleotide expression product comprising a nucleotide sequence that shares at least 50% sequence identity with the sequence set forth in any one of SEQ ID NO: 1, 3, 4, 5, 7, 9, 11, 13, 15, 16, 17, 19, 21, 23, 24, 25, 26, 28, 29, 30, 32, 33, 34, 35, 37, 38, 39, 40, 41, 42, 44, 46, 48, 50, 51, 52, 54, 55, 56, 57, 59, 62, 63, 64, 66, 68, 70, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 90, 91, 92, 93, 95, 96, 97, 99, 101, 103, 105, 107, 108, 109, 111, 113, 115, 117, 118, 119, 121, 123, 125, 126, 127, 129, 130, 131, 133, 135, 137, 139, 141, 143, 144, 145, 147, 148, 150, 151, 153, 155, 156, 158, 160, 161, 163, 164, 165, 167, 169, 170, 171, 173, 175, 176, 178, 180, 182, 184, 185, 186, 187, 188, 190, 192, 194, 195, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 233, 234, 236, 238, 239, 240, 241, 242, 243, 244, 246 or 248, or a complement thereof; (b) a gene having a polynucleotide expression product comprising a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in any one of SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249; (c) a gene having a polynucleotide expression product comprising a nucleotide sequence that encodes a polypeptide that shares at least 50% sequence similarity with at least a portion of the sequence set forth in SEQ ID NO: 22, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249, wherein the portion comprises at least 15 contiguous amino acid residues of that sequence; and (d) a gene having a polynucleotide expression product comprising a nucleotide sequence that hybridizes to the sequence of (a), (b), (c) or a complement thereof, under at least low stringency conditions.

2. A method according to claim 1, comprising comprise detecting aberrant expression of a stress marker polynucleotide selected from the group consisting of (a) a polynucleotide comprising a nucleotide sequence that shares at least 50% sequence identity with the sequence set forth in any one of SEQ ID NO: 1, 3, 4, 5, 7, 9, 11, 13, 15, 16, 17, 19, 21, 23, 24, 25, 26, 28, 29, 30, 32, 33, 34, 35, 37, 38, 39, 40, 41, 42, 44, 46, 48, 50, 51, 52, 54, 55, 56, 57, 59, 62, 63, 64, 66, 68, 70, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 90, 91, 92, 93, 95, 96, 97, 99, 101, 103, 105, 107, 108, 109, 111, 113, 115, 117, 118, 119, 121, 123, 125, 126, 127, 129, 130, 131, 133,

135, 137, 139, 141, 143, 144, 145, 147, 148, 150, 151, 153, 155, 156, 158, 160, 161, 163, 164, 165, 167, 169, 170, 171, 173, 175, 176, 178, 180, 182, 184, 185, 186, 187, 188, 190, 192, 194, 195, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 233, 234, 236, 238, 239, 240, 241, 242, 243, 244, 246 or 248, or a complement thereof; (b) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in any one of SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249; (c) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide that shares at least 50% sequence similarity with at least a portion of the sequence set forth in SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249, wherein the portion comprises at least 15 contiguous amino acid residues of that sequence; and (d) a polynucleotide comprising a nucleotide sequence that hybridizes to the sequence of (a), (b), (c) or a complement thereof, under at least low stringency conditions.

3. A method according to claim 1, comprising detecting aberrant expression of a stress marker polypeptide selected from the group consisting of: (i) a polypeptide comprising an amino acid sequence that shares at least 50% (sequence similarity with the sequence set forth in any one of SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249; (ii) a polypeptide comprising a portion of the sequence set forth in any one of SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249, wherein the portion comprises at least 5 contiguous amino acid residues of that sequence; (iii) a polypeptide comprising an amino acid sequence that shares at least 30% similarity with at least 15 contiguous amino acid residues of the sequence set forth in any one of SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78,

80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249; and (iv) a polypeptide comprising a portion of the sequence set forth in any one of SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249, wherein the portion comprises at least 5 contiguous amino acid residues of that sequence and is immuno-interactive with an antigen-binding molecule that is immuno-interactive with a sequence of (i), (ii) or (iii).

4. A method according to claim 1, wherein the aberrant expression is detected by: (1) measuring in a biological sample obtained from the test subject the level or functional activity of an expression product of at least one stress marker gene and (2) comparing the measured level or functional activity of each expression product to the level or functional activity of a corresponding expression product in a reference sample obtained from one or more normal subjects or from one or more subjects not under stress, wherein a difference in the level or functional activity of the expression product in the biological sample as compared to the level or functional activity of the corresponding expression product in the reference sample is indicative of the presence of a physiological response to stress in the test subject.

5. A method according to claim 4, further comprising diagnosing the presence, stage or degree of a physiological response to stress in the test subject when the measured level or functional activity of the or each expression product is 10% lower than the measured level or functional activity of the or each corresponding expression product.

6. A method according to claim 5, wherein the presence of a physiological response to stress is determined by detecting a decrease in the level or functional activity of at least one stress marker polynucleotide selected from (a) a polynucleotide comprising a nucleotide sequence that shares at least 50% sequence identity with the sequence set forth in any one of SEQ ID NO: 1, 3, 4, 7, 9, 11, 19, 21, 24, 25, 33, 34, 38, 39, 40, 41, 42, 50, 51, 56, 57, 59, 62, 63, 66, 70, 71, 73, 75, 79, 81, 83, 89, 90, 91, 92, 93, 97, 99, 105, 107, 108, 111, 119, 121, 122, 123, 129, 130, 137, 139, 140, 141, 142, 143 or 185, or a complement thereof; (b) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in any one of SEQ ID NO: 2, 8, 10, 12, 20, 22, 43, 58, 60, 67, 71, 72, 74, 76, 80, 82, 84, 94, 98, 100, 106, 112, 120, 122, 123, 124 or 138; (c) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide that shares at least 50% sequence similarity with at least a portion of the sequence set forth in SEQ ID NO: 2, 8, 10, 12, 20, 22,

43, 58, 60, 67, 71, 72, 74, 76, 80, 82, 84, 94, 98, 100, 106, 112, 120, 122, 123, 124 or 138, wherein the portion comprises at least 15 contiguous amino acid residues of that sequence; and (d) a polynucleotide comprising a nucleotide sequence that hybridizes to the sequence of (a), (b), (c) or a complement thereof, under at least low stringency conditions.

7. A method according to claim 4, further comprising diagnosing the presence, stage or degree of the physiological response to stress in the test subject when the measured level or functional activity of the or each expression product is 10% higher than the measured level or functional activity of the or each corresponding expression product.

8. A method according to claim 7, wherein the presence of a physiological response to stress is determined by detecting an increase in the level or functional activity of at least one stress marker polynucleotide selected from (a) a polynucleotide comprising a nucleotide sequence that shares at least 50% sequence identity with the sequence set forth in any one of SEQ ID NO: 5, 13, 15, 16, 17, 23, 26, 28, 29, 30, 32, 35, 37, 44, 46, 48, 52, 54, 55, 64, 68, 77, 85, 87, 95, 96, 101, 103, 113, 115, 117, 118, 125, 126, 131, 133, 135, 144, 145, 147, 148, 150, 151, 153, 155, 156, 158, 160, 161, 163, 164, 165, 167, 169, 170, 171, 173, 175, 176, 178, 180, 182, 183, 184, 186, 187, 188, 190, 192, 194, 195, 196, 198, 200, 202, 204, 206 or 210, or a complement thereof; (b) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in any one of SEQ ID NO: 6, 14, 18, 27, 31, 36, 45, 47, 49, 53, 65, 69, 78, 86, 88, 102, 104, 114, 116, 132, 134, 136, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 189, 191, 193, 197, 199, 201, 203, 205, 207 or 211; (c) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide that shares at least 50% sequence similarity with at least a portion of the sequence set forth in SEQ ID NO: 6, 14, 18, 27, 31, 36, 45, 47, 49, 53, 65, 69, 78, 86, 88, 102, 104, 114, 116, 132, 134, 136, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 189, 191, 193, 197, 199, 201, 203, 205, 207 or 211, wherein the portion comprises at least 15 contiguous amino acid residues of that sequence; and (d) a polynucleotide comprising a nucleotide sequence that hybridizes to the sequence of (a), (b), (c) or a complement thereof, under at least low stringency conditions.

9. A method according to claim 4, further comprising diagnosing the absence of a physiological response to stress when the measured level or functional activity of the or each expression product is the same as or similar to the measured level or functional activity of the or each corresponding expression product.

10. A method according to claim 4, wherein the measured level or functional activity of an individual expression product varies from the measured level or functional activity of an individual corresponding expression product by no more than about 5%.

11. A method according to claim 4, comprising measuring the level or functional activity of individual expression products of at least about 2 stress marker genes.

12. A method according to claim 4, comprising measuring the level or functional activity of individual expression products of at least 1 level one correlation stress marker gene selected from: (a) a polynucleotide comprising a nucleotide sequence that shares at least 50% sequence identity with the sequence set forth in any one of SEQ ID NO: 89, 90, 103, 125, 126, 163, 178, 182, 184 or 190, or a complement thereof; (b) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in any one of SEQ ID NO: 104, 179, 183 or 189; (c) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide that shares at least 50% sequence similarity with at least a portion of the sequence set forth in SEQ ID NO: 104, 179, 183 or 189, wherein the portion comprises at least 15 contiguous amino acid residues of that sequence; and (d) a polynucleotide comprising a nucleotide sequence that hybridizes to the sequence of (a), (b), (c) or a complement thereof, under at least low stringency conditions.

13. A method according to claim 4, comprising measuring the level or functional activity of individual expression products of at least 1 level two correlation stress marker gene selected from: (a) a polynucleotide comprising a nucleotide sequence that shares at least 50% sequence identity with the sequence set forth in any one of SEQ ID NO: 17, 23, 44, 52, 133, 135, 144, 147, 148, 151, 155, 192, 196, 202 or 206, or a complement thereof; (b) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in any one of SEQ ID NO: 18, 20, 45, 53, 134, 136, 149, 152, 193, 197 or 207; (c) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide that shares at least 50% sequence similarity with at least a portion of the sequence set forth in SEQ ID NO: 18, 20, 45, 53, 134, 136, 149, 152, 193, 197 or 207, wherein the portion comprises at least 15 contiguous amino acid residues of that sequence; and (d) a polynucleotide comprising a nucleotide sequence that hybridizes to the sequence of (a), (b), (c) or a complement thereof, under at least low stringency conditions.

14. A method according to claim 4, comprising measuring the level or functional activity of individual expression products of at least 1 level three correlation stress marker gene selected from: (a) a polynucleotide comprising a nucleotide sequence that shares at least 50% sequence identity with the sequence set forth in any one of SEQ ID NO: 5, 30, 37, 48, 54, 55, 64, 66, 70, 77, 79, 85, 91, 92, 95, 96, 101, 115, 117, 118, 121, 150, 153, 158, 164, 170, 180, 186 or198, or a complement thereof; (b) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in any one of SEQ ID NO: 6, 31, 49, 65, 67, 78, 80, 86, 102, 116, 122, 154, 159, 181 or 199; (c) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide that shares at least 50% sequence similarity with at least a portion of the sequence set forth in SEQ ID NO: 6, 31, 49, 65, 67, 78, 80, 86, 102, 116, 122, 154, 159, 181 or 199, wherein the portion comprises at least 15 contiguous amino acid residues of that sequence; and (d) a polynucleotide comprising a

nucleotide sequence that hybridizes to the sequence of (a), (b), (c) or a complement thereof, under at least low stringency conditions.

15. A method according to claim 4, comprising measuring the level or functional activity of individual expression products of at least 1 level four correlation stress marker gene selected from: (a) a polynucleotide comprising a nucleotide sequence that shares at least 50% sequence identity with the sequence set forth in any one of SEQ ID NO: 7, 15, 16, 19, 21, 24, 25, 26, 28, 35, 38, 39, 42, 46, 57, 68, 73, 81, 83, 97, 99, 107, 113, 123, 160, 165, 175, 187, 188, 194, 195 or 200, or a complement thereof; (b) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in any one of SEQ ID NO: 20, 22, 27, 29, 36, 42, 43, 58, 69, 74, 82, 84, 98, 100, 108, 114, 124, 166, 189 or 201; (c) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide that shares at least 50% sequence similarity with at least a portion of the sequence set forth in SEQ ID NO: 20, 22, 27, 29, 36, 42, 43, 58, 69, 74, 82, 84, 98, 100, 108, 114, 124, 166, 189 or 201, wherein the portion comprises at least 15 contiguous amino acid residues of that sequence; and (d) a polynucleotide comprising a nucleotide sequence that hybridizes to the sequence of (a), (b), (c) or a complement thereof, under at least low stringency conditions.

16. A method according to claim 4, comprising measuring the level or functional activity of individual expression products of at least 1 level five correlation stress marker gene selected from: (a) a polynucleotide comprising a nucleotide sequence that shares at least 50% sequence identity with the sequence set forth in any one of SEQ ID NO: 71, 3, 9, 11, 13, 32, 33, 34, 40, 41, 50, 51, 56, 59, 62, 63, 71, 75, 87, 93, 105, 111, 119, 127, 129, 130, 131, 137, 139, 141, 143, 145, 156, 161, 167, 169, 171, 173, 176, 185, 204 or 210, or a complement thereof; (b) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in any one of SEQ ID NO: 2, 4, 12, 14, 60, 61, 72, 76, 88, 94, 106, 112, 120, 128, 132, 138, 140, 142, 146, 157, 162, 168, 172, 174, 177, 205 or 211; (c) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide that shares at least 50% sequence similarity with at least a portion of the sequence set forth in SEQ ID NO: 2, 4, 12, 14, 60, 61, 72, 76, 88, 94, 106, 112, 120, 128, 132, 138, 140, 142, 146, 157, 162, 168, 172, 174, 177, 205 or 211, wherein the portion comprises at least 15 contiguous amino acid residues of that sequence; and (d) a polynucleotide comprising a nucleotide sequence that hybridizes to the sequence of (a), (b), (c) or a complement thereof, under at least low stringency conditions.

17. A method according to claim 4, wherein the biological sample comprises blood.

18. A method according to claim 4, wherein the biological sample comprises peripheral blood.

19. A method according to claim 4, wherein the biological sample comprises leukocytes.

20. A method according to claim 4, wherein the expression product is a RNA molecule.

21. A method according to claim 4, wherein the expression product is a polypeptide.

22. A method according to claim 4, wherein the expression product is the same as the corresponding expression product.

23. A method according to claim 4, wherein the expression product is a variant of the corresponding expression product.

24. A method according to claim 4, wherein the expression product or corresponding expression product is a target RNA or a DNA copy of the target RNA whose level is measured using at least one nucleic acid probe that hybridizes under at least low stringency conditions to the target RNA or to the DNA copy, wherein the nucleic acid probe comprises at least 15 contiguous nucleotides of a stress marker polynucleotide.

25. A method according to claim 24, wherein the measured level or abundance of the target RNA or its DNA copy is normalized to the level or abundance of a reference RNA or a DNA copy of the reference RNA that is present in the same sample.

26. A method according to claim 24, wherein the nucleic acid probe is immobilized on a solid or semi-solid support.

27. A method according to claim 24, wherein the nucleic acid probe forms part of a spatial array of nucleic acid probes.

28. A method according to claim 24, wherein the level of nucleic acid probe that is bound to the target RNA or to the DNA copy is measured by hybridization.

29. A method according to claim 24, wherein the level of nucleic acid probe that is bound to the target RNA or to the DNA copy is measured by nucleic acid amplification.

30. A method according to claim 24, wherein the level of nucleic acid probe that is bound to the target RNA or to the DNA copy is measured by nuclease protection assay.

31. A method according to claim 24, wherein the probe for detecting the stress marker polynucleotide comprises a sequence as set forth in any one of SEQ ID NO: 250-1807.

32. A method according to claim 24, wherein the expression product or corresponding expression product is a target polypeptide whose level is measured using at least one antigen-binding molecule that is immuno-interactive with the target polypeptide.

33. A method according to claim 24, wherein the measured level of the target polypeptide is normalized to the level of a reference polypeptide that is present in the same sample.

34. A method according to claim 24, wherein the antigen-binding molecule is immobilized on a solid or semi-solid support.

35. A method according to claim 24, wherein the antigen-binding molecule forms part of a spatial array of antigen-binding molecule.

36. A method according to claim 24, wherein the level of antigen-binding molecule that is bound to the target polypeptide is measured by immunoassay.

37. A method according to claim 4, wherein the expression product or corresponding expression product is a target polypeptide whose level is measured using at least one substrate for the target polypeptide with which it reacts to produce a reaction product.

38. A method according to claim 37, wherein the measured functional activity of the target polypeptide is normalized to the functional activity of a reference polypeptide that is present in the same sample.

39. A method according to claim 4, wherein a system is used to perform the method, which comprises at least one end station coupled to a base station., wherein the base station is caused (a) to receive subject data from the end station *via* a communications network, wherein the subject data represents parameter values corresponding to the measured or normalized level or functional activity of at least one expression product in the biological sample, and (b) to compare the subject data with predetermined data representing the measured or normalized level or functional activity of at least one corresponding expression product in the reference sample to thereby determine any difference in the level or functional activity of the expression product in the biological sample as compared to the level or functional activity of the corresponding expression product in the reference sample.

40. A method according to claim 39, wherein the base station is further caused to provide a diagnosis for the presence, absence or degree of a physiological response to stress.

41. A method according to claim 43, wherein the base station is further caused to transfer an indication of the diagnosis to the end station *via* the communications network.

42. A method according to claim 1, wherein detection of the aberrant expression is indicative of the presence or risk of a physiological response to stress.

43. A method according to claim 1, wherein the test subject is a horse.

44. A method for treating, preventing or inhibiting the development of stress in a subject, the method comprising detecting aberrant expression of at least one stress marker gene in the subject, and administering to the subject an effective amount of an agent that treats or ameliorates the symptoms or reverses or inhibits the development of stress in the subject, wherein the stress marker gene is selected from the group consisting of: (a) a gene having a polynucleotide expression product comprising a nucleotide sequence that shares at least 50% sequence identity with the sequence set forth in any one of SEQ ID NO: 1, 3, 4, 5, 7, 9, 11, 13, 15, 16, 17, 19, 21, 23, 24, 25, 26, 28, 29, 30, 32, 33, 34, 35, 37, 38, 39, 40, 41, 42, 44, 46, 48, 50, 51, 52, 54, 55, 56, 57, 59, 62, 63, 64, 66, 68, 70, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 90, 91, 92, 93, 95, 96, 97, 99, 101, 103, 105, 107, 108, 109, 111, 113, 115, 117, 118, 119, 121, 123, 125, 126, 127, 129, 130, 131, 133, 135, 137, 139, 141, 143, 144, 145, 147, 148, 150, 151, 153, 155, 156, 158, 160, 161, 163, 164, 165, 167, 169, 170, 171, 173, 175, 176, 178, 180, 182, 184,

185, 186, 187, 188, 190, 192, 194, 195, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 233, 234, 236, 238, 239, 240, 241, 242, 243, 244, 246 or 248, or a complement thereof; (b) a gene having a polynucleotide expression product comprising a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in any one of SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249; (c) a gene having a polynucleotide expression product comprising a nucleotide sequence that encodes a polypeptide that shares at least 50% sequence similarity with at least a portion of the sequence set forth in SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249, wherein the portion comprises at least 15 contiguous amino acid residues of that sequence; and (d) a gene having a polynucleotide expression product comprising a nucleotide sequence that hybridizes to the sequence of (a), (b), (c) or a complement thereof, under at least low stringency conditions.

45. An isolated stress marker polynucleotide selected from: (a) a polynucleotide comprising a nucleotide sequence that shares at least 50% sequence identity with the sequence set forth in any one of SEQ ID NO: 15, 16, 23, 24, 25, 28, 29, 32, 33, 34, 37, 38, 39, 40, 41, 50, 51, 54, 55, 62, 63, 89, 90, 91, 92, 95, 96, 107, 108, 117, 118, 125, 126, 129, 130, 143, 144, 147, 150, 155, 163, 164, 169, 170, 175, 184, 185, 186, 187, 194, 195, 232, 233, 238, 239, 240, 241, 242 or 243, or a complement thereof; (b) a polynucleotide comprising a portion of the sequence set forth in any one of SEQ ID NO: 15, 16, 23, 24, 25, 28, 29, 32, 33, 34, 37, 38, 39, 40, 41, 50, 51, 54, 55, 62, 63, 89, 90, 91, 92, 95, 96, 107, 108, 117, 118, 125, 126, 129, 130, 143, 144, 147, 150, 155, 163, 164, 169, 170, 175, 184, 185, 186, 187, 194, 195, 232, 233, 238, 239, 240, 241, 242 or 243, or a complement thereof, wherein the portion comprises at least 15 contiguous nucleotides of that sequence or complement; (c) a polynucleotide that hybridizes to the sequence of (a) or (b) or a complement thereof, under at least low stringency conditions; and (d) a polynucleotide comprising a portion of any one of SEQ ID NO: 15, 16, 23, 24, 25, 28, 29, 32, 33, 34, 37, 38, 39, 40, 41, 50, 51, 54, 55, 62, 63, 89, 90, 91, 92, 95, 96, 107, 108, 117, 118, 125, 126, 129, 130, 143, 144, 147, 150, 155, 163, 164, 169, 170, 175, 184, 185, 186, 187, 194, 195, 232, 233, 238, 239, 240, 241, 242 or 243, or a complement thereof, wherein the portion comprises at least 15 contiguous nucleotides of that sequence or complement and hybridizes to a sequence of (a), (b) or (c), or a complement thereof, under at least low stringency conditions.

46. A nucleic acid construct comprising a stress marker polynucleotide as claimed in claim 45, in operable connection with a regulatory element that is operable in a host cell.

47. An isolated host cell containing a nucleic acid construct as claimed in claim 46.

48. A probe comprising a nucleotide sequence that hybridizes under at least low stringency conditions to a polynucleotide as claimed in claim 45.

49. A probe as claimed in claim 48, wherein the probe comprise a nucleotide sequence that is capable of hybridizing to at least a portion of any one of SEQ ID NO: 15, 16, 23, 24, 25, 28, 29, 32, 33, 34, 37, 38, 39, 40, 41, 50, 51, 54, 55, 62, 63, 89, 90, 91, 92, 95, 96, 107, 108, 117, 118, 125, 126, 129, 130, 143, 144, 147, 150, 155, 163, 164, 169, 170, 175, 184, 185, 186, 187, 194, 195, 232, 233, 238, 239, 240, 241, 242 or 243 under at least low stringency conditions, wherein the portion is at least 15 nucleotides in length.

50. A probe as claimed in claim 49, comprising a sequence as set forth in any one of SEQ ID NO: 250-1807.

51. A solid or semi-solid support comprising at least one probe as claimed in claim 48 immobilized thereon.

52. Use of:

(i) one or more stress marker polynucleotides selected from the group consisting of (a) a polynucleotide comprising a nucleotide sequence that shares at least 50% (and at least 51% to at least 99% and all integer percentages in between) sequence identity with the sequence set forth in any one of SEQ ID NO: 1, 3, 4, 5, 7, 9, 11, 13, 15, 16, 17, 19, 21, 23, 24, 25, 26, 28, 29, 30, 32, 33, 34, 35, 37, 38, 39, 40, 41, 42, 44, 46, 48, 50, 51, 52, 54, 55, 56, 57, 59, 62, 63, 64, 66, 68, 70, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 90, 91, 92, 93, 95, 96, 97, 99, 101, 103, 105, 107, 108, 109, 111, 113, 115, 117, 118, 119, 121, 123, 125, 126, 127, 129, 130, 131, 133, 135, 137, 139, 141, 143, 144, 145, 147, 148, 150, 151, 153, 155, 156, 158, 160, 161, 163, 164, 165, 167, 169, 170, 171, 173, 175, 176, 178, 180, 182, 184, 185, 186, 187, 188, 190, 192, 194, 195, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 233, 234, 236, 238, 239, 240, 241, 242, 243, 244, 246 or 248, or a complement thereof; (b) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in any one of SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249; (c) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide that shares at least 50% (and at least 51% to at least 99% and all integer percentages in between) sequence similarity with at least a portion of the sequence set forth in SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31,

36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249, wherein the portion comprises at least 15 contiguous amino acid residues of that sequence; and (d) a polynucleotide comprising a nucleotide sequence that hybridizes to the sequence of (a), (b), (c) or a complement thereof, under at least low stringency conditions; or

(ii) one or more probes comprising a nucleotide sequence that hybridizes under at least low stringency conditions to a stress marker polynucleotide according to (i); or

(iii) one or more stress marker polypeptides selected from the group consisting of: (1) a polypeptide comprising an amino acid sequence that shares at least 50% (and at least 51% to at least 99% and all integer percentages in between) sequence similarity with the sequence set forth in any one of SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249; (2) a polypeptide comprising a portion of the sequence set forth in any one of SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249, wherein the portion comprises at least 5 contiguous amino acid residues of that sequence; (3) a polypeptide comprising an amino acid sequence that shares at least 30% (and at least 31% to at least 99% and all integer percentages in between) similarity with at least 15 contiguous amino acid residues of the sequence set forth in any one of SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249; and (4) a polypeptide comprising a portion of the sequence set forth in any one of SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207,

209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249, wherein the portion comprises at least 5 contiguous amino acid residues of that sequence and is immuno-interactive with an antigen-binding molecule that is immuno-interactive with a sequence of (1), (2) or (3); or

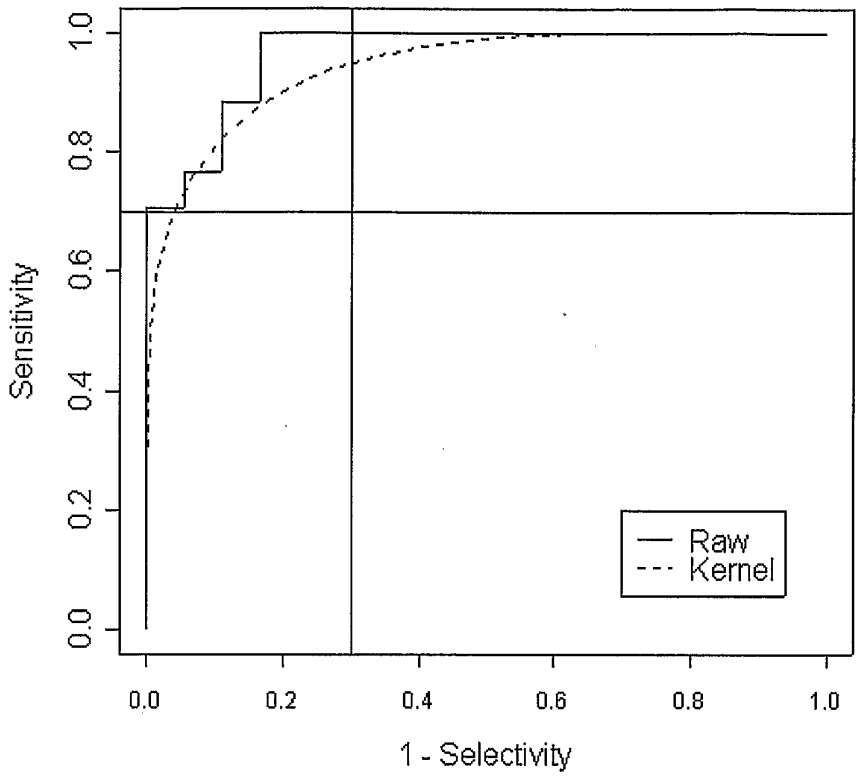
(iv) one or more antigen-binding molecules that are immuno-interactive with a stress marker polypeptide according to (iii),

in the manufacture of a kit for diagnosing the presence of a physiological response to stress in a subject.

53. A method according to claim 52, wherein the physiological response to stress is selected from the group consisting of: physical stress; mood disorders; anxiety disorders; inflammation; pain; chronic fatigue syndrome; stress-induced headache; cancer; human immunodeficiency virus (HIV) infections; neurodegenerative diseases; gastrointestinal diseases; eating disorders; supranuclear palsy; amyotrophic lateral sclerosis; a decrease in immune function or immunosuppression; hemorrhagic stress; stress-induced psychotic episodes; euthyroid sick syndrome; syndrome of inappropriate antidiarrhetic hormone (ADH); overeating or obesity; infertility; head traumas; spinal cord trauma; ischemic neuronal damage; excitotoxic neuronal damage; epilepsy; cardiovascular disorders; stroke; immune dysfunctions; restraint; behavioral (operant) conditioning; muscular spasms; urinary incontinence; senile dementia of the Alzheimer's type; multiinfarct dementia; amyotrophic lateral sclerosis; chemical dependencies and addictions; drug and alcohol withdrawal symptoms; osteoporosis; psychosocial dwarfism; hypoglycemia; hair loss; abnormal circadian rhythm; and disorders related to abnormal circadian rhythm.

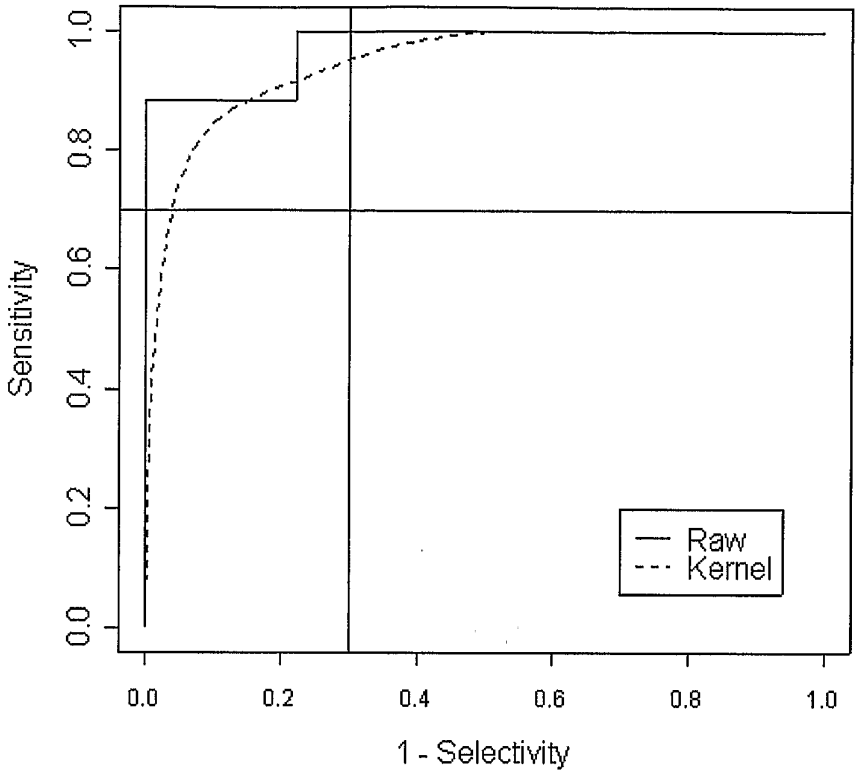
54. A method for diagnosing the presence of a physiological response to stress in a test subject, comprising detecting in the test subject aberrant expression of at least one stress marker polynucleotide selected from the group consisting of: (a) a polynucleotide comprising a nucleotide sequence that shares at least 50% sequence identity with the sequence set forth in any one of SEQ ID NO: 1, 3, 4, 5, 7, 9, 11, 13, 15, 16, 17, 19, 21, 23, 24, 25, 26, 28, 29, 30, 32, 33, 34, 35, 37, 38, 39, 40, 41, 42, 44, 46, 48, 50, 51, 52, 54, 55, 56, 57, 59, 62, 63, 64, 66, 68, 70, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 90, 91, 92, 93, 95, 96, 97, 99, 101, 103, 105, 107, 108, 109, 111, 113, 115, 117, 118, 119, 121, 123, 125, 126, 127, 129, 130, 131, 133, 135, 137, 139, 141, 143, 144, 145, 147, 148, 150, 151, 153, 155, 156, 158, 160, 161, 163, 164, 165, 167, 169, 170, 171, 173, 175, 176, 178, 180, 182, 184, 185, 186, 187, 188, 190, 192, 194, 195, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 233, 234, 236, 238, 239, 240, 241, 242, 243, 244, 246 or 248, or a complement thereof; (b) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in any one of SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102,

104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249; (c) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide that shares at least 50% sequence similarity with at least a portion of the sequence set forth in SEQ ID NO: 2, 6, 8, 10, 12, 14, 18, 20, 22, 27, 31, 36, 43, 45, 47, 49, 53, 58, 60, 61, 65, 67, 69, 72, 74, 76, 78, 80, 82, 84, 86, 88, 94, 98, 100, 102, 104, 106, 110, 112, 114, 116, 120, 122, 124, 128, 132, 134, 136, 138, 140, 142, 146, 149, 152, 154, 157, 159, 162, 166, 168, 172, 174, 177, 179, 181, 183, 189, 191, 193, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 245, 247 or 249, wherein the portion comprises at least 15 contiguous amino acid residues of that sequence; and (d) a polynucleotide comprising a nucleotide sequence that hybridizes to the sequence of (a), (b), (c) or a complement thereof, under at least low stringency conditions.



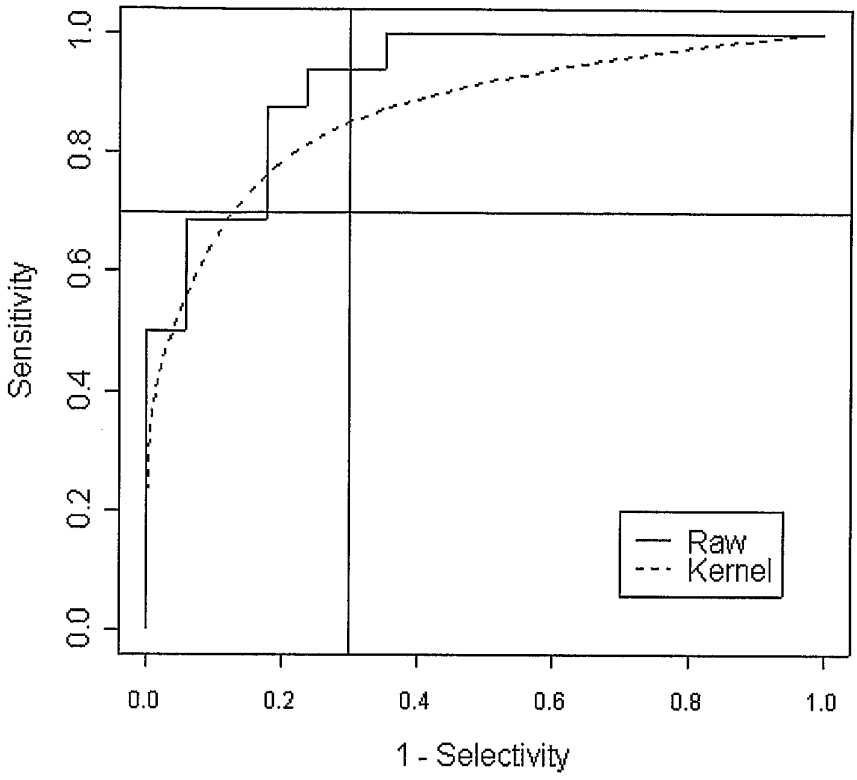
Day 28 versus Day 0

FIGURE 1



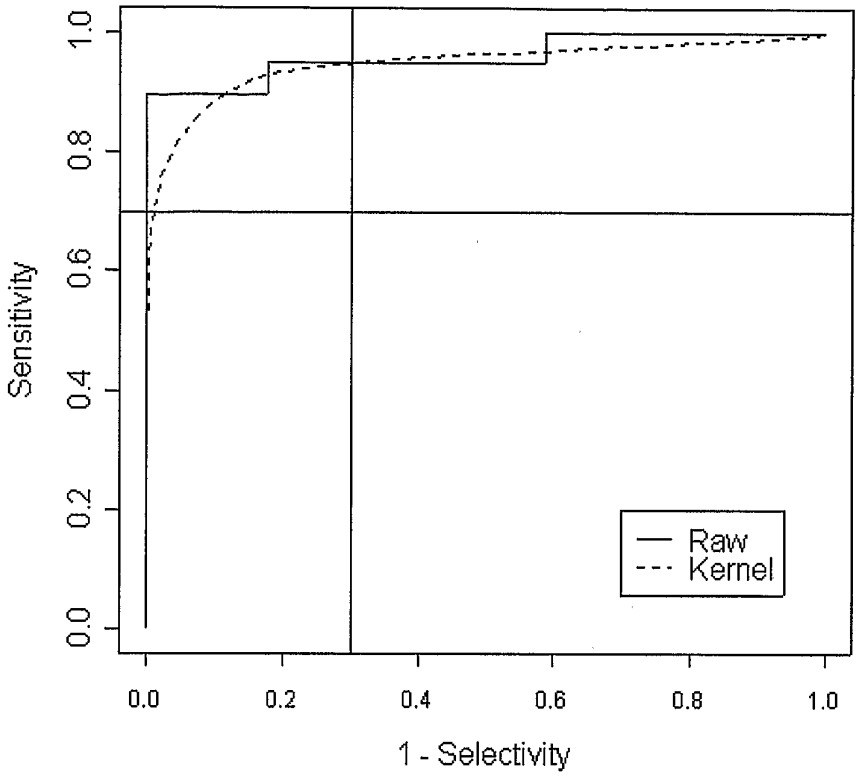
Day 28 versus Day 2

FIGURE 2



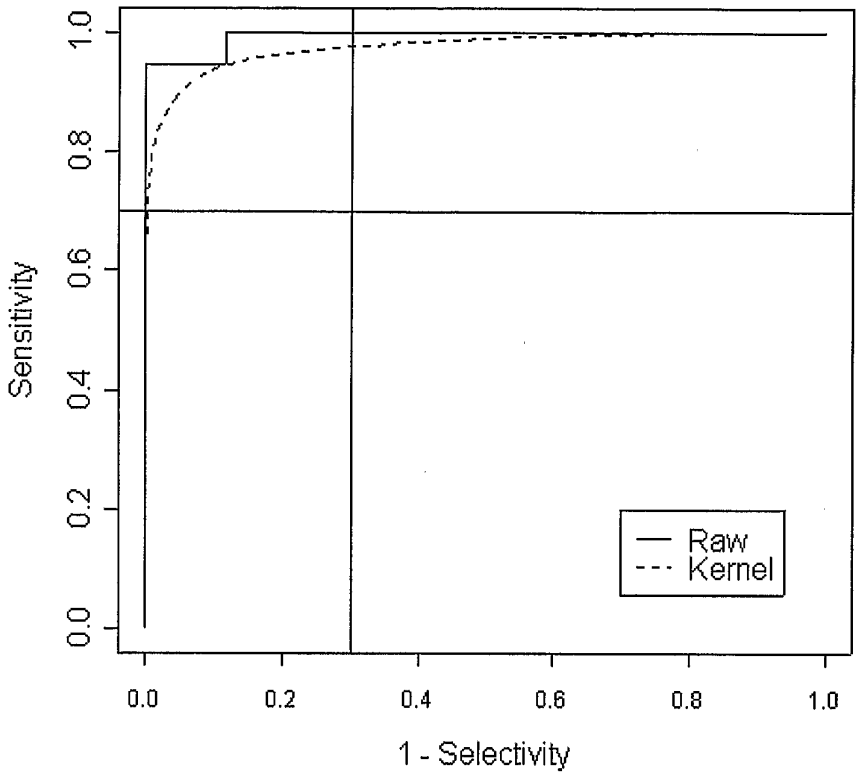
Day 28 versus Day 4

FIGURE 3



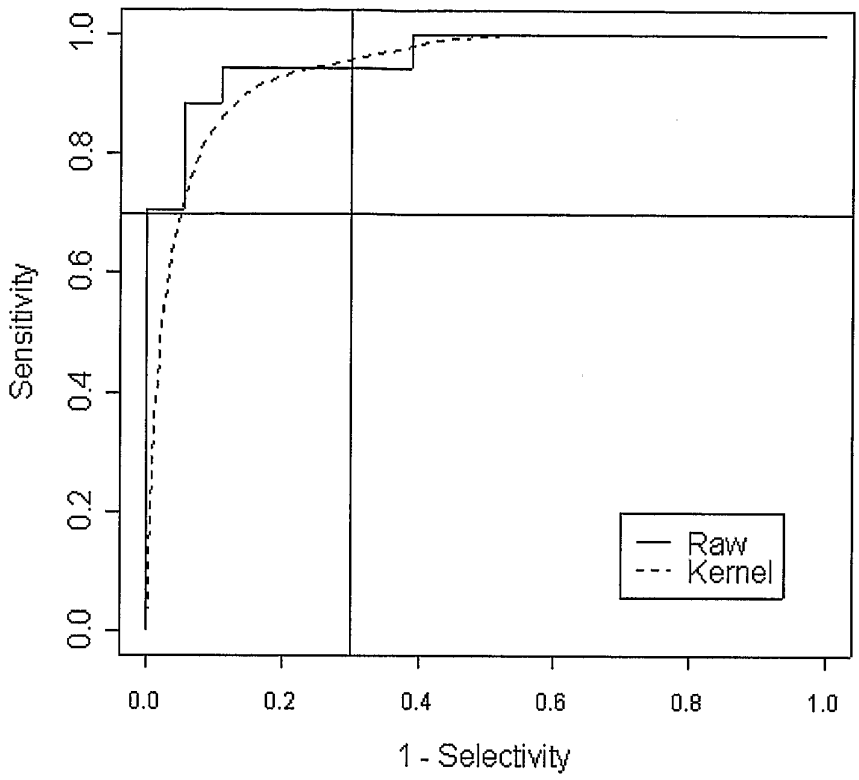
Day 28 versus Day 7

FIGURE 4



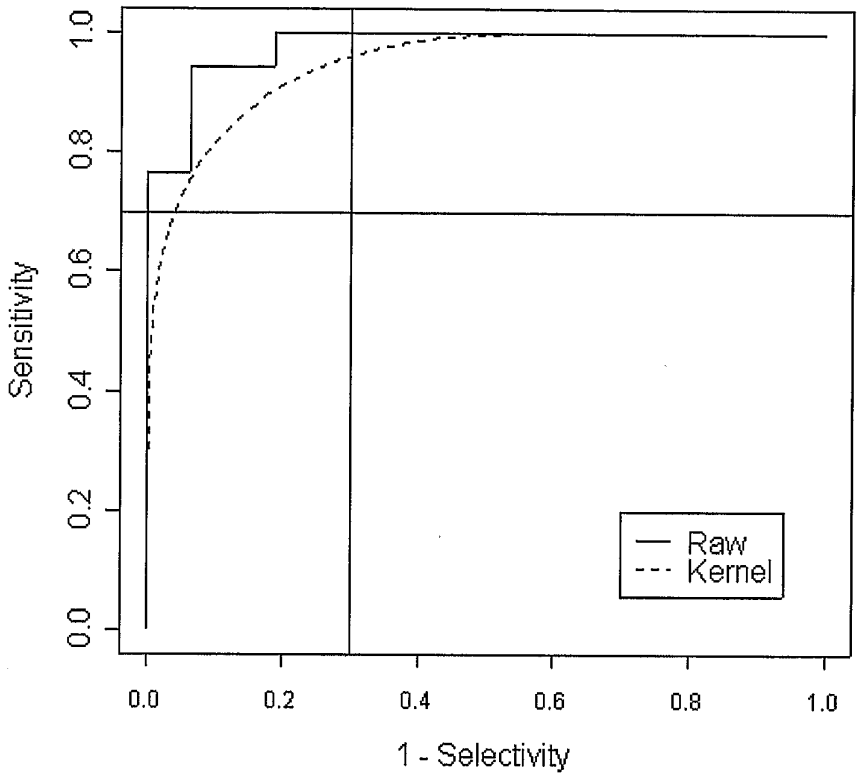
Day 28 versus Day 9

FIGURE 5



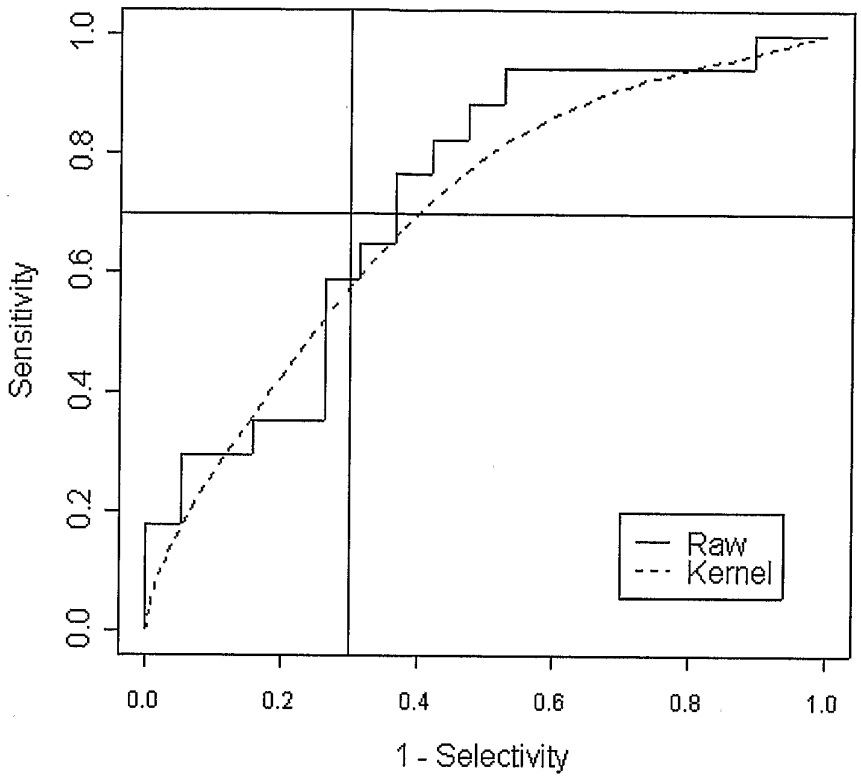
Day 28 versus Day 11

FIGURE 6



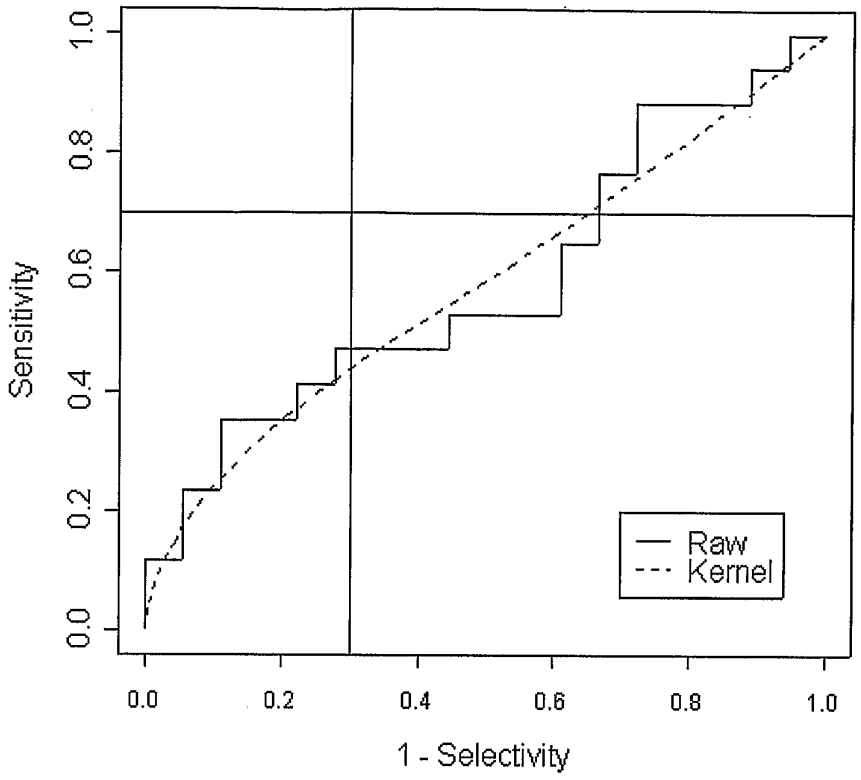
Day 28 versus Day 14

FIGURE 7



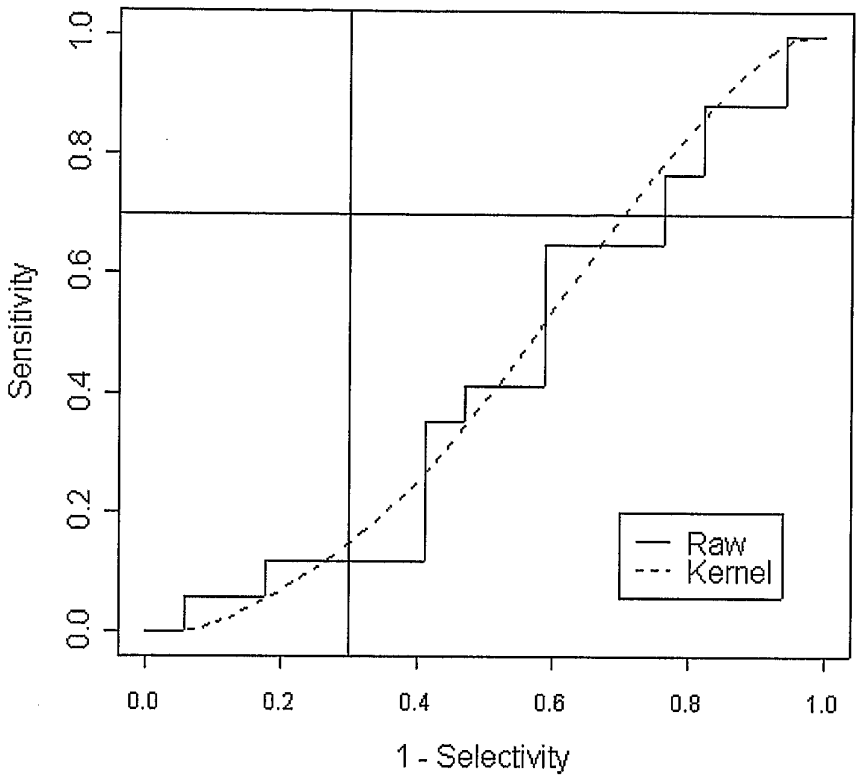
Day 28 versus Day 17

FIGURE 8



Day 28 versus Day 21

FIGURE 9



Day 28 versus Day 24

FIGURE 10