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(54) **Title:** POLYNUCLEOTIDE MARKER GENES AND THEIR EXPRESSION, FOR DIAGNOSIS OF ENDOTOXEMIA

(57) **Abstract:** The invention discloses isolated endotoxemia marker polynucleotides selected from any one of 163 different polynucleotide sequences, or variants thereof. Endotoxemia related conditions are diagnosed in a test subject by aberrant expression of at least one of the endotoxemia markers or variants thereof. Of practical use, is the early diagnosis of disease, determining those animals at risk of developing endotoxemia, monitoring of an animals immune response to the disease and the enablement of better treatments. Of particular interest is the diagnosis of laminitis in hoofed animals, including horses.

TITLE OF THE INVENTION

Polynucleotide Marker Genes and their Expression, for Diagnosis of Endotoxemia.

FIELD OF THE INVENTION

[0001] This invention relates generally to a method and apparatus for the diagnosis, detection of host response, monitoring, treatment and management of endotoxemia and endotoxemia-induced conditions in mammals. The invention also relates to the use of this method in monitoring, treatment and management of conditions that can lead to endotoxemia. The invention has practical use in early diagnosis, diagnosis of mild or sub-clinical endotoxemia, in the detection of specific cell immune responses as part of active or progressive disease, in monitoring clinically affected animals, and in enabling better treatment and management decisions to be made in clinically and sub-clinically affected animals. Additionally, the invention has practical use in monitoring patients in critical care or intensive care units for endotoxemia and in predicting clinical outcome.

BACKGROUND OF THE INVENTION

[0002] Endotoxemia (also called septic shock and septic syndrome) is generally considered to result from an inability of the host defense mechanisms to cope with foreign organisms, including gram positive and negative bacteria, viruses, fungi and parasites. The majority of endotoxemia cases are caused by gram negative bacteria (Glauser *et al.*, 1991, *Lancet* 338 (Sept) 732-736), in particular a product of gram negative bacteria called endotoxin or lipopolysaccharide (LPS), which is a component of the bacterial outer cell wall.

[0003] Because the main initiator of endotoxemia is endotoxin, many tests have been developed to measure these molecules in fluids, including the Limulus Amoebocyte Lysate (LAL) test (Cohen J., 2000, *Intensive Care Med.* 26: S51-S56), rabbit pyrogen test, and lethality in mice and chicken embryos (Hurley JC. *Clin Microbiol Reviews* 8(2): 268-292). However, measurement of endotoxin in fluids, especially blood, is a poor predictor of clinical outcome in endotoxemia for a number of reasons:

[0004] • The levels of endotoxin required to trigger the biological cascade of events leading to endotoxemia varies widely from patient to patient.

[0005] • The bioavailability of endotoxin varies from patient to patient depending upon the body's ability to detoxify or neutralize it.

[0006] • Some patients develop sensitivity to endotoxin, or are tolerant to endotoxin.

[0007] • Various biological fluids (and even fluid containers) contain agents that bind endotoxin that are capable of enhancing or limiting the biological effect of endotoxin, or can interfere with the measurement of endotoxin.

[0008] • Some endotoxins are more potent than others.

[0009] • The specificity and sensitivity of the LAL assay is at its limit when used for assaying endotoxin in blood or serum.

[0010] For these reasons, efforts have been made to develop assays for the determination of the biological effects of endotoxin - as a means of determining clinical outcome - including the measurement of molecules such as Tumor Necrosis Factor (TNF), C3a, C5a, Factor XII (Hageman Factor), interleukin-1 (IL-1), γ-interferon and various other cytokines, and the measurement of the level of activation of leukocytes. Such measurements have contributed to a "sepsis score" concept developed by Casey *et al.* (1993, *Ann Intern Med.* 119: 771-778).

[0011] However, none of these tests have been sufficiently sensitive, specific or practical enough to be used in routine clinical practice. In addition, the efficacy of available treatments also limits the practical use of such prognostic and monitoring tests.

[0012] Despite this, there are a number of features of endotoxemia that make early detection, monitoring, determination of clinical outcome, prognosis determination, early intervention and informed management of affected animals clinically and economically important, viz:

[0013] • Many and varied conditions can lead to endotoxemia.

[0014] • Endotoxemia can lead to many other conditions.

[0015] • Endotoxemia is often a peracute condition causing death if not correctly managed.

[0016] • It is estimated that 20-30% of human patients in intensive care units in the USA are affected and that more than 100,000 humans die each year in the USA alone (Young L & Glauser M (Eds) Gram negative septicemia and septic shock. WB Saunders Philadelphia (1991); Parrillo JE. 1990, *Ann Intern Med.* 113: 227-242).

[0017] • The extent of the condition in less developed countries is likely to be far higher due to poor hygiene and medical infrastructure.

[0018] • In up to 50% of cases an etiological agent is not determined.

[0019] • The condition is most common in hospitals in patients with other underlying diseases.

[0020] • The extent of subclinical disease and its effects on human health, animal husbandry, athletic performance, and ethical management are not known.

[0021] Apart from the direct detection of endotoxin, there have been many efforts to use secondary indicators of sepsis to diagnose and monitor this condition, including measuring heart rate, temperature, respiratory rate, cardiac output, systemic vascular resistance, plasma IL-6 levels, macrophage inflammatory protein-2, chemokine KC, protein C and C-reactive protein (Panacek *et al.*, 2004, *Crit Care Med.* 32: 2173-2182; Ulloa and Tracey, 2005, *Trends Mol Med.* 1:56-63).

[0022] Currently no panel of biomarkers is used to define sepsis in humans (Buras *et al.*, 2006, *Nature Reviews Drug Discovery*, 4: 854-865). However, a cytokine profile has been suggested (Ulloa *et al.*, 2005, *Trends Mol Biol.* 11: 56-63) Reasons for this are the complexity of the disease, difficulty in defining the stage of disease and the apparent existence of two distinct but not mutually exclusive phases of inflammatory and anti-inflammatory responses (Bone RC., 1996, *Crit Care Med.* 24: 1125-1128).

[0023] Given the current limitations of diagnostic, monitoring and prognostic procedures for endotoxemia, especially in sub-clinical or early-stages, there is a need for more effective modalities for early detection, diagnosis, monitoring, prognosis and management of the various phases of sepsis including, acute, peracute, early stage, advanced, and sub-clinical endotoxemia.

[0024] An example of a complication arising from endotoxemia is laminitis that causes profound lameness in hoofed animals. It occurs in perissodactyl and artiodactyl animals, including horses, cattle, goats, sheep and other hoofed animals (ungulates). It is believed the condition results from the action of endotoxin on tissues and the lamellae of the inner hoof wall. Failure of the lamellae results in separation of the inner hoof capsule from the pedal bone and the subsequent (weight-bearing) driving of the pedal bone through the hoof capsule, and crushing of the corium, sole and coronet (Sloet van Oldruitenborgh-Oosterbaan MM., 1999, *Vet Quarterly* 21(4) 121-127).

[0025] There are a number of features of laminitis that make early detection, monitoring, early intervention and informed management of affected animals clinically and economically important, viz:

[0026] • The exact cause of laminitis is not known.

[0027] • The extent of subclinical disease (often called the developmental stage; Hood DM., 1999, *Vet Clin Nth Amer Eq Pract* 15(2): 287-294) and its effects on animal husbandry, athletic performance, and ethical management are not known.

[0028] • The first 72 hours of the disease (developmental and acute stages) is the most critical period for monitoring. Animals that have not suffered major mechanical or structural failures at this stage are likely to recover.

[0029] • The pathogenesis of the disease is poorly understood.

[0030] • Laminitis is the largest killer of horses worldwide, usually as a result of euthanasia due to progressive disease that causes serious disability and pain.

[0031] • Present diagnostics are only partially effective once the disease is established, by which time preventative management or ameliorating therapies have little effect.

[0032] • There are few practical interventions available.

[0033] Thus, there is a need for more effective modalities for early diagnosis, diagnosis of mild or sub-clinical laminitis, in the detection of specific immune responses as part of active or progressive disease, and in monitoring animals clinically affected by laminitis. Such modalities would enable better treatment and management decisions to be made in clinically and sub-clinically affected animals prior to irreversible tissue damage.

[0034] Existing technology for diagnosing endotoxemia or for monitoring conditions that lead to endotoxemia or for evaluating sequelae of endotoxemia, is limited in that the detection of bacterial endotoxin in body fluids does not correlate well with clinical signs, and the sensitivity and specificity of these technologies is insufficient to be clinically useful. In addition, because the conditions are often peracute, advanced and irreversible tissue damage may have occurred (and possibly death) by the time endotoxin is able to be detected.

[0035] In addition, existing technologies for diagnosis or evaluation of laminitis are limited and are almost entirely reliant upon clinical evaluation and the detection of lameness. In many instances the lameness can be very subtle or sub-clinical. In addition, many of these clinical changes can only be observed in advanced stages of disease, at which time irreversible tissue damage has occurred, and where humane euthanasia is the only recourse.

SUMMARY OF THE INVENTION

[0036] The present invention represents a significant advance over current technologies for the management of affected animals. In certain advantageous embodiments, it relies upon measuring the level of certain markers in cells, especially circulating leukocytes, of the host rather than detecting endotoxin. As such, these methods are suitable for widespread screening of symptomatic and asymptomatic animals. In certain embodiments where circulating leukocytes are the subject of analysis, it is proposed that detection of a host response to endotoxemia and its sequelae (also referred to herein as "endotoxemia-related conditions") will be feasible at very early stages of its progression before extensive tissue damage has occurred.

[0037] Thus, the present invention addresses the problem of diagnosing endotoxemia-related conditions by detecting a host response 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 the presence of active disease or response to disease.

[0038] Accordingly, in one aspect, the present invention provides methods for diagnosing the presence of an endotoxemia-related condition in a test subject, especially in an equine test subject. These methods generally comprise detecting in the test subject aberrant expression of at least one gene (also referred to herein as an "endotoxemia 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% (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, 6, 7, 9, 10, 11, 13, 15, 16, 17, 18, 19, 21, 23, 25, 26, 27, 29, 31, 33, 35, 37, 38, 39, 41, 42, 43, 44, 45, 47, 49, 50, 52, 54, 56, 58, 60, 61, 63, 64, 66, 67, 68, 69, 70, 71, 73, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 86, 88, 90, 92, 93, 94, 96, 98, 100, 101, 102, 103, 104, 106, 107, 109, 110, 111, 113, 114, 115, 117, 119, 121, 122, 123, 124, 125, 126, 128, 130, 132, 134, 136, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 158, 160, 162, 164, 166, 168, 169, 170, 172, 173, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 193, 194, 195, 197, 199, 201, 203, 205, 206, 207, 209, 210, 211, 212, 214, 215, 216, 218, 220, 222, 223, 224, 225, 227, 229, 231, 233, 235, 236, 237, 239, 240, 242, 244, 245, 246, 248, 250, 252, 254, 255, 257, 259 260, 262, 264, 266, 268, 269, 270, 271, 272, 274, 276, 278, 279, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 305, 306, 307, 309, 311, 312, 314, 315, 316, 318, 320 321, 323 or 325, 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, 8, 12, 14, 20, 22, 24, 28, 30, 32, 34, 36, 40, 46, 48, 51, 53, 55, 57, 59, 62, 65, 72, 74, 78, 85, 87, 89, 91, 95, 97, 99, 105, 108, 112, 116, 118,

120, 127, 129, 131, 133, 135,138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 159, 161, 163, 165, 167, 171, 175, 177, 179, 181, 183, 185, 187, 189, 191, 196, 198, 200, 202, 204, 208, 213, 217, 219, 221, 226, 228, 230, 232, 234, 236, 238, 241, 243, 247, 249, 251, 253, 256, 258, 261, 263, 265, 267, 273, 275, 277, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324 or 326; (c) a gene having a polynucleotide expression product 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, 12, 14, 20, 22, 24, 28, 30, 32, 34, 36, 40, 46, 48, 51, 53, 55, 57, 59, 62, 65, 72, 74, 78, 85, 87, 89, 91, 95, 97, 99, 105, 108, 112, 116, 118, 120, 127, 129, 131, 133, 135,138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 159, 161, 163, 165, 167, 171, 175, 177, 179, 181, 183, 185, 187, 189, 191, 196, 198, 200, 202, 204, 208, 213, 217, 219, 221, 226, 228, 230, 232, 234, 236, 238, 241, 243, 247, 249, 251, 253, 256, 258, 261, 263, 265, 267, 273, 275, 277, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324 or 326, 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, medium, or high stringency conditions. In accordance with the present invention, these endotoxemia marker genes are aberrantly expressed in animals with an endotoxemia-related condition such as but not limited to an endotoxemia-induced condition, illustrative examples of which include shock, depression, abdominal discomfort, reduced pain threshold, laminitis and idiopathic conditions.

[0039] As used herein, polynucleotide expression products of endotoxemia marker genes are referred to herein as "endotoxemia marker polynucleotides." Polypeptide expression products of the endotoxemia marker genes are referred to herein as "endotoxemia marker polypeptides."

[0040] Thus, in some embodiments, the methods comprise detecting aberrant expression of an endotoxemia 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, 6, 7, 9, 10, 11, 13, 15, 16, 17, 18, 19, 21, 23, 25, 26, 27, 29, 31, 33, 35, 37, 38, 39, 41, 42, 43, 44, 45, 47, 49, 50, 52, 54, 56, 58, 60, 61, 63, 64, 66, 67, 68, 69, 70, 71, 73, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 86, 88, 90, 92, 93, 94, 96, 98, 100, 101, 102, 103, 104, 106, 107, 109, 110, 111, 113, 114, 115, 117, 119, 121, 122, 123, 124, 125, 126, 128, 130, 132, 134, 136, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 158, 160, 162, 164, 166, 168, 169, 170, 172, 173, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 193, 194, 195, 197, 199, 201, 203, 205, 206, 207, 209, 210, 211, 212, 214, 215, 216, 218, 220, 222, 223,

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[0041] In other embodiments, the methods comprise detecting aberrant expression of an endotoxemia 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, 8, 12, 14, 20, 22, 24, 28, 30, 32, 34, 36, 40, 46, 48, 51, 53, 55, 57, 59, 62, 65, 72, 74, 78, 85, 87, 89, 91, 95, 97, 99, 105, 108, 112, 116, 118, 120, 127, 129, 131, 133, 135,138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 159, 161, 163, 165, 167, 171, 175, 177, 179, 181, 183, 185, 187, 189, 191, 196, 198, 200, 202, 204, 208, 213, 217, 219, 221, 226, 228, 230, 232, 234, 236, 238, 241, 243, 247, 249, 251, 253, 256, 258, 261, 263, 265, 267, 273, 275, 277, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324 or 326; (ii) a polypeptide comprising a portion of the sequence set forth in any one of SEQ ID NO: 2, 8, 12, 14, 20, 22, 24, 28, 30, 32, 34, 36, 40, 46, 48, 51, 53, 55, 57, 59, 62, 65, 72, 74, 78, 85, 87, 89, 91, 95, 97, 99, 105, 108, 112, 116, 118, 120, 127, 129, 131, 133, 135,138, 140,

142, 144, 146, 148, 150, 152, 154, 156, 159, 161, 163, 165, 167, 171, 175, 177, 179, 181, 183, 185, 187, 189, 191, 196, 198, 200, 202, 204, 208, 213, 217, 219, 221, 226, 228, 230, 232, 234, 236, 238, 241, 243, 247, 249, 251, 253, 256, 258, 261, 263, 265, 267, 273, 275, 277, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324 or 326, 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, 8, 12, 14, 20, 22, 24, 28, 30, 32, 34, 36, 40, 46, 48, 51, 53, 55, 57, 59, 62, 65, 72, 74, 78, 85, 87, 89, 91, 95, 97, 99, 105, 108, 112, 116, 118, 120, 127, 129, 131, 133, 135,138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 159, 161, 163, 165, 167, 171, 175, 177, 179, 181, 183, 185, 187, 189, 191, 196, 198, 200, 202, 204, 208, 213, 217, 219, 221, 226, 228, 230, 232, 234, 236, 238, 241, 243, 247, 249, 251, 253, 256, 258, 261, 263, 265, 267, 273, 275, 277, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324 or 326; and (iv) a polypeptide comprising a portion of the sequence set forth in any one of SEQ ID NO: 2, 8, 12, 14, 20, 22, 24, 28, 30, 32, 34, 36, 40, 46, 48, 51, 53, 55, 57, 59, 62, 65, 72, 74, 78, 85, 87, 89, 91, 95, 97, 99, 105, 108, 112, 116, 118, 120, 127, 129, 131, 133, 135,138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 159, 161, 163, 165, 167, 171, 175, 177, 179, 181, 183, 185, 187, 189, 191, 196, 198, 200, 202, 204, 208, 213, 217, 219, 221, 226, 228, 230, 232, 234, 236, 238, 241, 243, 247, 249, 251, 253, 256, 258, 261, 263, 265, 267, 273, 275, 277, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324 or 326, 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).

[0042] Typically, such 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 endotoxemia 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 lacking disease, 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 an endotoxemia-related condition in the test subject. In some embodiments, the methods further comprise diagnosing the presence, stage or degree of an endotoxemia-related condition in the test subject 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 functional activity of an individual corresponding expression product., which is hereafter referred to as "aberrant expression." In illustrative examples of this type, the presence of an endotoxemia-related condition is determined by detecting a **decrease** in the level or functional activity of at least one endotoxemia 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, 6, 7, 11, 13, 15, 16, 17, 18, 19, 21, 25, 26, 35, 37, 38, 41, 42, 43, 44, 50, 52, 54, 58, 60, 63, 64, 69, 70, 71, 73, 77, 79, 80, 81, 82, 83, 86, 92, 93, 96, 98, 100, 101, 102, 103, 104, 106, 115, 117, 128, 134, 137, 141, 143, 153, 155, 158, 162, 164, 166, 174, 182, 186, 188, 190, 195, 197, 199, 201, 205, 206, 207, 209, 210, 211, 214, 215, 216, 222, 223, 240, 244, 246, 248, 259, 260, 269, 272, 280, 282, 284, 286, 290, 298, 300, 302, 305, 306, 307, 309, 312, 314, 315, 316, 318, 320, 321, 323, 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: 8, 12, 14, 20, 22, 36, 51, 53, 55, 59, 65, 72, 74, 78, 87, 97, 99, 105, 116, 118, 129, 135, 138, 142, 144, 154, 156, 159, 163, 165, 167, 175, 183, 187, 189, 191, 196, 198, 200, 202, 208, 217, 241, 247, 249, 261, 273, 281, 283, 285, 287, 291, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324; (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: 8, 12, 14, 20, 22, 36, 51, 53, 55, 59, 65, 72, 74, 78, 87, 97, 99, 105, 116, 118, 129, 135, 138, 142, 144, 154, 156, 159, 163, 165, 167, 175, 183, 187, 189, 191, 196, 198, 200, 202, 208, 217, 241, 247, 249, 261, 273, 281, 283, 285, 287, 291, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324, 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.

[0043] In other illustrative examples, the presence of an endotoxemia-related condition is determined by detecting an **increase** in the level or functional activity of at least one endotoxemia 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, 9, 10, 23, 27, 29, 31, 33, 39, 45, 47, 49, 56, 61, 66, 67, 68, 75, 76, 84, 88, 90, 94,

107, 109, 110, 111, 113, 114, 119, 121, 122, 123, 124, 125, 126, 130, 132, 136, 139, 145, 147, 149, 151, 157, 160, 168, 169, 170, 172, 173, 176, 178, 180, 184, 192, 193, 194, 203, 212, 218, 220, 224, 225, 227, 229, 231, 233, 235, 236, 237, 239, 242, 245, 250, 252, 254, 255, 257, 262, 264, 266, 268, 270, 271, 274, 276, 278, 279, 288, 292, 294, 296, 304, 311, 325, 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, 24, 28, 30, 32, 34, 40, 46, 48, 57, 62, 85, 89, 91, 95, 108, 112, 120, 127, 131, 133, 140, 146, 148, 150, 152, 161, 171, 177, 179, 181, 185, 204, 213, 219, 221, 226, 228, 230, 232, 234, 238, 243, 251, 253, 256, 258, 263, 265, 267, 275, 277, 289, 293, 295, 297, 326; (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: 8, 12, 14, 20, 22, 36, 51, 53, 55, 59, 65, 72, 74, 78, 87, 97, 99, 105, 116, 118, 129, 135, 138, 142, 144, 154, 156, 159, 163, 165, 167, 175, 183, 187, 189, 191, 196, 198, 200, 202, 208, 217, 241, 247, 249, 261, 273, 281, 283, 285, 287, 291, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324wherein 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.

[0044] In some embodiments, the method further comprises diagnosing the absence of an endotoxemia-related condition 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.".

[0045] 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, 45, 46, 47, 48, 49 or 50 endotoxemia marker polynucleotides. For example, the methods may comprise measuring the level or functional activity of an endotoxemia marker polynucleotide either alone or in combination with as much as 49, 48, 47, 46, 45, 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 endotoxemia marker polynucleotide(s). In another example, the methods may comprise measuring the level or functional activity of an endotoxemia marker polypeptide either alone or in combination with as

much as 49, 48, 47, 46, 45, 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 endotoxemia 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 endotoxemia marker genes that have a very high correlation ($p<0.001$)with the presence or risk of an endotoxemia-related condition (hereafter referred to as "**level one correlation endotoxemia 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: 11, 23, 29, 35, 43, 44, 68, 81, 82, 84, 104, 105, 107, 119, 130, 136, 147, 155, 174, 192, 193, 245, 254, 255, 262, 264, 270, 271, 279, 296, 325, 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: 12, 24, 30, 36, 85, 108, 120, 131, 148, 156, 175, 256, 263, 265, 297, 326; (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: 12, 24, 30, 36, 85, 108, 120, 131, 148, 156, 175, 256, 263, 265, 297, 326, 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.

[0046] 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 endotoxemia marker genes that have a high correlation ($p<0.005$)with the presence or risk of an endotoxemia-related condition (hereafter referred to as "**level two correlation endotoxemia 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, 7, 9, 10, 17, 18, 21, 25, 26, 33, 54, 61, 64, 79, 80, 90, 94, 115, 117, 121, 122, 125, 126, 143, 160, 162, 164, 172, 173, 178, 184, 186, 194, 199, 205, 206, 225, 229, 242, 244, 252, 257, 259, 274, 276, 282, 284, 288, 294, 306, 316, 318, 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, 22, 34, 55, 62, 65, 91, 95, 116, 118, 127, 144, 161, 163, 165, 179, 185, 187, 200, 226, 230, 243, 253, 258, 275, 277, 283, 285, 289, 295, 317, 319; (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, 22, 34, 55, 62, 65, 91, 95, 116, 118, 127, 144, 161, 163, 165, 179, 185, 187, 200, 226, 230, 243, 253, 258, 275, 277, 283, 285, 289, 295, 317, 319, 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.

[0047] 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 endotoxemia marker genes that have a medium correlation ($p<0.05$)with the presence or risk of an endotoxemia-related condition (hereafter referred to as "**level three correlation endotoxemia 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: 3, 4, 5, 6, 13, 15, 16, 27, 31, 37, 38, 39, 41, 42, 45, 47, 49, 52, 56, 58, 63, 66, 67, 69, 70, 71, 77, 83, 86, 88, 96, 98, 100, 101, 106, 109, 110, 111, 113, 114, 128, 132, 134, 137, 139, 141, 145, 149, 151, 153, 157, 158, 166, 168, 169, 176, 180, 188, 190, 197, 203, 207, 209, 210, 211, 214, 215, 218, 220, 222, 223, 224, 231, 233, 236, 237, 239, 240, 241, 246, 250, 260, 266, 268, 269, 272, 278, 280, 286, 290, 292, 300, 304, 309, 312, 314, 315, 321, 323 , 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: 14, 28, 32, 40, 46, 48, 53, 57, 59, 72, 78, 87, 89, 97, 99, 112, 129, 133, 135, 138, 140, 142, 146, 150, 152, 154, 159, 167, 177, 181, 189, 191, 198, 204, 208, 219, 221, 232, 234, 238, 247, 251, 261, 267, 273, 281, 287, 291, 293, 301, 310, 313, 322, 324; (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: 14, 28, 32, 40, 46, 48, 53, 57, 59, 72, 78, 87, 89, 97, 99, 112, 129, 133, 135, 138, 140, 142, 146, 150, 152, 154, 159, 167, 177, 181, 189, 191, 198, 204, 208, 219, 221, 232, 234, 238, 247, 251, 261, 267, 273, 281, 287, 291, 293, 301, 310, 313, 322, 324, 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.

[0048] 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 endotoxemia marker genes that have a moderate correlation (significant at 72 hours post-induction only and $p<0.05$)with the presence or risk of an endotoxemia-related condition (hereafter referred to as "**level four correlation endotoxemia 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: 19, 50, 60, 73, 75, 92, 93, 102, 103, 123, 124, 170, 182, 195, 201, 212, 216, 227, 235, 248, 298, 302, 305, 307, 311, 320, 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, 51, 74, 76, 171, 183, 196, 202, 213, 217, 228, 249, 299, 303, 308; (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, 51, 74, 76, 171, 183, 196, 202, 213, 217, 228, 249, 299, 303, 308, 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.

[0049] In some embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level one correlation endotoxemia 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 endotoxemia 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 endotoxemia marker gene and the level or functional activity of an expression product of at least 1 level two endotoxemia 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 endotoxemia marker genes and the level or functional activity of an expression product of at least 1 level two correlation endotoxemia 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 endotoxemia marker gene and the level or functional activity of an expression product of at least 2 level two correlation endotoxemia marker genes.

[0050] In some embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level one correlation endotoxemia marker gene and the level or functional activity of an expression product of at least 1 level three correlation endotoxemia 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 endotoxemia marker genes and the level or functional activity of an expression product of at least 1 level three correlation endotoxemia 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 endotoxemia marker gene and the level or functional activity of an expression product of at least 2 level three correlation endotoxemia 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 endotoxemia marker gene and the level or functional activity of an expression product of at least 3 level three correlation endotoxemia marker genes.

[0051] In some embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level one correlation endotoxemia marker gene and the level or functional activity of an expression product of at least 1 level four correlation endotoxemia 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 endotoxemia marker genes and the level or functional activity of an expression product of at least 1 level four correlation endotoxemia 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 endotoxemia marker gene and the level or functional activity of an expression product of at least 2 level four correlation endotoxemia 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 endotoxemia marker gene and the level or functional activity of an expression product of at least 3 level four correlation endotoxemia 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 endotoxemia marker gene and the level or functional activity of an expression product of at least 4 level four correlation endotoxemia marker genes.

[0052] In some embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level two correlation endotoxemia 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 endotoxemia 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 endotoxemia marker gene and the level or functional activity of an expression product of at least 1 level three correlation endotoxemia 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 endotoxemia marker genes and the level or functional activity of an expression product of at least 1 level three correlation endotoxemia 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 endotoxemia marker gene and the level or functional activity of an expression product of at least 2 level three correlation endotoxemia 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 endotoxemia marker gene and the level or functional activity of an expression product of at least 3 level three correlation endotoxemia 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 endotoxemia marker gene and the level or functional activity of an expression product of at least 4 level three correlation endotoxemia marker genes.

[0053] In some embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level two correlation endotoxemia marker gene and the level or functional activity of an expression product of at least 1 level four correlation endotoxemia 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 endotoxemia marker genes and the level or functional activity of an expression product of at least 1 level four correlation endotoxemia 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 endotoxemia marker gene and the level or functional activity of an expression product of at least 2 level four correlation endotoxemia 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 endotoxemia marker gene and the level or functional activity of an expression product of at least 3 level four correlation endotoxemia 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 endotoxemia marker gene and the level or functional activity of an expression product of at least 4 level four correlation endotoxemia 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 endotoxemia marker gene and the level or functional activity of an expression product of at least 5 level four correlation endotoxemia marker genes.

[0054] In some embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level two correlation endotoxemia 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 endotoxemia 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 endotoxemia marker gene and the level or functional activity of an expression product of at least 1 level five correlation endotoxemia 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 endotoxemia marker genes and the level or functional activity of an expression product of at least 1 level five correlation endotoxemia 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 endotoxemia marker gene and the level or functional activity of an expression product of at least 2 level five correlation endotoxemia 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 endotoxemia marker gene and the level or functional activity of an expression product of at least 3 level five correlation endotoxemia 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 endotoxemia marker gene and the level or functional activity of an expression product of at least 4 level five correlation endotoxemia 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 endotoxemia marker gene and the level or functional activity of an expression product of at least 5 level five correlation endotoxemia marker genes.

[0055] In some embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level three correlation endotoxemia 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 endotoxemia 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 endotoxemia marker gene and the level or functional activity of an expression product of at least 1 level four correlation endotoxemia 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 endotoxemia marker genes and the level or functional activity of an expression product of at least 1 level four correlation endotoxemia 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 endotoxemia marker gene and the level or functional activity of an expression product of at least 2 level four correlation endotoxemia 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 endotoxemia marker gene and the level or functional activity of an expression product of at least 3 level four correlation endotoxemia 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 endotoxemia marker gene and the level or functional activity of an expression product of at least 4 level four correlation endotoxemia 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

endotoxemia marker gene and the level or functional activity of an expression product of at least 5 level four correlation endotoxemia marker genes.

[0056] In some embodiments, the methods comprise measuring the level or functional activity of an expression product of at least 1 level four correlation endotoxemia 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 endotoxemia 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 endotoxemia 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 endotoxemia 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 endotoxemia 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 endotoxemia 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 endotoxemia marker genes.

[0057] Advantageously, the biological sample comprises blood, especially peripheral blood, which suitably 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.

[0058] 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 hybridists under at least low, medium, or high stringency conditions to the target RNA or to the DNA copy, wherein the nucleic acid probe comprises at least 15 contiguous nucleotides of an endotoxemia marker polynucleotide. In these embodiments, 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. 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.

[0059] 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).

[0060] 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.

[0061] In some embodiments, a system is used to perform the diagnostic methods as broadly described above, 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 or degree of endotoxemia-related conditions. 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.

[0062] In another aspect, the invention contemplates use of the methods broadly described above in the monitoring, treatment and management of conditions that can lead to endotoxemia, illustrative examples of which include retained placenta, meningitis, endometriosis, shock, toxic shock (i.e., a sequelae to tampon use), gastroenteritis, appendicitis, ulcerative colitis, Crohn's disease, inflammatory bowel disease, acid gut syndrome, liver failure and cirrhosis, failure of colostrum transfer in neonates, ischemia (in any organ), bacteraemia, infections within body cavities such as the peritoneal, pericardial, thecal, and pleural cavities, burns, severe wounds, excessive exercise or stress, hemodialysis, conditions involving intolerable pain (e.g., pancreatitis, kidney stones), surgical operations, and non-healing lesions.

In these embodiments, the diagnostic methods of the invention are typically used at a frequency that is effective to monitor the early development of an endotoxemia-related condition to thereby enable early therapeutic intervention and treatment of that condition. In illustrative examples, the diagnostic methods are used at least at 1, 2, 3, 4,5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23 or 24 hour intervals.

[0063] In yet another aspect, the present invention provides methods for treating, preventing or inhibiting the development of an endotoxemia-related condition in a subject. These methods generally comprise detecting aberrant expression of at least one endotoxemia 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 the endotoxemia-related condition in the subject. Representative examples of such treatments or agents include but are not limited to, antibiotics, steroids, intravenous fluids, vasoactives, palliative support for damaged or distressed organs (e.g. oxygen for respiratory distress, fluids for hypovolemia) and close monitoring of vital organs.

[0064] In still another aspect, the present invention provides isolated polynucleotides, referred to herein as "endotoxemia 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: 3, 4, 9, 15, 16, 17, 18, 25, 26, 37, 38, 41, 42, 43, 44, 49, 63, 66, 67, 68, 69, 70, 75, 76, 79, 80, 81, 82, 83, 92, 93, 100, 101, 102, 103, 106, 109, 110, 113, 114, 121, 122, 123, 124, 125, 136, 157, 168, 169, 172, 173, 192, 193, 194, 205, 206, 209, 210, 211, 214, 215, 222, 223, 224, 235, 236, 239, 244, 245, 254, 259, 268, 269, 270, 271, 278, 279, 304, 305, 306, 311, 314, 315 or 320, or a complement thereof; (b) a polynucleotide comprising a portion of the sequence set forth in any one of SEQ ID NO: 3, 4, 9, 15, 16, 17, 18, 25, 26, 37, 38, 41, 42, 43, 44, 49, 63, 66, 67, 68, 69, 70, 75, 76, 79, 80, 81, 82, 83, 92, 93, 100, 101, 102, 103, 106, 109, 110, 113, 114, 121, 122, 123, 124, 125, 136, 157, 168, 169, 172, 173, 192, 193, 194, 205, 206, 209, 210, 211, 214, 215, 222, 223, 224, 235, 236, 239, 244, 245, 254, 259, 268, 269, 270, 271, 278, 279, 304, 305, 306, 311, 314, 315 or 320, 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: 3, 4, 9, 15, 16, 17, 18, 25, 26, 37, 38, 41, 42, 43, 44, 49, 63, 66, 67, 68, 69, 70, 75, 76, 79, 80, 81, 82, 83, 92, 93, 100, 101, 102, 103, 106, 109, 110, 113, 114, 121, 122, 123, 124, 125, 136, 157, 168, 169, 172, 173, 192, 193, 194, 205, 206, 209, 210, 211, 214, 215, 222, 223, 224, 235, 236, 239, 244, 245, 254, 259, 268, 269, 270, 271, 278, 279, 304, 305, 306, 311, 314, 315 or 320, 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.

[0065] In yet 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.

[0066] In still 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.

[0067] 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, 8, 12, 14, 20, 22, 24, 28, 30, 32, 34, 36, 40, 46, 48, 51, 53, 55, 57, 59, 62, 65, 72, 74, 78, 85, 87, 89, 91, 95, 97, 99, 105, 108, 112, 116, 118, 120, 127, 129, 131, 133, 135,138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 159, 161, 163, 165, 167, 171, 175, 177, 179, 181, 183, 185, 187, 189, 191, 196, 198, 200, 202, 204, 208, 213, 217, 219, 221, 226, 228, 230, 232, 234, 236, 238, 241, 243, 247, 249, 251, 253, 256, 258, 261, 263, 265, 267, 273, 275, 277, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324 or 326, 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, 8, 12, 14, 20, 22, 24, 28, 30, 32, 34, 36, 40, 46, 48, 51, 53, 55, 57, 59, 62, 65, 72, 74, 78, 85, 87, 89, 91, 95, 97, 99, 105, 108, 112, 116, 118, 120, 127, 129, 131, 133, 135,138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 159, 161, 163, 165, 167, 171, 175, 177, 179, 181, 183, 185, 187, 189, 191, 196, 198, 200, 202, 204, 208, 213, 217, 219, 221, 226, 228, 230, 232, 234, 236, 238, 241, 243, 247, 249, 251, 253, 256, 258, 261, 263, 265, 267, 273, 275, 277, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324 or 326 under at least low, medium or high 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, 6, 7, 9, 10, 11, 13, 15, 16, 17, 18, 19, 21, 23, 25, 26, 27, 29, 31, 33, 35, 37, 38, 39, 41, 42, 43, 44, 45, 47, 49, 50, 52, 54,

56, 58, 60, 61, 63, 64, 66, 67, 68, 69, 70, 71, 73, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 86, 88, 90, 92, 93, 94, 96, 98, 100, 101, 102, 103, 104, 106, 107, 109, 110, 111, 113, 114, 115, 117, 119, 121, 122, 123, 124, 125, 126, 128, 130, 132, 134, 136, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 158, 160, 162, 164, 166, 168, 169, 170, 172, 173, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 193, 194, 195, 197, 199, 201, 203, 205, 206, 207, 209, 210, 211, 212, 214, 215, 216, 218, 220, 222, 223, 224, 225, 227, 229, 231, 233, 235, 236, 237, 239, 240, 242, 244, 245, 246, 248, 250, 252, 254, 255, 257, 259 260, 262, 264, 266, 268, 269, 270, 271, 272, 274, 276, 278, 279, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 305, 306, 307, 309, 311, 312, 314, 315, 316, 318, 320 321, 323 or 325 under at least low, medium or high stringency conditions, wherein the portion is at least 15 nucleotides in length. Representative probes for detecting the endotoxemia marker polynucleotides according to the resent invention are set forth in SEQ ID NO: 326-2315 (see Table 2).

[0068] 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.

[0069] In a further aspect, the present invention provides isolated polypeptides, referred to herein as "endotoxemia 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 an endotoxemia marker gene as broadly described above, for example, especially an endotoxemia 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: 3, 4, 9, 15, 16, 17, 18, 25, 26, 37, 38, 41, 42, 43, 44, 49, 63, 66, 67, 68, 69, 70, 75, 76, 79, 80, 81, 82, 83, 92, 93, 100, 101, 102, 103, 106, 109, 110, 113, 114, 121, 122, 123, 124, 125, 136, 157, 168, 169, 172, 173, 192, 193, 194, 205, 206, 209, 210, 211, 214, 215, 222, 223, 224, 235, 236, 239, 244, 245, 254, 259, 268, 269, 270, 271, 278, 279, 304, 305, 306, 311, 314, 315 or 320; (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).

[0070] Still a further aspect of the present invention provides an antigen-binding molecule that is immuno-interactive with an endotoxemia marker polypeptide as broadly described above.

[0071] 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.

[0072] Still another aspect of the invention provides the use of one or more endotoxemia 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 endotoxemia 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 diagnosing the presence of an endotoxemia-related condition in a subject.

[0073] In still other aspects, the invention is directed to the use of the diagnostic methods as broadly described above, or one or more endotoxemia 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 endotoxemia marker polypeptides as broadly described above, or the use of one or more antigen-binding molecules as broadly described above, for diagnosing an endotoxemia-related condition animals (vertebrates), mammals, non-human mammals, animals, such as horses involved in load bearing or athletic activities (e.g., races) and pets (e.g., dogs and cats).

[0074] The aspects of the invention are directed to animals (vertebrates), mammals, non-human mammals, animals, such as horses involved in load bearing or athletic activities (e.g., races) and pets (e.g., dogs and cats).

BRIEF DESCRIPTION OF THE DRAWINGS

[0075] Figure 1 is a graphical representation of a receiver operating curve (ROC) for comparison of gene expression 24 hours post-induction. The ROC curve generated from these data demonstrated that 24 hours post-induction, was well separated from 0 hours. The sensitivity and selectivity using two principal components are 1.00 and 1.00 respectively.

[0076] Figure 2 is a graphical representation of ROC for comparison of gene expression 72 hours post-induction. The ROC curve generated from these data demonstrated that 72 hours post-induction, was well separated from 0 hours. The sensitivity and selectivity using two principal components are 0.667 and 1.00 respectively. Using four principal components this can be improved to 0.883 and 1 respectively (not shown).

DETAILED DESCRIPTION OF THE INVENTION

1. Definitions

[0077] 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.

[0078] 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.

[0079] The term "aberrant expression," as used herein to describe the expression of an endotoxemia marker gene, refers to the overexpression or underexpression of an endotoxemia marker gene relative to the level of expression of the endotoxemia marker gene or variant thereof in cells obtained from a healthy subject or from a subject lacking endotoxemia, and/or to a higher or lower level of an endotoxemia marker gene product (e.g., transcript or polypeptide) in a tissue sample or body fluid obtained from a healthy subject or from a subject lacking endotoxemia. In particular, an endotoxemia marker gene is aberrantly expressed if the level of expression of the endotoxemia 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% than the level of expression of the endotoxemia marker gene by cells obtained from a healthy subject or from a subject without endotoxemia, and/or relative to the level of expression of the endotoxemia marker gene in a tissue sample or body fluid obtained from a healthy subject or from a subject without endotoxemia.

[0080] 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.

[0081] 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.

[0082] 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.

[0083] 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.

[0084] 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.

[0085] 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.

[0086] 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.

[0087] 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.

[0088] 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.

[0089] 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.

[0090] 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.

[0091] 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.

[0092] As used herein, the term "functional activity" generally refers to the ability of a molecule (e.g., a transcript or polypeptide) to perform its designated function including a biological, enzymatic, or therapeutic function. In certain embodiments, the functional activity of a molecule corresponds to its specific activity as determined by any suitable assay known 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] By "housekeeping gene" is meant a gene that is expressed in virtually all cells since it is fundamental to the any cell's functions (e.g., essential proteins and RNA molecules).

[0097] "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.

[0098] 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.

[0099] 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.

[0100] 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.

[0101] 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).

[0102] 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.

[0103] By "obtained from" is meant that a sample such as, for example, a nucleic acid extract or polypeptide extract is isolated from, or derived from, a particular source. For instance, the extract may be isolated directly from a biological fluid or tissue of the subject.

[0104] 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.

[0105] 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 fiber 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.

[0106] 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.

[0107] The term "pathogen" is used herein in its broadest sense to refer to an organism or an infectious agent whose infection of cells of viable animal tissue elicits a disease response.

[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 hybridize and serve as a site for the initiation of synthesis. By "substantially complementary", it is meant that the primer is sufficiently complementary to hybridize with a target polynucleotide. Desirably, the primer contains no mismatches with the template to which it is designed to hybridize 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 hybridize 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 A *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 of endotoxemia. 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 hybridize 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] The term "treat" is meant to include both therapeutic and prophylactic treatment.

[0125] 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.

[0126] 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

[0127] 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 endotoxemia and uses therefor*

[0128] The present invention concerns the early detection, diagnosis, or prognosis of endotoxemia or its sequelae (also referred to herein as "endotoxemia-related conditions"). Markers of endotoxemia, 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 with or susceptible to endotoxemia, are disclosed. These markers are indicators of endotoxemia-related conditions and, when differentially expressed as compared to their expression in normal subjects or in subjects lacking endotoxemia-related conditions, are diagnostic for the presence of those conditions in tested subjects. Such markers provide considerable advantages over the prior art in this field. In certain advantageous embodiments where leukocytes (e.g., peripheral blood cells) are used for the analysis, it is possible to diagnose active endotoxemia-related conditions before serum antibodies to endotoxin, or endotoxaemia-causing agent are detected.

[0129] It will be apparent that the nucleic acid sequences disclosed herein will find utility in a variety of applications in detection, diagnosis, prognosis and treatment of endotoxemia-related conditions. Examples of such applications within the scope of the present disclosure comprise amplification of endotoxemia markers using specific primers, detection of endotoxemia markers by hybridization 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.

[0130] The identified endotoxemia 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.

[0131] 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 marker genes or 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.

[0132] 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 endotoxemia markers of interest. It will be recognized that full-length genes may be obtained using the full-length or 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 endotoxemia marker genes using the detection methods described herein, and are part of the invention.

[0133] One of ordinary skill in the art could select segments from the identified marker genes for use in 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, 5, 7, 8, 10, 12, 14, 16, 17, 18, 20, 22, 24, 26, 27, 28, 30, 32, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 52, 54, 55, 56 or 57 (see Table 1).

4. Nucleic acid molecules of the invention

[0134] As described in the Examples and in Tables 1, the present disclosure provides 179 markers of endotoxemia, identified by GeneChip® analysis of blood obtained from normal horses and from horses with clinical evidence of an endotoxemia-related condition. Of the 179 markers identified, 121 comprise coding regions sequences (see the markers relating to SEQ ID NO: 1, 5, 6, 7, 11, 13, 19, 21, 23, 27, 29, 31, 33, 35, 39, 45, 47, 50, 52, 54, 56, 58, 60, 61, 64, 71, 73, 77, 78, 84, 86, 88, 90, 94, 96, 98, 102, 103, 104, 107, 111, 115, 117, 119, 126, 128, 130, 132, 134, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 158, 160, 162, 164, 166, 170, 174, 176, 178, 180, 182, 184, 186, 188, 190, 195, 197, 199, 201, 203, 207, 212, 216, 218, 220, 225, 227, 229, 231, 233, 237, 240, 242, 246, 248, 250, 252, 255, 257, 260, 262, 264, 266, 272, 274, 276, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 307, 309, 312, 316, 318, 321, 323 or 325) and 58 comprise 5' and/or 3' untranslated sequences only (see the markers relating to SEQ ID NO: 3, 4, 9, 15, 16, 17, 18, 25, 26, 37, 38, 41, 42, 43, 44, 49, 63, 66, 67, 68, 69, 70, 75, 76, 79, 80, 81, 82, 83, 92, 93, 100, 101, 102, 103, 106, 109, 110, 113, 114, 121, 122, 123, 124, 125, 136, 157, 168, 169, 172, 173, 192, 193, 194, 205, 206, 209, 210, 211, 214, 215, 222, 223, 224, 235, 236, 239, 244, 245, 254, 259, 268, 269, 270, 271, 278, 279, 304, 305, 306, 311, 314, 315 or 320). These sequences, which are presented in Table 1, are diagnostic for the presence, stage or degree of an endotoxemia-related condition (also referred to herein as "endotoxemia marker polynucleotides"). Sequence analysis has revealed that the endotoxaemia marker genes can be classified into subgroups. For example, several endotoxaemia marker genes encode membrane associated polypeptides involved in the immune response (e.g., SEQ ID NO. 59, 219, 230, 253, 285, and 295), whereas others encode cytoplasm associated polypeptides (e.g., SEQ ID NO: 217, 241, 247, 265, 267, 287, and 291), while still others encode extracellular polypeptides (e.g., SEQ ID NO: 30, 85, 108, 127, 140, and 226), whereas still others encode nuclear polypeptides (e.g., 8, 12, 20, 28, 40, 55, 281, 283 and 313) and still others encode cytoskeleton molecules (e.g., SEQ ID NO: 105 and 213).

[0135] 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.

[0136] 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, 5, 7, 8, 10, 12, 14, 16, 17, 18, 20, 22, 24, 26, 27, 28, 30, 32, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 52, 54, 55, 56 or 57 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 diagnose an endotoxemia-related condition. 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.

[0137] 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 endotoxemia marker genes are presented in Tables 2.

[0138] 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 labeled 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).

[0139] The present invention provides substantially full-length cDNA sequences as well as EST and partial cDNA sequences that are useful as markers of endotoxemia-related condition. 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 "endotoxemia marker polynucleotides." Additionally, the present invention includes within its scope isolated or purified expression products of endotoxemia marker polynucleotides (i.e., RNA transcripts and polypeptides).

[0140] 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 endotoxaemia 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.

[0141] The present invention also encompasses portions of the full-length or substantially full-length nucleotide sequences of the endotoxemia marker genes or their transcripts or DNA copies of these transcripts. Portions of an endotoxemia marker nucleotide sequence may encode polypeptide portions or segments that retain the biological activity of the native polypeptide. Alternatively, portions of an endotoxemia marker nucleotide sequence that are useful as hybridization probes generally do not encode amino acid sequences retaining such biological activity. Thus, portions of an endotoxemia 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 endotoxemia marker polypeptides of the invention.

[0142] A portion of an endotoxemia marker nucleotide sequence that encodes a biologically active portion of an endotoxemia 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 endotoxemia marker polypeptide. Portions of an endotoxemia marker nucleotide sequence that are useful as hybridization probes or PCR primers generally need not encode a biologically active portion of an endotoxemia marker polypeptide.

[0143] Thus, a portion of an endotoxemia marker nucleotide sequence may encode a biologically active portion of an endotoxemia 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 an endotoxemia marker polypeptide can be prepared by isolating a portion of one of the endotoxemia marker nucleotide sequences of the invention, expressing the encoded portion of the endotoxemia marker polypeptide (e.g., by recombinant expression *in vitro*), and assessing the activity of the encoded portion of the endotoxemia marker polypeptide. Nucleic acid molecules that are portions of an endotoxemia 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 endotoxemia marker nucleotide sequence.

[0144] The invention also contemplates variants of the endotoxemia 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 endotoxemia 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 an endotoxemia 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.

[0145] The endotoxemia 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 endotoxemia 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 endotoxemia 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.

[0146] In certain embodiments, an antigen-binding molecule of the invention is encoded by a polynucleotide that hybridizes to a disclosed nucleotide sequence under very high stringency conditions. One embodiment of very high stringency conditions includes hybridizing 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.

[0147] Other stringency conditions are well known in the art and a skilled addressee 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.

[0148] 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:

[0149] $T_m = 81.5 + 16.6 (\log_{10} M) + 0.41 (\%G+C) - 0.63 (\%\ formamide) - (600/length)$

[0150] 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.

[0151] 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

[0152] The present invention also contemplates full-length polypeptides encoded by the endotoxemia marker genes of the invention as well as the biologically active portions of those polypeptides, which are referred to collectively herein as "endotoxemia marker polypeptides." Biologically active portions of full-length endotoxemia 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 an endotoxemia 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 endotoxemia marker polypeptides. Typically, portions of a full-length endotoxemia 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 endotoxemia marker polypeptide include peptides comprising amino acid sequences sufficiently similar to or derived from the amino acid sequences of a (putative) full-length endotoxemia marker polypeptide, for example, the amino acid sequences shown in SEQ ID NO: 2, 4, 6, 9, 11, 13, 15, 19, 21, 23, 25, 29, 31, 33, 51, 53 or 58, which include less amino acids than a full-length endotoxemia 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 endotoxemia marker polypeptide. A biologically active portion of a full-length endotoxemia 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 or 3000, 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.

[0153] The present invention also contemplates variant endotoxemia 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 endotoxemia marker polyeptide 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.

[0154] An endotoxemia 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 an endotoxemia 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 endotoxemia 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 endotoxemia 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.

[0155] Variant endotoxemia marker polypeptides may contain conservative amino acid substitutions at various locations along their sequence, as compared to the parent endotoxemia 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:

[0156] 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.

[0157] 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.

[0158] 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).

[0159] 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.

[0160] 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.

[0161] 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.

[0162] 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.

[0163] 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.

[0164] 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 endotoxemia marker polypeptide can readily be determined by assaying its activity. Conservative substitutions are shown in Table 4 below 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.

[0165] 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).

[0166] Thus, a predicted non-essential amino acid residue in an endotoxemia 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 an endotoxemia 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.

[0167] Accordingly, the present invention also contemplates variants of the naturally-occurring endotoxemia 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 endotoxemia marker polypeptide sequence as, for example, set forth in any one of SEQ ID NO: 2, 4, 6, 9, 11, 13, 15, 19, 21, 23, 25, 29, 31, 33, 51, 53 or 58. 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 endotoxemia marker polypeptide sequence as, for example, set forth in any one of SEQ ID NO: 2, 4, 6, 9, 11, 13, 15, 19, 21, 23, 25, 29, 31, 33, 51, 53 or 58. 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 endotoxemia marker polypeptide are contemplated. endotoxemia marker

polypeptides also include polypeptides that are encoded by polynucleotides that hybridize under stringency conditions as defined herein, especially high stringency conditions, to the endotoxemia marker polynucleotide sequences of the invention, or the non-coding strand thereof, as described above.

[0168] In one embodiment, variant polypeptides differ from an endotoxemia 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, 4, 6, 9, 11, 13, 15, 19, 21, 23, 25, 29, 31, 33, 51, 53 or 58 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.

[0169] 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 an endotoxemia 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.

[0170] 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 an endotoxemia marker polypeptide as, for example, set forth in any one of SEQ ID NO: 2, 4, 6, 9, 11, 13, 15, 19, 21, 23, 25, 29, 31, 33, 51, 53 or 58, and has the activity of that endotoxemia marker polypeptide.

[0171] Endotoxemia 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 an endotoxemia 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 endotoxemia marker polypeptide; and (d) isolating the endotoxemia 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, 4, 6, 9, 11, 13, 15, 19, 21, 23, 25, 29, 31, 33, 51, 53 or 58 or a variant thereof.

[0172] 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.

[0173] The regulatory element will generally be appropriate for the host cell employed for expression of the endotoxemia 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.

[0174] 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.

[0175] The expression vector may also include a fusion partner (typically provided by the expression vector) so that the endotoxemia 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 endotoxemia marker polynucleotide into an expression vector so that the translational reading frames of the fusion partner and the endotoxemia 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.

[0176] 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 endotoxemia marker polypeptide from the fusion construct.

The liberated polypeptide can then be isolated from the fusion partner by subsequent chromatographic separation.

[0177] 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.

[0178] 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 practicing 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.

[0179] Recombinant endotoxemia marker polypeptides may be produced by culturing a host cell transformed with a chimeric construct. The conditions appropriate for expression of the endotoxemia 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.

[0180] Recombinant endotoxemia 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 endotoxemia 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

[0181] The invention also provides antigen-binding molecules that are specifically immuno-interactive with an endotoxemia 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 an endotoxemia 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.

[0182] 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 endotoxemia marker polypeptides of the invention.

[0183] 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

stabilized Fv fragment comprises a disulfide stabilized 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 disulfide 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).

[0184] Phage display and combinatorial methods for generating anti-endotoxemia 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 endotoxemia marker polypeptides. They can also be used to detect and/or isolate the endotoxemia marker polypeptides of the invention. Thus, the invention also contemplates the use of antigen-binding molecules to isolate endotoxemia 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-endotoxemia marker polypeptide antigen-binding molecules are attached to a suitable resin, the resin is contacted with a sample suspected of containing an endotoxemia marker polypeptide, and the endotoxemia 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.).

[0185] 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- endotoxemia marker polypeptide antigen-binding molecule (e.g., monoclonal antibody) can be used to detect endotoxemia 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 endotoxemia marker polypeptides levels in biological samples (including whole cells and fluids) for diagnosing the presence, absence, degree, or stage of development of endotoxemia. 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.

[0186] 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 endotoxemia marker gene expression or the presence of endotoxemia marker polynucleotides

[0187] The present invention is predicated in part on the discovery that: horses with clinical evidence of endotoxemia-related conditions have aberrant expression of certain genes (referred to herein as "endotoxemia marker genes") whose transcripts include, but are not limited to, SEQ ID NO: 1, 3, 4, 5, 6, 7, 9, 10, 11, 13, 15, 16, 17, 18, 19, 21, 23, 25, 26, 27, 29, 31, 33, 35, 37, 38, 39, 41, 42, 43, 44, 45, 47, 49, 50, 52, 54, 56, 58, 60, 61, 63, 64, 66, 67, 68, 69, 70, 71, 73, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 86, 88, 90, 92, 93, 94, 96, 98, 100, 101, 102, 103, 104, 106, 107, 109, 110, 111, 113, 114, 115, 117, 119, 121, 122, 123, 124, 125, 126, 128, 130, 132, 134, 136, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 158, 160, 162,

164, 166, 168, 169, 170, 172, 173, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 193, 194, 195, 197, 199, 201, 203, 205, 206, 207, 209, 210, 211, 212, 214, 215, 216, 218, 220, 222, 223, 224, 225, 227, 229, 231, 233, 235, 236, 237, 239, 240, 242, 244, 245, 246, 248, 250, 252, 254, 255, 257, 259 260, 262, 264, 266, 268, 269, 270, 271, 272, 274, 276, 278, 279, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 305, 306, 307, 309, 311, 312, 314, 315, 316, 318, 320 321, 323 or 325, as compared to normal horses or to horses lacking endotoxemia-related conditions.

[0188] Accordingly, in certain embodiments, the invention features a method for diagnosing the presence, absence, degree or stage of an endotoxemia-related condition in a subject, which is typically of equine origin, by detecting aberrant expression of an endotoxemia marker gene in a biological sample obtained from the subject. Accordingly, in order to make such diagnoses, it will be desirable to qualitatively or quantitatively determine the levels of endotoxemia marker gene transcripts or the level or functional activity of endotoxemia marker polypeptides. In some embodiments, the presence, degree, or stage of development of an endotoxemia-related condition is diagnosed when an endotoxemia marker gene product is expressed at a detectably lower level in the biological sample as compared to the level at which that gene is expressed in a reference sample obtained from normal subjects or from subjects lacking that condition. In other embodiments, the presence, degree, or stage of development of an endotoxemia-related condition is diagnosed when an endotoxemia marker gene product is expressed at a detectably higher level in the biological sample as compared to the level at which that gene is expressed in a reference sample obtained from normal subjects or from subjects lacking that condition. Generally, such diagnoses are made when the level or functional activity of an endotoxemia marker gene product in the biological sample varies from the level or functional activity of a corresponding endotoxemia 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%. 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 endotoxemia 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 endotoxemia 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 endotoxemia 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 labelled 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 polymerisation. 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] Vincent and Kong disclose a method termed helicase-dependent isothermal DNA amplification (HDA) (Vincent and Kong, EMBO Reports, 5(8):795-800, 2004). This method uses DNA helicase to separate DNA strands and hence does not require thermal cycling. The entire reaction can be carried out at one temperature and this method should have broad application to point-of-care DNA diagnostics.

[0199] 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.

[0200] 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).

[0201] 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).

[0202] Depending on the format, the endotoxemia 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).

[0203] In some embodiments, amplification products or "amplicons" are visualized in order to confirm amplification of the endotoxemia 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-labelled 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 endotoxemia 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.

[0204] 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.

[0205] 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 lacking an endotoxemia-related condition. In this way, it is possible to correlate the amount of a endotoxemia marker nucleic acid detected with the progression or severity of the disease.

[0206] 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.

[0207] 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 analysing 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 endotoxemia 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 endotoxemia 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.

[0208] 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.

[0209] 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.

[0210] 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 functionalised 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.

[0211] 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.

[0212] 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.

[0213] 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 endotoxemia 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.*

[0214] 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*).

[0215] 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.

[0216] Usually the target endotoxemia 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.

[0217] 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)

[0218] Radioactive reporter molecules include, for example, ^{32}P, which can be detected by an X-ray or phosphoimager techniques.

[0219] 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.

[0220] 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).

[0221] 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. Hybridisation 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.

[0222] A hybridization mixture containing the target endotoxemia 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.

[0223] 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 optimizing 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.

[0224] 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 color 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 endotoxemia 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

[0225] Consistent with the present invention, the presence of an aberrant concentration of an endotoxemia marker protein is indicative of the presence, degree, or stage of development of an endotoxemia-related condition. Endotoxemia marker protein levels in biological samples can be assayed using any suitable method known in the art. For example, when an endotoxemia 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., coloured, 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).

[0226] 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 an endotoxemia 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.

[0227] 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.

[0228] 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).

[0229] 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 polymerisable 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).

[0230] 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 recognise 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.

[0231] 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.

[0232] 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.

[0233] 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).

[0234] 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.

[0235] 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.

[0236] 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.

[0237] 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.

[0238] In certain embodiments, the techniques used for detection of endotoxemia 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.

[0239] 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 endotoxemia marker expression products, together with indications of the actual status of the individuals (e.g., presence, absence, degree, or stage of development of an endotoxemia-related condition) 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

[0240] All the essential materials and reagents required for detecting and quantifying endotoxemia maker 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) an endotoxemia marker polynucleotide (which may be used as a positive control), (ii) a primer or probe that specifically hybridizes to an endotoxemia 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) an endotoxemia marker polypeptide (which may be used as a positive control), (ii) an antigen-binding molecule that is immuno-interactive with an endotoxemia 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 an endotoxemia marker gene.

8. Methods of treatment or prophylaxis

[0241] The present invention also extends to the management of endotoxaemia-related conditions, or prevention of further progression of endotoxaemia-related conditions, or assessment of the efficacy of therapies in subjects following positive diagnosis for the presence,

or stage of endotoxaemia-related conditions in the subjects. Generally, the management of endotoxaemia-related conditions is highly intensive and can include identification and amelioration of the underlying cause and aggressive use of therapeutic compounds such as, vasoactive compounds, antibiotics, steroids, antibodies to endotoxin, and anti tumour necrosis factor agents. In addition, palliative therapies[1] aimed at restoring and protecting organ function can be used such as intravenous fluids and oxygen.

[0242] Typically, the therapeutic 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 endotoxaemia. 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 endotoxaemia, the medical practitioner or veterinarian may evaluate severity of any symptom associated with the presence of endotoxaemia including tachycardia, fever, chills, vomiting, diarrhoea, skin rash, headaches, confusion, muscle aches, seizures. In any event, those of skill in the art may readily determine suitable dosages of the therapeutic agents and suitable treatment regimens without undue experimentation.

[0243] The therapeutic agents may by administered in concert with adjunctive (palliative) therapies to increase oxygen supply to major organs, increase blood flow to major organs and/or to reduce the inflammatory response. Illustrative examples of such adjunctive therapies include non steroidal-anti inflammatory drugs (NSAIDs), intravenous saline and oxygen.

[0244] 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.

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[1] Cohen J & Glauser MP. Lancet 338: 736-739 (1991).

EXAMPLES

EXAMPLE 1

IDENTIFICATION OF SPECIFIC DIAGNOSTIC GENES FOR ENDOTOXAEMIA-RELATED CONDITIONS

Experimental Disease Trial Design

[0245] A clinical trial was performed on three blocks of fours horses each. The first block consisted of four horses that were dosed orally with 12.5 mg/kg of oligofructose[2] as part of the trial procedure described by Pollitt[3] which is specifically designed to induce endotoxaemia and subsequent acute laminitis. The second block consisted of four horses that underwent the same trial procedure but were dosed with normal saline (0.9%) solution (controls). The same four horses in the second block then underwent the trial procedure (following a period of recovery) for a second time but were dosed with oligofructose (block three). All horses were stalled under the same conditions for the duration of the procedure (120 hours).

[0246] Endotoxaemia-related conditions in horses (including laminitis) can be induced experimentally and one of the more reliable methods of induction is by carbohydrate overload through oral dosing with oligofructose.

[0247] Blood samples were collected at four time points – Hour 0 prior to dosing and at hours 24, 48, and 72 hours after dosing. The sample at Hour 0 acted as a control for each horse.

[0248] The following tests and observations were undertaken at all of the above time points:

[0249] (i) physical examination, rectal temperature, digital pulse, hoof temperature, heart and respiratory rate, faecal pH, hoof shifting; and

[0250] (ii) haematology and biochemistry.

[0251] Blood samples from each of the animals on Hours 0, 24, 48 and 72 of the trial were analysed 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 Diagnostic Marker Genes" below) reveals a number of specific genes that differ in expression between animals before and after

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[2] Raftilose®, Orafti Active Food Ingredients, Aanndorenstraat, B-3300 Tienen, Belgium.
[3] van Eps A & Pollitt CC. Equine Vet J. 36(3):255-60 (2004).

experimental induction of endotoxaemia and laminitis from Hour 24 following dosing. It is possible to design an assay that measures the RNA level in the sample from the expression of at least one and desirably at least two endotoxaemia marker genes, representative transcript sequences of which are set forth in SEQ ID NO: 1, 3, 4, 5, 6, 7, 9, 10, 11, 13, 15, 16, 17, 18, 19, 21, 23, 25, 26, 27, 29, 31, 33, 35, 37, 38, 39, 41, 42, 43, 44, 45, 47, 49, 50, 52, 54, 56, 58, 60, 61, 63, 64, 66, 67, 68, 69, 70, 71, 73, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 86, 88, 90, 92, 93, 94, 96, 98, 100, 101, 102, 103, 104, 106, 107, 109, 110, 111, 113, 114, 115, 117, 119, 121, 122, 123, 124, 125, 126, 128, 130, 132, 134, 136, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 158, 160, 162, 164, 166, 168, 169, 170, 172, 173, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 193, 194, 195, 197, 199, 201, 203, 205, 206, 207, 209, 210, 211, 212, 214, 215, 216, 218, 220, 222, 223, 224, 225, 227, 229, 231, 233, 235, 236, 237, 239, 240, 242, 244, 245, 246, 248, 250, 252, 254, 255, 257, 259 260, 262, 264, 266, 268, 269, 270, 271, 272, 274, 276, 278, 279, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 305, 306, 307, 309, 311, 312, 314, 315, 316, 318, 320 321, 323 or 325.

Materials and Methods

Blood Collection

[0252] 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

[0253] 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.

[0254] 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.

Generation of Gene Expression Data

Choice of Method

[0255] 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:

[0256] • GeneChip® analysis using Affymetrix technology.

[0257] • Real-Time Polymerase Chain Reaction (TaqMan™ from Applied Biosystems for example).

[0258] 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.

[0259] 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.

[0260] 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.

[0261] 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 analyzed simultaneously.

[0262] The methodology for GeneChip® data generation and analysis and Real Time PCR is presented below in brief.

GeneChip® Data Generation

cDNA & cRNA Generation

[0263] 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).

[0264] The steps are:

[0265] • A total of 3 μg of total RNA is used as a template to generate double stranded cDNA.

[0266] • cRNA is generated and labeled using biotinylated Uracil (dUTP).

[0267] • biotin-labeled cRNA is cleaned and the quantity determined using a spectrophotometer and MOPS gel analysis.

[0268] • labeled cRNA is fragmented to ~ 300bp in size.

[0269] • RNA quantity is determined on an Agilent "Lab-on-a-Chip" system (Agilent Technologies).

Hybridization, Washing & Staining

[0270] The steps are:

[0271] • 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.

[0272] • The final volume (80 μL) of the hybridization cocktail is added to the GeneChip® cartridge.

[0273] • The cartridge is placed in a hybridization oven at constant rotation for 16 hours.

[0274] • The fluid is removed from the GeneChip® and stored.

[0275] • The GeneChip® is placed in the fluidics station.

[0276] • The experimental conditions for each GeneChip® are recorded as an .EXP file.

[0277] • All washing and staining procedures are carried out by the Affymetrix fluidics station with an attendant providing the appropriate solutions.

[0278] • The GeneChip® is washed, stained with steptavidin-phycoerythin dye and then washed again using low salt solutions.

[0279] • 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

[0280] The scanner and MAS 5 software generates an image file from a single GeneChip® called a .DAT file (see figure overleaf).

[0281] The .DAT file is then pre-processed prior to any statistical analysis.

[0282] Data pre-processing steps (prior to any statistical analysis) include:

[0283] • .DAT File Quality Control (QC).

[0284] • .CEL File Generation.

[0285] • Scaling and Normalization.

.DAT File Quality Control

[0286] 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.

[0287] 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

[0288] 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.

[0289] All .CEL files generated from the GeneChips® are subjected to specific quality metrics parameters.

[0290] 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 GeneChips®.

Analysis of GeneChip® Data

[0291] Two illustrative approaches to normalising data may be used:

[0292] • Affymetrix MAS 5 Algorithm.

[0293] • Robust Multi-chip Analysis (RMA) algorithm of Irizarry (Irizarray *et al.*, 2002, *Biostatistics* (in print)).

[0294] Those of skill in the art will recognise that many other approaches might be adopted, without materially affecting the invention.

Affymetrix MAS 5 Algorithm

[0295] .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.

[0296] 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.

[0297] 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.

[0298] 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

[0299] Median chip intensity was calculated using the Affymetrix MAS5 algorithm, but with a scale factor fixed at one.

RMA Algorithm

[0300] This algorithm quantifies the expression of a set of chips, rather than of a single chip. It estimates background intensities using a robust statistical model applied to perfect match probe data. It does not make use of mis-match probe data. Following implicit background correction, chips are processed using Quantile Quantile normalization (Rizarray *et al.*, 2002, *Biostatistics* (in print)).

DNA Extraction

[0301] 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.

[0302] Determination of DNA quantity and quality is necessary prior to proceeding and can be achieved using a spectrophotometer or agarose gel electrophoresis.

Genotyping Analysis

[0303] 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). An illustrative method for genotyping using allele-specific PCR is described here.

Primer Design

[0304] 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

[0305] 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

[0306] 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. Thus, homozygotes and heterozygotes can be determined.

Real-Time PCR Data Generation

[0307] 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:

[0308] 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.

[0309] 2. Primers should be 15-30 bases in length.

[0310] 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.

[0311] 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.

[0312] 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.

[0313] 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).

[0314] 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.

[0315] 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),

[0316] 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,

[0317] 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.

[0318] (See also the general principles of PCR Primer Design by InVitroGen.)

General Method:

[0319] 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 normalizer,

[0320] 2. Multiplex PCR will only work properly if the control primers are limiting (ABI control reagents do not have their primers limited),

[0321] 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,

[0322] 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,

[0323] 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:

[0324] 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.

[0325] 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).

[0326] 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:

[0327] 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]

Reagents	Volume
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

* If a PDAR is used, 2.5 μL of primer + probe mix used.

[0328] 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:

[0329] Reverse transcription (by MuLV) 48° C for 30 min.

[0330] AmpliTaq activation 95° C for 10 min.

[0331] 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.)

[0332] 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:

[0333] Make sure the following before starting a run:

[0334] 1. Cycle parameters are correct for the run.

[0335] 2. Choice of spectral compensation is correct (*off* for singleplex, *on* for multiplex reactions).

[0336] 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.

[0337] 4. No Template Control is labeled as such (for accurate ΔRn calculations).

[0338] 5. The choice of dye component should be made correctly before data analysis.

[0339] 6. You must save the run before it starts by giving it a name (not leaving as untitled). Also at the end of the run, first save the data before starting to analyze.

[0340] 7. 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.

[0341] 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.)

[0342] 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:

[0343] At the end of each reaction, the recorded fluorescence intensity is used for the following calculations:

[0344] 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.

[0345] There are three illustrative methods to quantitate the amount of template:

[0346] 1. Absolute standard method: In this method, a known amount of standard such as in vitro translated RNA (cRNA) is used.

[0347] 2. Relative standard: Known amounts of the target nucleic acid are included in the assay design in each run,

[0348] 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: .

[0349] 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 (normalizer). 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.

[0350] 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.

[0351] As long as the target and normalizer have similar dynamic ranges, the comparative C_T method ($\Delta\Delta C_T$ method) is the most practical method. It is expected that the normalizer 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 normalizer:

[0352] $\Delta C_T = C_T$ (target) - C_T (normalizer)

[0353] This value is calculated for each sample to be quantitated (unless, the target is expressed at a higher level than the normalizer, 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:

[0354] comparative expression level = $2^{-\Delta\Delta CT}$

[0355] 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).

[0356] 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.

[0357] Recommendations on Procedures:

[0358] 1. Use positive-displacement pipettes to avoid inaccuracies in pipetting,

[0359] 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.

[0360] 3. The optimal concentrations of the reagents are as follows:

[0361] 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.

[0362] 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.

[0363] 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.

[0364] iv. The optimal probe concentration is 50-200 nM, and the primer concentration is 100-900 nM. Ideally, each primer pair should be optimized 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.

[0365] 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° C for Polymerase activation, and 40 cycles of 15 sec at 95° C (denaturation) and 1 min at 60° 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° C (reverse transcription with conventional reverse transcriptase) and 5 min at 95° C (reverse transcriptase inactivation).

[0366] 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).

[0367] 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.

[0368] 7. The dynamic range of a primer/probe system and its normalizer 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 normalizer real-time RT-PCRs for the same range of total RNA concentrations.

[0369] 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.

[0370] 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.

[0371] 10. TaqMan Universal PCR master mix should be stored at 2 to 8° C (not at –20° C).

[0372] 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.

[0373] 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.

[0374] 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).

[0375] 14. It is ideal to run duplicates to control pipetting errors but this inevitably increases the cost.

[0376] 15. If multiplexing, the spectral compensation option (in Advanced Options) should be checked before the run.

[0377] 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.

[0378] 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).

[0379] 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.

[0380] 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).

[0381] 20. A small ΔRn value (or greater than expected C_T value) indicates either poor PCR efficiency or low copy number of the target.

[0382] 21. A standard deviation >0.16 for C_T value indicates inaccurate pipetting.

[0383] 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.

[0384] 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.

[0385] 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.

[0386] 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.

EXAMPLE 2

IDENTIFICATION OF DIAGNOSTIC MARKER GENES AND PRIORITY RANKING OF GENES

[0387] For experimental groups, differences in gene expression between animals before and after experimental induction of endotoxaemia were analysed using the empirical Bayes approach of Lonnstedt and Speed (Lonnstedt and Speed, 2002, *Statistica Sinica* **12**: 31–46).

[0388] The objectives were to: (a) identify changes in gene expression during the acute endotoxaemic phase of disease, and (b) evaluate the diagnostic potential of these changes, for detecting enodtoxaemia.

[0389] Comparison between dosed and control horses involved some information which is within horses (i.e. some information is available from the longitudinal comparison of horses which were used both as controls and as treated animals), and some information which is between horses (involving cross-sectional comparisons between horses which were dosed and horses which were not). In addition, some planed samples were not available. The result is an unbalanced, non-orthogonal mixed effects study.

[0390] Gene expression data were generated, and quality metrics were generated for each chip. Only chips providing high quality data and passing all quality metrics were used in subsequent analyses. The chips were then processed using the RMA (Robust Multichip Analysis) algorithm as implemented in the R Bioconductor project. Following calculation of expression measures, the distribution of the chips was compared using Box and Whisker plots, kernel density estimates and MA plots. Outliers were removed from further analyses.

[0391] Results obtained were corroborated using Microarray Analysis Software 5.0 (provided by Affymetrix) and a list of "housekeeping" genes to scale the data. Housekeeping genes were determined *a priori* by identifying those genes that vary the least in gene expression across healthy horses of various breed, age, sex, and geographical location, and across horses with various diseases.

[0392] Positive horses at each time point were compared with all horses at time zero, and negative horses at the time point concerned. For example, horses which were positive at 24 hours were compared with all horses at day 0, and negative horses at 24 hours. Two

approaches were used for each comparison: univariate comparisons made gene at a time, and multivariate comparisons using the entire gene set. For the univariate comparisons, the analysis of each gene was made on a linear mixed model, in which horse was a random effect and time (time 0 vs current time) and status (control or induced) were fixed effects. Individual p values were adjusted using the Holm step down procedure (Holm, S. 1979, *Scandinavian Journal of Statistics* 6: 65–70) to provide strong control of the Family-Wise Error Rate (FWER). For multivariate analyses, a composite strategy was employed involving, reduced space linear discriminate analysis, support vector machines and classification tree techniques. Genes that showed statistically significant differences before and after experimental induction of endotoxaemia were tabulated for each day post dosing.

[0393] A list of genes ranked by p value for comparisons made between hours 0 and 24, 48 and 72 post-dosing is shown in Table 5. This analysis is based on two-group comparisons (Hour 0 versus hours 24, 48, and 72) with p Values adjusted using Holm's and the FDR method. Results are based on the full outcome from the empirical Bayes method.

[0394] Using linear mixed models, and at 24 hours, 159 genes were statistically significant when Holm's correction was applied and 995 genes following FDR adjustment. Using classification and regression trees, 829 of the 3105 genes on the GeneChip™ separated the groups perfectly with a p value of 0.002.

[0395] Using linear mixed models, and at 72 hours, no genes were statistically significant when Holm's correction was applied and 62 genes following FDR adjustment. Using classification and regression trees, 125 of the 3105 genes on the GeneChip™ separated the groups perfectly with a p value of 0.001.

[0396] Using linear mixed models, and at 120 hours, no genes were statistically significant when either Holm's correction or FDR adjustment were applied. Using classification and regression trees, 7 of the 3105 genes on the GeneChip™ separated the groups perfectly with a p value of 0.019.

[0397] The genes listed in Table 5 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 significant genes ($p<0.05$) is based on increasing t value for the first time point (24 hours) followed by ranking on increasing t value at 72 hours. Note, some genes are significant for both 24 and 72 hours, others are significant for either 24 or 72 hours.

EXAMPLE 3

DEMONSTRATION OF DIAGNOSTIC POTENTIAL TO DETERMINE ENDOTOXAEMIA

[0398] In addition, 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. 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.

[0399] Cross-validated discriminant function scores were used to estimate a receiver operator curve. The receiver operator curve was calculated by moving a critical threshold along the axis of the discriminant function scores. Both raw empirical ROCs were calculated, and smoothed ROCs using Lloyd's method (Lloyd, C.J. 1998, *Journal of the American Statistical Association* **93**: 1356–1364). Curves were calculated for the comparison of clinically normal and clinically affected animals. Separate curves were calculated, using gene expression at each day post-inoculation. The area under the receiver operator curve was calculated by the trapezoidal rule, applied to both the empirical ROC and the smoothed ROC.

[0400] The ROC curve provides a useful summary of the diagnostic potential of an assay. A perfect diagnostic assay has an ROC curve which is a horizontal line passing through the point with sensitivity and specificity both equal to one. The area under the ROC curve for such a perfect diagnostic is 1. A useless diagnostic assay has a ROC curve which is given by a 45 degree line through the origin. The area for such an uninformative diagnostic is 0.5.

[0401] The ROC curves for the analysis based on comparisons between time point 0 and time points 24 hours and 72 hours are presented Figures 1-2, respectively. The diagnostic capability is very high.

EXAMPLE 4

PREDICTIVE GENE SETS

[0402] Although about 180 genes have been identified as having diagnostic potential, a much fewer number are generally required for acceptable diagnostic performance.

[0403] Table 6 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 (Figueirodo M.A. Adeaptive Sparseness for Supervised Learning).

[0404] Table 7 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 endotoxemia marker genes can be made.

[0405] Table 8 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 endotoxemia marker genes can be made.

[0406] Table 9 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 endotoxemia marker genes can be made.

[0407] Table 10 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 endotoxemia marker genes can be made.

[0408] Table 11 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 endotoxemia marker genes can be made.

[0409] Table 12 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 endotoxemia marker genes can be made.

[0410] Table 13 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 endotoxemia marker genes can be made.

[0411] Table 14 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 endotoxemia marker genes can be made.

[0412] Table 15 shows the cross-validated classification success obtained from a linear discriminant analysis based on 12 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 endotoxemia marker genes can be made.

[0413] Table 16 shows the cross-validated classification success obtained from a linear discriminant analysis based on 13 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 endotoxemia marker genes can be made.

[0414] Further numbers of genes introduced noise (and subsequently lower specificity and sensitivity) through observational overload compared to the number of variables.

[0415] The genes listed in Table 5 are ranked in order of their t statistic - 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.

EXAMPLE 5

DEMONSTRATION OF SPECIFICITY

[0416] The specificity of the endotoxemia signature was examined by training a classifier on the trial data only and running the classifier over a large gene expression dataset of over 850 GeneChips®. Gene expression results in the database were obtained from samples from horses with various diseases and conditions including; clinical, induced acute and chronic EPM, herpes virus infection, degenerative osteoarthritis, stress, *Rhodococcus* infection, endotoxemia, laminitis, gastric ulcer syndrome, animals in athletic training and clinically normal animals.

[0417] Three classifiers were generated. All were based on the comparison of positives at 24 hours with all horses at time zero, and negative horses at 24 hours. The first used all the genes on the GeneChip™. The second used only those genes that were statistically significant (Holm's adjusted p value <0.05). The third was based on all of the genes except for 45 that had been identified as being involved in at least one other gene signature for disease. The latter was the most specific. It was able to identify all eight endotoxemic horses in the

database. It also identified five other horses, one with severe gastritis, one with botulism, another with Wobbler syndrome and two others with an unknown diagnosis.

[0418] Using this method and a gene signature of 159 genes, a specificity of 99% for endotoxemia was obtained from a population sample size of over 850.

EXAMPLE 7

GENE ONTOLOGY

[0419] 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. Table 17 lists and groups the genes based on these criteria. See also Table 1, which contains sequence information for each gene.

[0420] The disclosure of every patent, patent application, and publication cited herein is hereby incorporated herein by reference in its entirety.

[0421] 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.

[0422] 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:
WBC001D02.bFSP_20012908.abd	Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12).	1 GCGGGCAAGGCGGGCGGAGCGCACTGGAACTCAAGGGGGCGCACAGCGGCGCGCTCGCAC 61 CGCTCGGCTCCGCGCGGCTCTAGGAGGTGGCGGCGGTGGCGGTGGCGGCGGTGGCGGCGG 121 CGGCGGCGGCGGGGGCGCAGGGCTGAGCGAGCGTCCGGGTTCCGGGGCTCCGGGGAAGGCG 181 GTTGCAGCTCCTGAGTGCAGCGCGGCTTCCTGCCACTGTCCCGGCCCGGCCACCTCTCTG 241 TCATGGCTCTGGCGGACAGCACACGTGGATTACCCAACGGGGGCGGCGGCGGGGGCGGCA 301 GTGGCTCCTCGTCGTCCTCCGCGGAGCCACCGCTCTTCCCCGACATCGTGGAGCTGAACG 361 TGGGGGGCCAGGTGTACGTGACCCGGCGCTGCACGGTGGTGTCGGTGCCCGACTCGCTGC 421 TCTGGCGCATGTTCACGCAGCAGCAGCCGCAGGAGCTGGCCCGGGACAGCAAAGGCCGCT 481 TCTTTCTGGACCGGGACGGCTTCCTCTTCCGCTACATCCTGGATTACCTGCGGGACTTGC 541 AGCTCGTGCTGCCCGACTACTTCCCCGAGCGCAGCCGGCTGCAGCGCGAGGCCGAGTACT 601 TCGAGCTGCCAGAGCTCGTGCGCCGCCTCGGGGCGCCCCAGCAGCCCGGCCCGGGGCCGC 661 CGCCCTCGCGGCGCGGGGTGCACAAGGAGGGCTCGCTGGGTGACGAGCTGCTGCCGCTTG 721 GCTACTCGGAGCCCGAACAGCAGGAGGGCGCCTCTGCCGGGGCGCCGTCGCCCACGCTGG 781 AGCTGGCTAGCCGCAGTCCGTCCGGGGGCGCGGCGGGCCCGCTGCTCACGCCGTCCCAGT 841 CGCTGGACGGCAGCCGGCGCTCGGGCTACATCACCATCGGCTACCGCGGCTCCTACACCA 901 TCGGGCGGGACGCGCAGGCGGACGCCAAGTTCCGGCGAGTGGCGCGCATCACCGTTTGCG 961 GAAAGACGTCGCTGGCCAAGGAGGTGTTTGGGGACACCCTGAACGAAAGCCGGGACCCCG 1021 ACCGTCCCCCGGAGCGCTACACCTCGCGCTATTACCTCAAGTTCAACTTCCTGGAGCAGG 1081 CCTTCGACAAGCTGTCCGAGTCGGGCTTCCACATGGTGGCGTGCAGCTCCACGGGCACCT 1141 GCGCCTTTGCCAGCAGCACCGACCAGAGCGAGGACAAGATCTGGACCAGCTACACCGAGT 1201 ACGTCTTCTGCAGGGAGTGAGCTCCCCAGACCCCCTCGCCACTCCAGCGCCCAGTCCTTC 1261 TCCTGCCCGAGAGATGATTACAGAGCCTCTTGTCCCACCTTTGTCCCCTGGCTGCTGCCC 1321 TCCCATTCTCCCCCTCCAGTAGTAGCTGGGTGAGACCTGTCCGCCCACCTTCCCTCCACT 1381 ACAGAACCTGCAGCCGCAAATCCTCTGGGCTGCTTCGTCTTCTTTGGACCTCCTGAACCG 1441 AGAGAACCCAGAGGAACCCCCACCCCACCCCCACCTACCACTCCATGCTTTCTCTACTCC 1501 CTGCCTCAAACCACCCCTCCCCCAGATGGTACTTCAGTTTGGATCTATTGGGGGAGTGTG 1561 GCCACAGACCGGGGGATGATTGAATTGTTCAGAACCTGATTGGACCGTGTCCAATGTGCG 1621 GAAGATTTCCTTGAAATCTTCTCAAGCTCTTATGACTCACTGGGGGTTTAAGAGATCAGG 1681 ATTGGTTCCACTGTCTGGGGTTAGTGTTTTACAAGGTCATTACACAGTCTTTTTGACCTC 1741 TTTTGAAGGTAGAGTTTTAGAAGGCTGGATGGAAGATTCTGAGCCTGGAATTAGGACCCC 1801 ATGGAGGCAGTTCAGTAACTAAACTAATAAAGTTTTGAAAAGTTACACGTAAAGTAGAAG 1861 AATCTAGTGCGTGGGACAGTAAAGGATCCTTTCTCGTACAGAATAAAAGGTCTCAGCCTG 1921 TAGCTTAAACTTATAGAAAGTGATCCGCCTGCCTGCAGAGGCGCCCTTTTCAGCTGCTGC 1981 TCGCCAGAAGCCCTTGATTCCACTGGTTGACATGGCAGCAGTTACTGGCAAGAGGGAGAA 2041 AGGACGCTGCCGCCTAAGAGTGCAAGGCTGCTCAGGTCTCCAAGCGCCGTAGGAGGTCAC 2101 CTGGCAGTGACTGTAGGGAGCTGGGTCATAGTGCACGTCGTGGGTATTAGGAAAGCCTGT 2161 ATTCTTTCAATGAATGTCAGTAGGACCTTCCTTTAGCTGTAAGACTTGGTGGGCGGGGTG 2221 GGGTGGGGAGGGAGGAAAGGGTAGGAAGGGTGGGAAGGGAGAAGCAGACATAGTCATTTA	SEQ ID NO:1

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2281 TGATTTGAAAGTTGGAAGTTTGTACCATCTGTTTGAGTATATGCACATTTAAAAAATATC	
		2341 ATATAGTAAATGCAAACATGCCAAGTATTTTATAAAGATTAATAACAGACCTACTCTTAA	
		2401 CTGGCAGTTTGAACTAACTGTGTTGAGTCCTAAACTTAGAAGTTGCTGATACTTACATAA	
		2461 CCTAACCAAAGAGCTATCCAGTAGGGTTTTAGTTTGTGAACTTTATTTTCCTGTTGATTA	
		2521 TAAATCCTGATTTTTAAGATCTATTTACTTGAGCAAAATATGTTTGATTTCGGTTAGTTA	
		2581 GACTTAAGATCTCTTATTAAAAGTCCTTACTTTCTCCAAGCCCAGTCAATGTTGACTTCT	
		2641 GGGCAAACCTGAAAATGCCACTTCTTTCATGCAGATTCTTTGAAGTTAAGATGGAATCTT	
		2701 TTCGAGTGATAGAGCTGCAGAGATATAGAAGCTCCATGGGCTGCCCATCTGTAGATAGCT	
		2761 GTAAAATGGAATATTTTTAATTGAAGGCAAAAAAGTGCTTAAAAGTGAGCTGAGCAATAA	
		2821 AATGGTCCAATAATAGGTAAATGCAACAGAAACAGAAGGAGACCTGGTTGCCTTATACCT	
		2881 TTACGCGAACACGGAATAAACTCCCACTGCACATCCTGTCTACACCATAAGTGGAGGGAA	
		2941 ATAAACCTCGTCATGCTCCATGCTGTGAGGCTCCTTTGGATATTCTGTGATGACCGAGAA	
		3001 GCCTATTTTGTTTTGTTTTCAACATCTTTATCCGAAGTACGTTTTTTAAAGATTTTGTAAG	
		3061 AGTCGTTTTTCAGTGTTTAAATTAGCGCTATTTTTCCTTCTTTTTAAAATGAATCTTGTA	
		3121 CTGTATCTTACTATGTCTGTAACAGGTGTTAAGAATTGAAACAGTTTTATTCTTAGATTC	
		3181 ATGCGATCCAGTCTGTATATACCATATATAAACATTTTACATGAATCATTTAGTTTTTTA	
		3241 ATTCATTTACTAATGCTATATAAAATTTCCTATATTACCCCAGTAATTTGCATCAGCTGGTT	
		3301 TATATACTAAAGCAACATGTTTTGATGAGTTTCTTACATCCTTATCGAGGAATTGGGTTA	
		3361 GGAAAAAATACATAATTGTAAAACTGAGTTTGCTGTAATTATACTTTTTTCTTGAGTATT	
		3421 AGTTGTATTACTAATCATATGTTGATTAACTGTCTACTTAAAGTCAAGGTACCTGTATTT	
		3481 TTAATCCACTAATTTTTTTTTAGTTGGGAAATAGATTTCAAGTCTTTTATTAGACTAACA	
		3541 TTTTTTGAGAAGTAAAATTGACTTTATATACAAAGCCTGTAATTTTAGGCGAAATGGAAG	
		3601 CAGAAATCTAGGAAGTTGTGCTTGCTTGTATGGTCTCAGACTAAGTAATGCATCAGAATT	
		3661 CATCTGTTTGAAGCCTGAAATAATTTAGGACTCTGATTCACTGACCAAAAGTCAGTGTTG	
		3721 CAGAGATTTCTCTACCCCGTATGGTATTTGTTAGATTGTTCAACAGGAAGCACATGATT	
		3781 GAGAACATCTTGGGACAGACCAAAACCACTGACAGATGGCAAGGCTCGGCGATTCTGATT	
		3841 TCCCTTCTCAAATCTGCTCAACTCCAAGAGTCTTGAGAAACTGCTAAAATTTTGCCTCTG	
		3901 TCACTCAAGTCTTCACAAATGTTATCTTGTAAACCTTTGAGGTGAACTATTCCACTGTCTT	
		3961 GTACATAGGCATCTTATTCACTGCACCCTGTCACACCCAGCACCCCCCGCCCCGCACATT	
		4021 ATTTGAAAGACTGGGAATTTAATGGTTAGGGACAGTAAATCTACTTCTTTTTCCAGGGAC	
		4081 GACTGTCCCCTCTAAAGTTAAAGTCAATACAAGAAAACTGTCTATTTTTAGCCTAAAGTA	
		4141 AAGGCTGTGAAGAAAATTCATTTTACATTGGGTAGACAGTAAAAAACACAAGTAAAATACT	
		4201 TGACATGAGCACCTTTAGATCCCTTCCCCTCCCATGGGCTTTGGGCCACAGAATGAACCTT	
		4261 TGAGGCCTGTAAAGTGGATTGTAATTTCCTATAAGCTGTAATAGTGGAGGTATTGTGGGT	
		4321 TCATTTGAGTAAGCCCTCCAAGATACCATTCAAATAACCTGGGAGAAGTCTCATAAATTA	
		4381 TTCAGATAATTATCACTGCATGAATCTGATTCAGAGGCATGCATTTACATATGTTGCCCT	
		4441 AATTACCATTTGATGATCATAAATACAACTGAATGACATTGGACTTTTAGTAACAAACTT	
		4501 AATTTTTAAAAAAGTGTAGACAATGGTGGTTAAAAAAAAAAAAAACAGGTGCCAGGTTCT	
		4561 GTGTGTTTGCACCAAGTAATTGACATGTTTTTTGTTTAATACATGTGGACCATGAACAGT	
		4621 ATTCATTCTACTTTTTCAAATGATATGCTGTAGAAAATATTCCTTGAAGATGTGAGATTT	
		4681 AAAAATTTTCCCTTTCAATGTTGTTTAATTGTATTTCTTACTTGGTTTTTTTGATTGA	
		4741 TAGCACAGTGATAAATCATAATACTAGACAAAATTGTCTTCTCTTTCAAACCAGAGCCAT	
		4801 ATATATGTCTGTATATATGGGACCTACTGCTTCTCTGAGGAAATGCATAATCTGTTAATA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		4861 TCAGACAAAATGAGCAATTGGCAGTGCTCATAATATTCCAATTTTTATTGGAATTTTC 4921 GATGGAATGTTATTTCATATAAAGCCATGTAAGGTGAAACTTTGATAACTTTTTACTCTTC 4981 AAGTTAGGGTAAATTCTGATCCCAATATTCAATTCATTTGTGTACTCCCACATGCAAAATG 5041 CTAAATTACAATGCAGACATTAAGAAAAAGTATTGACTGGAGGGGTTGAATTCCTTGAGA 5101 ATTTATTTTATAGTCTAAATCACAAATACTTTACTCAATTTAGTTTTTAAAATAGTAAAC 5161 TGAATATTTTTGTGTTAAGCCTATCAGAGTCAATCCTTCGTTTGGAATTGTTTTCCTGTT 5221 TTTCCTTACTATAAATCATTTTAAAAACTGAATTCATTTTCTTAGATGGCATAAGTCTGTC 5281 TCTTGAGAAATAAGTAAAATACTCCTATTTTCAGTATCTGTAGCACCTGAAATAGGTCTT 5341 TGTATAGCCAGAAACAAGTTATGTTGAAGTTAGCTTTTCTTTGTCAACAGTTTTGGACAA 5401 TAAAAATCTGAAAGTATTAACACTTGATTTTCTACTGGGGCCCTTCAACTTGGTTGGAA 5461 GAAATTCAACCAGAATATCTACATTAGAGTATAATCATGTGTGGTAGGAAGATGGACTAG 5521 TTAATCAAGATTTGTTGTCACTTAAATTTTTTGTGATTTTTTTCCAAGCCAGTTTTTTA 5581 AATTCTAAATGTGTTTTGAGGTATGGGTACATTAATTGTAATGTAAACTATTATACAACT 5641 GTTTTTGCGACTTTATAGGCAGGTAAATTTTGCTATTACTATTGAATACAAATGACAATT 5701 CATTTATGACCACTCAAACAGCGTTAGTAACCATTTAGTGACAAGGATTAAAACATCCA 5761 TCTGGATGTTAATTTTGAAGATGTAAATTATATGTTGTTTAAATTTTTCCAGGCATCTGA 5821 AAACCTTATCTGCTAGACAATGTAAGATTCACACAGAGTTATCTGGGATTCTGATTTTTT 5881 AAATAGTACATATCATTAAACCATTTTCTCTAAATGTAAGAAGAGCAGAAAAAATCTTAT 5941 AAGATTATCAGATTTTTCTAATGACACAGAAATGTAAGAAAAAAATCCCTTTATATTGAA 6001 AAAAGATGCAGTCAAAGTCTTTTCAGACATGCCCAAACTTTGAGAATTCCTTCACCATC 6061 TAATGCTATAAAGATTTTTGTTCTTCCTGTTCACAACCAGTTGTATAACAGAAATACTAG 6121 CTACTGTTTTCCTTCCTGTGTGTGAAGTAATGAATCATTGATTATGTGACTTGTTATGTA 6181 TTCAATTAAACACTAAAGAATAAAACATTCACTCCTTT 1 M A L A D S S T R G L P N G G G G G G G S 1 ATGGCTCTGGCGGACAGCACACGTGGATTACCCAACGGGGGCGGCGGCGGGGGCGGCAGT 21 G S S S S S A E P P P L F P D D I V E L N V 61 GGCTCCTCGTCGTCCTCCGCGGAGCCACCGCTCTTCCCCGACATCGTGGAGCTGAACGTG 41 G G Q V Y V T R R C T V V S V P D S L L 121 GGGGGCCAGGTGTACGTGACCCGGCGCTGCACGGTGGTGTCGGTGCCCGACTCGCTGCTC 61 W R M F T Q Q Q P Q E L A R D S K G R F 181 TGGCGCATGTTCACGCAGCAGCCAGCCGCAGGAGCTGGCCCGGGACAGCAAAGGCCGCTTC 81 F L D R D G F L F R Y I L D Y L R D L Q 241 TTTCTGGACCGGGACGGCTTCCTCTTCCGCTACATCCTGGATTACCTGCGGGACTTGCAG 101 L V L P D Y F P E R S R L Q R E A E Y F 301 CTCGTGCTGCCCGACTACTTCCCCGAGCGCAGCCGGCTGCAGCGCGAGGCCGAGTACTTC 121 E L P E L V R R L G A P Q Q P G P G P P	SEQ ID NO:2

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		361 GAGCTGCCAGAGCTCGTGCGCCGCCTCGGGGCGCCCCAGCAGCCCGGCCCGGGGCCGCCG	
		141 P S R R G V H K E G S L G D E L L P L G 421 CCCTCGCGGCGCGGGGTGCACAAGGAGGGCTCGCTGGGTGACGAGCTGCTGCCGCTTGGC	
		161 Y S E P E Q Q E G A S A G A P S P T L E 481 TACTCGGAGCCCGAACAGCAGGAGGGCGCCTCTGCCGGGGCGCCGTCGCCCACGCTGGAG	
		181 L A S R S P S G G A A G P L L T P S Q S 541 CTGGCTAGCCGCAGTCCGTCCGGGGGCGCGGCCGCCTGCTCACGCCGTCCCAGTCG	
		201 L D G S R R S G Y I T I G Y R G S Y T I 601 CTGGACGGCAGCCGGCGCTCGGGCTACATCACCATCGGCTACCGCGGCTCCTACACCATC	
		221 G R D A Q A D A K F R R V A R I T V C G 661 GGGCGGGACGCGCAGGCGGACGCCAAGTTCCGGCGAGTGGCGCGCATCACCGTTTGCGGA	
		241 K T S L A K E V F G D T L N E S R D P D 721 AAGACGTCGCTGGCCAAGGAGGTGTTTGGGGACACCCTGAACGAAGCCGGGACCCCGAC	
		261 R P P E R Y T S R Y Y L K F N F L E Q A 781 CGTCCCCCGGAGCGCTACACCTCGCGCTATTACCTCAAGTTCAACTTCCTGGAGCAGGCC	
		281 F D K L S E S G F H M V A C S S T G T C 841 TTCGACAAGCTGTCCGAGTCGGGCTTCCACATGGTGGCGTGCAGCTCCACGGGCACCTGC	
		301 A F A S S T D Q S E D K I W T S Y T E Y 901 GCCTTTGCCAGCAGCACCGACCAGAGCGAGGACACAAGATCTGGACCAGCTACACCGAGTAC	
		321 V F C R E - 961 GTCTTCTGCCAGGGAGTGA	
WBC001E10.bFSP_20012908.abd	No Homology	1 GACTGGGAACAGCAAGTGCAAAGTTCCTGTGGCAGAAATGTGCCTGGCAAGGAGGCCTG 61 CATGGCTGGAGCATTGTGAGCTGGTGGGAGAATGGAGAACAGGAAGAGATGATGGGGTAC 121 CTCGCGTCTTCATCGGTAAAGACTGTATAGGTGGATGCACTGACCTACTCAACATGCATC 181 AGAGTGGGCAGCTGTTGACACGGCTAAAGCAAATTGGAGCTCTAGAATAATTACAGAGCT 241 GATCCCAGACTGATGTCCCCCTGAGAGCTGAATAGCATTGCAATGATGACAGCACTTCCT 301 GGTGGATGGATCAGGGGCTACCTTTACCCAGCTACAGCAGCTGTTTACTTCTGAAATATG 361 TTACCAAAAAAGGAGGGGTGGGGGTTGGCAAAAATAGCTTTTTCTTTTTTGATTTAGTG 421 TTAAAAGTGGCTCAACTTGCCCCAAATCACAGATCTGAGAAGTTGATGGATGTCTTGGG 481 TTTCTTCTGGATCGGCCCTTTGGTTCCAAAAGACCGTGACAGTCATGGCCTAGAATTCA 541 CTCACTGACTCAAAAGATGTTCTCTCTTTGGCACATGTTTCTTATGATTGTCCTCCAT	SEQ ID NO:3

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		601 GCGCCGGGCCTCGTCTACCTCTAAGCCAGTGTTTCGCAACCAAGTTTATCCCAAGCCCCT 661 CAGGATGAATCTGTAGTTGGTTTTCTGCTACTACCTGAAAATTATTTGTTGAGTTTGGC 721 TTTATGGAGTTTGTACT	SEQ ID NO:4
		1 GCATGTGTCTCCCTGGTTACCATCCTCACTCCACCCCACTCCTATCTTGAGAATCGTTTG 61 CTCTGAAACAGTGTTCTCAACCTTGACAAATTCACAGCTCTCACAGGAAATGTTCAACAG 121 TTAAGAAATTGGAGAAGTGAATTAAGAAATGAGGGCCTGAGGGCCCCATTTGAGAAAGT 181 CCGCAGGAAACATTAAGCACTGTTGGCCTCCTGGTGCCCAGTGATCGGAGGTCCAGGTGG 241 AGATGCCGTGATCATCTCTTGCCTAAGATGCTCATCCAGGTCATCCTGAACAAGTATGTG 301 TTAATTTGCTTAGATTATGAACCAAAGTAAAACATGAAATTTAAAACGTTATCACAGAAA 361 ACTTACAACTCCCTCCCCCAAGGGTATGTCTGTGAAAGTAGCCAAATTTAAGAAACACGG 421 TCCTAAATTATTTTCTCTCCTCTTTTTCCCTACTCTCTGCAGTCTTTAGGGT 481 CTGTGATGTTTGTTGTTCTAGCATTGCAAGAGTAAGTTAATTTCCTTCTGCAGTCTTTAGGGT 541 GAATGTTAATTTCTTTTCTAATAAAGAAGTACCCAGAGATGAAAAAAAAAAAAAAAAAA	SEQ ID NO:5
WBC001F10.bFSP_20012908.abd	No Homology	1 CTTTTTCAAAATAGGTCTCTAGGAAAACCAGCAGAACATTAGCCTGTGCAGAGCCATCG 61 TTTGGGAGCACACTCTTCCGTTACGCTTGGCACGCAGATCTCCCCTGTGGTGGGATTTCT 121 TTCTTTTTTGTTGTTTTTCCTTTTGTTTCAAGGGGGTACTTCCCCCCTATTTTCTCTTT 181 TCCCTTGATACAAGTTGTAGATGAAATAGGAGAAAGCCCTTGTTGCTATAGATGTGTGTG 241 CAGTCTGGCAGCCTTAAGCCCACCTGGGCACTTTTAGAAAAAAAACAAAAAACACCAAAA 301 AAAACAGTGTCATATGTATTAATGATCCAGGTGGTTTTTAGTCTTTCCTGATGATGGGGT 361 GTTCATGTTAGTTTCTTTTCTTGAAAACCCTATTTCAACATTAGGCAAAGTAGCTAAGAGC 421 CTTTTGTTTTGGTAAATTAGTGGGGAAATGGCATTTTAAGAGGACTCTCTTCTCAAAGAA 481 CTTAGCTGAGAGTCGAATTCTTCTCTTTTCCAGCTGATGAAGCTAAGTGGGTATCCCAGA 541 AATGTTTGTTTTTCTGAAGGGGAGTACTCCAGGCCATCACTGAAGCTGTCTCCAGGCAGAG 601 AGTTAGCACACTTTCTACACCTTGTAGAATTCTGGGCTGTAGCATTACTCTGATTTTCTG 661 TCTAATGAAGGCAGAGATGCTGGTAGTTTAAAATTTTTATTTTAGGACTTATCTGTACT 721 CTGAATTTTCA	SEQ ID NO:6
		1 TAAATGAAAATCTGTAGATTCTCTCCTCCCCTAATCCCAGAAAACGAAACCAAATAATGT 61 TTTTTGAAATTGTTTCTAGGATTTCAAAGTGAAAAATGATGGTACTATCCAAAATTCTTT 121 ATTTCAGAACATGACAATAGATTCCTTTAATGTAGGCTCAAGATCAAAACAGCATGTCCT 181 GTAAGCTCAGATAGACTCTGTTGACTCCAAGGGTTTTGATCAGTATCATAACAAACTTTT 241 CCCTTTGACATGCTCTGATTTTTGTTGTTGGGGGGAGGGCGTGTGTGTGTGCGTGTG 301 TGTGTGTGTGCGCGCGCGCGTGTGTGTGCGGTGTCCACCAGTATCAGTGCCTGCCTGCGT 361 TAGGAGAATTACATTCCTGGTTCTGTATGAGGAGAAGGGTGTATAAAGCAACATGAAACA 421 TTACCCCTCATTTTGTTTTTAAAGGACAAACTAATGTTAATTGTTCTCAGAACTGGATTTT 481 CTTCCTCAAAATTAAAAGTTTTCTTTTCTTTGGATTTAATGAAGTATTGCTAGCTGAAG 541 CCAGTTTGACATGGTGAGAGAGATGTCAGACTGATGAAAGGTGTGCAGCCTGATTTAAAA 601 CCAACCCCGAACCCTTTTAAAGAACATAAAACATATT	
WBC001F11.bFSP_20	Homo sapiens		

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
012908.abd	retinoblastoma-like 2 (p130), mRNA	1 AGCGGGCAGGCGCGGTGCGGGCGGCGACGGGCGGGCGCTTCGCCGTTTGAATGGCTGCG 61 GGCCCGGGCCCTCACCTCACCTGAGGTCCGGCCGCCCAGGGGTGCGCTATGCCGTCGGGA 121 GGTGACCAGTCGCCACCGCCCCCGCCTCCCCCTCCGGCGGCGGCAGCCTCGGATGAGGAG 181 GAGGAGGACGACGGCGAGGCGGAAGACGCCGCGCCGCCTGCCGAGTCGCCCACCCCTCAG 241 ATCCAGCAGCGGTTCGACGAGCTGTGCAGCCGCCTCAACATGGACGAGGCGGCGCGGGCC 301 GAGGCCTGGGACACGCTACCGCAGCATGAGCGAAAGCTACACGCTGGAGGGAAATGATCTT 361 CATTGGTTAGCATGTGCCTTATATGTGGCTTGCAGAAAATCTGTTCCAACTGTAAGCAAA 421 GGGACAGTGGAAGGAAACTATGTATCTTTAACTAGAATCCTGAAATGTTCAGAGCAGAGC 481 TTAATCGAATTTTTTAATAAGATGAAGAAGTGGGAAGACATGGCAAATCTACCCCCACAT 541 TTCAGAGAACGTACTGAGAGATTAGAAAGAAACTTCACTGTTTCTGCTGTAATTTTTAAG 601 AAATATGAACCCATTTTTCAGGACATCTTTAAATACCCTCAAGAGGAGCAACCTCGTCAG 661 CAGCGAGGAAGGAAACAGCGGCGACACAGCCCTGTACTGTGTCTGAAATTTTCCATTTTTGT 721 TGGGTGCTTTTTATATATGCAAAAGGTAATTTCCCCATGATTAGTGATGATTTGGTCAAT 781 TCTTATCACCTGCTGTGTGCTTTGGACTTAGTTTATGGAAATGCACTTCAGTGTTCT 841 AATCGTAAAGAACTTGTGAACCCTAATTTTAAAGGCTTATCTGAAGATTTTCATGCTAAA 901 GATTCTAAACCTTCCTCTGACCCCCCTTGTATCATTGAGAAACTGTGTTCCTTACATGAT 961 GGCCTAGTTTTGGAAGCAAAGGGGATAAAGGAACATTTCTGGAAACCCTATATTAGGAAA 1021 CTTTATGAAAAAAAGCTCCTTAGGGAAAAGAAGAAATCTCACTGGGTTCTAGAACCT 1081 GGGAACTTTGGAGAGAGTTTTAAAGCCATCAATAAGGCCTATGAGGAGTATGTTTTATCT 1141 GTTGGGAATTTAGATGAGCGGATATTTCTTGGAGAGGATGCTGAGGAGGAAATTGGGACT 1201 CTCTCAAGGTGTCTGAACGCTGGTTCAGGAACAGAGACTGCTGAAAGGGTGCAGATGAAA 1261 AACATCTTACAGCAGCATTTTGACAAGTCCAAAGCACTTAGAATCTCCACACCACTAACT 1321 GGTGTTAGTACATTAAGGAGAATAGCCCTTGTGTGACTCCAGTTTCTACAGCTACGCAT 1381 AGCTTGAGTCGTCTTCACACCATGCTGACAGGCCTCAGGAATGCACCAAGTGAGAAACTG 1441 GAACAGATTCTCAGGACATGTTCCAGAGATCCAACCCAGGCTATTGCTAACAGACTGAAA 1501 GAAATGTTTGAAATATATTCTCAGCATTTCCAGCCAGACGAGGATTTCAGTAATTGTGCT 1561 AAAGAAATTGCCAGCAAACATTTTCGTTTTGCGGAGATGCTTTACTATAAAGTATTAGAA 1621 TCTGTTATTGAGCAGGAACAAAAAAGACTAGGAGACATGGATTTATCTGGTATTCTGGAA 1681 CAAGATGCGTTCCACAGATCTCTCTTGGCCTGCTTGAGGTCGTCACTTTTTCTTAT 1741 AAGCCTCCTGGGAATTTTCCATTTATTACTGAAATATTTGATGTGCCTCTTTTATCATTTT 1801 TATAAGGTGATAGAAGTATTCATTAGAGCAGAAGATGGCCTTTGTAGAGAGGTGGTAAAA 1861 CACCTTAATCAGATTGAAGAACAGATCTTAGATCATTTGGCATGGAAACCAGAGTCTCCA 1921 CTCTGGGAAAAAATTAGAGACAATGAAAACAGAGTTCCTACATGTGAAGAGGTCATGCCA 1981 CCTCAGAACCTGGAAAGGGCAGATGAAATTTGCATTGCTGGCTCCCCTTTGACTCCCAGA 2041 AGGGTGACTGAAGTTCGTGCTGATACTGGAGGACTTGGAAGGAGCATATAACATCTCCAACC 2101 ACATTATACGATAGGTACAGCTCCCCACCAGCCAGCACACTACCAGAAGGCGGCTATTTGTT 2161 GAGAATGATAGCCCCCTCTGATGGAGGGACGCCTGGGCGCATGCCCCCCACAGCCCCTAGTC 2221 AATGCTGTCCCTGTGCAGAATGTATCTGGGGAGACTGTTTCTGTCACACCAGTTCCTGGA 2281 CAGACTTTGGTCACCATGGCAACCGCCACTGTCACAGCCAACAATGGGCAAACGGTAACC 2341 ATTCCTGTGCAAGGTATTGCCAATGAAAATGGAGGGATAACATTCTTCCCTGTCCAAGTC 2401 AATGTTGGGGGGCAGGCACAAGCTGTGACAGGCTCCATCCAGCCCCTCAGTGCTCAGGCC 2461 CTGGCTGGAAGTCTGAGCTCTCAACAGGTGACAGGAACAACTTTGCAAGTCCCTGGTCAA 2521 GTGGCCATTCAACAGATTTCCCCAGGTGGCCAACAGCAGAAGCAAGGCCAGTCTGTAACC	SEQ ID NO:7

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2581 AGCAGTAGTAATAGACCCAGGAAGACCAGCTCTTTATCGCTTTTCTTTAGAAAGGTATAC 2641 CATTTAGCAGCTGTCCGCCTTCGGGATCTCTGTGCCAAACTAGATATTTCAGATGAATTG 2701 AGGAAAAAAATCTGGACCTGCTTTGAATTCTCCATAATTCAGTGTCCTGAACTTATGATG 2761 GACAGACATCTGGACCAGTTATTAATGTGTGCCATTTATGTGATGGCAAAGGTCACAAAA 2821 GAAGATAAGTCCTTCCAGAACATTATGCGTTGTTATAGGACTCAGCCGCAGGCCCCGGAGC 2881 CAGGTGTATAGAAGTGTTTTGATAAAAGGAAAAAGAAAAAGAAGAAATTCTGGCAGCAGT 2941 GATAGCAGAAGCCATCAGAATTCTCCAACAGAACTAAACAAAGATAGAACCAGTAGAGAC 3001 TCCAGTCCAGTTATGAGGTCAAGCAGCACCTTGCCAGTTCCACAGCCCAGCAGTGCTCCT 3061 CCCACACCTACTCGCCTCACAGGTGCCAACAGTGACATGGAAGAAGAGGAGGGAGAC 3121 CTCATTCAGTTCTACAACAACATCTACATCAAACAGATTAAGACATTTGCCATGAAGTAC 3181 TCACAGGCAAATATGGATGCTCCTCCTCGCTCTCCCTATCCATTTGTAAGAACAGGCTCT 3241 CCTCGCCGAATACAGTTGTCTCAAAATCATCCTGTCTACATTTCCCCACATAAAAATGAA 3301 ACAATGCTTTCTCCTCGTGAAAAGATTTTCTACTTCAGCAACACAGTCCTTCAAAGAGA 3361 CTAAGAGAAATTAACAGTATGATCCGGACAGGAGAAACTCCAACCAAAAAGCGAGGGATT 3421 CTTTGGAAGACGGAAGTGAATCACCTGCAAAAAGAATTTGCCCAGAAAATCATTCTGCC 3481 TTACTGCGCCGTCTACAAGATGTAGCTAATGACCGAGGTTCCCACTGAGGTTAGTCCATG 3541 GTATTGAAACTGTCTTCTCACAAACTCTGTTTAGCAGCATCATTTAATGCATGCTCGATT 3601 ATGGGGCTCTTTCCCTTAATCCTTCCAGTATCCATAGGATATTCTGACTCATCCCAACTG 3661 CCTTTTTCCTACCATTCAGTGCTTGCCCTCAAGGCTGCTTAGAATCCAAACTTGGATTT 3721 TTGACTCTGGCAAAGCTTTTAGAAATACTGCAAGAAATGATGTGTACCCAAACGTGAGC 3781 ATAGGAGGCTTCTGTTGACGTACTCCAACAGAAGAACTGTTTTCAAGTTCATTCCTACCC 3841 GTTTGTGGTCACCTTTGGCCCTCACAAAAAGTAAACACAAAACTAGGTATTTTGTCCTA 3901 AAACACCTGGTAGGAGTGTGTGATTTTTTGCATTCCTGACAAAGGAGAGCACACCCAGGT 3961 TTGGAGGTCCTAGGTCATTAGCCCTCGTCTCCCGTTCCCTTTGTGCACATCTTCCCTCTC 4021 CCCATTCGGTGTGGTGCAGTGTGAAAAGTCCTTGATTGTTCGGGTGTGCAATGTCTGAGT 4081 GAACCTGTATAAGTGGAGGCACTTTAGGGCTGTAAAATGCATGATTTTTGTAACCCAGATT 4141 TTGCTGTATATTTGCGATGGCACTTTCTACAATGTGAACTTTATTAAGTATATAAACTTCT 4201 AGGCTAAACATTCAATATCTTCTTTGATGCTTTTGTACTTTTTTAAATTGTTAAAGCCC 4261 CAGTAGCCACCTTTTGGGCATATTTGAAATTCTCCAGTTTTTGATTATTAAGAGGGATCA 4321 GCTGGCTAAGTAAAGATTTTAAATCAAGTTGAATTAAGGGGATTAATAGGAAAATTATGA 4381 CCTCTTCCTTTAGGAGGCAGTTATCCNAAAGACATGTCTATTAAGGTGATATATTTTAA 4441 ATATCTTTGAGTGTGTTCCTGGCAGTTTAAGAAATAGTTGGAGAATTTAGGTTTTTATT 4501 AGTACACAGTACCATTTATACAAATTAGAAAATGTTATTTAACAGCTATTGAATTATCTA 4561 TATACACCTTTATTAATCGCTATTGTTCCAGCAGTTTTAACGTTGAACGAATAATCTTAT 4621 TAGGGAGAAAATTCAATTGTAAATTGAATCAGTATATAACAAAGTTACTAGGTAACTTCAC 4681 ATTGCTCTGAAAGAAATATGGAACTTACACTGTTCAATTAGAATAGTGTTCTGCAAAAAT 4741 ATTTATAAAACCTCTCAGATACTGCTACTGTAATTTTATATGAAAATAAGTGTATTTTTC 4801 AATAAAGCATTTATAAATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	SEQ ID NO:8
		1 M P S G G D Q S P P P P P P P P A A A A 1 ATGCCGTCGGGAGGTGACCAGTCGCCACCGCCCCCGCCTCCCCCTCCGGCGGCGGCAGCC 21 S D E E E E E D D G E E A E D A A P P A E S	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		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 GCGGCGCGGCCGAGGCCTGGACAGCTACCGCAGCATGAGCGAAAGCTACACGCTGGAG	
		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 ACTGTAAGCAAAGGACAGTGGAAGGAAACTATGTATCTTTAACTAGAATCCTGAAATGT	
		121 S E Q S L I E F F N K M K K W E D M A N 361 TCAGAGCCAGAGCTTAATCGAATTTTTTAATAAGATGAAGAAGTGGGAAGACATGGCAAAT	
		141 L P P H F R E R T E E R L E R N F T V S A 421 CTACCCCCACATTTCAGAGAACGTACTGAGAGATTAGAAGAAACTTCACTGTTTCTGCT	
		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 CAACCTCGTCAGCAGCGAGGAAGGAAACAGCGGCGACAGCCCTGTACTGTGTCTGAAATT	
		201 F H F C W V L F I Y A K G N F P M I S D 601 TTCCATTTTTGTTGGGTGCTTTTTATATATGCAAAAGGTAATTTCCCCATGATTAGTGAT	
		221 D L V N S Y H L L L C A L D L V Y G N A 661 GATTTGGTCAATTCTTATCACCTGCTGCTGTGTGCTTTGGACTTAGTTTATGGAAATGCA	
		241 L Q C S N R K E L V N P N F K G L S E D 721 CTTCAGTGTTCTAATCGTAAAGAACTTGTGAACCCTAATTTTAAGGCTTATCTGAGAT	
		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 TCCTTACATGATGGCCTAGTTTTGGAAGCAAAGGGATAAAGGAACATTTCTGGAAACCC	
		301 Y I R K L Y E K K L L K G K E E N L T G 901 TATATTAGGAAACTTTATGAAAAAAAGCTCCTTAAGGGAAAAGAAGAAAATCTCACTGGG	

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 AACAGACTGAAAGAAATGTTTGAAATATATTCTCAGCCATTCCAGCCAGACGAGGATTTC	
		481 S N C A K E I A S K H F R F A E M L Y Y 1441 AGTAATTGTGCTAAAGAAATTGCCAGCAAACATTTCGTTTGCGGAGATGCTTTACTAT	
		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 ACTTTTCTTATAAGCCTCCTGGGAATTTTCCATTTATTACTGAAATATTTGATGTGCCT	
		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	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		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	
		641 L T P R R V T E V R A D T G G L G R S I 1921 TTGACTCCCAGAAGGGTGACTGAAGTTCGTGCTGATACTGGAGGACTTGGAAGGAGCATA	
		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 CAGCCCCTAGTCAATGCTGTCCCTGTGCAGAATGTATCTGGGGAGACTGTTTCTGTCACA	
		721 P V P G Q T L V T M A T A T V T A N N G 2161 CCAGTTCCTGGACAGACTTTGGTCACCATGGCAACCGCCACTGTCACAGCCAACACAATGGG	
		741 Q T V T I P V Q G I A N E N G G I T F F 2221 CAAACGGTAACCATTCCTGTGCAAGGTATTGCCAATGAAATGGAGGGATAACATTCTTC	
		761 P V Q V N V G G Q A Q A V T G S I Q P L 2281 CCTGTCCAAGTCAATGTTGGGGGCAGGCACAAGCTGTGACAGGCTCCATCCAGCCCCTC	
		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	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		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	
		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 GCCATGAAGTACTCACAGGCAAATATGGATGCTCCTCCGCTCTCCCTATCCATTTGTA	
		1041 R T G S P R R I Q L S Q N H P V Y I S P	
		3121 AGAACAGGCTCTCCTCGCCGAATACAGTTGTCTCAAAATCATCCTGTCTACATTTCCCCA	
		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 CCTTCAAAGACTAAGAGAAATTAACAGTATGATCCGGACAGGAGAAACTCCAACCAAA	
		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	
WBC003D11.bFSP_20011309.abd	No Homology	1 GGACCTTTGGCACAAACACTGAAAAGAGTTATGTTGATAATCAGAAGTGATTGATGGAGC	SEQ ID NO:9
		61 AGAATTCCAGCGTTTCATGGAGAGTTGAAGTACATGATGACAAAACCCTTGGGAAAACCT	
		121 TCTAATTTCTTGGGACATTTCAAGGAAGCAACATCCCCCCTTTCTTCCAGGAACTTTTTTG	
		181 TGACTTGACTAGGACTCGCACTGCTCCCAAAGTTATCGCCATCCCACCTTGCTCTCCGTC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		241 TCCCATAAAATCTTGAGGGCCACCGGAGAGGAGGCGAATTTTAAATGTAGATCTCCTC 301 CCTTCCACAGCCAGTCTCAAACACACCTACTCAAGGTGTGGTCCATGGACCAGAAGCATG 361 AGCATCATTTTGTTAGAAAAGCAGCATCAAAGGTACCACCGCAGATCTTCGGAACCAGAA 421 CCTGCATTTTAACAAGATCCCCAGGGAATTTGTGTTGTACACAGGAGTGAATGTTCTGGC 481 ATATTCTAGAGTAATCTTTTGTTTTCCATGCTGACAGAAGAGCTTGTCTTTAAACTAGG 541 CAGGAAAACATATCCTCGACTTTGGACTTTGCATCTGCCATTCTCTCCTTCCTAGGACAA 601 CTTTCCTCANAATCGGACTAATTTCTACCCTCTCTTCGAGTCTCAGCATAGTCATCAATT 661 TCACCAGGAAGCATTCTCTGAATCTCTTGAAGTAGGATTAGGTGTCACCTCTGTGTCCC 721 TCTAAGGCTTCATGATTTCTAGCCTTGTGTGATCATTTCTTCTCTTCTTGAGTGTCTCCA 781 ACTGGACTGTGAGCTCCATAATTACAGGGAATGGCATTCAGTTGATTCTCCATAAATAAG 841 TTGAATGAATGAATGATTACTTTCCATTTTGAAGATGAAGAATTTGAGGC 1 ACCATTCCTGCTCTCACTATGGCTTGGCCTTGAGACTTGCTTTGGCTAATGGAATGTCAG 61 CAAGTGTGACTCAGACAGAGTGTGCATTCCTTCTTGCCCGTTACACGATAAGTCTCGCTT 121 GTTCTTGCACCCCTGCCTCCGCCATGAGAATGTGCCCAGGCTGAACTGCTGGAGGGATGT 181 GAAAAATGTATGGAAGACAGTTAAGTCATTCCATTATACCAGCTGAGGTTGTCCTTAATC 241 AGCCATCGGACCAACTTGTAGCTGACTACAGTCACATCCATGAGCCCAGTCAAGATCAGC 301 AGACCTGCCCGGGCAACCCAGACTCAGGAGCCACAATCAAGTACCATTATTTTAGGGCAC 361 AGAGTTTCAGGAGTGGTTTGTTAACGAAGTATTCTTGGTGGAAGTTGCTAACTGATTCAG 421 CAACCAATGGATTGTCAATGTTTTTGCATTTGACTGCAACAATTTGGAACATACAAGAGG 481 GTGATTCGCATCTTCATTTCCTCTTAGCTGTCAGGATCTGTAAATCTAAAACGCTTTGAA 541 TAAAGTTCTTTCTTCTGACAGAAAAAAAAAAA	SEQ ID NO:10
WBC004E04.bFSP_20011309.abd	Homo sapiens TRAF-interacting protein with a forkhead-associated domain, mRNA (cDNA clone MGC:20791 IMAGE:4763971)	1 gagaggacgt gctctgccag ccagtgggaa ggcaggccgc gcgcgcggga gcgcgggagg 61 atcggcggct cgcggtcact ggtccctggc tcggttcccc gcaccccggg gctcacactt 121 acccgcgcgg aggagcagcg gccgggtgtc cacccccatc ctgcgcccag tctcctcgat 181 tcccctcgct ctgagccggg agagccgaac agctgaagag agttcactga ctcccccagcc 241 ccaggtgggc cttgtgcaca tcatgaccag ttttgaagat gctgacacag aagagacagt 301 aacttgtctc cagatgacgg tttaccatcc tggccagttg cagtgtggaa tatttcagtc 361 aataagtttt 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 atctcccaaga tcactcttgc aagaaaacaa 721 ctggccacca cacaggccca taccggagta tggcacttac tcgctctgct cctcccaaag 781 cagttctccg acagaaatgg atgaaaatga gtcatgaaca cagaaagtct aagaggagaa 841 atatgatgga tgaagagctc tgtagatgct gtatagacac taaataagag ttgattaggg 901 tagtatatta tagtcatctg ttatgctgtg aaatttggaa ttcaaaattt tgaagtctgt 961 aaattgtgtt agtcattaac ttagtcacct gttgtattct ggatctacac aaaattatct 1021 taagtgctct tattaatctg tgaggattaa tatacaaaaa gtatcctttg agatgaagtc 1081 gtgttctcaa aataaggtta tattatttcc ttttctgct tgattttcat cttgtgtttt	SEQ ID NO:11

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1141 gctttgtttt tgtaaggaac catcctttgg tttggtcaca tcagttcaca acagccattt 1201 gttttcaagg tcaaggctcc aggcagttg ttactggtgt ttgcagcctg tcagtacttg 1261 cagtactgga atagttcta ggctagtgtc tgcggtcac tgtggtttta gcatgggagg 1321 acttatttga gaaatactac cttactttc tatgatttct tttacagag ttatagtgtg 1381 tttatccta agatgacagt tctctttgtc tatattcagc atctaagaca aatatttaaa 1441 cattttaaag aaccactgtg ttaagtttag gattatttac ttaccaaatt agaagtttga 1501 ctttatgtg ttatacacaa tctttaaatt tcacgaattc acctttttaa tagtatccat 1561 gtacataata aaatcaaagt ttaattaaaa aaaaaaaaa aaaa 1 M T S F E D A D T E E T V T C L Q M T V 1 ATGACCAGTTTTGAAGATGCTGACACAGAAGACAGTAACTTGTCTCCAGATGACGGTT 21 Y H P G Q L Q C G I F Q S I S F N R E K 61 TACCATCCTGGCCAGTTGCAGTGTGGAATATTTCAGTCAATAAGTTTTAACAGAGAAA 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 CAGGACAAACAGGTTTCCCGAGTTCAGTTTTCTCTGCAGCTGTTTAAAAATTCAACAGC 81 S V L S F E I K N M S K K T N L I V D S 241 TCAGTTCTCTCCTTTGAAATAAAAATATGAGTAAAAAGACCAATCTGATCGTGGACAGC 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 TTTATTTTATCTCCAAGATCACTCTTGCAAGAAACAACTGGCCACCACACAGGCCCATA 161 P E Y G T Y S L C S S Q S S S P T E M D 481 CCGGAGTATGGCACTTACTCGCTCTGCTCCCCAAAGCAGTTCTCCGACAGAAATGGAT 181 E N E S - 541 GAAAATGAGTCATGA	SEQ ID NO:12
WBC004G01.bFSP_20011309.abd	Homo sapiens neural precursor cell expressed, developmentally	1 agcggagggg ggagccggaa gcccagcgcg gagccggccg cggccccctg ttgtgttgct 61 gcggagaggt acttggatgc atttacagg ttagcctcac ttgagctgtt gtcctgcaag 121 taaagtgtat ttttggtgat tgaaagttgg agaactttca tttcagctga gtggtgtagt	SEQ ID NO:13

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
	down-regulated 1	181 tgaattggtt cctgtagccg ctgtccctaa acccaggccg acgttaccgc cttgtgtcct 241 gactgctagc tttcgacggg accgtctttg agggactcat gtaaagtctc tcccttaatg 301 ctcagttctt agaagaccga ggcgcagtca tgcaggaaaa cctcagattt gcttcatcag 361 gagatgatat taaaatatgg gatgcttcat ctatgacatt ggtggataaa ttcaacccac 421 acacatcacc acatggaatc agctcaatat gttggagcag caataataac tttttagtaa 481 cagcatcttc cagtggcgac aaaatagttg tctcaagttg caaatgtaaa cctgttccac 541 ttttagagct tgctgaaggg caaaagcaga catgtgtcaa tttaaattct acatctatgt 601 atttggtaag cggaggccta aataacactg ttaatatttg ggatttaaaa tcaaaaggag 661 ttcatcgatc tcttaaggat taaagatcaa gtaacttgtg taacatacaa ttggaatgat 721 tgctacattg cttctggatc tcttagtggt gaaattattt tacacagtgt aaccactaat 781 ttatctagta ctccttttgg ccatggtagt aaccagtctg ttcggcactt gaagtactcc 841 ttgtttaaga aatcactact gggcagtgtt tcggataatg gaatagtaac tctctgggat 901 gtaaatagtc agagtccata ccataacttt gacagtgtac acaaagctcc agcgtcaggc 961 atctgttttt ctcctgtcaa tgaattgctc tttgtaacca taggcttgga taaaagaatc 1021 atcctctatg acacttcaag taagaagcta gtgaaaactt tagtggctga cactcctcta 1081 actgcggtag atttcatgcc tgatggagcc actttggcta ttggatcttc ccgggggaaa 1141 atatatcaat atgatttaag aatgttgaaa tcaccagtta agaccatcag tgctcacaag 1201 acatctgtgc agtgtatagc atttcagtac tccactgttc ttactaagtc aagtttaaat 1261 aaaggctgtt caaataagcc cacaacagtg aacaaacgaa gtgttaatgt gaatgctgct 1321 agtggaggag ttcagaattc cggaattgtc agagaagcac ctgccacgtc cattgccaca 1381 gttctaccac aacctatgac atcagctatg gggaaaggaa cagttgctgt tcaagaaaaa 1441 gcaggtttgc ctcgaagcat aaacacagac actttatcta aggaaacaga cagtggaaaa 1501 aatcaggatt tctccagctt tgatgatact gggaaaagta gtttaggtga catgttctca 1561 cctatcagag atgatgctgt agttaacaag ggaagtgatg agtccatagg caaaggagat 1621 ggctttgact ttctaccgca gttgaactca gtgtttcctc caagaaaaaa tccagtaact 1681 tcaagtactt cagtattgca ttctagtcct cttaatgttt tatgggatct ccagggaaag 1741 aggaaaatga aaaccgtgat ctaacagctg agtctaagaa aatatatatg ggaaaacagg 1801 aatctaaaga ctccttcaaa cagttagcaa agttggtcac atctggtgct gaaagtggaa 1861 atctaaatac ctctccatca tctaaccaaa caagaaattc tgagaaattt gaaaagccag 1921 agaatgaaat tgaagcccag ttgtatatgtg aaccccaat caatggatcc tcaactccaa 1981 atccaaagat agcatcttct gtcactgctg gagttgccag ttcactctca gaaaaaatag 2041 ccgacagcat tggaaataac cggcaaaatg caccattgac ttccattcaa attcgtttta 2101 ttcagaacat gatacaggaa acgttggatg actttagaga agcatgccat agggacattg 2161 tgaatttgca agtggagatg attaaacagt ttcatatgca actgaatgaa atgcattctt 2221 tgctggaaag atactcagtg aatgaaggtt tagtggctga aattgaaaga ctacgagaag 2281 aaaacaaaag attacgggcc cacttttgaa atttcagtga atacctttaat gttctgtaat 2341 ttgggaagtt tctggcaaca cagaactaca tagaatcagt attgttttca tggcctccag 2401 ggaaaaaatg ttttcaagt aagagtaaaa gggtgatggg attttatacc aacaactgtt 2461 tcatcttaaa aatatgtata ttttatatt aaaaattgta cagtatgtca tctacccaat 2521 aggaaagtca acaggatctt tatttttga aagctttagc catccactaa gtgccctttt 2581 tcataagaga agaaaattgt gcataaaaat tggttatgtt tgttttttag tcatctttt 2641 taacatatat tttgattga caaattgcct ttcaaatttt tgggctagt tgagatttaa 2701 agagtttgat atgcttccta ttttatggga gaaagtaatt ttaaaatggc aattggtgtt	SEQUENCE IDENTIFIER:

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2761 tctaagccat tgactaataa aacataggct tggctagtaa ttatttttgtt aacttgatga 2821 agtcaagtat gactattatt tattgtacat ttgataagac aatttttgga atttgaatt 2881 gcacaaatta catgatatct tttgcattta tgttactata ttgtacttct gacaaatctt 2941 tatcctggg tggtatttt aagatatctt tacctataaa aagtgtttaa ggttcatagg 3001 actcgacaag agctatctgg tgattttctc attagtaaca tgcaacgttg tactgcaaaa 3061 tttcaatcaa catgacaact tataatgagt ggagatttca tattagatac taaatattat 3121 agtattattt ctatttttctt tttccaaata agaagcttgg attatttttat tttgtggtct 3181 ttatcattaa ctttaattct ttctgtactg tgtataatat ttttatatta ttggccttac 3241 cataaaatta tttagaaagg ttgtcaaaat aagttatacc tcttttggcaa tagatagatg 3301 tgtacatcta cctactatga tctacaattt taggttaagt gaagcttggg ggggctactg 3361 acttggttac cttcttgtct cttgtcccaa agatttaaac tatgtacctt tgtatagctc 3421 ttctgcccca ttttgacttc tgagatgaaa gtatttacta aaatttaaaaa aaaaaaaaca 3481 aaaaacaaac ctttagctca ctaactttat ggtttctgta agtgatggaa atttttaagg 3541 atatatttaa taagcataaa cttactaata attacttcca aaaataaaaa caggaatatt 3601 acttttaaag aaaaaaaaaa aaa 1 M Q E N L R F A S S G D D I K I W D A S 1 ATGCAGGAAAACCTCAGATTTGCTTCATCAGGAGATGATATTAAAATATGGGATGCTTCA 21 S M T L V D K F N P H T S P H G I S S I 61 TCTATGACATTGGTGGATAAATTCAACCCACACACATCACCACATGGAATCAGCTCAATA 41 C W S S N N N F L V T A S S S G D K I V 121 TGTTGGAGCAGCAATAATAACTTTTTAGTAACAGCATCTTCCAGTGGCGACAAAATAGTT 61 V S S C K C K P V P L L E L A E G Q K Q 181 GTCTCAAGTTGCAAATGTAAACCTGTTCCACTTTTAGAGCTTGCTGAAGGGCAAAAGCAG 81 T C V N L N S T S M Y L V S G G L N N T 241 ACATGTGTCAATTTAAATTCTACATCTATGTATTTGGTAAGCGGAGGCCTAAATAACACT 101 V N I W D L K S K R V H R S L K D H K D 301 GTTAATATTTGGGATTTAAAATCAAAAAGAGTTCATCGATCTCTTAAGGATCATAAAGAT 121 Q V T C V T Y N W N D C Y I A S G S L S 361 CAAGTAACTTGTGTAACATACAATTGGAATGATTGCTACATTGCTTCTGGATCTCTTAGT 141 G E I I L H S V T T N L S S T P F G H G 421 GGTGAAATTATTTTACACAGTGTAACCACTAATTTATCTAGTACTCCTTTTGGCCATGGT 161 S N Q S V R H L K Y S L F K K S L L G S 481 AGTAACCAGTCTGTTCGGCACTTGAAGTACTCCTTGTTTAAGAAATCACTACTGGCAGT	SEQ ID NO:14

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		181 V S D N G I V T L W D V N S Q S P Y H N 541 GTTTCGGATAATGGAATAGTAACTCTCTGGGATGTAAATAGTCAGAGTCCATACCATAAC	
		201 F D S V H K A P A S G I C F S P V N E L 601 TTTGACAGTGTACACAAAGCTCCAGCGTCAGGCATCTGTTTTTCTCCTGTCAATGAATTG	
		221 L F V T I G L D K R I I L Y D T S S K K 661 CTCTTTGTAACCATAGGCTTGGATAAAAGAATCATCCTCTATGACACTTCAAGTAAGAAG	
		241 L V K T L V A D T P L T A V D F M P D G 721 CTAGTGAAAACTTTAGTGGCTGACACTCCTCTAACTGCGGTAGATTTCATGCCTGATGGA	
		261 A T L A I G S S R G K I Y Q Y D L R M L 781 GCCACTTTGGCTATTGGATCTTCCCGGGGGAAAATATCAATATGATTTAAGAATGTTG	
		281 K S P V K T I S A H K T S V Q C I A F Q 841 AAATCACCAGTTAAGACCATCAGTGCTCACAAGACATCTGTGCAGTGTATAGCATTTCAG	
		301 Y S T V L T K S S L N K G C S N K P T T 901 TACTCCACTGTTCTTACTAAGTCAAGTTTAAATAAAGGCTGTTCAAATAAGCCCACAACA	
		321 V N K R S V N N V N A A S G G G V Q N S G I 961 GTGAACAAACGAAGTGTTAATGTGAATGCTGCTAGTGGAGGAGTTCAGAATTCCGGAATT	
		341 V R E A P A T S I A T V L P Q P M T S A 1021 GTCAGAGAAGCACCTGCCACGTCCATTGCCACAGTTCTACCACAACCTATGACATCAGCT	
		361 M G K G T V A V Q E K A G L P R S I N T 1081 ATGGGGAAAGGAACAGTTGCTGTTCAAGAAAAAGCAGGTTTGCCTCGAAGCATAAACACA	
		381 D T L S K E T D S G K N Q D F S S F D D 1141 GACACTTTATCTAAGGAAACAGACAGTGGAAAAAATCAGGATTTCTCCAGCTTTGATGAT	
		401 T G K S S L G D M F S P I R D D A V V N 1201 ACTGGGAAAAGTAGTTTAGGTGACATGTTCTCACCTATCAGAGATGATGCTGTAGTTAAC	
		421 K G S D E S I G K G D G F D F L P Q L N 1261 AAGGGAAGTGATGAGTCCATAGGCAAAGGAGATGGCTTTGACTTTCTACCGCAGTTGAAC	
		441 S V F P P R K N P V T S S T S V L H S S 1321 TCAGTGTTTCCTCCAAGAAAAAATCCAGTAACTTCAGTACTTCAGTATTGCATTCTAGT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		461 P L N V F M G S P G K E E N E N R D L T 1381 CCTCTTAATGTTTTTATGGGATCTCCAGGGAAAGAGGAAATGAAAACCGTGATCTAACA	
		481 A E S K K I Y M G K Q E S K D S F K Q L 1441 GCTGAGTCTAAGAAAATATATATGGGAAAACAGGAATCTAAAGACTCCTTCAAACAGTTA	
		501 A K L V T S G A E S G N L N T S P S S N 1501 GCAAAGTTGGTCATCTGGTGCTGAAGTGGAAATCTAAATACCTCTCCATCATCTAAC	
		521 Q T R N S E E K F E K P E E N E E I E E A Q L I 1561 CAAACAGAAATTCTGAGAAATTTGAAAGCCAGAGAATGAAATTGAAGCCCAGTTGATA	
		541 C E P P P I N G S S T P N P K I A S S V T 1621 TGTGAACCCCCAATCAATGGATCCTCAACTCCAAATCCAAGATAGCATCTTCTGTCACT	
		561 A G V A S S L S E K I A D S I G N N R Q 1681 GCTGGAGTTGCCAGTTCACTCTCAGAAAAAATAGCCGACAGCATTGGAAATAACCGGCAA	
		581 N A P L T S I Q I R F I Q N M I Q E T L 1741 AATGCACCATTGACTTCCATTCAAATTCGTTTTATTCAGAACATGATACAGGAAACGTTG	
		601 D D F R E A C H R D I V N L Q V E M I K 1801 GATGACTTTAGAGAAGCATGCCATAGGGACATTGTGAATTTGCAAGTGGAGATGATTAAA	
		621 Q F H M Q L N E M H S L L E R Y S V N E 1861 CAGTTTCATATGCAACTGAATGAAATGCATTCTTTGCTGGAAAGATACTCAGTGAATGAA	
		641 G L V A E I E R L R E E N K R L R A H F 1921 GGTTTAGTGGCTGAAATTGAAGACTACGAGAAGAAAACAAAGATTACGGGCCCACTTT	
		661 - 1981 TGA	
WBC004G09.bfSP_20011309.abd	No homology	1 GGACGAAAAATTTACCAAATTGCAGATAGCAAGCCTAGGAGGAATAGCTAATTCACAGG 61 TGATAGAATTAAGAGTTTAAAAGATTTTTTGACAAACTGGAATACTATCTGGAAATGACT 121 AGGATAGAAATTTGCCAAGAACAATTGAGTGGTTAGGTTTTTTAAAATATTAATCAAGAA 181 TATCTGTTGTGTGCTGAGTACCTGACATACATTATAGGCAGCATCTCTTGCAGGATTAGT 241 GATAGCCCAGTTTACAGCTGGAGAAATTAAAGTTTGGAGAAAATAAGGTAACTTGTCCAAA 301 GCCAGAATATAGTAAATCGAAGGTACAAGTTTAATATGGAGAGTTTCTAACTTGAAAAGC 361 TTTCGAGTGAAAAGAATCTAGACTTCACCAGTCAGTTGCTCACAAAGTCAGTGGAAACCA 421 ATTAGAAAAGCTGGTAGAAAAGCTAATAAATTATAGACTGTTTGAACAGTTGTGTCCAGA 481 TTGAGGGAGATAATAGCCCTCCCACCATTCTCCATGCAGATCATACCACCCCAAAGTAGC	SEQ ID NO:15

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		541 TCTTTAATCAGTAGGTACAAAAATCCATTATCATTATAGTATATGCTTAAAATATTTTTA 601 TGCACTTAGAAATGCTAAAAATTTAGATATAGCCTAAAGCAAATAAAACTTTGGCTTTTT 661 AAAGATTAAAGTAGGCTAGTCTTTTTTTAAAAAAAAGTAGAAAACTAGTATGCTGGCTTG 721 AAATATAGAGTTATGTGTCATTTCAAGTATTTTAATTGCACCTTAGTGAAATTACATATT 781 TTATGTAGATTTATTTGAGTACTATTGAATGTATTTCTTTATTACAATATTACTGGAAT	
		1 TTTGGAGAAATAAGGTAACTTGTCCAAAGCCAGAATATAGTAAATCGAAGGTACAAGTTT 61 AATATGGAGAGTTTCTAACTTGAAAAGCTTTCGAGTGAAAAGAATCTAGACTTCACCAGT 121 CAGTTGCTCACAAAGTCAGTGGAAACCAATTAGAAAAGCTGGTAGAAAAGCTAATAAATT 181 ATAGACTGTTTGAACAGTTGTGTCCAGATTGAGGGAGATAATAGCCCTCCCACCATTCTC 241 CATGCAGATCATACCACCCCAAAGTAGCTCTTTAATCAGTAGGTACAAAAATCCATTATC 301 ATTATAGTATATGCTTAAAATATTTTTATGCACTTAGAAATGCTAAAAATTTAGATATAG 361 CCTAAAGCAAATAAAACTTTGGCTTTTTAAAGATTAAAGTAGGCTAGTCTTTTTTTAAAA 421 AAAAGTAGAAAACTAGTATGCTGGCTTGAAATATAGAGTTATGTGTCATTTCAAGTATTT 481 TAATTGCACCTTAGTGAAATTACATATTTTATGTAGATTTATTTGAGTACTATTGAATGT 541 ATTTCTTTATTACAATATTACTGGAATCCTTTACACTGTTACCTGCTTAGGAATAAATAA 601 TTCTAAAAGAAAATGTAAAAAAAAAAAAAAAAAACTCGAG	SEQ ID NO:16
WBC005D09.bFSP_20012109.abd	No homology		
		1 GCGTAAAGCATTTTTCTTAGCCTTTCCTTTGTCTTGATCTGTTGTTAACAAGATTAATAC 61 TGCCAGACTTAAAATATTCTACTGTTGGGCTAAAAGGAATACAACTTAGATTGCACAAAA 121 CTTTTGCTTTTTAGAGAAAATATAACTCAGCTGTCTTTTAAAAGAGCTGTGTTGTTATCT 181 ACAAGACTATTTGCAGTCTTTTTTTCAGAGCAGATTCTAACAGTTGTGAATGGTTTAAAA 241 AATAGAAAATTACTAAAATATTAGTTTTGGGGGTTTTATAGAGGGAGAAAAACAAAACAG 301 GACCAAAGTTTATGTGCCTTCTTCAGTAGTCTTAATTGACCTTTTCTTCCTATTTGAGAC 361 TGAGGTAGCGTCAGTATTCTGGTTTTCAGGAAATATGTACTATATAGTTTTCGAAGAATG 421 TTATCCCACAGGCTGTTCATAGAAGCAAAGAACTGTAACTGTGTCCATGAAGTCTCGGTT 481 ACACTTTTGCCTTTGTCACATAATATTCAGTGTATAGCATCGTGCAAGTCCAGGACAGAG 541 CTGCTCTGAAGCTTTGTGGTAGTCATCCCAGTTTTTGTAACCTGAGGCGTATGTTCCAGA 601 GAACAGGGATATGTGTGGTCCCGTGACCTTGGTGATGATAGTCATGATTGCAAGCTCTTT 661 ATGGCAAGCTTAAATCAGCACTGTAAACAGATTTTTGTTGTGTTATTTTCGGTTCTCGAA 721 TCTATGTAGTAGTTGTAATAATAAATATTTAAATAGCTATTTTTGATGTCATTTAAAAAA 781 AAATCATCCCCTGGCCTTTTTCCCCCTCTTACCATGTTAC	SEQ ID NO:17
		1 CCTGGTCTGCCACTGTCAGCGTGACCTTGGCCTCAGTTCTCCTAGTCTCTAAGGTCCCTT 61 CTAACTTTCATGTCAGACAAGGTTCTTTTCATTTGACATTTTGAAAGGATAATGAGCTTT 121 AAAGTAAGTCTTGGTAAGGTGATATTTTAGGCAATCTTTCTTCTCCTTATCGCTTACAGT 181 GTTCTTAGAATTCTTTGAATATCATGAGAACCTCGTGTCTGTTCTGATTCCCTCCTCCTT 241 CCCTGATGCTAAATTTCCAATTGATATCAAACTGTCAACCTACCAAAAGAGATATTGTGG 301 CTTGTGGGTATTGCTGTCTTGTTTTTGATATGTTCTTGTATTGACTGCCCATTGGCCTGA 361 AAATACTCATTGTTAAACCTAAAAAAAAAAATCACTTTTCTTTCCCACTGACTGTTTTTTC 421 TGCTTGTTGTAAGAATCAAACGAGATATTGTATGTGAAAGCACCTTGTAAACTGTAACCT 481 ATCAATGTAAACTGTTAAGGTGTGTTGTTATTTCATTAATTACTTCTTTGTTCAGAATGA	SEQ ID NO:18

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		541 AATTTCCTACGCACTACTGTAGCTAGGAAATGCTGAAAACAACTGTGTTTTTTAATTAAT 601 CATAACTGCAAATTAAAGTATCTTCAAAGGATAGAAAAAAAATAAAAAAAAAAAAAAAAA 661 AAAAAC	
WBC005E06.bFSP_20012109.abd	*Homo sapiens* modulator of estrogen induced transcription, mRNA (cDNA clone IMAGE:4864860)	1 caagtggcca aacatcagaa tcgattaaaa aaagtgaaga aaagaagcga ataagttcca 61 agagtccagg acatatggta atactagacc aaactaaagg agatcattgt agaccatcaa 121 gaagaggaag atatgagaaa attcatggaa gaagtaagga aaaggagaga gctagtctag 181 ataaaaaaag agataaagac tacagaagga aagagatctt gccttttgaa aagatgaagg 241 aacaaaggtt gagagaacat ttagttcgtt ttgaaaggct gcgacgagca atggaacttc 301 gaagacgaag agagattgca gagagagagc gtcgagagcg agaacgcatt agaataattc 361 gtgaacggga agaacgggaa cgcttacaga gagagagaga gcgcctagaa attgaaaggc 421 aaaaactaga gagagagaga atggaacgcg aacgcttgga aagggaacgc attcgtattg 481 aacaggaacg tcgtaaggaa gctgaacgga ttgctcgaga aagagaggaa ctcagaaggc 541 aacaacagca gcttcgttat gaacaagaaa aaaggaattc cttgaaacgc ccacgtgatg 601 tagatcatag gcgagatgat ccttactgga gcgagaataa aaagttgtct ctagatacag 661 atgcacgatt tggccatgga tccgactact ctcgccaaca gaacagattt aatgactttg 721 atcaccgaga gaggggcagg tttcctgaga gttcagcagt acagtcttca tcttttgaaa 781 ggcgggatcg ctttgttggt caaagtgagg ggaaaaaagc acgacctact gcacgaaggg 841 aagatccaag cttcgaaaga tatcccaaaa atttcagtga ctccagaaga aatgagcctc 901 caccaccaag aaatgaactt agagaatcag acaggcgaga agtacgaggg gagcgagacg 961 aaaggagaac ggtgattatt catgacaggc ctgatatcac tcatcctaga catcctcgag 1021 aggcagggcc caatccttcc agacccacca gctggaaaag tgaaggaagc atgtccactg 1081 acaaacggga aacaagagtt gaaaggccag aacgatctgg gagagaagta tcagggcaca 1141 gtgtgagagg cgctcccccc gggaatcgta gcagcgcttc ggggtacggg agcagagagg 1201 gagacagagg agtcatcaca gaccgaggag gtggatcaca gcactatcct gaggagcgac 1261 atgtggttga acgccatgga cgggacacaa gcggaccaag gaaagagtgg catggtccac 1321 cctctcaagg gcctagctat catgatacga ggcgaatggg tgacggccgg gcaggagcag 1381 gcatgataac ccaacattca agtaacgcat ccccaattaa tagaattgta caaatcagtg 1441 gcaattccat gccaagagga agtggctccg gatttaagcc atttaagggt ggacctccgc 1501 gacgattctg aaaatgagct ctctgccaag gttttaagat aatttattga aatctcctgt 1561 aaactttact tgactactta tgaagaggac ctctgacttg cttgagagtt ctgtcagact 1621 tttcttttta aaaatttaac atgattgctt ttctcaattt tggagaagat gtttaaatag 1681 ttctgttgta acttttaata gttttgtgta tcattcaact ttttttcttg cagcaccgag 1741 gcacatttga aaagatggaa ttgaagtcgt tttgtttaac gctgtgtgaa tataaagagt 1801 agtttgcagc tgtgtggtag tggtttaatt tgcagcctta gctctgtggt gtctggctct 1861 agagttactt ctttttacca agcattttca gcctccattt tgaaggctgt ctacacttaa 1921 gaagtcttag ctgtctaatt tttagagaat aagattgttc attgcatttc tgagtattat 1981 gtaacctatt tttgcagaag gtactgttac attaagtgca tctgtgtatc ctggtttaaa 2041 aaaatgtaat ctttttttgaa ataaaccttc atattctgta tagttgctaa agtgttgaga 2101 acctttttaa ttgtaaaatg agaaccgatt ttcagtttag tgtagcagca cacttgttca 2161 ggtttgcatg gtatgaaacc aaatagattc atgaaacctt ggccatgagg tttgtttcac 2221 aaggttctta gaccgagttg tgcaggtaag tgcactttta ggtaatctgc actgtttgtt	SEQ ID NO:19

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2281 tgatggataa attccatctc tgggaattgt gtgggtatta atgtttccat gttcccaact 2341 atgttgagaa gtggaaaaaa acccaggttc tagatgggtg aatcagttgg gttttgtaaa 2401 tacttgtatg tggggaagac attgttgtct ttttgtgaaa ataaaaatcc acacctggaa 2461 aaaaaaaaaa aaa 1 M V I L D Q T K G D H C R P S R R G R Y 1 ATGGTAATACTAGACCAAACTAAAGGAGATCATTGTAGACCATCAAGAAGAGGAAGATAT 21 E K I H G R S K E K E R A S L D K K R D 61 GAGAAAATTCATGGAAGAAGTAAGGAAAAGGAGAGAGCTAGTCTAGATAAAAAAAGAGAT 41 K D Y R R K E I L P F E K M K E Q R L R 121 AAAGACTACAGAAGGAAAGAGATCTTGCCTTTTGAAAAGATGAAGGAACAAAGGTTGAGA 61 E H L V R F E R L R R A M E L R R R R E 181 GAACATTTAGTTCGTTTTGAAAGGCTGCGACGAGCAATGGAACTTCGAAGACGAAGAGAG 81 I A E R E R R E R E R I R I I R E R E E 241 ATTGCAGAGAGAGAGCGTCGAGAGCGAGAACGCATTAGAATAATTCGTGAACGGGAAGAA 101 R E R L Q R E R E R L E I E R Q K L E R 301 CGGGAACGCTTACAGAGAGAGAGAGAGCGCCTAGAAATTGAAAGGCAAAAACTAGAGAGA 121 E R M E R E R L E R E R I R I E Q E R R 361 GAGAGAATGGAACGCGAACGCTTGGAAAGGGAACGCATTCGTATTGAACAGGAACGTCGT 141 K E A E R I A R E R E E L R R Q Q Q Q L 421 AAGGAAGCTGAACGGATTGCTCGAGAAAGAGAGGAACTCAGAAGGCAACAACAGCAGCTT 161 R Y E Q E K R N S L K R P R D V D H R R 481 CGTTATGAACAAGAAAAAAGGAATTCCTTGAAACGCCCACGTGATGTAGATCATAGGCGA 181 D D P Y W S E N K K L S L D T D A R F G 541 GATGATCCTTACTGGAGCGAGAATAAAAAGTTGTCTCTAGATACAGATGCACGATTTGGC 201 H G S D Y S R Q Q N R F N D F D H R E R 601 CATGGATCCGACTACTCTCGCCAACAGAACAGATTTAATGACTTTGATCACCGAGAGAGG 221 G R F P E S S A V Q S S S F E R R D R F 661 GGCAGGTTTCCTGAGAGTTCAGCAGTACAGTCTTCATCTTTTGAAAGGCGGGATCGCTTT 241 V G Q S E G K K A R P T A R R E D P S F 721 GTTGGTCAAAGTGAGGGGAAAAAAGCACGACCTACTGCACGAAGGGAAGATCCAAGCTTC	SEQ ID NO:20

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		261 E R Y P K N F S D S R R N E P P P P R N 781 GAAAGATATCCCAAAAATTTCAGTGACTCCAGAAGAAATGAGCCTCCACCACCAAGAAAT 281 E L R E S D R R R E V R G E E R D E E R R T V 841 GAACTTAGAGAATCAGACAGGCGAGAAGTACGAGGGAGCGAGCGAAGGAGAACGGTG 301 I I H D R P D I T T H P R H P R E A G P N 901 ATTATTCATGACAGGCCTGATATCACTCATCCTAGACATCCTCGAGAGGCAGGGCCCAAT 321 P S R P T S W K S E G S M S T D K R E T 961 CCTTCCAGACCCACCAGCTGGAAAAGTGAAGGAAGCATGTCCACTGACAAACGGGAAACA 341 R V E R P E R S G R E V S S G H S V R G A 1021 AGAGTTGAAAGGCCAGAACGATCTGGGAGAGAAGTATCAGGGCACAGTGTGAGAGGCGCT 361 P P G N R S S A S G Y G S R E G D R G V 1081 CCCCCTGGGAATCGTAGCAGCGCTTCGGGGTACGGGAGCAGAGAGGGAGACAGAGGAGTC 381 I T D R G G G S Q H Y P E E R H V V E R 1141 ATCACAGACCGAGGAGGTGGATCACAGCACTATCCTGAGGAGCGACATGTGGTTGAACGC 401 H G R D T S G P R K E W H G P P S Q G P 1201 CATGGACGGGACACAAGCCGACCAAGGAAAGAGTGGCATGGTCCACCCTCTCAAGGGCCT 421 S Y H D T R R M G D G R A G A G M I T Q 1261 AGCTATCATGATACGAGGCGAATGGGTGACGGCCGGGCAGGAGCAGGCATGATAACCCAA 441 H S S N A S P I N R R I V Q I S G N S M P 1321 CATTCAAGTAACGCATCCCCAATTAATAGAATTGTACAAATCAGTGGCAATTCCATGCCA 461 R G S G S G F K P F K G G P P R R F - 1381 AGAGGAAGTGGCTCCGGATTTAAGCCATTTAAGGGTGGACCTCCGCGACGATTCTGA	
WBC005F01.bFSP_20012109.abd	Homo sapiens vaccinia related kinase 2, mRNA (cDNA clone MGC:34431 IMAGE:5221315).	1 GGGCCGCTGCACTGCGAGGCCGACGCAGCTGGAGAGAAGTTAGGCAGGTCCTAGGGAGGG 61 CAGGCTCGAGTGCTGGGCCCGCCTCCCCGCGGACTGTAGGCCCGGGGCTCCGCCTCGT 121 CGCAGCGGCAGGTAGGAGGCGGTGCGCGCGGCCCGGCGACGGGGATCCTGAGGCCCGAA 181 GTGATGCCACCAAAAAGAAATGAAAAATACAAACTTCCTATTCCATTTCCAGAAGGCAAG 241 GTTCTGGATGATATGGAAGGCAATCAGTGGTACTGGGCAAGAAGATTGGCTCTGGAGGA 301 TTTGGATTGATATATTTAGCTTTCCCCACAAATAAACCAGAGAAAGATGCAAGACATGTA 361 GTAAAAGTGGAATATCAAGAAAATGGCCCGTTATTTTCAGAACTTAAATTTTATCAGAGA	SEQ ID NO:21

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		421 GTTGCAAAAAAAGACTGTATCAAAAGTGGATAGAACGCAAACAACTTGATTATTTAGGA	
		481 ATTCCTCTGTTTTATGGATCTGGTCTGACTGAATTCAAGGGAAGAAGTTACAGATTTATG	
		541 GTAATGGAAAGACTAGGAATAGATTTACAGAAGATCTCAGGCCAGAATGGTACCTTTAAA	
		601 AAGTCAACTGTCCTGCAATTAGGTATCCGAATGTTGGATGTACTGGAATATATACATGAA	
		661 AATGAATATGTTCATGGTGATGTAAAAGCAGCAAATCTACTTTTGGGTTACAAAAATCCA	
		721 GACCAGGTTTATCTTGCAGATTATGGACTTTCCTACAGATATTGTCCCAATGGGAACCAC	
		781 AAACAGTATCAGGAAAATCCTAGAAAAGGCCATAATGGGACAATAGAGTTTACCAGCTTG	
		841 GATGCCCACAAGGGAGTAGCCTTGTCCAGACGAAGTGACGTTGAGATCCTCGGCTACTGC	
		901 ATGCTGCGGTGGTTGTGTGGGAAACTTCCCTGGGAACAGAACCTGAAGGACCCTGTGGCT	
		961 GTGCAGACTGCTAAAACAAATCTGTTGGACGAGCTCCCCCAGTCAGTGCTTAAATGGGCT	
		1021 CCTTCTGGAAGCAGTTGCTGTGAAATAGCCCAATTTTTGGTATGTGCTCATAGTTTAGCA	
		1081 TATGATGAAAAGCCAAACTATCAAGCCCTCAAGAAAATTTTGAACCCTCATGGAATACCT	
		1141 TTAGGACCACTGGACTTTTCCACAAAGGACAGAGTATAAATGTCCATACTCCAAACAGT	
		1201 CAAAAAGTTGATTCACAAAAGGCTGCAACAAAGCAAGTCAACACAAGGCACACAATAGGTTA	
		1261 ATCGAAAAAAAAGTCCACAGTGAGAGAAGCGCTGAGTCCTGTGCAACATGGAAAGTGCAG	
		1321 AAAGAGGAGAAACTGATTGGATTGAACAATGAAGCAGCTCAGGAAAACACAAGGAGA	
		1381 AGACAAAAATATTGTAAGTCTCAAGAATTTCTGAATGAACGAAAAAGTTCTCCACAAAAA	
		1441 TCTAGTGGCATACAATTCCCAAATTCATTTTATGAAACCCATCCAGATTTTACCAGTGAA	
		1501 GATATATTCAACAAGTCAAGATCTCCAACTTGGTATACATATGCTTCTACGCCTGGTATG	
		1561 GAGGTCACAGACTTAGAAAGTTCTACAGGATTTTGGCTTACTCAGTTTGCTCTTAGTGAA	
		1621 GAGACAAAGGCAGATGTGTATTATTATGGCTTCATCATTCTTTTTCTTTTGGTATTAGTA	
		1681 TGTCTTGCTTTATATTTCTCTGAAGATGATACCAAAATTCCTTTTGATAATTTTTTAAG	
		1741 TTTCCAGCTCTTCACCGAAATGTTGTATTCTTATTTCAGTGTTTCCTTCCAGACATTTTT	
		1801 AAGGTAATTGGCTTTAAAAGAGAACATATTTTAACAAAGTTTGTGGACACTCTAAAAAA	
		1861 TAAAATTGCTTTGTACTAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	
		1921 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	
		1 M P P K R N E K Y K L P I P F P E G K V	SEQ ID NO:22
		1 ATGCCACCAAAAGAAATGAAAAATACAAACTTCCTATTCCATTTCCAGAAGGCAAGGTT	
		21 L D D M E G N Q W V L G K K I G S G G G F	
		61 CTGGATGATATGGAAGGCAATCAGTGGGTACTGGGCAAGAAGATTGGCTCTGGAGGATTT	
		41 G L I Y L A F P T N K P E K D A R H V V	
		121 GGATTGATATATTTAGCTTTCCCCACAAATAAACCAGAGAAAGATGCAAGACATGTAGTA	
		61 K V E Y Q E N G P L F S E L K K F Y Q R V	
		181 AAAGTGGAATATCAAGAAAATGGCCCGTTATTTCAGAACTTAAATTTTATCAGAGAGTT	
		81 A K K D C I K K W I E R K Q L D Y L G I	
		241 GCAAAAAAGACTGTATCAAAAGTGGATAGAACGCAAACAACTTGATTATTTAGGAATT	
		101 P L F Y G S G L T E F K G R S Y R F M V	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		301 CCTCTGTTTTATGGATCTGGTCTGACTGAATTCAAGGGAAGAAGTTACAGATTTATGGTA 121 M E R L G I D L Q K I S G Q N G T F K K 361 ATGGAAAGACTAGGAATAGATTTACAGAAGATCTCAGGCCAGAATGGTACCTTTAAAAAG 141 S T V L Q L G I R M L D V L E Y I H E N 421 TCAACTGTCCTGCAATTAGGTATCCGAATGTTGGATGTACTGGAATATATACATGAAAAT 161 E Y V H G D V K A A N L L L G Y K N P D 481 GAATATGTTCATGGTGATGTAAAAGCAGCAAATCTACTTTTGGGTTACAAAAATCCAGAC 181 Q V Y L A D Y G L S Y R Y C P N G N H K 541 CAGGTTTATCTTGCAGATTATGGACTTTCCTACAGATATTGTCCCAATGGGAACCACAAA 201 Q Y Q E N P R K G H N G T I E F T S L D 601 CAGTATCAGGAAAATCCTAGAAAAGGCCATAATGGGACAATAGAGTTTACCAGCTTGGAT 221 A H K G V A L S R R S D V E I L G Y C M 661 GCCCACAAGGGAGTAGCCTTGTCCAGACGAAGTGACGTTGAGATCCTCGGCTACTGCATG 241 L R W L C G K L P W E Q N L K D P V A V 721 CTGCGGTGGTTGTGTGGGAAACTTCCCTGGGAACAGAACCTGAAGGACCCTGTGGCTGTG 261 Q T A K T N L L D E L P Q S V L K W A P 781 CAGACTGCTAAAACAAATCTGTTGGACGAGCTCCCCCAGTCAGTGCTTAAATGGGCTCCT 281 S G S S C C E I A Q F L V C A H S L A Y 841 TCTGGAAGCAGTTGCTGTGAAATAGCCCAATTTTTGGTATGTGCTCATAGTTTAGCATAT 301 D E K P N Y Q A L K K I L N P H G I P L 901 GATGAAAAGCCAAACTATCAAGCCCTCAAGAAAATTTTGAACCCTCATGGAATACCTTTA 321 G P L D F S T K G Q S I N V H T P N S Q 961 GGACCACTGGACTTTTCCACAAAAGGACAGAGTATAAATGTCCATACTCCAAACAGTCAA 341 K V D S Q K A A T K Q V N K A H N R L I 1021 AAAGTTGATTCACAAAAGGCTGCAACAAAGCAAGTCAACAAGGCACACAATAGGTTAATC 361 E K K V H S E R S A E S C A T W K V Q K 1081 GAAAAAAAAGTCCACAGTGAGAGAAGCGCTGAGTCCTGTGCAACATGGAAAGTGCAGAAA 381 E E K L I G L M N N E A A Q E N T R R R 1141 GAGGAGAAACTGATTGGATTGATGAACAATGAAGCAGCTCAGGAAAACACAAGGAGAAGA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		401 Q K Y C K S Q E F L N E R K S S P Q K S 1201 CAAAAATATTGTAAGTCTCAAGAATTTCTGAATGAACGAAAAAGTTCTCCACAAAAATCT 421 S G I Q F P N S F Y E T H P D F T S E D 1261 AGTGGCATACAATTCCCAAATTCATTTTATGAAACCCATCCAGATTTTACCAGTGAAGAT 441 I F N K S R S P T W Y T Y A S T P G M E 1321 ATATTCAACAAGTCAAGATCTCCAACTTGGTATACATATGCTTCTACGCCTGGTATGGAG 461 V T D L E S S T G F W L T Q F A L S E E 1381 GTCACAGACTTAGAAAGTTCTACAGGATTTTGGCTTACTCAGTTTGCTCTTAGTGAAGAG 481 T K A D V Y Y Y G F I I L F L L V L V C 1441 ACAAAGGCAGATGTGTATTATTATGGCTTCATCATTCTTTTTCTTTTGGTATTAGTATGT 501 L A L Y F L - 1501 CTTGCTTTATATTTTTCTCTGA	
WBC005F10.bFSP_20012109.abd	Polymeric immunoglobulin receptor 3 precursor (PIGR3)	1 ggtgcgacca agccctggct ccagtcttag cgggtatctg cccaccatgg ccctggtgct 61 gatcctccag ctgctgaccc tctggcctct gtgtcacaca gacatcactc cgtctgtccc 121 cccagcttca taccacccta agccatggct gggagctcag ccggctacag ttgtgacccc 181 tggggtcaac gtgaccttga gatgccgggc acccaaccc gcttggagat ttggactttt 241 caagcctgga gagatcgctc ccctctcttt ccgggatgtg tcctccgagc tggcagaatt 301 ctttctggag gaggtgactc cagcccaagg gggaagttac cgctgctgct accgaaggcc 361 agactgggag 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 601 gggcgcccgc gccccggca cctacagctg ctactatcac acgcctccg cgccctacgt 661 gctgtcgcag cgcagcgagg tgctggtcat cagctgggaa gatctggct cctccgacta 721 cacccgggg aacctagtcc gcctgggct ggccgggctg gtcctcatct ccctgggcgc 781 gctggtcact tttgactggc gcagtcagaa ccgcgctcct gctggtatcc gcccctgagc 841 cccaggagca ctgcagcccg agacttccaa cctgagtggc ggagaagctg ggaccctggg 901 ctggactgtc ctttcctgca gcccacagt cctgctggct gagctccgcg gaacggtcct 961 tgaccccgc tgtgccctgt gctgtagctt ctttccaggc ctttcccaag gagtagctga 1021 aaggaagacg cgattagtgg ttaagacttc caagccagaa gacagaggct 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 ggggacaata agggaataaa agctggcgag cgcggcaccc 1321 caccagagtc tgcttccacg ttgtgggagc ttgttctct tgctctacac aataaatctt	SEQ ID NO:23

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1381 gctgctgctt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1 M A L V L I L Q L 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 ACAGTTGTGACCCCTGGGGTCAACGTGACCTTGAGATGCCGGGCACCCCAACCCGCTTGG 61 R F G L F K P G E I A P L L F R D V S S 181 AGATTTGGACTTTTCAAGCCTGGAGAGATCGCTCCCCTTCTCTTCCGGGATGTGTCCTCC 81 E L A E F F L E E V T P A Q G G S Y R C 241 GAGCTGGCAGAATTCTTTCTGGAGGAGGTGACTCCAGCCCAAGGGGGAAGTTACCGCTGC 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 CTGCTGGTGACAGAGGAGCTGCCGCGGCCGTCGCTGGTGGCGCTGCCCGGGCCGGTGGTG 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 GACTTCACGCTGCTGGGCGCCCCGCCCCCGGCACCTACAGCTGCTACTATCACACGCCC 201 S A P Y V L S Q R S E V L V I S W E D S 601 TCCGCGCCCTACGTGCTGTCGCAGCGCAGCGAGGTGCTGGTCATCAGCTGGGAAGACTCT 221 G S S D Y T R G N L V R L G L A G L V L 661 GGCTCCTCCGACTACACCCGGGGAACCTAGTCCGCCTGGGGCTGGCCGGGCTGGTCCTC 241 I S L G A L V T F D W R S Q N R A P A G 721 ATCTCCCTGGGCGCTGGTCACTTTTGACTGGCGCAGTCAGAACCGCGCTCCTGCTGGT 261 I R P - 781 ATCCGCCCCCTGA	SEQ ID NO:24

Gene Name	GenBank HomoLogy	DNA SEQUENCE // DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
WBC007A08.bFSP_20 010110.abd	No Homology	1 GTTTCATCCGTTCTGTGAGGCTCTGCGGCATCTGCCAGATAGCAAACAGGCCTCATGCAG 61 GCAGATTAGGGCCTAAAGCAGATCAGAAGGCTTTGTAAAAGACCTCCCTGAGCCATCCCT 121 CTGCAGTGTTGGCTCAAGGCCACATGTCGTTTAGTCACAGCAAAGAGTAGACAGTTAGGA 181 AAAGCAAATGTCTTTTTATTTTCTACATCTCCTCCCCTCAGATAGGGAGCTATGACTC 241 AGTTGCACCTAAGAATACTGTAATTTGACTCTGTAATTGCCTTTGCTTCCCAAACCTGGG 301 AATCAATGGAAAGGCAGGGAATGTTCCTCTTCTGTGGCCAGGTTCTGTTCTTTGCAATTA 361 CAGCAAATTTTTAAAAATGCAAAGGCAGTTGTTGGTCCGCAGGGCTTGGCCAGTTATGTG 421 GTAGATACAGAGGCTAGCAGACAATTTGAGGATCCCGCTGTAATAATAAATGGCAGCTAG 481 CATTCGTTGACCATGTATTTATATGTCAGGCACTGAGCTAGGCAGGCTCTCTCTATATGG 541 CAGCTCCAAACTTCACAATAACTGTGAGTTAAGTACTTTATCTTCATTTCATAGATGAAG 601 AAACAGGTTCGGAGAGAAAAAGTTCTTTCCCAAGCCAGTACAGCTAGTAAGTGGTAGAAT 661 CAGGATTCATAGTGTCACCATATGGGACCAATGTTTATAGGGAAAAGGAAAATTACAAGT 721 CTTCTTAAAATGAAGTGGCCAGCTTTTCTTGCACAGACTAAATAACTCTAACTGGCATTT 781 TTCGGTTGGGAAACAGCTGAATTAGTAGTTAAGTCTGACAGCCAAGTGAGTTTTAGAAAC 841 CGCAGCGTGGAGCATGCACTCCCCCACACCATCTGCTGTGTTGATTAGCAGTCCTGCCTC 901 AGTCTCTTTCTTT 1 AAGAAGAAATAGATAATCTGAATAGCGCTATGTCTATTAAAACTTAATAGCTCTGGGGGG 61 TGTAGGTATTATTGTCCTCATTTTACAGATAAGGAAACTGAGGCTCAGAGAGAAAGTC 121 TGTTGCTCAAGGTAGCAAAGCTAAAATATGGCAGAGCTAGGATTCAAATCCAGGTCTTCT 181 GATTCTCATTCCAGTGCCCTTTCAGTATACCGTGTTGCCTCTAAAGATTGCAGCTCCTTA 241 TTTACTGGAAAGTTGTTCCTGCCCAGTCCACACCCTCCCACCCCATCTTCCTCGAGCCCT 301 CTGTCTGTGTTTTCATCAGGATTATATTCATTGTATTTGGAATCCGTGTTCTTTTTTGTG 361 TTGGGAAAAACAAATCTCTTCTACCAGCTTGCACTCAGACCAACTTGGAAAAAAAAAGTT 421 TAAATGCTGTTGCAGATGTACACTTAAAAATGTGAAGTTTGTAGCTTTAACTTTTGTAA 481 CTAAAATTAATAACACTGGCTTAAGTGCTGACTAGAAATGCTATTTTATAAAGTTTGGAT 541 GTAAATAATCAGTCGAGGTCAGCAGTTTGTATATGTATGAGACAGCTTCCTCCATTGCCT 601 TTTTTTTTAAATTTGAAATGCTTTCTCTGTGCTTTCGTTAGAATTGTTGTTCTTCCTCTT 661 TCCTACACCGTGTCACCTTTGTTTTAAATAAACTGTCCTTCGGAAAAAAAAAAAAAAAA 721 A	SEQ ID NO:25 SEQ ID NO:26
WBC007F03.bFSP_20 010110.abd	Homo sapiens mRNA for enolase 1 variant, clone: adSE00169	1 agtatctgtg ggtacccgga gcacggagat ctcgccggct ttacgttcac ctcggtgtct 61 gcagcaccct ccgcttcctc tcctaggcga cgagacccag tggctagaag ttcaccatgt 121 ctattctcaa gatccatgcc agggagatct ttgactctcg cgggaatccc actgttgagg 181 ttgatcttct cacctcaaaa ggtctcttca gagctgctgt gcccagtggt gcttcaactg 241 gtatctatga ggccctagag ctccgggaca atgataagac tcgctatatg gggaagggtg 301 tctcaaaggc tgttgagcac atcaataaaa ctattgcgcc tgccctggct agcaagaaac 361 tgaacgtcac agaacaagag aagattgaca aactgatgat cgagatggat ggaacagaaa 421 ataaatctaa gtttggtgcg aacgccattc tgggggtgtc cttgccgtc tgcaaagctg 481 gtgccgttga gaaggggtc ccctgtacc gccacatcgc tgacttggct ggcaactctg	SEQ ID NO:27

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		541 aagtcatcct gccagtcccg gcgttcaatg tcatcaatgg cggttctcat gctggcaaca 601 agctggccat gcaggagttc atgatcctcc cagtcggtgc agcaaacttc agggaagcca 661 tgcgcattgg agcagaggtt taccacaacc tgaagaatgt catcaaggag aaatatggga 721 aagatgccac caatgtgggg gatgaaggcg ggtttgctcc caacatcctg gagaataaag 781 aaggcctgga gctgctgaag actgctattg ggaaagctgg ctacactgat aaggtggtca 841 tcggcatgga cgtagcggcc tccgagttct tcaggtctgg gaagtatgac ctggacttca 901 agtctcccga tgaccccagc aggtacatct cgcctgacca gctggctgac ctttgaccag gatgactggg 961 ccttcatcaa ggactaccca gtggtgtcta tcgaagatcc ctttgaccag gatgactggg 1021 gagcttggca gaagttcaca gccagtgcag gaatccaggt agtgggggat gatctcacag 1081 tgaccaaccc aaagaggatc gccaaggccg tgaacgagaa gtcctgcaac tgcctcctgc 1141 tcaaagtcaa ccagattggc tccgtgaccg agtctcttca ggcgtgcaag ctggcccagg 1201 ccaatggttg gggcgtcatg gtgtctcatc gttcgggggga gactgaagat acttcatcg 1261 ctgacctggt tgtgggggctg tgcactgggc agatcaagac tggtgcccct tgccgatctg 1321 agcgcttggc caagtacaac cagctcctca gaattgaaga ggagctgggc agcaaggcta 1381 agtttgccgg caggaacttc agaaacccct tggccaagta agctgtgggc aggcaagccc 1441 ttcggtcacc tgttggctac acagaccctc cccctcgtgt cagctcaggc agctcgaggc 1501 ccccgaccaa cacttgcagg ggtccctgct agttagcgcc ccaccgccgt ggagttcgta 1561 ccgcttcctt agaacttcta cagaagccaa gctcctgga gccctgttgg cagctctagc 1621 tttgcagtcg tgtaattggc ccaagtcatt gttttctcg cctcactttc caccaagtgt 1681 ctagagtcat gtgagcctcg tgtcatctcc gggtggccca caggctagat ccccggtggt 1741 tttgtgctca aaataaaaag cctcagtgac ccatgaaaaa aaaaaaaaaa aaa 1 M S I L K I H A R E I F D S R G N P T V 1 ATGTCTATTCTCAAGATCCATGCCAGGGAGATCTTTGACTCTCGCGGGAATCCCACTGTT 21 E V D L F T S K G L F R A A V P S G A S 61 GAGGTTGATCTCTTCACCTCAAAAGGTCTCTTCAGAGCTGCTGTGCCCAGTGGTGCTTCA 41 T G I Y E A L E L R D N D K T R Y M G K 121 ACTGGTATCTATGAGGCCCTAGAGCTCCGGGACAATGATAAGACTCGCTATATGGGGAAG 61 G V S K A V E H I N K T I A P A L A S K 181 GGTGTCTCAAAGGCTGTTGAGCACATCAATAAAACTATTGCGCCTGCCCTGGCTAGCAAG 81 K L N V T E Q E K I D K L M I E M D G T 241 AAACTGAACGTCACAGAACAAGAGAAGATTGACAAACTGATGATCGAGATGGATGGAACA 101 E N K S K F G A N A I L G V S L A V C K 301 GAAAATAAATCTAAGTTTGGTGCGAACGCCATTCTGGGGGTGTCCCTTGCCGTCTGCAAA 121 A G A V E K G V P L Y R H I A D L A G N 361 GCTGGTGCCGTTGAGAAGGGGGTCCCCCTGTACCGCCACATCGCTGACTTGGCTGGCAAC	SEQ ID NO:28

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		141 S E V I L P V P A F N V I N G G S H A G 421 TCTGAAGTCATCCTGCCAGTCCCGGCGTTCAATGTCATCAATGGCGGTTCTCATGCTGGC 161 N K L A M Q E F M I L P V G A A N F R E 481 AACAAGCTGGCCATGCAGGAGTTCATGATCCTCCCAGTCGGTGCAGCAAACTTCAGGGAA 181 A M R I G A E V Y H N L K N V I K E K Y 541 GCCATGCGCATTGGAGCAGAGGTTTACCACAACCTGAAGAATGTCATCAAGGAGAAATAT 201 G K D A T N V G D E G G F A P N I L E N 601 GGGAAAGATGCCACCAATGTGGGGATGAAGGCGGGTTTGCTCCCAACATCCTGGAGAAT 221 K E G L E L L K T A I G K A G Y T D K V 661 AAAGAAGGCCTGGAGCTGCTGAAGACTGCTATTGGGAAAGCTGGCTACACTGATAAGGTG 241 V I G M D V A A S E F F R S G K Y D L D 721 GTCATCGGCATGGACGTAGCGGCCTCCGAGTTCTTCAGGTCTGGGAAGTATGACCTGGAC 261 F K S P D D P S R Y I S P D Q L A D L Y 781 TTCAAGTCTCCCGATGACCCCAGCAGGTACATCTCGCCTGACCAGCTGGCTGACCTGTAC 281 K S F I K D Y P V V S I E D P F D Q D D 841 AAGTCCTTCATCAAGGACTACCCAGTGGTGTCTATCGAAGATCCCTTTGACCAGGATGAC 301 W G A W Q K F T A S A G I Q V V G D D L 901 TGGGGAGCTTGGCAGAAGTTCACAGCCAGTGCAGGAATCCAGGTAGTGGGGGATGATCTC 321 T V T N P K R I A K A V N E K S C N C L 961 ACAGTGACCAACCCAAAGAGGATCGCCAAGGCCGTGAACGAGAAGTCCTGCAACTGCCTC 341 L L K V N Q I G S V T E S L Q A C K L A 1021 CTGCTCAAAGTCAACCAGATTGGCTCCGTGACCGAGTCTCTTCAGGCGTGCAAGCTGGCC 361 Q A N G W G V M V S H R S G E T E D T F 1081 CAGGCCAATGGTTGGGGCGTCATGGTGTCTCATCGTTCGGGGAGACTGAAGATACCTTC 381 I A D L V V G L C T G Q I K T G A P C R 1141 ATCGCTGACCTGGTTGTGGGCTGTGCACTGGGCAGATCAAGACTGGTGCCCCTTGCCGA 401 S E R L A K Y N Q L L R I E E E L G S K 1201 TCTGAGCGCTTGGCCAAGTACAACCAGCTCCTCAGAATTGAAGAGGAGCTGGGCAGCAAG 421 A K F A G R N F R N P L A K -	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1261 GCTAAGTTTGCCGGCAGGAACTTCAGAAACCCCTTGGCCAAGTAA	
WBC008A10.bFSP_20 010110.abd	Homo sapiens matrix metalloproteinase 8 (neutrophil collagenase) (MMP8) , mRNA.	1 GCTCGCCAGGGAAGGGCCCTACCCAGAGGACAGAAAGAAGCCAGGAGGGGTAGAGTTTG 61 AAGAGAAGATCATGTTCTCCCTGAACGCTTCCATTTCTGCTCTTACTCCATGTGCAGA 121 TTTCCAAGGCCTTTCCTGTATCTTCTAAAGAGAAAAATACAAAAACTGTTCAGGACTACC 181 TGGAAAAGTTCTACCAATTACCAAGCAACCAGTATCAGTCTACAAGGAAGAATGGCACTA 241 ATGTGATCGTTGAAAAGCTTAAAGAAATGCAGCGATTTTTTGGGTTGAATGTGACGGGGA 301 AGCCAAATGAGGAAACTCTGGACATGATGATAAAAAGCCTCGCTGTGGAGTGCCTGACAGTG 361 GTGGTTTTATGTTAACCCCAGGAAACCCCAAGTGGGAACGCACTAACTTGACCTACAGGA 421 TTCGAAACTATACCCCACAGCTGTCAGAGGCTGAGGTAGAAAGAGCTATCAAGGATGCCT 481 TTGAACTCTGGAGTGTTGCATCACCTCTCATCTTCACCAGGATCTCACAGGGAGAGGCAG 541 ATATCAACATTGCTTTTTACCAAAGAGATCACGGTGACAATTCTCCATTTGATGGACCCA 601 ATGGAATCCTTGCTCATGCCTTTCAGCCAGGCCAAGGTATTGGAGGAGATGCTCATTTTG 661 ATGCCGAAGAAACATGGACCAACACCTCCGCAAATTACAACTTGTTTCTTGTTGCTGCTC 721 ATGAATTTGGCCATTCTTTGGGGCTCGCTCACTCCTCTGACCCTGGTGCCTTGATGTATC 781 CCAACTATGCTTTCAGGGAAACCAGCAACTACTCACTCCCTCAAGATGACATCGATGGCA 841 TTCAGGCCATCTATGGACTTTCAAGCAACCCTATCCAACCTACTGGACCAAGCACACCCA 901 AACCCTGTGACCCCAGTTTGACATTTGATGCTATCACCACACTCCGTGGAGAAAIACTTT 961 TCTTTAAAGACAGGTACTTCTGGAGAAGGCATCCTCAGCTACAAAGAGTCGAACTCAATT 1021 TCATTTCTCTGTTCTGGCCATCCTTGCCAAATGGTATACAGGCGGCTTATGAGGATTTTG 1081 ACAGGGACCTAATTTTCCTATTTAAAGGCAACCAATACTGGGCTCTGAATGGCTATGACA 1141 TTCAGCAAGGTTATCCCAAGGACATATCAAACTACGGCTTCCCAAGCAGTGTCCAAGCAA 1201 TTGATGCAGCTGTTTCCTATAGGAGTAAAACATACTTCTTTGTAAATGATCAATCTGGA 1261 GATATGATAACCAAAGACGATCCATGGAAGCAGGTTATCCCCAAAGCATAGCAAGTACCT 1321 TTCCAGGAATAGGAAGCAGAATTGATGCAGTTTTCCAGCAAGATGACTTCTTTTTTCT 1381 TCAGCGGACCAGTTTATTATGCATTTGATCTTAATACTCAGAGAGTTACTAGGGTTGCAA 1441 GAATCAATAAATGGCTTAACTGTAGACGAAGTTGAAGCAAAATCAAATGTGGCTGTATCC 1501 ACTTTCAGAATGTTGAAGGGAAGTTCAGCATGCATTTTCGTTACATTGTGTCCTGCTTAT 1561 ACTTTCTCAATATTAAGTCATTGTTTCCCATCACTGTATCCATTCTACCTGTCCTCCGT 1621 GAAAATATGTTTGGAATATTCCACTATTTGCAGAGGCTTATTCAGTTCTTACACATTCCA 1681 TCTTACATTAGTGATTCCATCAAGAGAAGGAAAGTAAGCCTTTTTGTCACCTCAATATT 1741 TACTATTTCAATACTTACATATCTGACTTCTAGGATTTATTGTTATATTACTTGCCTATC 1801 TGACTTCATACATCCCTCAGTTTCTTAAAATGTCCTATGTATATCTGCTACATGCAATTT 1861 AGCACTGGATTTAGGTTATAAGTAAGATTATATAAACAAGATAGATAGTACTCCTTGCGTT 1921 TATTGAAAATCTGGTGCTATTTTCCACTCTTGGAAAGAAATATTGTTGATATGTATTGTG 1981 AGTTGAATTGTGTTCCCCAAAAAAGCTATGTGCAAGTCCCAACCTCGGGTACCTATGAAT 2041 GTGAGCTTACCAGGGTCTTTGCAGATGTAAATAGTTAAGTTAAGGTGAGATCACACTGAA 2101 TTAGGGTGGGCTCTAAATCCATTATGACTGTTGTTCTTATAAGAAGAAGAGCATAGCC 2161 ACCTAGGGGAGGAGGCCGTGTGAAGACAGAGGCAGAGATTGGAGTGACGCATCTCCAAGC 2221 CAA 1 M F S L K T L P F L L L L H V Q I S K A	SEQ ID NO:29 SEQ ID NO:30

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1 ATGTTCTCCCTGAAGACGCTTCCATTTCTGCTCTTACTCCATGTGCAGATTTCCAAGGCC	
		21 F P V S S K E K N T K T V Q D Y L E K F	
		61 TTTCCTGTATCTTCTAAAGAGAAAAATACAAAAACTGTTCAGGACTACCTGGAAAAGTTC	
		41 Y Q L P S N Q Y Q S T R K N G T N V I V	
		121 TACCAATTACCAAGCAACCAGTATCAGTCTACAAGGAAGAATGGCACTAATGTGATCGTT	
		61 E K L K E M Q R F F G L N V T G K P N E	
		181 GAAAAGCTTAAAGAAATGCAGCGATTTTTTGGGTTGAATGTGACGGGGAAGCCAAATGAG	
		81 E T L D M M K K P R C G V P D S G G F M	
		241 GAAACTCTGGACATGATGAAAAAGCCTCGCTGTGGAGTGCCTGACAGTGGTGGTTTTATG	
		101 L T P G N P K W E R T N L T Y R I R N Y	
		301 TTAACCCCAGGAAACCCCAAGTGGGAACGCACTAACTTGACCTACAGGATTCGAAACTAT	
		121 T P Q L S E A E V E R R A I K D A F E L W	
		361 ACCCCACAGCTGTCAGAGGCTGAGGTAGAAAGAGCTATCAAGGATGCCTTTGAACTCTGG	
		141 S V A S P L I F T R I S Q G E A D I N I	
		421 AGTGTTGCATCACCTCTCATCTTCACCAGGATCTCACAGGGAGAGGCAGATATCAACATT	
		161 A F Y Q R D H G D N S P F D G P N G I L	
		481 GCTTTTTACCAAAGAGATCACGGTGACAATTCTCCATTTGATGGACCCAATGGAATCCTT	
		181 A H A F Q P G Q G I G G D A H F D A E E	
		541 GCTCATGCCTTTCAGCCAGGCCAAGGTATTGGAGGAGATGCTCATTTTGATGCCGAAGAA	
		201 T W T N T S A N Y N L F L V A A H E F G	
		601 ACATGGACCAACACCTCCGCAAATTACAACTTGTTTCTTGTTGCTGCTCATGAATTTGGC	
		221 H S L G L A H S S D P G A L M Y P N Y A	
		661 CATTCTTTGGGGCTCGCTCACTCCTCTGACCCTGGTGCCTTGATGTATCCCAACTATGCT	
		241 F R E T S N Y S L P Q D D I D G I Q A I	
		721 TTCAGGGAAACCAGCAACTACTCACTCCCTCAAGATGACATCGATGGCATTCAGGCCATC	
		261 Y G L S S N P I Q P P T G P S T P K P C D	
		781 TATGGACTTTCAAGCAACCCTATCCAACCTACTGGACCAAGCACACCCAAACCCTGTGAC	
		281 P S L T F D A I T T L R G E I L F F K D	
		841 CCCAGTTTGACATTTGATGCTATCACCACACTCCGTGGAGAAATACTTTTCTTTAAGAC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		301 R Y F W R R H P Q L Q R V E L N F I S L 901 AGGTACTTCTGGAGAAGGCATCCTCAGCTACAAAGAGTCGAACTCAATTTCATTTCTCTG 321 F W P S L P N G I Q A A Y E D F D R D L 961 TTCTGGCCATCCTTGCCAAATGGTATACAGGCGGCTTATGAGGATTTTGACAGGGACCTA 341 I F L F K G N Q Y W A L N G Y D I Q Q G 1021 ATTTTCCTATTTAAAGGCAACCAATACTGGGCTCTGAATGGCTATGACATTCAGCAAGGT 361 Y P K D I S N Y G F P S S V Q A I D A A 1081 TATCCCAAGGACATATCAAACTACGGCTTCCCAAGCAGTGTCCAAGCAATTGATGCAGCT 381 V S Y R S K T Y F F V N D Q F W R Y D N 1141 GTTTCCTATAGGAGTAAAACATACTTCTTTGTAAATGATCAATTCTGGAGATATGATAAC 401 Q R R S M E A G Y P Q S I A S T F P G I 1201 CAAAGACGATCCATGGAAGCAGGTTATCCCCAAAGCATAGCAAGTACCTTTCCAGGAATA 421 G S R I D A V F Q Q D D F F L F F S G P 1261 GGAAGCAGAATTGATGCAGTTTTCCAGCAAGATGACTTCTTTCTTTTCTTCAGCGGACCA 441 V Y Y A F D L N T Q R V T R V A R I N K 1321 GTTTATTATGCATTTGATCTTAATACTCAGAGAGTTACTAGGGTTGCAAGAATCAATAAA 461 W L N C R R S - 1381 TGGCTTAACTGTAGACGAAGTTGA	
WBC008A12.bFSP_20010110.abd	Homo sapiens cDNA FLJ33312 fis, clone BNGH42005968, weakly similar to DIPZ PROTEIN.	1 AGTTTAATTACGTCCCCGGGAACTGCGCCGATTTGGACTTTTGGCACTTGGACCTATGCT 61 TTAAAAAGAAAAAAGTGTCATTGGCGTGGAGTGGGGCTAGTGGAGGGTGAGGTGAATGCG 121 CCGTTTGGAAACCACAGGACAGTGAACGTTTCGTCTCTCCCAGCGAGACTCTCCCGCGGG 181 CCCGGCGGCCGCATCGGGAGCCCGGCGGAAACATGGCGGCGCCCGGAGGCCGGGGCCGCA 241 GCCTCTCCGGCCTGCTCCCCGCGCAGACCTCGCTAGAGTACGCCCTGCTCGACGCCGTTA 301 CCCAGCAGGAGAAGGACAGCCTGGTCTACCAGTATCTGCAGAAGGTGGACGGCTGGGAGC 361 AGGACTTGTCAGTACCCGAGTTTCCGGAAGGATTAGAATGGCTGAACACAGAAGAACCTA 421 TTTCTGTCTACAAGGATCTATGTGGAAAAATAGTCGTCCTTGATTTCTTCACCTACTGCT 481 GCATAAACTGTATTCACCTATTGCCTGATCTCCATGCATTAGAACACACATACTCTGATA 541 AAGATGGTCTTCTTATTATTGGTGTTCACTCGGCTAAGTTTCCAAATGAAAAAGTCCTGG 601 ATAACATTAAGAGTGCTGTTCTTCGATACAACATCACCCACCCTATGGTTAATGATGCAG 661 ATGCCAGCCTTTGGCAAGAACTAGAAGTTTCCTGCTGGCCAACTCTAGTCATACTTGGAC 721 CTCGTGGAAACATGTTGTTTTCTTTGATTGGAGAGGGACACAAAGATAAATTATTTTTAT	SEQ ID NO:31

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		781 ATACTTCAATTGCTTTAAAGTATTACAAAGACAGGGGGCAGATCAGATCAGATAAAATTG 841 GAATAAAACTCTATAAAGATTCTTTGCCACCTTCACCATTGCTATTTCCTGGCAAAGTAA 901 CAGTAGACCAAGTTACTGATAGATTGGTAATAGCAGACACTGGACATCATAGAATTTTGG 961 TCGTTTGGAAGAATGGACAAATTCAATATAGCATTGGAGGACCCAACCCTGGAAGAAAAG 1021 ATGGAATATTTTCAGAATCAACTTTTAATTCTCCACAGGGTGTAGCCATAATGAATAATA 1081 TCATATATGTGGCAGACACTGAAAACCACCTTATAAGAAAGATTGACCTAGAAGCTGAGA 1141 AGGTGAGCACTGTGTAGCTGGTATTGGAATTCAAGGTACAGATAAAGAAGGTGGAGCAAAAG 1201 GAGAACAGCAGCCCATTAGTTCCCCTTGGGATGTGGTTTTTGGAACATCAGGTTCAGAGG 1261 TCCAACGAGATGACATTCTGTGGATAGCCATGGCAGGGACTCATCAGATATGGCACTCC 1321 TGTTGGACTCTGGCAGACTACCAAAGAAAAATGAGTTAAAAAAAGGAACCTGCTTCAGT 1381 TTGCTGGAAGTGGAAATGAAGAGAATCGAAATAATGCATATCCTCACAAGGCAGGTTTTG 1441 CCCAACCTTCAGGTCTTTCTGTGGCCTCAGAAGATCCCTGGAGCTGCCTGTTCGTAGCAG 1501 ATAGTGAGAGCAGCACCGTGAGAACCGTCTCACTGAAGGATGGAGCCGTGAAGCACCTTG 1561 TGGGAGGAGAAAGAGACCCCATGGACTTATTTGCTTTTGGTGATGTTGATGGAGTAGGAA 1621 TCAATGCAAAGCTTCAGCACCCACTTGGAGTAACTTGGGACAAGAAAAGGAATTTAGTTT 1681 ATGTGGCAGACTCTTATAATCACAAGATTAAAGTTGTGGATCCCAAAACGAAAACCTGTA 1741 CAACATTAGCAGGAACTGGAGATGCAAGTAATGTTATCAGTTCCAGTTTTACTCAGTCAA 1801 CTTTTAATGAGCCAGGAGGCTTGTGTATTGGAGAGAATGGTCAGTTATTATATGTAGCAG 1861 ACACCAATAATCATCAGATTAAAGTGATGGATTTAGAAACAAAAATGATTTCTGTGCTCC 1921 CACTCTTCACATCTGAAAACACTGTGGTAGATGGCCCATTCCCAGAAGAAAAACAGAAGA 1981 CATTACCCAGACTACCTAAATCTGCTCCAGCCGTTAAACTCTCCCCAGTGGCTGCATCTC 2041 CAGGACAGACTCTTCAGTTCAAGCTGAGATTAGACCTCCCATCGGGAGCAAAACTAACTG 2101 AAGGAGCACCCAGTTGCTGGTTTCTAACAGCTGAAGGCAATGAATGGCTTCTTCAAGGAC 2161 AGATACCATCTGGAGAAATAGAGAGCATTTCCAATCAACCCACAATCTCACTACAGATTC 2221 CTGGAGATTGTGTATCGCTTGAAGCTGTTATATCTGTCAGCGTGTTTCTTTACTACTGTA 2281 GCGCAGACAGCAGTGCCTGTATGATGAAGGGAATTTTGTTCAGTCAGCCTTTACAAATAA 2341 GCGCTACGCAACAAGGTTGCATAGCTCCAGTAGAGCTCCAATATGTATTTTAGCAAGCAA 2401 GCTAGCTAGCAACCCATTGCCACACCACTCTACTGTCTCCCATCCTGACTATCACTGTAATTT 2461 AAGGAAAGAAAACTTTATTTCTGCCTCTGGATACCAAGAAACCCATTGCTGAGTTCTAGC 2521 CACTGATCTTTAAAATAAAGCTATGCTCCTT 1 M A A P G G R G R S L S G G L L P A Q T S 1 ATGGCGGCGCCCGGAGGCCGGGGCCGCAGCCTCTCCGGCCTGCTCCCCGCGCAGACCTCG 21 L E Y A L L D A V T Q Q E K D S L V Y Q 61 CTAGAGTACGCCCTGCTCGACGCCGTTACCCAGCAGGAGAAGGACAGCCTGGTCTACCAG 41 Y L Q K V D G W E Q D D L S V P E F P E G 121 TATCTGCAGAAGGTGGACGGCTGGGAGCAGGACTTGTCAGTACCCGAGTTTCCGGAAGGA 61 L E W L N T E E P I S V Y K D L C G K I 181 TTAGAATGGCTGAACACAGAAGAACCTATTTCTGTCTACAAGGATCTATGTGGAAAAATA	SEQ ID NO:32

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		81 V V L D F F T Y C C I N C I H L L P D L	
		241 GTCGTCCTTGATTTCTTCACCTACTGCTGCATAAACTGTATTCACCTATTGCCTGATCTC	
		101 H A L E H T Y S D K D G L L I I G V H S	
		301 CATGCATTAGAACACACATACTCTGATAAAGATGGTCTTCTTATTATTGGTGTTCACTCG	
		121 A K F P N E K V L D N I K S A V L R Y N	
		361 GCTAAGTTTCCAAATGAAAAAGTCCTGGATAACATTAAGAGTGCTGTTCTTCGATACAAC	
		141 I T H P M V N D A D A S L W Q E L E V S	
		421 ATCACCCACCCTATGGTTAATGATGCAGATGCCAGCCTTTGGCAAGAACTAGAAGTTTCC	
		161 C W P T L V I L G P R G N M L F S L I G	
		481 TGCTGGCCAACTCTAGTCATACTTGGACCTCGTGGAAACATGTTGTTTCTTTGATTGGA	
		181 E G H K D K L F L Y T S I A L K Y Y K D	
		541 GAGGGACACAAAGATAAATTATTTTTATATACTTCAATTGCTTTAAAGTATTACAAAGAC	
		201 R G Q I R D N K I G I K L Y K D S L P P	
		601 AGGGGGCAGATCAGAGATAATAAAATTGGAATAAAACTCTATATAAAGATTCTTTGCCACCT	
		221 S P L L F P G K V T V D Q V T D R L V I	
		661 TCACCATTGCTATTTCCTGGCAAAGTAACAGTAGACCAAGTTACTGATAGATTGGTAATA	
		241 A D T G H H R I L V V W K N G Q I Q Y S	
		721 GCAGACACTGGACATCATAGAATTTTGGTCGTTTGGAAGAATGGACAAATTCAATATAGC	
		261 I G G P N P G R K D D G I F S E S T F N S	
		781 ATTGGAGGACCCAACCCTGGAAGAAAAGATGGAATATTTTCAGAATCAACTTTTAATTCT	
		281 P Q G V A I M N N I I Y V A D T E N H L	
		841 CCACAGGGTGTAGCCATAATGAATAATATCATATATGTGGCAGACACTGAAAACCACCTT	
		301 I R K I D L E A E K V S T V A G I G I Q	
		901 ATAAGAAAGATTGACCTAGAAGCTGAGAAGGTGAGCACTGTAGCTGGTATTGGAATTCAA	
		321 G T D K E G G A K G E Q Q P I S S P W D	
		961 GGTACAGATAAGAAGGTGGAGCAAAAGGAGAACAGCAGCCCATTAGTTCCCCTTGGGAT	
		341 V V F G T S G S E V Q R D D I L W I A M	
		1021 GTGGTTTTTGGAACATCAGGTTCAGAGGTCCAACGAGATGACATTCTGTGGATAGCCATG	
		361 A G T H Q I W A L L L D S G R L P K K N	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1081 GCAGGGACTCATCAGATATGGCACTCCTGTTGGACTCTGGCAGACTACCAAAGAAAAAT	
		381 E L K K G T C L Q F A G S G N E E N R N	
		1141 GAGTTAAAAAAAGGAACCTGCCTTCAGTTTGCTGGAAGTGGAAATGAAGAGAATCGAAAT	
		401 N A Y P H K A G F A Q P S G L S V A S E	
		1201 AATGCATATCCTCACAAGGCAGGTTTTGCCCAACCTTCAGGTCTTTCTGTGGCCTCAGAA	
		421 D P W S C L F V A D S E S S T V R T V S	
		1261 GATCCCTGGAGCTGCCTGTTCGTAGCAGATAGTGAGAGCAGCACCGTGAGAACCGTCTCA	
		441 L K D G A V K H L V G G E R D P M D L F	
		1321 CTGAAGGATGGAGCCGTGAAGCACCTTGTGGGAGGAGAAAGAGACCCCATGGACTTATTT	
		461 A F G D V D G V G I N A K L Q H P L G V	
		1381 GCTTTTGGTGATGTTGATGGAGTAGGAATCAATGCAAAGCTTCAGCACCCACTTGGAGTA	
		481 T W D K K R N L V Y V A D S Y N H K I K	
		1441 ACTTGGGACAAGAAAAGGAATTTAGTTTATGTGGCAGACTCTTATAATCACAAGATTAAA	
		501 V V D P K T K T C T T L A G T G D A S N	
		1501 GTTGTGGATCCCAAACGAAAACCTGTACAACATTAGCAGGAACTGGAGATGCAAGTAAT	
		521 V I S S S F T Q S T F N E P G G L C I G	
		1561 GTTATCAGTTCCAGTTTTACTCAGTCAACTTTTAATGAGCCAGGAGGCTTGTGTATTGGA	
		541 E N G Q L L Y V A D T N N H Q I K V M D	
		1621 GAGAATGGTCAGTTATTATATGTAGCAGACACCAATAAATCATCAGATTAAAGTGATGAT	
		561 L E T K M I S V L P L F T S E N T V V D	
		1681 TTAGAAACAAAAATGATTTCTGTGCTCCCACTCTTCACATCTGAAAACACTGTGGTAGAT	
		581 G P F P E E K Q K T L P R L P K S A P A	
		1741 GGCCCATTCCCAGAAGAAAAACAGAAGACATTACCCAGACTACCTAAATCTGCTCCAGCC	
		601 V K L S P V A A S P G Q T L Q F K L R L	
		1801 GTTAAACTCTCCCCAGTGGCTGCATCTCCAGGACAGACTCTTCAGTTCAAGCTGAGATTA	
		621 D L P S G A K L T E G A P S C W F L T A	
		1861 GACCTCCCATCGGGAGCAAAACTAACTGAAGGAGCACCCAGTTGCTGGTTTCTAACAGCT	
		641 E G N E W L L Q G Q I P S G E I E S I S	
		1921 GAAGGCAATGAATGGCTTCTTCAAGGACAGATACCATCTGGAGAAATAGAGAGCATTTCC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		661 N Q P T I S L Q I P G D C V S L E A V I 1981 AATCAACCCACAATCTCACTACAGATTCCTGGAGATTGTGTATCGCTTGAAGCTGTTATA 681 S V S V F L Y Y C S A D S S A C M M K G 2041 TCTGTCAGCGTGTTTCTTTACTACTGTAGCGCAGACAGCAGTGCCTGTATGATGAAGGGA 701 I L F S Q P L Q I S A T Q Q G C I A P V 2101 ATTTTGTTCAGTCAGCCTTTACAAATAAGCGCTACCGCAACAAGGTTGCATAGCTCCAGTA 721 E L Q Y V F - 2161 GAGCTCCAATATGTATTTTAG	
WBC008D09.bFSP_20010110.abd	Homo sapiens cDNA: FLJ21472 fis, clone COL04936.	1 CATCACCCTTTTTAACATTGTTTACACATCACTGCCTGTTTTAGCCATGGGGATTTTGA 61 CCAGGATGTGAGTGACCAGAACAGCGTGGACTGTCCCCAGCTCTACAAACCAGGACAGCT 121 GAATCTGCTTTTTTAACAAGCGTAAATTTTCCATTTGCGTGTTGCATGGAATCTACACCTC 181 ATTAGTCCTTTTTCTTCATCCCCTATGGGGCCTTTTACACGTGGCTGGAGAAGATGGCA 241 ACATATTGCTGACTACCAGTCCTCTGCAGTTACATGGCCACATCTTTGGTCATTGTGTC 301 AGTGTGCAGATAGCCTTGGATACCAGTTACTGGACTTTCATTAATCACGTCTTCATCTGG 361 GGGAGCATTGCCATTTATTTCTCCATTTTATTTACAATGCACAGTAATGGCATCTTTGGC 421 ATCTTCCCAAACCAGTTTCCATTTGTTGGTAATGCACGACATTCCCTGACCCAGAAGTGC 481 ATCTGGCTTGTAATTCTCTTACAACAGTGGCTTCAGTTATGCCAGTGGTGGCATTCAGA 541 TTTTTGAAGGTGGATTTATACCCAACCCTGAGTGATCAGATCCGCCGGTGGCAGAAGGCT 601 CAAAAGAAGGCAAGGCCTCCAAGTAGCCGAAGGCCTCGGACCCGCAGGTCAAGCTCAAGA 661 AGGTCTGGATATGCTTTTGCTCACCAAGAAGGCTATGGAGAGCTTATCACATCTGGAAAA 721 AATATGCGAGCTAAAAAATCCACCCCCAACATCAGGGCTGGAAAAGACACATTATAATAGC 781 ACTAGCTGGATTGAAAATTTATGTAAGAAAACCACAGACACCGTGAGCAGCTTTAGCCAG 841 GATAAAACAGTGAAACTGTGAGTCAATATGAATTTAAACCACGTAGTTATCTTTTCACTT 901 CAGGTGGAGCTGAAATTCTGCTGGCTCCAGAGTTTGAGATTTGAGGCAAGAGGTGGGGCA 961 GGCAGATTGCCTCACTTAACTTAAATCTGCGGCAGACAACTGCCAGTGCCCATCAAACAG 1021 GAGTGTGCGCTATGGAAAACCAGGCCAGATGGTCACTGTCGAATTCGTGATTTGGTGGAC 1081 AAAACACTCGCTGTTACAAGTACAGATTTTTTTTTTTTTAAATCAACCTAGATACCAAT 1141 GGACCTGAACTTCAGAATCTTATTTATGGAGAAAAACTTGTAGTCTGCATATACATTGA 1201 ATGAATCTTCAGATGGATAAAACGGTGCAATCAAAAGGTAATCAAAATATCCCAGCTGAA 1261 GAGTGTGCTTGTTGCACAGATAAACACGTATAGGTAAGCTCAGCCTTTCCCAGGATATGCT 1321 TTTAAGATTTAAAATGCGTCCTAAGGTGCTTTCAGACTAAGAGCAGCTTGTCACTTTCCA 1381 GTCTTGATATCTACCTGTGTGTTCAACTGAGACAACACATCCCCTTCCGGCCTGAAGAGT 1441 AGAGGAATGTGTTGGTGTTCCTCATTTTTCTACTAGTTTAGAGATGAAGTAGAGTGAGCA 1501 TCTTTACAGTGGGATGGGCTGGTAATGTGGTCAAATTTATTCAAAAAGCTCTCAGTCTGT 1561 GTCATGTAAGGACATGCTTATGAAATGTGAGAGAGGCTCGCCACTAAGTATTCTAAATAC 1621 TTTTCAATGGCTTTTCTAACAACCTCAGTAGTAATTTGCTGAGCATCATCCAGACCATTA 1681 ATAGAACCAGCAAAGCACTGGAATTTCACCCTTTAATGATTGTTTTTCATATAGTATATG	SEQ ID NO:33

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1741 GGCAAATACCTTCCAAGTTTCCAATTTTAAAAGTTCAGATTTGAAACCAAACAGATTAA 1801 TAAACAATCTCTTTCATTACTATTTAAAACTCAGGTTTAGATTGTTTAAAATTAGTTGC 1861 TTTTGATACTCAGCTGTCATGTTATAATTCAAACATGTAGTAAACATATGTAGGTAAGG 1921 TTGTTTTTTTGGAGATGTTGCAGCTCAAATTTCAGTCCACATATGAATCATCAGTGTATT 1981 TTCCATAAAGTGATTCGGGCATATTTGTGTGAAAACCTCAGTTCTGTCACTTCTTACCTC 2041 TATAAACTTGGACGATAATGAAAAAAAAAAAAAAAAAA 1 M A T S L V I V V S V Q I A L D T S Y W 1 ATGGCCACATCTTTGGTCATTGTGGTCAGTGTGCAGATAGCCTTGGATACCAGTTACTGG 21 T F I N H V F I W G S I A I Y F S I L F 61 ACTTTCATTAATCACGTCTTCATCTGGGGGAGCATTGCCATTTATTTCTCCATTTTATTT 41 T M H S N G I F G I F P N Q F P F V G N 121 ACAATGCACAGTAATGGCATCTTTGGCATCTTCCCAAACCAGTTTCCATTTGTTGGTAAT 61 A R H S L T Q K C I W L V I L L T T V A 181 GCACGACATTCCCTGACCCAGAAGTGCATCTGGCTTGTAATTCTCTTACAACAGTGGCT 81 S V M P V V A F R F L K V D L Y P T L S 241 TCAGTTATGCCAGTGGTGGCATTCAGATTTTTGAAGGTGGATTTATACCCAACCCTGAGT 101 D Q I R R W Q K A Q K K A R P P S S R R 301 GATCAGATCCGCCGGTGGCAGAAGGCTCAAAGAAGGCAAGGCCTCCAAGTAGCCGAAGG 121 P R T R R S S S R R S G Y A F A H Q E G 361 CCTCGGACCCGCAGGTCAAGCTCAAGAAGGTCTGGATATGCTTTTGCTCACCAAGAAGGC 141 Y G E L I T S G K N M R A K N P P P T S 421 TATGGAGAGCTTATCACATCTGGAAAAAATATGCGAGCTAAAAATCCACCCCCAACATCA 161 G L E K T H Y N S T S W I E N L C K K T 481 GGGCTGGAAAAGACACATTATAATAGCACTAGCTGGATTGAAAATTTATGTAAGAAAACC 181 T D T V S S F S Q D K T V K L - 541 ACAGACACCGTGAGCAGCTTTAGCCAGGATAAAACAGTGAAACTGTGA	SEQ ID NO:34
WBC009F04.bFSP_20 010310.abd	Homo sapiens integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29	1 AGCGGGAGTCGCGGAACAGCAGGCCCGAGCCCACCGCGCCGGGCCCCGGACGCCGCGCGG 61 AAAAGATGAATTTACAACCAATTTTCTGGATTGGACTGATCAGTTCAGTTTGCTGTGTGT 121 TTGCTCAAACAGATGAAAATAGATGTTTAAAAGCAAATGCCAAATCATGTGGAGAATGTA 181 TACAAGCAGGGCCAAATTGTGGGTGGTGCACACAAATTCAACATTTTTACAGGAAGGAATGC 241 CTACTTCTGCACGATGTGATGATTTAGAAGCCTTAAAAAAGAAGGGTTGCCCTCCAGATG	SEQ ID NO:35

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
	includes MDF2, MSK12), transcript variant 1A, mRNA (cDNA clone MGC:17220 IMAGE:3924411).	301 ACATAGAAAATCCCAGAGGCTCCAAAGATATAAAGAAAAATAAAAATGTAACCAACCGTA 361 GCAAAGGAACAGCAGAAGCTCAAGCCAGAGGATATTACTCAGATCCAACCACAGCAGT 421 TGGTTTTGCGATTAAGATCAGGGAGCCACAGACATTTACATTAAAATTCAAGAGAGCTG 481 AAGACTATCCCATTGACCTCTACTACCTTATGGACCTGTCTTACTCAATGAAAGACGATT 541 TGGAGAATGTAAAAAGTCTTGGAACAGATCTGATGAATGAAATGAGGAGGATTACTTCGG 601 ACTTCAGAATTGGATTTGGCTCATTTGTGGAAAAGACTGTGATGCCTTACATTAGCACAA 661 CACCAGCTAAGCTCAGGAACCCTTGCACAAGTGAACAGAACTGCACCAGCCCATTTAGCT 721 ACAAAAATGTGCTCAGTCTTACTAATAAGAGAAGTATTTAATGAACTTGTTGGAAAAC 781 AGCGCATATCTGGAAATTTGGATTCTCCAGAAGGTGGTTTCGATGCCATCATGCAAGTTG 841 CAGTTTGTGGATCACTGATTGGCTGGAGGAATGTTACACGGCTGCTGGTGTTTTCCACAG 901 ATGCCGGGTTTCACTTTGCTGGAGATGGGAAACTTGGTGGCATTGTTTTACCAAATGATG 961 GACAATGTCACCTGGAAAATAATATGTACACAATGAGCCATTATTATGATTATCCTTCTA 1021 TTGCTCACCTTGTCCAGAAACTGAGTGAAAATAATATTCAGACAATTTTTGCAGTTACTG 1081 AAGAATTTCAGCCTGTTTACAAGGAGCTGAAAAACTTGATCCCTAAGTCAGCAGTAGGAA 1141 CATTATCTGCAAATTCTAGCAATGTAATTCAGTTGATCATTGATGCATACAATTCCCTTT 1201 CCTCAGAAGTCATTTTGGAAAACGGCAAATTGTCAGAAGGAGTAACAATAGTTACAAAT 1261 CTTACTGCAAGAACGGGGTGAATGGAACAGGGGAAAATGGAAGAAAATGTTCCAATATTT 1321 CCATTGGAGATGAGGTTCAATTTGAAATTAGCATAACTTCAAATAAGTGTCCAAAAAAGG 1381 ATTCTGACAGCTTTAAAATTAGGCCTCTGGGCTTTACGGAGGAAGTAGAGGTTATTCTTC 1441 AGTACATCTGTGAATGTGAAATGCCAAAGCGAAGGCATCCCTGAAAGTCCCAGTGTCATG 1501 AAGGAAATGGGACATTTGAGTGTGGCGCGTGCAGTGCAATGAAGGGCGTGTTGTGATAGAC 1561 ATTGTGAATGCAGCACAGATGAAGTTAACAGTGAAGACATGGATGCTTACTGCAGGAAAG 1621 AAAACAGTTCAGAAATCTGCAGTAACAATGGAGAGTGCGTCTGCGGACAGTGTGTTTGTA 1681 GGAAGAGGGATAATACAAATGAAATTTATTCTGGCAAATTCTGCAGTGTGATAATTTCA 1741 ACTGTGATAGATCCAATGGCTTAATTGTGGAGGAAATGGTGTTTGCAAGTGTCGTGTGT 1801 GTGAGTGCAACCCCAACTACACTGGCAGTGCATGTGACTGTTCTTTGGATACTAGTACTT 1861 GTGAAGCCAGCAACGGACAGATCTGCAATGGCCGGGCATCTGTGAGTGTGGTGTCTGTA 1921 AGTGTACAGATCCGAAGTTTCAAGGGCAAACGTGTGAGATGTGTCAGACCTGCCTTGGTG 1981 TCTGTGCTGAGCATAAGAATGTGTTCAGTGCAGAGCCTTTAATAAAGGAGAAAAGAAAG 2041 ACACATGCGCCCAGGAATGTTCACATTTCAACATTACCAAGGTTGAAAATCGGGACAAGT 2101 TACCTCAGCCAGGCCAGGTTGATCCCCTGTCTCACTGTAAGGAGAAGGATGTGGATGACT 2161 GCTGGTTCTATTTCACGTATTCAGTGAATGGGAACAATGAGGCCATTGTTCACGTTGTGG 2221 AGACTCCAGAGTGCCCCACTGGTCCAGACATCATTCCAATTGTAGCTGGTGTGGTTGCTG 2281 GAATTGTTCTTATTGGCCTTGCATTGCTGCTGATTTGGAAGCTTTTAATGATAATTCATG 2341 ACAGAAGGGAATTTGCCAAATTTGAGAAGGAAAAAATGAATGCCAAATGGGACACGGGTG 2401 AAAATCCTATTTATAAGAGTGCTGTGACAACTGTTGTCAATCCGAAGTACGAGGGAAAAT 2461 GAGCACTCGCTGTGTGCAAATTTCACAACACTGAATGCAAAGCAGTACTTTTCCTAGTCACA 2521 GTAAGGTAGCTGTAGGGCTGTACCGCCATGGGGTTACTCATGTGCCGGTTTTGAAAGTGT 2581 ACAATATGTATAATTTTAAAAATTTGTTATTATTTTGAAAATAATGTTATCATCAATGCC 2641 AGGGACTGACCAGAGACTTGAGACAGGATGGTTGTCCTCATCATAAGGTCACGTGGTGCC 2701 TTTTTGACCTTTTACTCCTGGGCTGTTGAAATCAAGTTCTTATTGGATCGAGTGGTGTGT 2761 CTACAGTGATGGAAGGGCAGTAGTTAAAATAATGAGTATGATGAGAGTTTCTATTAATCA 2821 CGTATTAAAACTGATCTTTAGCTTTACAGATATGTCAGTTTTCAGTTATACAGAATCCAC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2881 AGTAAATTTCTGCTACCTAGTTTAGAATTGTTTTAAATCTGTTATTTTGCTATTTGCCTG 2941 TTAGACATGACTGATGACATATCTGAAAGACAAGTATGTTGAGAGTTGCTGGTGTAAAAT 3001 ACGTTTGAAATAGTTGATCTACAGAGGCCATGGGACAAAGTCAGAGAGTTAGAAAGGGAA 3061 ACCATAGCTTTAAAACCTGTGTGCCATTTTGAGAGTTACTTAATCTGGTAACTTTTATG 3121 CCTTCTTTTATAAATTCAAGCCTTCAGGAAAAGTATTGGGAAATTTTCTGCAAAAAAGT 3181 CCTTGATTTAGCATTATTTACATAAAGGCCTTAATTTCCATAGTACTTGCTGAATTGGGG 3241 ACCTTTGGGTGAATTTGTTTTTATTCATTTTATTTTGTTTGAAGCCTGGTGCTTTTTACCA 3301 CCTCTTCTAATCATTTAATGTATTTGTTTGCAATTTGGGGGTAAGACTTTTTTTATGAGT 3361 ACTTTTTCTTTGAAGTTTTAGCGGTCAATTTGCCTTTTTAATGAACGTGTGAAGTTGTAC 3421 TGTGGCTTACGCAACAGCTGTCACTTAAGCGACTCTCTTATTTTCAGGCAGTGCCGTAATAG 3481 ACCGCTGTATAGTTACTTCTCACTGTCAGAGCTGCCCATTTTGTTTCATACCAGTCACAT 3541 CCTTGTTTTAAGTGCCTTTTAAATTTTAACAGTTCACTTTTTACATGCTGTTTACTGAAGT 3601 TATTTATTAAAATATGCCTAAAATACTTAAATCGGAAAAAAAAAAAAAAAAA	SEQ ID NO:36
		1 M N L Q P I F W I G L I S S V C C V F A 1 ATGAATTTACAACCAATTTTCTGGATTGGACTGATCAGTTCAGTTTGCTGTGTGTTTGCT 21 Q T D E N R C L K A N A K S C G E C I Q 61 CAAACAGATGAAAATAGATGTTTAAAGCAAATGCCAAATCATGTGGAGAATGTATACAA 41 A G P N C G W C T N S T F L Q E G M P T 121 GCAGGGCCAAATTGTGGGTGGTGCACAAATTCAACATTTTTACAGGAAGGAATGCCTACT 61 S A R C D D L E A L K K K G C P P D D I 181 TCTGCACGATGTGATGATTTAGAAGCCTTAAAAAAGAAGGGTTGCCCTCCAGATGACATA 81 E N P R G S K D I K K N K N V T N R S K 241 GAAAATCCCAGAGGCTCCAAAGATATAAAGAAAAATAAAAATGTAACCAACCGTAGCAAA 101 G T A E K L K P E D I T Q I Q P Q Q L V 301 GGAACAGCAGAAGCTCAAGCCAGAGGATATTACTCAGATCCAACCACAGCAGTTGGTT 121 L R L R S G E P Q T F T L K F K R A E D 361 TTGCGATTAAGATCAGGGGAGCCACAGACATTTACATTAAAATTCAAGAGAGCTGAAGAC 141 Y P I D L Y Y L M D L S Y S M K D D L E 421 TATCCCATTGACCTCTACTACCTTATGGACCTGTCTTACTCAATGAAAGACGATTTGGAG 161 N V K S L G T D L M N E M R R I T S D F 481 AATGTAAAAAGTCTTGGAACAGATCTGATGAATGAAATGAGGAGGATTACTTCGGACTTC 181 R I G F G S F V E K T V M P Y I S T T P 541 AGAATTGGATTTGGCTCATTTGTGGAAAAGACTGTGATGCCTTACATTAGCACAACACCA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		201 A K L R N P C T S E Q N C T S P F S Y K 601 GCTAAGCTCAGGAACCCTTGCACAAGTGAACAGAACTGCACCAGCCCATTTAGCTACAAA	
		221 N V L S L T N K G E V F N E L V G K Q R 661 AATGTGCTCAGTCTTACTAATAAAGGAGAAGTATTTAATGAACTTGTTGGAAAACAGCGC	
		241 I S G N L D S P E G G F D A I M Q V A V 721 ATATCTGGAAATTTGGATTCTCCAGAAGGTGGTTTCGATGCCATCATGCAAGTTGCAGTT	
		261 C G S L I G W R N V T R L L V F S T D A 781 TGTGGATCACTGATTGGCTGGAGGAATGTTACACGGCTGCTGGTGTTTTCCACAGATGCC	
		281 G F H F A G D G K L G G I V L P N D G Q 841 GGGTTTCACTTTGCTGGAGATGGGAAACTTGGTGGCATTGTTTTACCAAATGATGGACAA	
		301 C H L E N N M Y T M S H Y Y D Y P S I A 901 TGTCACCTGGAAAATATATGTACACAATGAGCCATTATTATGATTATCCTTCTATTGCT	
		321 H L V Q K L S E N N I Q T I F A V T E E 961 CACCTTGTCCAGAAACTGAGTGAAAATAATATTCAGACAATTTTTGCAGTTACTGAAGAA	
		341 F Q P V Y K E L K N L I P K S A V G T L 1021 TTTCAGCCTGTTTACAAGGAGCTGAAAAACTTGATCCCTAAGTCAGCAGTAGGAACATTA	
		361 S A N S S N V I Q L I I D A Y N S L S S 1081 TCTGCAAATTCTAGCAATGTAATTCAGTTGATCATTGATGCATACAATTCCCTTTCCTCA	
		381 E V I L E N G K L S E G V T I S Y K S Y 1141 GAAGTCATTTTGGAAAACGGCAAATTGTCAGAAGGAGTAACAATAAGTTACAAATCTTAC	
		401 C K N G V N G T G E N G R K C S N I S I 1201 TGCAAGAACGGGGTGAATGGAACAGGGGAAAATGGAAGAAAATGTTCCAATATTTCCATT	
		421 G D E V Q F E I S I T S N K C P K K D S 1261 GGAGATGAGGTTCAATTTGAAATTAGCATAACTTCAAATAAGTGTCCAAAAAAGGATTCT	
		441 D S F K I R P L G F T E E V E V I L Q Y 1321 GACAGCTTTAAAATTAGGCCTCTGGGCTTTACGGAGGAAGTAGAGGTTATTCTTCAGTAC	
		461 I C E C E C Q S E G I P E S P K C H E G 1381 ATCTGTGAATGTGAATGCCAAAGCGAAGGCATCCCTGAAAGTCCCAAGTGTCATGAAGGA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		481 N G T F E C G A C R C N E G R V G R H C 1441 AATGGGACATTTGAGTGTGGCGCGTGCAATGAAGGCGTGTTGGTAGACATTGT	
		501 E C S T D E V N S E D M D A Y C R K E N 1501 GAATGCAGCACAGATGAAGTTAACAGTGAAGACATGGATGCTTACTGCAGGAAAGAAAAC	
		521 S S E I C S N N G E C V C G Q C V C R K 1561 AGTTCAGAAATCTGCAGTAACAATGGAGAGTGCGTCTGCGGACAGTGTGTTTGTAGGAAG	
		541 R D N T N E I Y S G K F C E C D N F N C 1621 AGGGATAATACAAATGAAATTTATTCTGGCAAATTCTGCGAGTGTGATAATTTCAACTGT	
		561 D R S N G L I C G G N G V C K C R V C E 1681 GATAGATCCAATGGCTTAATTTGTGGAGGAAATGGTGTTTGCAAGTGTCGTGTGTGAG	
		581 C N P N Y T G S A C D C S L D T S T C E 1741 TGCAACCCCAACTACACTGGCAGTGCATGTGACTGTTCTTTGGATACTAGTACTTGTGAA	
		601 A S N G Q I C N G R G I C E C G V C K C 1801 GCCAGCAACGGACAGATCTGCAATGGCCGGGGCATCTGTGAGTGTGGTGTCTGTAAGTGT	
		621 T D P K F Q G Q T C E M C Q T C L G V C 1861 ACAGATCCGAAGTTTCAAGGGCAAACGTGTGAGATGTGTCAGACCTGCCTTGGTGTCTGT	
		641 A E H K E C V Q C R A F N K G E K K D T 1921 GCTGAGCATAAAGAATGTGTTCAGTGCAGAGCCTTTAATAAGGAGAAAGAAAGACACA	
		661 C A Q E C S H F N I T K V E N R D K L P 1981 TGCGCCCAGGAATGTTCACATTTCAACATTACCAAGGTTGAAAATCGGGACAAGTTACCT	
		681 Q P G Q V D P L S H C K E K D V D D C W 2041 CAGCCAGGCCAGGTTGATCCCCTGTCTCACTGTAAGGAGAAGGATGTGGATGACTGCTGG	
		701 F Y F T Y S V N G N N E A I V H V V E T 2101 TTCTATTTCACGTATTCAGTGAATGGGAACAATGAGGCCATTGTTCACGTTGTGGAGACT	
		721 P E C P T G P D I I P I V A G V V A G I 2161 CCAGAGTGCCCCACTGGTCCAGACATCATTCCAATTGTAGCTGGTGTGGTTGCTGGAATT	
		741 V L I G L A L L L I W K L L M I I H D R 2221 GTTCTTATTGGCCTTGCATTGCTGCTGATTTGGAAGCTTTTAATGATAATTCATGACAGA	
		761 R E F A K F E K E K M N A K W D T G E N	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2281 AGGGAATTTGCCAAATTTGAGAAGGAAAAAATGAATGCCAAATGGGACACGGGTGAAAAT 781 P I Y K S A V T T V V N P K Y E G K - 2341 CCTATTTATAAGAGTGCTGTGACAACTGTTGTCAATCCGAAGTACGAGGGAAAATGA	
WBC009H07.bFSP_20010310.abd	No Homology	1 ATCCTCGTGCCGGGAGTGCAGATCCTTTGAACCATTGTTATGGTAGGACAGGCCCCTTCA 61 ACGGCCTGGGGAGCTGGAATAAGCTGGCTTACTGTTTGGAATCGTGCTGGTGGGTCAGAT 121 GTCTCTAGTTCTAGTAAAAAGCAACTGGAGTCTCCTGGGAGAAACTTCGGGAAGCAGAGT 181 TGTGTTAGGTAAGGCTCTGCTGACATTGCACAGTTTTAGACGAACGTTGGCACAGGATGT 241 TAGATTTCTGTGACAAGTTCATCTACCTATTTTAGTAAGCACATAGTTCTCCAGCTAAAA 301 TTTGAATTCTTCTTGAAATAAAAGAAGATGAAATGAAAGAATAATTCTTGAAATATCACT 361 CAAATACCCCCAGCATGTTGTGAGCTTCCTGTAAGTGGTGGGTTACAAATCTGCTGGGTG 421 CCAAGTGCTGGATAGTGCTGGGTGGCTGTGTAGGAACCCCCTTGGCTTGCGTGTGAAGGC 481 TTGCAGATTGCCAGGAGGCTCCAGCTAATGAGTTTTAGGTAGAGCCTGGAAAGCTGTGTG 541 TTAAACTTCTTTCCAAGGAATTCTGGTCACCAGGCGGCTTGGGAACGATGAGGGCAGGCC 601 ACATAGGATATGTTAGGCAGGAAAGAAACACCCTTTTAAAAGACAAGGGTAGAAGAGGAG 661 TGAAATACTTGGAACTCAGAACTAGCAAGAGAGTTGACAGATTTCCTATGATCTTTGGAA 721 ACTGTCTTCACTGATGAAAGTACACCGCTTTTGTAGACTATCTGATTAGAGGGCATTGTG 781 CTGCTTTTGTGAAGGGAAAGTGGCCGTGGTGGTGGAGATGTCAAAGACTTGGACAAGGGA 841 GCAGGGGCTGCCTAATTTCAAAGTCTGGTTTT	SEQ ID NO:37
		1 ACTTGTAGTGGTGACAGTTTAGAGAGTCTAAAACTCTGTAAGGTTGTAAAGGAGGCGTGA 61 CAAAACCAGCTGGAGTCAGGAACTGCTTCCACTCTGCTCATGCAACAGCCGAGTTAAGAA 121 ATAAGTGTTCCCCAGAATGCACACTGTGCTGCCACCCCCAGGTGACATTCTTTCCAGGTA 181 CATTTGACACCTCTTCTCGCACATCCTGTTCACCTGTTGGTGACCACACCCNTGGTCTCA 241 TGCGAGATTTAGTACACCTGCACAGTCCCTTCTCAGGGGCAGACCTCCTCCTGACGGCCT 301 CCGCCAGTGAGTTGCAGCCACCCGATGTTGCGTTTGGAAGTGTTTGTTGCTCCCGTTGGA 361 GAAAGTATTTGCATAAGCATTTCATGTGTCTAGTGTGGCATTTCTGGATGCGGCTGTCAC 421 AGCAGTGTTATTGGTAGTTAATCTTACTGCAAGGTGAACAGTATGGCTGTTTGCTTTGTC 481 CTTGCCATGGCGTTCTTAGAAAGTACCCTGTCTTTCAATATTGGTTTTTTCAACATGAAT 541 ATATTCTACTTACAAACTCGTTTTGCTTCTTTGTATATAATTTGCCTTGGGTTTATTGTG 601 CACAGTTTATTTAGTTATGTTTTCGTGTATTATCAGGAGCAATTTGATAAGTACATGTGA 661 ATAACCTCCTGTAAATGAATTTTATAACAAAATGTACTAAAATATTTTCTCAAAAAAAAA 721 AAAAAAAAA	SEQ ID NO:38
WBC011D03.bFSP_20010510.abd.	Homo sapiens nuclear autoantigen GS2NA mRNA.	1 GGGGAAGGGCAGATGGAGGAGGGATTGTAATGGCGGCAGCCGGCAGCTCCCTGCTCTGAC 61 CCACGGCAGGCACACAGCAACGACCCCTTCCCCGCCCCTCTCCCGGCCGGCCTCCGCCCC 121 GCAGCCAGCGCGGGGCCACCCTCTCCGGCCCTTCCCCCAGCTGTCGGCGTCTCGCCCTGC 181 GCCCCGGCCGGGGCCCCACACACAATGGACGAGCTTGCCGGAGGCGGTGGTGGCGGCCCG 241 GGGATGGCGGCCCCTCCCCGGCAGCAGCAGGGACCTGGGGGGAACCTGGGCCTTTCGCCC 301 GGGGGGAACGGAGCGGCGGGCGGCGGGGGTCCTCCGGCCTCCGAGGGAGCGGGTCCCGCG	SEQ ID NO:39

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		361 GCAGGCCCCGAGCTGTCCCGGCCGCAGCAGAACACTATCCCGGGATACTGCACTACATC	
		421 CAGCACGAGTGGGCTCGGTTCGAGATGGAGCGGCGCACTGGGAGGTGGAACGGCCCGAA	
		481 CTGCAGGCCCGGATTGCATTTCTACAAGGCGAAAGAAAAGGTCAAGAGAACCTGAAGAAG	
		541 GACTTAGTAAGAAGAATAAAGATGTTAGAGTATGCATTAAACAAGAAAGGGCAAAATAT	
		601 CACAAATTAAAATATGGCACGGAACTGAACCAAGGTGACTTGAAAATGCCAACCTTTGAG	
		661 TCAGAAGAAACCAAAGACACAGAGGCTCCCACAGCACCTCAGAATAGCCAGTTAACGTGG	
		721 AAGCAAGGCAGACAGCTTTTAAGACAGTATCTTCAGGAAGTAGGTTATACAGATACAATA	
		781 TTAGATGTCCGGTCTCAGCGGTAAGGTCATTACTTGGACTATCTAATTCAGAACCAAAT	
		841 GGATCAGTAGAAACAAAGAATTTAGAACAGATCCTGAATGGAGGTGAATCTCCTAAGCAA	
		901 AAGGGACAAGAAATAAAAAGCCCCTCTGGTGATGTTCTTGAGACATTCAATTCTTAGAA	
		961 AATGCTGATGACAGTGATGAAGAAGAGGAAAATGACATGATTGAAGGCATCCCAGAAGGA	
		1021 AAGGACAAACATCGGATGAATAAACACAAAATAGGTAATGAAGGTTTAGCTGCTGACCTA	
		1081 ACTGATGATCCTGATACTGAAGAAGCACTTAAAGAGTTTGATTTTTAGTCACTGCTGAA	
		1141 GATGGTGAAGGAGCTGGAGAAGCACGGAGTTCAGGGGATGGCACAGAATGGGCTGAACCA	
		1201 ATAACGTTTCCATCTGGAGGAGGCAAGTCATTTATTATGGTTCTGATGATGTTTTGTTA	
		1261 AGTGTACTGGGCCTTGGAGACCTTGCAGACTTGACGGTAACAAATGATGCAGACTATAGT	
		1321 TATGATTTGCCTGCCAATAAAGATGCCTTTCGAAAGACATGGAACCCCAAGTATACACTA	
		1381 CGTAGCCATTTTGATGGAGTACGGGCATTAGCTTTCCATCCTGTAGAACCTGTGCTGGTT	
		1441 ACTGCCTCTGAGGACCATACTCTCGAAACTTTGGAACTTGCAAAAACAGTTCCTGCCAAA	
		1501 AAGAGTGCCTCTTTGGATGTAGAGCCTATCTACACATTTAGGGCCCACATTGGTCCTGTT	
		1561 CTATCATTAGCTCTTAGTTCTAATGGAGAACAATGTTTTAGTGGTGGTATTGATGCAACC	
		1621 ATCCAGTGGTGGAATATGCCTAGCCCTAACGTGGATCCATATGACACATATGAGCCAAAT	
		1681 GTTCTAGCTGGCACTTTAGTTGCTCATACAGATGCTGTCTGGGTCTTTGCTTATAGTGGC	
		1741 ATAAAAAATCAGTTACTGTCTTGTTCAGCAGATGGCACTGTTAGGTTATGGAATCCGCAA	
		1801 GAAAAATTGCCGTGTATTTGCACTTACAATGGAGATAAAAAGCATGGAATACCTACATCA	
		1861 GTTGACTTTATAGGCTGTGATCCAGCTCATATGGTAACCTCTTTCAACACTGGTAGTGCA	
		1921 GTAATTTATGATTTAGAAACATCACAGTCATTGGTGATACTTTCATCACAGGTAGATTCT	
		1981 GGTTTACAATCTAATAATCATATCAACAGAGTAGTAAGTCATCCCACACTTCCTGTTACA	
		2041 ATAACTGCTCATGAAGATAGACACATCAAATTTTTTGACAATAAAACGGGTAAAATGATC	
		2101 CATTCTATGGTAGCTCACTTGGATGCTGTTACAAGTCTAGCAGTAGATCCTAATGGAATC	
		2161 TATTAAATGTCTGGAAGCCATGATTGTTCTATTAGATTGTGGAATTTGGACAGCAAGACA	
		2221 TGTGTGCAAGAAATAACAGCACATAGGAGAAAATTAGATGAATCAATTTATGATGTTGCT	
		2281 TTCCATCCATCAAAGCATATATTGCCAGTGCAGGGGCTGATGCCCTGGCCAAAGTGTTT	
		2341 GTGTGAATCAACAGAAGCTCACATTCTAACAGCAGACTTGCGTGGACAGAAAGAGGGTCT	
		2401 GCATCACTGCCATCAGAAAGCTTCCTGATATGACACTACATGTGATCTGCCTGGTGAAGG	
		2461 CTATTGAGGACAGGCATAAATTGGTAGAAATCACATCTTAATGTCAGGCTCATTAATTTA	
		2521 ATTGTAATTACTGTATTTTGTGGGACAAAAAAAAGGACTCCAGTATTTGTGGCCTGTACT	
		2581 GGATATGAACTGAGCGTATGTCTGTTTTTTAGGTATCTTTAAGCCAATGTGGAGTCTGAC	
		2641 CTTACAAAAAAGTTTTTTTTCTCTTCTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	
		2701 ATTTTGGACTCTGTGTGCTGCCTTAGGGTTAGGAATGTGGTGCTCTTGTTGGGGGGAAGT	
		2761 GAGCTCCAAGAGTAGCTTTTTTTTCATCTCTTAGTGATCTTCTGTTTATCAGTTGAATGCC	
		2821 ACAGATTCCCTTTTAAACTTATTTTGCTTTAAAAAAAAAAAAAAAAGAAAAAGAAAATTT	
		2881 AACTTAAAATATTTTAGCATTAGTTGCACAAAATGTTTGGATAAAATTCTAGTTTTTATA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2941 AGTCTTTTTATATATTTAGCCTGTCACAACAGTGCTCAAGATTGTATTGAAGTTTTTCTG 3001 CATTATACAACCCTAAAACACAGAGATCTCACTGACCCGTTGCCCTGTAACCACTTTCTT 3061 TCCTTCTTTTGCCTAATACAGCTCAGCTAAGTCCTTCCATAAAGATGCTAAATAACTTTC 3121 ATCATCACATAAATGTCTTCATAAACCAAGGACTATTAAGTGTATTAAAATGAAACAGTG 3181 GGGTTTAGTACTCCAAATGAACTCTTAAAGAAAAAAACTAATCTTGGCATCCTATCACTA 3241 TGTGATATTTTGTACATCTTACTGTATTCACAAGTTTATTTATCAAGGATTATCCATCTT 3301 GCTAATGGCCTATTATTTATTTCACTTTTTGTTGGTCTTTATATCCTTTTATTAATGTGC 3361 TAAAGGAACCTGTATATCTATTTTGGAACTCTTTGAATAGTCTAAAATAGACTAAAAATG 3421 GAGTATTTTATAGTTTAAATTACAAACCAAGGTGGTTCCCCCTAAGATATATATCTTGGT 3481 TTACCATGATTCCAAACAAAACTAACTTGTTTAAAAATATTTGGAGTAAAGTTTTATTTG 3541 CATTACAAATAGGATACAAAAATAGTTGAATCAGGATACAGAAATCTGCTGTGTTTTGAC 3601 TAGTTATCCCTGTTTTATTTTTTTAGATGTGCTTAATTTATGGTGTAACTAAAGATTTTG 3661 TTTGTGTAATGCATGATTAAGACAATAAAGTATTTTTTCTAGTCTTCCGAGAAACTTTTC 3721 TGATCAGTTTGCGAGTTTTGATGAGTTTTGTAAGGTTTTTGTTTTACAAACTATGAATCA 3781 GCAAATTTTTAAGATTGTACCACATAGCAAACATACAGCTGTTGAAAAATAATGTATATA 3841 AAATGCATATAATAAATATTAAATTGTGTACCTGTA	
		1 M D E L A G G G G G G P G M A A P P R Q 1 ATGGACGAGCTTGCCGGAGGCGGTGGTGGCGGCCCGGGGATGGCGGCCCCTCCCCGGCAG	SEQ ID NO:40
		21 Q Q G P G G N L G L S P G G N G A A G G 61 CAGCAGGGACCTGGGGGGAACCTGGGCCTTTCGCCCGGGGGGAACGGAGCGGCGGGCGGC	
		41 G G P P A S E G A G P A A G P E L S R P 121 GGGGGTCCTCCGGCCTCCGAGGGAGCGGGTCCCGCGGCAGGCCCCGAGCTGTCCCGGCCG	
		61 Q Q N T I P G I L H Y I Q H E W A R F E 181 CAGCAGAACACTATCCCGGGGATACTGCACTACATCCAGCACGAGTGGGCTCGGTTCGAG	
		81 M E R A H W E V E R A E L Q A R I A F L 241 ATGGAGCGGGCGCACTGGGAGGTGGAACGGGCCGAACTGCAGGCCCGGATTGCATTTCTA	
		101 Q G E R K G Q E N L K K D L V R R I K M 301 CAAGGCGAAAGAAAAGGTCAAGAGAACCTGAAGAAGGACTTAGTAAGAAGAATAAAGATG	
		121 L E Y A L K Q E R A K Y H K L K Y G T E 361 TTAGAGTATGCATTAAAACAAGAAAGGGCAAAATATCACAAATTAAAATATGGCACGGAA	
		141 L N Q G D L K M P T F E S E E T K D T E 421 CTGAACCAAGGTGACTTGAAAATGCCAACCTTTGAGTCAGAAGAAACCAAAGACACAGAG	
		161 A P T A P Q N S Q L T W K Q G R Q L L R 481 GCTCCCACAGCACCTCAGAATAGCCAGTTAACGTGGAAGCAAGGCAGACAGCTTTTAAGA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		181 Q Y L Q E V G Y T D T I L D V R R S Q R V 541 CAGTATCTTCAGGAAGTAGGTTATACAGATACAATATTAGATGTCCGGTCTCAGCGGGTA	
		201 R S L L G L S N S E P N G S V E T K N L 601 AGGTCATTACTTGGACTATCTAATTCAGAACCAAATGGATCAGTAGAAACAAAGAATTTA	
		221 E Q I L N G G E S P K Q K G Q E I K R P 661 GAACAGATCCTGAATGGAGGTGAATCTCCTAAGCAAAAGGGACAAGAAATAAAAAGGCCC	
		241 S G D V L E T F N F L E N A D D S D E E 721 TCTGGTGATGTTCTTGAGACATTCAATTTCTTAGAAAATGCTGATGACAGTGATGAAGAA	
		261 E E N D M I E G I P E G K D K H R M N K 781 GAGGAAAATGACATGATTGAAGGCATCCCAGAAGGAAAGGACAAACATCGGATGAATAAA	
		281 H K I G N E G L A A D L T D D P D T E E 841 CACAAAATAGGTAATGAAGGTTTAGCTGCTGACCTAACTGATGATCCTGATACTGAAGAA	
		301 A L K E F D F L V T A E D G E G A G E A 901 GCACTTAAAGAGTTTGATTTTTTAGTCACTGCTGAAGATGGTGAAGGAGCTGGAGAAGCA	
		321 R S S G D G T E W A E P I T F P S G G G 961 CGGAGTTCAGGGGATGGCACAGAATGGGCTGAACCAATAACGTTTCCATCTGGAGGAGGC	
		341 K S F I M G S D D V L L S V L G L G D L 1021 AAGTCATTTATTATGGGTTCTGATGATGTTTTGTTAAGTGTACTGGGCCTTGGAGACCTT	
		361 A D L T V T N D A D Y S Y D L P A N K D 1081 GCAGACTTGACGGTAACAAATGATGCAGACTATAGTTATGATTTGCCTGCCAATAAAGAT	
		381 A F R K T W N P K Y T L R S H F D G V R 1141 GCCTTTCGAAAGACATGGAACCCCAAGTATACACTACGTAGCCATTTTGATGGAGTACGG	
		401 A L A F H P V E P V L V T A S E D H T L 1201 GCATTAGCTTTCCATCCTGTAGAACCTGTGCTGGTTACTGCCTCTGAGGACCATACTCTG	
		421 K L W N L Q K T V P A K K S A S L D V E 1261 AAACTTTGGAACTTGCAAAAAACAGTTCCTGCCAAAAAGAGTGCCTCTTTGGATGTAGAG	
		441 P I Y T F R A H I G P V L S L A L S S N 1321 CCTATCTACACATTTAGGGCCCACATTGGTCCTGTTCTATCATTAGCTCTTAGTTCTAAT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		461 G E Q C F S G G I D A T I Q W W N M P S 1381 GGAGACAATGTTTTAGTGGTGGTATTGATGCAACCATCCAGTGGTGGAATATGCCTAGC 481 P N V D P Y Y D T Y E P N V L L A G T L V A 1441 CCTAACGTGGATCCATATGACACATATGAGCCAAATGTTCTAGCTGGCACTTTAGTTGCT 501 H T D A V W G L A Y Y S G I K N Q L L S C 1501 CATACAGATGCTGTCTGGGGTCTTGCTTATAGTGGCATAAAAAATCAGTTACTGTCTTGT 521 S A D G T V R L W N P Q E K L P C I C T 1561 TCAGCAGATGGCACTGTTAGGTTATGGAATCCGCAAGAAAAATTGCCGTGTATTTGCACT 541 Y N G D K K H G I P T S V D F I G C D P 1621 TACAATGGAGATAAAAAGCATGGAATACCTACATCAGTTGACTTTATAGGCTGTGATCCA 561 A H M V T S F N T G S A V I Y D L E T S 1681 GCTCATATGGTAACCTCTTTCAACACTGGTAGTGCAGTAATTTATGATTTAGAAACATCA 581 Q S L V I L S S Q V D S G L Q S N N H I 1741 CAGTCATTGGTGATACTTTCATCACAGGTAGATTCTGGTTTACAATCTAATAATCATATC 601 N R V V S H P T L P V T I T A H E D R H 1801 AACAGAGTAGTAAGTCATCCCACACTTCCTGTTACAATAACTGCTCATGAAGATAGACAC 621 I K F F D N K T G K M I H S M V A H L D 1861 ATCAAATTTTTTGACAATAAAACGGGTAAAATGATCCATTCTATGGTAGCTCACTTGGAT 641 A V T S L A V D P N G I Y - 1921 GCTGTTACAAGTCTAGCAGTAGATCCTAATGGAATCTATTAA	
WBC011F05.bFSP_20010510.abd	No Homology	1 GGCCGCCGCCACTGTTGGGCTCTCCTTTCAGTCGTCATTTTTAAGGAAAGAAGGGTACTA 61 TGTTTATTGTTAAAATTTCACAGAAAATTTTTGTCTGATGAATTTATTAGTCTTCATTTT 121 GAGGGTAAAAGAATTTTAGAAAATGCAAATATTCTGTAAAAAATTTAGATTTTTGATATT 181 TTGGGAAAAGTTGATGAAAGCAACCTCAGATAAAAATTTTCTGAAAACCATCAATGTGGT 241 CACGATACAGACTTCAGTGTGCTGTTCCTGGTCGCGGGTGTAACGGAGGAGGGGTTCCAA 301 CGCAGTTTGTGCCGGGAAATCCGAGTGCGCGCCCAAAGGAGAGGTTGGCCGCGGTGGCGG 361 CAGCAGCACCTCCCTGCACCTCACTTCTTAAAGCCAAGATTAGTTTTATGCCCTCCTCCT 421 TTCTGGGGTATTTGACTTTCTAGTTCATGATAGAAAATCCTCTTTGCTTTGCCAGTCGAT 481 CCCACTTGGTTAGATGACTTGGTAAGGGGGATGGATGTCCAGGAGTAAATGAACCTTGAC 541 TGTGTCTTACACTTGCAATGATATTTATAATTTTGGTCATTAAAACATTTTAATTAGTG 601 GCCAGAATATAAAACTTCCTTTCTCTTGGGAAAAGTCTTGTAGCCACTGGGAGTTGGGC 661 AGGTAGTCACACGGAACTCAGCAGTCACTAGATGTTCTTCCTTCTCACCAGTGCTTG	SEQ ID NO:41

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		721 AGCTTTCACAGTGGACTTGATTGAGTTGTCAATTTAGTGGTAATAAATGAGCTGTACGTT 781 GGTCCC	
			SEQ ID NO:42
		1 GTGACTTGAGCACGGTTTAGTTTAGTCTTCACCTTGGCTGTCACCTTCCAGAGGGTGTGT 61 GCACAGACCCTGGGGCACACACAGCACTGAGCACCACGAGGATGCCCAAGACCGAGCAAC 121 AGCAAGGGCTGGTTTCTCCCGGTGTTACAAACCACACAAGCAGACGTCTCTGAGCGTTT 181 CCAGTGTTTTATCCAAATAAAAACTCTACTAGGGCTCTTGCTGACTTCAGTGCCTTTTGT 241 AAATCATTTTTGATTTTCCTCAACTTGCTTTTTGGGAATAGGCAGTGATGCTAAGTGGAG 301 GTAAGTGAGATTCTTTCTCCTCGTTAAGTTTTGTTCTTAAAACTTCTACATTGAAACTTG 361 TATTTAAAATAGCTTATTTCTTTCACGTGATAACAAGACAGGTCAGGAATATGGAATCAA 421 GATTTAGATTTTAAAATTCAAAAGGTTGTTACACAGGGTGTTTCCACTTGTGTAGCAGTG 481 GAATCTAGATATAAGACAGAAAAACACATTCTCTTCTTAAAGACCAACGGCATTTTTAAAA 541 GGCATCTTTGTTTCTCAACAGAAATCGGAATACAGATGTTATATTCACAGTCATAACCTGT 601 TTCCTCTAAGATCTTGCTATACTGTCCTGTATATTGTTGTAAATATTCAGATGGAAATTA 661 AAATGGTGTTTTTTGCCCTAAAAAAAAAAAAAAAAA	
WBC012A03.bFSP_20010810.abd	No Homology		SEQ ID NO:43
		1 GGAAGCTTTGAACTGTGCTGACTCTTCTGTTTGGGGAAGGAGGTTGTTTTCTGTGTGCCT 61 CAGAATATGACGGCTGCCAAACCATTACCTCCACCTAAAGCAGTGTAACACCAGAGCGTT 121 CAGTCCCAGATCAGATCCTTTTAGGACAGAAGTGTGTTTCCTCATTTTGGAGTGGAGCTG 181 TGAGTGGATGCATGCTCTGTCAGCTTGCATTTGTCCACTCTCTGTGCAGGCTCCGTGAGA 241 GTCTCAGAGCTGGGCCGGGCCACATGCATCAGGTCCTTCTCTCCTCTGGGTGTCCTCGGG 301 GGCACCTTGGGCCTGAGTCTCCCTCCAAGAGGCAGAAAGTGAGTCTGGTGGACTAGAGAT 361 CTCACCCATTCTGTGGGCTGGGGTTCCAGGCAGCCCAGCTGTCACCTGGGAACATCTGGA 421 GGAGGGTTGGCCCTCAGCACTCAGCGGGTGCCCGTGGTGTGGAGGATCCACAGTCAGCCC 481 ATGTGAATGAGCTACAGGAAGTGGTAATCACGTGTAGAAAAAATAAAAGCCTGGGAGGCT 541 GCAAACAGAACAGAATTCTTGTTTCATGAGGCACAGGAGCATTGCTACCACCAGTCTCAG 601 AGCACTGTGAAGGGACACACAGATCCCAGAATAGTCAGGAAAAGGTTTCACTATAACCAA 661 GAAGTCATGTTAGTGATGTGTTAGTCACAGACAGCACCCACAAACCTGGGCACTTGGCAG 721 ACGCGTACCAGCTTTGCGTACGTCCTGGGCAGAGAGCTGGTTCCACACCATTTGCATGGT 781 CTGCAGGAGCTTCTGCTACTGAATCCATGTTGGGTGGTTGATGGGGAGCAGCCCCCTGGGA 841 TGGGCCTGCTGGGATTGTTCATCCTATCAGTGTATTTGGTGTCCTCCTCTTCTCTGTT	
			SEQ ID NO:44
		1 TGCATGCGCAGAGCCCCTCTCAATGGGAGGAGAGGTGAGTAGGAGGAGGAAGGTTAGCAG 61 TGCCCTGAGTGATGTCCAGTTCCATTAGACACTCTGTCCCCATCTTCCCAACAGTCTATG 121 TGGAAGGAAAGGAAAGAATTTACTCTGTTAGGAATCTCTCGAAGAAAATTTGAAACCTG 181 TGAGTCACAGTCAAAGAAACTTATCCACGAAACATAATTCATGTTTTCATGAGTCCTATA 241 GATGTTTGAGTCAGAAGAAGGAGGGAGGTGACTGTGAGAAATCGCCCCTTTTTATTC 301 AACATCTGGGGATTGCAAATGCAGAAGGAAATCTATTTGGTTAGGCCTAGGCCATGCCTT 361 GGCTGAGTATAAAATACTCTTAGTCGTGAAGGCTCAGATAGTCTGTACGTGAACTGCTCCA 421 AGCGGGGTTACTGGCACATGTACAGAGGCATTCAGCGTGGACTGTGCCTGAGACCGACAG 481 GGCGGAGGATTCGATCCCAGTGAGAGCTGAGTCATTTGTTACAGGTATGAACGCCCAAGG 541 AAATTACCTTTTAGCAAAAGAAAGTTAAATGATTTAACAGTCCCCATATGTGTTAATGTC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		601 TCACATGTATTTGTATCATAACGTGTAACATAATTGTGGAACAAAAATATCTACAATAAA 661 TCTTTTAGTATTTGTGAAAAAAAAAAAAAAAAAAA	
WBC012B04.bFSP_20010810.abd	Homo sapiens EGF-like-domain, multiple 5 (EGFL5)	1 ATGGCGGCAGAGACCTCGCAAGGCTGCGACCAGGCTCTCTGGAGCAGCAGAGGGCATGCC 61 AAGCTCTACATCGTCGCTGCCGCTGCCCTCTCCCATCGCGGGTTCCCGCGCTGGTCCCCG 121 CCCGAGCTGGGCCCGGTGGAGCAGATGACTAGGCCCGGCGTCTGCCGCGCGGGGCGCATC 181 CTTTGTCTGCTCCGCGGCGCCCGGTGCCCGAGGCCCGCGCCCACACTCTTTGGGCAGACAA 241 AGCCGGGGCCGCCGCCGAGCCCGGCGGCTAGAGCTGGGCTCCGCACCACCCTTCTCCCGCC 301 TCACGGACCCCCCCCTCCTCCTGGACGTCCTCTGATTGGCCTACGGGGCTACAAAGAGGCC 361 GGGAAGCGGGCGGATCACGTGGGCGACTGTGCTTCCCATTGGCGACGGCTCCCACGGC 421 CCAGGCCCCGAGGACCGGGCCCCCGCGCGCCACCGTCCACCGACCCCTGGCTGCGACTTC 481 TCCAGCCCAGTCCCCGGAGACCACCCCTCTTTGGGCGACTGCTGGACCCTCTTCCACCAC 541 CTTTCAGGCGCCGCGCTCGGCCCCTCGCCGACCACCCCCTCCGGCGGCGGAACGCACTTCGAC 601 CACCTCTCAGGCGCCGACCAGACCCGCGCCGCCACCACCTTTCGACGACCACTGGCCCGGC 661 GCCGACCACCCCTGTAGCGACCACCGTACCGGCGCCCACGACTCCCCGGACCCCGACCCC 721 CGATCTCCCCAGCAGCAGCAACAGCAGCGTCCTCCCCCACCCCACCTGCCACCGAGGCCCC 781 CTCTTCGCCTCCTCCAGAGACCAGAATGGGCGCAAACTTTTGGGTTGGGTTCGCGCACCC 841 AGCCTCTCTGCCTGGGTTATTTGGGGAAGTTTGAAAGCCCGCATAGTACCTCCTTCAACC 901 ACTGGGTCAAAAGCTGAGGAGTATGTATGTAACTGCTCTGTGGTTGGAAGCCTGAATGTG 961 AATCGCTGCAACCAGACCACAGGGCAGTGTGAGTGTCGGCCAGGTTATCAGGGGCTTCAC 1021 TGTGAAACCTGCAAAGAGGGCTTTTACCTAAATTACACTTCTGGCTCTGTCAGCCATGT 1081 GACTGTAGTCCACATGGAGCTCTCAGCATACCGTGCAACAGTTCTGGGAAATGCCAGTGC 1141 AAAGTGGGTGTCATTGGCTCTATATGTGACCGATGCCAAGATGGATATTATGGCTTTAGT 1201 AAGAATGGCTGCTTGCCCTGCCAATGCAATAATCGGTCTGCCAGTTGCGATGCCCTCACA 1261 GGTGCTTGTTTAAACTGCCAGGAAAATAGCAAAGGAAATCACTGTGAAGAATGTAAAGAA 1321 GGATTTTATCAGAGTCCTGATGCCACTAAAGAATGTCTTCGCTGCCCTTGTTCAGCAGTG 1381 ACATCTACAGGCAGCTGCTCTATAAAATCGAGTGAATTGGAACCTGAATGTGACCAGTGT 1441 AAAGATGGTTACATAGGCCCGAACTGCAATAAATGTGAAAATGGCTATTACAATTTTGAC 1501 AGCATCTGTAGAAAGTGCCAATGTCACGGCCATGTGGACCCAGTTAAAACTCCAAAGATT 1561 TGTAAGCCCGAGAGTGGTGAGTGCATCAACTGCCTCCATAACACCACTGGGTTTTGGTGT 1621 GAGAACTGCCTAGAAGGTTATGTTCACGACCTCGAGGGAAATTGCATCAAGAAAGAAGTT 1681 ATTCTTCCAACACCTGAAGGTTCTACCATTTTGGTTTCCAATGCCTCTTTGACCACATCA 1741 GTGCCCACCCCTGTTATAAATAGTACTTTTACCCCTACAACCCTGCAGACTATCTTTTCA 1801 GTAAGCACTTCTGAAAACAGCACTTCAGCTTTAGCTGATGTATCATGGACCCAATTTAAC 1861 ATCATCATTTTGACAGTCATCATCATTGTTGTGGTGCTGCTAATGGGATTTGTGGGGCT 1921 GTATATATGTACCGCGAGTACCAAAACCGGAAACTCAATGCCCCCTTTGGACCATCGAG 1981 CTGAAAGAAGACAATATCAGTTTCAGCAGCTACCATGACAGCATTCCCAATGCAGATGTT 2041 TCGGGATTGTTGGAAGATGATGGCAATGAAGTGGCTCCCAATGGGCAGCTGACCCTGACG 2101 ACGCCCATACATAACTACAAAGCCTAAGGAGCTAGAACTGTTCTGAATTGTTAACCACA 2161 GTGCTTGCTAAGACAGAGTCAGCCCCTGGGCCAGACAAAGCCTGGCTAGAGTTTGCTGAG 2221 AAAGCAAAGGCAAATAGTGCATCTGAAATTTTCAGGTACAAATTTGTAATGCGCTTAGCC	SEQ ID NO:45

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2281 TATCTATTGCTCTTAGTTTTCCCATGAAGATCTGAAGCGTTCACTGTCATTAGGACTTGA	
		2341 AGTAAAGTATATTTTTGTACCAAACCACATGGGAGTATGGAAAGGCTGAACCCCATAGTG	
		2401 CAGCCCAAAACCACTTTGACCTCCAGATAGACTCCTGGGGAAGCATTCACCAAGCCAGTG	
		2461 GTAACAAGATGATGAATGTGGAGGGGGAAAAGACTGCTGGAAGACTTCATCTCCATTCCT	
		2521 GAAACATTTTTTTTAAAACAGTGTCAGGGATTATATTCGTTTTACTATACAAAAGGACAT	
		2581 CATTGAGGAAAAGCTTGTTTCTAGGCTGTATCACAGTAAATAATCTTGATTGTTCTAGA	
		2641 ACAGGGGTAGAAAAGTCCCAAGATCTTCAGAAGGGCTTGGTTTTTTCCTCCCAGGATTCT	
		2701 TGCTCAGTGATGAGTTGAAAGCACAGGATAAGCTTCTAAGGGAGGAAGGCAGCATTGGGG	
		2761 AGCAGGAGGCTGATGGTCCTCCTCCAGGGTCTCAGTGTAAATGATAAATTGTCTAAAAATA	
		2821 AGGAATATTCCTGCCTCTAGAGAAATAAGGTGTACATAGTTAATGTAGCATATCTGGTCG	
		2881 ACGTTGTATTTGTATCTATTTGTAAAAAAAAAAATCATGTCATATTTTATCATCTGGAATT	
		2941 TATTTGTACAGCAGTTAATGGTGTTGTAAAAAGAAAAAATATGGGATTGCTTAAAATACT	
		3001 GTAAAATAGATGGCAATATTGCTAGAGCTGGGACTCTGGTGAGCATCCGTCATTTTTAGT	
		3061 CCTTCTTGAGGACATTGCTGAATTTATAAGAGGTCGAATGTTTCTTCTTTCCTTTCTC	
		3121 AGTCTAAAAGTAGAGTATATATGCTCTTTGACTTACTATGATTCAAGCAATAGATTTTGAA	
		3181 GTCAGTAATCGTTAAGCTGGGACATAGGATGCATTCTCCCAAAACATTAATCTAATTAGA	
		3241 CATTAGCCACCCTATATATTTTACATAGATTAATATAAAACATATCCTCATTAAAAAATG	
		3301 TTTTTCTTGAATGTAAAAGATAGTCTTCCAAAGGATAGAAATATTTTAGTTCCAAGAGAA	
		3361 AAGCCATCATATTACTTGGGATCTGTAGTTTTCATGCCTATAGAAATATTTATAATCCTCC	
		3421 CTCACCCCAAATAAAAAATCTCCTACATGTGAACATAGCCTGTCACTCATTTGCCATGAG	
		3481 GTATGTGCCATCTCCCTGCAGTGCTATAGTTCTCCCATTGTCTTCCTGTCTGGTTAATGA	
		3541 GCAGCTTTGTAGATGGGTGTGTCTAGTTAGTTCTTGCTTTTTGATGGAGTTTTTTCCTAG	
		3601 AGGCCAACTACTGTTGCTCTCGTTTATTATGATATTGACATTTTGGGTTAAGCAAGGTGG	
		3661 GTGGGAAAGGTGGTCAGATGTTAAATATAACTTATTAGGAGGAACAGTGAACTGTGAAGT	
		3721 GGTTAGAAAAAAAAATAAAAACTTCTTATTAGATTAGACCTAGGAAATTCAAGCTGACCCC	
		3781 TTTGCCTAACTTCCCTAGAGAAAAACCTAGAACTTGGTCATCCCTTTATAGGAGACCCCT	
		3841 AAGTTGTTCTCAGGGTTTGGAGATGATGTTCTGGAGGGAGTACAAGCAAATAATCTACTT	
		3901 CTGGTAATCTGAGGGTGCTTTGCGTATTTGGCCATTGCTCAGAAGAATAGAGGTTACATT	
		3961 ATATTACATTATATGAAAATTATTTAGTTTTTCTATAGCCCTTTGTAGTTTGCAAAGCAC	
		4021 TTTTCCATATGTGTGTCCTCTCTTCCACACCATAGCCCCCTGAGGAAGTAATTGTTGTCCC	
		4081 CCATTTTATAGATGAAAAGGCTGAGGCACAGAGGAGCTAAATATCTTGTTCAAGGCTATA	
		4141 CAATGTGTGTGATTATTAGGCTTGGAATCAGGGCCTCTAACTCTAAAGCACATGTTTTTT	
		4201 CAACTATATGCAGAAATTGCCTAGCCATGGACACACAAGAAAGCTGGGAGGAAGAGTTCTAC	
		4261 TTGTGGATGTTTTTTAATTTTTTTTAAATATCAGGAGCAATCCAGGGCCATACAGCTATGA	
		4321 AGCACTTAGTGAAAAGAACACAAGAAGATTTACTAACTGAAGTTAGTATTAGTGATTAGA	
		4381 AAACAAAACTGCCAGTTTGTGCTTCATTAAGGTGAACTCATCTCTCCAAGCAGGAAGGGA	
		4441 AAATTTGCTTTCCCTAGCAGTTGCTGCATATGTGTGTACAGACTGCACAATTCTAAGAAA	
		4501 TTGTGCAAAATGGCATACCTGTCTTTCTCCCAGATACACCGCCCCCCTGCCCCCCCAAAA	
		4561 AAGGTCAGGATTAAAGGTGGTGAGAAGTGAACATTTATTAAACAGAAGTTAAACCAATAG	
		4621 AGAGAAAGGAGGTTTGTTGGAGTCTAAGAGGATTTTGACCATGTAGAAATTCCTTGAAAC	
		4681 AGACCTTAAAAGGTATTGAAAAATTGAATCACAAGAAAGTTTACCTTTAAATACTTGTT	
		4741 AATGGCTCCCTAGATCATGGTTATAATTTTTCTCAATGGGAAAAAAAGTCTTAAAATTTGT	
		4801 TTTAAATAAGATCCTCTAATGTCTCGAGCTTTTTGATTCTGGAAATAATTTGCTTTAAAA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		4861 TATAAATCAATCAGAAAGTGATCTACCACTGAAATCATTCTAGGAAACTAGCATGGATG 4921 CACTGCACAATGTTCTTTCCTCTAAAGGCATGGGCCCCATAAACTGTGGCATCTGGCAGC 4981 AGGATGCCATCAGTCCTTTAGAAAGCCTAATTTTGGGCCGGGTGCGTGGCTCACGCCTG 5041 TAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCACAAGGTCAGGAGTTCGAGACCA 5101 GCCTGGTCAACATGGCGAAATCCCGTCTCTACTAAAAACACAAAAATTAGCCGGGTGTAC 5161 GTGCCTGTAGTCTCAGCTACTTGGGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGG 5221 CAGAGGTTACAGTGAGCCGAGATGGCGCCATTTCACTCCAGCCTGGGCGACAGAGCAAGA 5281 CTCTGTCTCAAAAAAAAGGAGAAAAAGAAAGCCTAATATTGGGAGAATGTTTGTGTAAG 5341 GATTGGAAATCTGTTTATTTTTAAATAAGATAGCACTGATGTGAATCTTATTTGGAAATT 5401 ACAGATACTGCCATTAAGCGATGCTTTTATCTTCATTAATTCATTTGTGGTAAGCGCCTAT 5461 GCATTTCTGATGGTTAGGTGCCCTAGGTAGTGTTAAGTATGTCCGTGTCCTCCCTTACTC 5521 CCCTCTCGCTCCCTCTACCCTCTATCCCCTAGGGTTCTTTTATTAATGGAATTTCTCCAT 5581 TTATAGAGAAAAAATGACATTTGAAAACTAAAGCTCATTTATATTAATACTAAGGTCCTG 5641 TGGGCCTAGTGCGTTACTCTTCCCAGTGATACCTAGATTTTAAGAGTAGAGAACAGAGGA 5701 AACATGGGATGAGAGGAGAGAGGTTTTTTAGACAACATTTGTAGACACCTCAAATTATAT 5761 CACTGTTCTCTAGCTCCCAATATGCCTGGGAAAATTGGCCTTTAAAGCAATGCTCACTGAC 5821 CTGCTAGTTCGTTTTGGTCAGCTGAGTACCATCAGGATATTTAACCTTTAAGTGCTGTT 5881 TTGGGAGTAGAAAACTAAAGCAACAATACTTCCTCTTGACAGCTTTGATTGGAATGGGGT 5941 TATTAGATCATTCACCTTGGTCCTACACTTTTAGGATGCTTGGTGAACATCACACCACT 6001 TATCATGAACATTCCCTGGTTCCTATATTTTGGGCTATGTGGGTAGGAATTGTTACTTGT 6061 TACTGCAGCAGCAGCCCTAGAAAGTAAGCCCAGGGCTTCAGATCTAAGTTAGTCCAAAAG 6121 CTAAATGGTTTAAAGTTAAGTTTTAATACTAGGCACAAGCACTCTGTAATACGTTAAATT 6181 TCAGCCCAAGCAATTAGGAAATGTTTCTGAAACATTAGACTTATATTTACGTCACTAAAA 6241 TTCTAACACAAATTTTAAAACCGTGTCTCATACATATGCTGTACTAGGCTTCCTGATGCA 6301 TTTCTAAATTTGTGTATGATTTGAATATATGAAAGAATTTATACAAGAGTGTTATTTAAA 6361 ATTATTAAAAATAAATGTATATAATTTGTACCTATTGTAGATTTGTTGTTTACTTTTTTG 6421 TGTGGTCAGAGTTGTTTCATGTCTTCAAATACATGCCAAGGATCATTTACTTTCAGCCCA 6481 CTTCATAAAAATCTTTGAACTCTT 1 M A A E T S Q G C D Q A L W S S R G H A 1 ATGGCGGCAGAGACCTCGCAAGGCTGCGACCAGGCTCTCTGGAGCAGCAGAGGGCATGCC 21 K L Y I V A A A A L S H R G V P A R S P 61 AAGCTCTACATCGTCGCTGCCGCTGCCCTCTCCCATCGCGGGGTTCCCGCGCGGTCCCCG 41 P E L G P V E Q M T R P G V C R A G R I 121 CCCGAGCTGGGCCCGGTGGAGCAGATGACTAGGCCCGGCGTCTGCCGCGCGGGGCGCATC 61 L C L L R G A R C P R P A P H S L G R Q 181 CTTTGTCTGCTCCGCGGCGCCCGGTGCCCGAGGCCCGCGCCCCACTCTTTGGGCAGACAA 81 S R G R R E P G G L E L G S H H P S P A 241 AGCCGGGGCCGCCGCGAGCCCGCGGGCTAGAGCTGGGCTCGCACCACCCTTCTCCCGCC	SEQ ID NO:46

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		101 S R T A P S P G R P L I G L R G Y K E A 301 TCACGGACCGCCCCCTCTCCTGGACGTCCTCTGATTGGCCTACGGGGCTACAAAGAGGCC	
		121 G K R A D H V G G D C G F P L G D G S H G 361 GGGAAGCGGGCGGATCACGTGGGCGACTGTGGCTTCCCATTGGCGACGGCTCCCACGGC	
		141 P G P E D R A P A R H R P P T P G C D F 421 CCAGGCCCCGAGGACCGGGCCCCCGCGCGCCACCGTCCACCGACCCCTGGCTGCGACTTC	
		161 S S P V P G D H P S L G D C W T L F H H 481 TCCAGCCCAGTCCCCGGAGACCACACCCTCTTTGGGCGACTGCTGGACCCTCTTCCACCAC	
		181 L S G A A R P L A D H P S G G G T H F D 541 CTTTCAGGCGCCGCTCGGCCCCTCGCCGACCACCCCTCCGGCGCGGAACGCACTTCGAC	
		201 H L S G A D Q T R A D H P F D D H W P G 601 CACCTCTCAGGCGCCGACCAGACCCGCGCCGACCACCCTTTCGACGACCACTGGCCCGGC	
		221 A D H P C S D H R T G A H D S P D P D P 661 GCCGACCACCCCTGTAGCGACCACCGTACCGGCGCCCACGACTCCCCGGACCCCGACCCC	
		241 R S P Q Q Q Q Q R P P H P T C H R G P 721 CGATCTCCCCAGCAGCAACAGCAGCGTCCTCCCCACCCCACCTGCCACCGAGGCCCC	
		261 L F A S S R D Q N G R K L L G W V R A P 781 CTCTTCGCCTCCTCCAGAGACCAGAATGGGCGCAAACTTTGGGTTGGGTTCGCGCACCC	
		281 S L S A W V I W G S L K A R I V P P S T 841 AGCCTCTCTGCCTGGGTTATTTGGGGAAGTTTGAAAGCCCGCATAGTACCTCCTTCAACC	
		301 T G S K A E E Y V C N C S V V G S L N V 901 ACTGGGTCAAAAGCTGAGGAGTATGTATGTAACTGCTCTGTGGTTCGAAGCCTGAATGTG	
		321 N R C N Q T T G Q C E C R P G Y Q G L H 961 AATCGCTGCAACCAGACCACAGGGCAGTGTGAGTGTCGGCCAGGTTATCAGGGCTTCAC	
		341 C E T C K E G F Y L N Y T S G L C Q P C 1021 TGTGAAACCTGCAAGAGGGCTTTACCTAAATTACACTTCTGGCTCTGTCAGCCATGT	
		361 D C S P H G A L S I P C N S S G K C Q C 1081 GACTGTAGTCCACATGGAGCTCTCAGCATACCGTGCAACAGTTCTGGGAAATGCCAGTGC	

Gene Name	GenBank HomoIogy	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		381 K V G V I G S I C D R C Q D G Y Y G F S 1141 AAAGTGGGTGTCATTGGCTCTATATGTGACCGATGCCAAGATGGATATTATGGCTTTAGT	
		401 K N G C L P C Q C N N R S A S C D A L T 1201 AAGAATGGCTGCTTGCCCTGCCAATGCAATAATCGGTCTGCCAGTTGCGATGCCCTCACA	
		421 G A C L N C Q E N S K G N H C E E C K E 1261 GGTGCTTGTTTAAACTGCCAGGAAAATAGCAAAGGAAATCACTGTGAAGAATGTAAAGAA	
		441 G F Y Q S P D A T K E C L R C P C S A V 1321 GGATTTTATCAGAGTCCTGATGCCACTAAAGAATGTCTTCGCTGCCCTTGTTCAGCAGTG	
		461 T S T G S C S I K S S E L E P E C D Q C 1381 ACATCTACAGGCAGCTGCTCTATAAAATCGAGTGAATTGGAACCTGAATGTGACCAGTGT	
		481 K D G Y I G P N C N K C E N G Y Y N F D 1441 AAAGATGGTTACATAGGCCCGAACTGCAATAAATGTGAAAATGGCTATTACAATTTTGAC	
		501 S I C R K C Q C H G H V D P V K T P K I 1501 AGCATCTGTAGAAAGTGCCAATGTCACGGCCATGTGGACCCAGTTAAAACTCCAAAGATT	
		521 C K P E S G E C I N C L H N T T G F W C 1561 TGTAAGCCCGAGAGTGGTGAGTGCATCAACTGCCTCCATACACCACTGGGTTTTGGTGT	
		541 E N C L E G Y V H D L E G N C I K K E V 1621 GAGAACTGCCTAGAAGGTTATGTTCACGACCTCGAGGGAAATTGCATCAAGAAAGAAGTT	
		561 I L P T P E G S T I L V S N A S L T T S 1681 ATTCTTCCAACACCTGAAGGTTCTACCATTTTGGTTTCCAATGCCTCTTTGACCACATCA	
		581 V P T P V I N S T F T P T T L Q T I F S 1741 GTGCCCACCCCTGTTATAAATAGTACTTTTACCCCTACAACCCTGCAGACTATCTTTTCA	
		601 V S T S E N S T S A L A D V S W T Q F N 1801 GTAAGCACTTCTGAAAACAGCACTTCAGCTTTAGCTGATGTATCATGGACCCAATTTAAC	
		621 I I I L T V I I I V V V L L M G F V G A 1861 ATCATCATTTTGACAGTCATCATCATTGTTGTGGTGCTGCTAATGGGATTTGTGGGGCT	
		641 V Y M Y R E Y Q N R K L N A P F W T I E 1921 GTATATATGTACCGCGAGTACCAAAACCGGAAACTCAATGCCCCCTTTGGACCATCGAG	
		661 L K E D N I S F S S Y H D S I P N A D V	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1981 CTGAAAGAAGACAATATCAGTTTCAGCAGCTACCATGACAGCATTCCCAATGCAGATGTT 681 S G L L E D D G N E V A P N G Q L T L T 2041 TCGGGATTGTTGGAAGATGATGGCAATGAAGTGGCTCCCAATGGGCAGCTGACCCTGACG 701 T P I H N Y K K A - 2101 ACGCCCATACATAACTACAAAGCCTAA	
WBC012C10.bFSP_20010810.abd	H.sapiens mRNA for inwardly rectifing potassium channel Kir4.2.	1 GCAGTAGCAGAATCCCATGGTAGCCAGGTGGGTGAAGGGAGCGAGGACGTCCCACCTGC 61 CTTGAAGAAGACGCCTTCTGACCTGCTGAGTGAGTGACCAGGTGGTCCCAAGAGCCTGAC 121 GATGGACGCCATGCACATCAACACATGTCCAGTGCTCCTCTGGTGAAGCACACTGCTGGAGC 181 TGGACTCAAGACCAACAGGCCCCGAGTCATGTCCAAGAGTGGACACAGCAACGTGAGAAT 241 CGACAAGGTGGATGGCATCTACTTACTCTACCTTCAAGACTTGTGGACGACCGTGATCGA 301 CATGAAGTGGAGGTACAAGCTCACCCTCTTTGCAGCCACCTTTGTGATGACCTGGTTCCT 361 GTTCGGAGTAATCTATTACGCCATTGCATTTATTCACGGGGACTTAGAGCCCAGTGAGCG 421 TATTTCAAATCACACCCCCTGCATCATGAAAGTGGACTCTCTCACAGGGCATTTCTCTT 481 TTCCCTGGAATCCCAGACAACCATTGGCTATGAGTTCGCTCCATCACGGAGGAATGTCC 541 TCATGCCATTTTCCTGTTGGTCGCTCAGTTGGTCATCACGACCTTGATTGAGATCTTCAT 601 CACGGCACCTTCCTGGCAAAAATCGCCAGACCCAAAAAGCGGGCAGAGACCATCAAGTT 661 CAGCCACTGTGCTGTCATCACCAAGCAGAATGGGAAGCTGTGCTTGGTGATTCAGGTAGC 721 CAATATGAGGAAGAGCCTCTTGATTCAGTGCCAGCTCTCTGGCAAGCTCCTGCAGACCCA 781 CGTCACCAAGGAGGGGGAGCGGATTCTCCTCAACCAAGCCACTGCCAAATTCCACGTGGA 841 CTCCTCCTCTGAGAGCCCCTTCCTCATTCTGCCCATGACATTCTACCATGTGCTGGATGA 901 GACGAGCCCCCTGAGAGACCTCACACCCCAAAACCTAAAGGAGAAGGAGTTTGAGCTTGT 961 GGTCCTCCTCTCAATGCCACTGTGGAATCCACCAGCGCTGTCTGCCAGAGCCGAACATCTTA 1021 TATCCCAGAGGAAATCTACTGGGGTTTTGAGTTTGTGTGCCTGTGGTATCTCTCTCCAAAAA 1081 TGGAAAATATGTGGCTGATTTCAGTCAGTTCGAACAGATCCGGAAGAGCCCGGACTGCAC 1141 CTTTTATTGCGCAGATGCTGAGAAGCAGAAACTTGAGGAGAAGTACAGGCAGGAGGACCA 1201 GAGGGAAAGAGAACTGAGGACCCTTTGTTACAGCAGAGCAACGTCTGACGGCAGTGGTG 1261 TCACTGCTGTTTAACTCTGCGAGCTGTTTCCACATCTGAGCTCGCTCCAAAAGCAAAGGT 1321 CGCTGTGAAAGCAAAACTGTGTGGATGCACTCTCAAAAAACCTCACAGGCTACAAACTTG 1381 ATCTTTTCCTTTGATCTGGTGGCTAAACAAGCATTTCCATGTTTGAGAGGCTTCCTTTTA 1441 AATGCTTTGTCTGAAGCAAACTCTCAAAATTCAGATTTTCTAAAGTGGGGCTACATTTCG 1501 AAGAACTTGGTGTAGAGCAATTGAAAAAATGTCCTGCTGGATGGACAGACATTGATGCTG 1561 ACATTGAAAGGAACGGCATTTCTATACAAGATTATTAGCTGTAATACAAGATATTTATTT 1621 AACCAATGACCTTATGGCTGAGAGTTGAATTGTGGTTCAGTATTCATTGATCTCACTGCT 1681 TTAAAACATGCTCCTTTTGTTCAAGCAG 1 M D A M H I N M S S A P L V K K H T A G A 1 ATGGACGCCATGCACATCAACATGTCCAGTGCTCCTCTGGTGAAGCACACTGCTGGAGCT 21 G L K T N R P R V M S K S G H S N V R I	SEQ ID NO:47 SEQ ID NO:48

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		61 GGACTCAAGACCAACAGGCCCCGAGTCATGTCCAAGAGTGGACACAGCAACGTGAGAATC	
		41 D K V D G I Y L L Y L Q D L W T T V I D	
		121 GACAAGGTGGATGGCATCTACTTACTCTACCTTCAAGACTTGTGGACGACCGTGATCGAC	
		61 M K W R Y K L T L F A A T F F V M T W F L	
		181 ATGAAGTGGAGGTACAAGCTCACCCTCTTTGCAGCCACCTTTGTGATGACCTGGTTCCTG	
		81 F G V I Y Y A I A F I H G D L E P S E E R	
		241 TTCGGAGTAATCTATTACGCCATTGCATTTATTCACGGGGACTTAGAGCCCAGTGAGCGT	
		101 I S N H T P C I M K V D S L T G A F L F	
		301 ATTTCAAATCACACCCCCTGCATCATGAAAGTGGACTCTCTCACAGGGGCATTTCTCTTT	
		121 S L E S Q T T I G Y G V R S I T E E C P	
		361 TCCCTGGAATCCCAGACAACCATTGGCTATGGAGTTCGCTCCATCACGGAGGAATGTCCT	
		141 H A I F L L L V A Q L V I T T L I E I F I	
		421 CATGCCATTTTCCTGTTGGTCGCTCAGTTGGTCATCACGACCTTGATTGAGATCTTCATC	
		161 T G T F L A K I A R P K K R A E T I K F	
		481 ACGGGCACCTTCCTGGCAAAAATCGCCAGACCCAAAAAGCGGCAGAGACCATCAAGTTC	
		181 S H C A V I T K Q N G K L C L V I Q V A	
		541 AGCCACTGTGCTGTCATCACCAAGCAGAATGGGAAGCTGTGCTTGGTGATTCAGGTAGCC	
		201 N M R K S L L I Q C Q L S G K L L Q T H	
		601 AATATGAGGAAGAGCCTCTTGATTCAGTGCCAGCTCTCTGGCAAGCTCCTGCAGACCCAC	
		221 V T K E G E R I L L N Q A T A K F H V D	
		661 GTCACCAAGGAGGGGGAGCGGATTCTCCTCAACCAAGCCACTGCCAAATTCCACGTGGAC	
		241 S S S E S P F L I L P M T F Y H V L D E	
		721 TCCTCCTCTGAGAGCCCCTTCCTCATTCTGCCCATGACATTCTACCATGTGCTGGATGAG	
		261 T S P L R D L T P Q N L K E K E F E L V	
		781 ACGAGCCCCCTGAGAGACCTCACACCCCAAAACCTAAAGGAGAAGGAGTTTGAGCTTGTG	
		281 V L L N A T V E S T S A V C Q S R T S Y	
		841 GTCCTCCTCAATGCCACTGTGGAATCCACCAGCGCTGTCTGCCAGAGCCGAACATCTTAT	
		301 I P E E I Y W G F E F V P V V S L S K N	
		901 ATCCCAGAGGAAATCTACTGGGGTTTTGAGTTTGTGCCTGTGGTATCTCTCTCCAAAAAT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		321 G K Y V A D F S Q F E Q I R K S P D C T 961 GGAAAATATGTGGCTGATTTCAGTCAGTTCGAACAGATCCGGAAGAGCCCGGACTGCACC 341 F Y C A D A E K Q K L E E K Y R Q E D Q 1021 TTTTATTGCGCAGATGCTGAGAAGCAGAAACTTGAGGAGAAGTACAGGCAGGAGGACCAG 361 R E R E L R T L L L Q Q S N V - 1081 AGGGAAAGAGAACTGAGGACCCTTTTGTTACAGCAGAGCAACGTCTGA	
WBC012E05.bFSP_20010810.abd	No homology.	1 GAAAACAGTGGCTGCAAAGCACCCCAAAAAGCCTTTCAAGTGCCTTCTGTTAATATTGAT 61 TTATACGGTTTAAATGTGCCTGATTCTTCCAGGAAAATCTCAATTATTGCACTCAGCTCC 121 ATTTCTACCTGTTCCATTACCCAAGATAATAAATTAGTTACTGCGTTGTAAAGACAGTGG 181 TCTCTTCTTTGTTCGTTAAAATAAGGTTGTGTTTCTCTGTTTACATTAATGAAGTCTGAA 241 TTTAAAATGGTGATAAAACCAAGATTTAGTACTTTCTAAACTCAAGGAAATTATTTCTAG 301 ACATGAGGTAATTCTTTTAAATTTAAACTGTTGTACAGATCCCTTAAATGTTCTTGTTAA 361 GTACCTACTATTCTGCTGAACTTTAAAAGTTAATTCCCACATTTACAGGAATCTATGATA 421 TTTAAACATTTTTTATTGCTCATTAATGTTTCTGAGTATAATATATATGCCTTATTTTTA 481 GACTTGTAAAATGTATGAAATCTCACTAGTGCACGGACATCTGTGAAGTTAGCAGTGAGT 541 TGGAATTTTAAATGACTATGTGAAGGATACGCAAAATATGTTAACTCTTGTTACTTTTGT 601 ATGTGATTGTATAAGCATGTGACTGTATTATAACATTGTTCACTTTGAAAACTAATATAG 661 ATATGCTTGATTCTGAACAATAAGTGTGACTTGTATTGAACAGTTTATAGACTGTGTTCC 721 TTATTTAACACAATTATGAATTCTTCCACTCGTTCATAATTTGTACATCTCACTGCTTAG 781 CTTAGATTCAAGTCTGTGTTTATGCATTTATGTACCTGCTGATCATCACTGTGTACTCAG 841 AATTACTGTAGGAGTATTCTGACTCTAACATGGACTTTTAAAAATCTTTCAATAACCTGC 901 CAGTGGGATATGCTCACTGATCTGTGCTTAAGTTGAAGATATAACTTGTCTTGAAGGATA 961 TTTAAATATTTAGAGATCATGCTTGCGTTACTAGGACGTTGTCTGTGATGGTGTCCACGT 1021 GTGGAGGAGCCGTGTGCTGGTGACAGCCAGCTTTGTCTGTCCTGCCTTCTCTTCAGGTGC 1081 AGCCTTACTGGTCCTCACCTTCATGACCGTCCTGACTGTATATTTTCAAGTCAGCCTTGC 1141 TGGATTTGGAGTCTTACTGACTTTGTGTTTTTGTAGTTGAAGTTATGGAAATGCTTTTTG 1201 ATTTGTATTTAGATATTGAAGTCATTCATCAGATAGCACATTTGTATGTCTGAGCCTCAT 1261 GTACCTATTTGAAGTCATATTTTTAAAAATATATTTACAGGTTTATTTGTGACTTTTTAT 1321 CATTTCTTCAAATATTTCATGTTTACATTAAAAAAATTCCCAGAGAACCAAAAAA	SEQ ID NO:49
WBC012E07.bFSP_20010810.abd	Pinin, desmosome associated protein (PNN)	1 GGCTGTCAGTCCTTTCGCGCCTCGGCGGCGCGGCATAGCCCGGCTCGGCCTGTAAAGCAG 61 TCTCAAGCCTGCCGCAGGGAGAAGATGGCGGTCGCCGTGAGAACTTTGCAGGAACAGCTG 121 GAAAAGGCCAAAGAGAGTCTTAAGAACGTGGATGAGAACATTCGCAAGCTCACCGGGCGG 181 GATCCGAATGACGTGAGGCCCATCCAAGCCAGATTGCTGGCCCTTTCTGGTCCTGGTGGA 241 GGTAGAGGACGTGGTAGTTTATTACTGAGGCGTGGATTCTCAGATAGTGGAGGAGGACCC 301 CCAGCCAAACAGAGAGACCTTGAAGGGGCAGTCAGTAGGCTGGGCGGGGAGCGTCGGACC 361 AGAAGAGAATCACGCCAGGAAAGCGACCCGGAGGATGATGATGTTAAAAAGCCAGCATTG	SEQ ID NO:50

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		421 CAGTCTTCAGTTGTAGCTACCTCCAAAGAGCGCACACGTAGAGACCTTATCCAGGATCAA	
		481 AATATGGATGAAAAGGGAAAGCAAGGAACCGGCGAATATTTGGCTTGTTGATGGGTACC	
		541 CTTCAAAAATTTAAACAAGAATCCACTGTTGCTACTGAAAGGCAAAAGCGGCGCCAGGAA	
		601 ATTGAACAAAAACTTGAAGTTCAGGCAGAAGAGAGAAAGCAGGTTGAAAATGAAAGG	
		661 AGAGAACTGTTTTGAAGAGAGGCGTGCTAAACAGACAGAACTGCGGCTTTTGGAACAGAAA	
		721 GTTGAGCTTGCGCCAGCTGCAAGAAGAATGGAATGAACATAATGCCAAAATAATTAAATAT	
		781 ATAAGAACTAAGACAAAGCCCCATTTGTTTTATATTCCTGGAAGAATGTGTCCAGCTACC	
		841 CAAAAACTAATAGAAGAGTCACAGAGAAAAATGAACGCTTTATTTGAAGGTAGACGCATC	
		901 GAATTTGCAGAACAAATAAATAAATATGAGGCTAGGCCTAGAAGACAATCAATGAAGGAA	
		961 AAAGAGCATCAGGTGGTGCGTAATGAAGAACAGAAGGCGGAACAAGAAGAGGGTAAGGTG	
		1021 GCTCAGCGAGAGGAAGAGTTGGAGGAGACAGGTAATCAGCACACAATGATGTAGAAATAGAG	
		1081 GAAGCAGGAGAGGAAGAGGAAAAGGAAATAGCGATTGTTCATAGTGATGCAGAGAAAGAA	
		1141 CAGGAGGAGGAAGAACACAAAAACAGGAAATGGAGGAGTTAAGATGGAGGAGGAAACTGAGGTA	
		1201 AGGGAAAGTGAGAAGCAGCAGGATAGTCAGCCTGAAGAAGTTATGGATGTGCTAGAGATG	
		1261 GTTGAGAATGTCAAACATGTGTAATTGCTGACCAGGAGGTAATGGAAACTAATCGAGTTGAA	
		1321 AGTGTAGAACCTTCAGAAAATGAAGCTAGCAAAGAATTGGAACCAGAAATGGAATTTGAA	
		1381 ATTGAGCCAGATAAAGAATGTAAATCCCTTTCTCCTGGGAAAGAGAATGTCAGTGCTTTA	
		1441 GACATGGAAAAGGAGTCTGAGGAAAAAGAAGAAAAAGAATCTGAGCCCCAACCTGAGCCT	
		1501 GTGGCTCAACCTCAGCCTCAGTCTCAGCCCCAGCTTCAGCTTCAATCCCAGTCCCAACCA	
		1561 GTACTCCAGTCCCAGCCTCCCTCTCAGCCTGAGGATTTGTCATTAGCTGTTTTACAGCCA	
		1621 ACACCCCAAGTTACTCAGGAGCAAGGCATTTACTACCTGAGAGGAAGGATTTTCCTGTA	
		1681 GAGTCTGTAAAACTCACTGAGGTACCAGTAGAGCCAGTCTTGACAGTACATCCAGAGAGC	
		1741 AAGAGCAAAACCAAAACTAGGAGCAGAAGTAGAGGTCGAGCTAGAAATAAAACAAGCAAG	
		1801 AGTAGAAGTCGAAGCAGTAGCAGTAGCAGTTCTAGTAGCAGTTCAACCAGTAGCAGCAGT	
		1861 GGAAGTAGTTCCAGCAGTGGAAGTAGTAGCAGTCGCAGTAGTTCCAGTAGCAGCTCCAGT	
		1921 ACAAGTGGCAGCAGCAGCAGAGATAGTAGCAGTAGCACTAGTAGTAGTGAGAGTAGA	
		1981 AGTCCGAGTAGGGGCCGGGGACATAACAGAGATAGAAAGCACACGAGAAGGAGCGTGGATCGG	
		2041 AAGCGAAGGGATACTTCAGGACTAGAAAGAAGTCACAAATCTTCAAAAGGTGGTAGTAGT	
		2101 AGAGATACGAAAGGATCAAAGGATAAGAATTCCCGGTCCGACAGGAAAAGGTCTATATCC	
		2161 GAGAGTAGTCGATCAGGCAAAAGATCGTCGAGAAGTGAAAGAGACCGAAAATCAGACAGG	
		2221 AAAGACAAAAGGCGTTAATGGAAGAAGCCAGGCTTTCTTAGCCTATTCTTTGCAGCAGAA	
		2281 GATTTCTTGATGAGTAAAAGGATTACCTTTCCTTGTAAGGAGGATGCTGCCTTAAGAATT	
		2341 GCATGTTGTAAAAAATCTTTTTGGAAAATACAGACTGTTGTTTACCAGACATTCTTGTA	
		2401 CTTTTTGCATAATTTTGTAAGAGTTATTTATCAAAATTATGTGAGGTTCCAAAATATGTA	
		2461 AAATAATATAATAAAAAAAGATTAACATCCCTTGTCATCTTTTTTAAATATCCTATACT	
		2521 CTGCAGTAAGAATGTATATTTTAATAGGTAAATCTTTAAGTCTGTTCCCTTCTAATTCTG	
		2581 TATCATACATTGCTTTTGTAGAAATAAATGTGCATTTCTTTTCATTAGTTTTGAGATGTCC	
		2641 TCGTTGACGCTTGTATAATAAATATCCTCTTGATACCATTTTCAGCTTTTATCACTAGAT	
		2701 ACTGAACGTGATTAGAATGTCTTTGAAAGTTTCCTCACTTTTATTTGCCTTAGGCAGTTA	
		2761 TTTTGAGTTGTCAAAATCAGATCTTTGCAGCTTTGAGGGGGAACATAATAGTTCTCCGTG	
		2821 AAATCATTTACTGTTTTTCTAATCTCCCTTGTTATTTTAATCTAAGCATTTTCCCCTCC	
		2881 TCATCTTTAACCACGTATTTGGTAGATAACTTAAAATAGTATAATTTGGTTGCATTTT	
		2941 CTTCATGATTATGGGAGCATCATTCTTTTGTCTCCATGGTTACTTGTGTGATACAGCATA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		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	SEQ ID NO:51
		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	
		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 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 AGGAACCGGCGAATATTTGGCTTGTTGATGGGTACCCTTCAAAAATTTAAACAAGAATCC	
		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 L F E E R R 541 GCAGAAGAAGAGAGAAAGCAGGTTGAAAATGAAAGGAGAGAACTGTTTGAAGAGAGGCGT	
		201 A K Q T E L R L L E Q K V E L A Q L Q E 601 GCTAAACAGACAGAACTGCGGCTTTTGGAACAGAAAGTTGAGCTTGCGCAGCTGCAAGAA	
		221 E W N E H N A K I I K Y I R T K T K P H 661 GAATGGAATGAACATAATGCCAAAATAATTAAATATATAAGAACTAAGACAAAGCCCCAT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		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 I E E F A E Q I N K 781 AGAAAAATGAACGCTTTATTTGAAGGTAGACGCATCGAATTTGCAGAACAAATAAATAAA	
		281 M E A R P R R Q S M K E K E H Q V V R N 841 ATGGAGGCTAGGCCTAGAAGACAATCAATGAAGGAAAAAGAGCATCAGGTGGTGCGTAAT	
		301 E E Q K A E E Q E E G K V A Q R E E E L E 901 GAAGAACAGAAGGCGGAACAAGAAGAGGGTAAGGTGGCTCAGCGAGAGGAAGAGTTGGAG	
		321 E T G N Q H N D V E E I E E E A G E E E E E K 961 GAGACAGGTAATCAGCACAATGATGTAGAAATAGAGGAAGCAGGAGAGGAAGAGGAAAAG	
		341 E I A I V H S D A E E K E Q E E E E E Q K Q 1021 GAAATAGCGATTGTTCATAGTGATGCAGAGAAAGAACAGGAGGAAGAACAAAAACAG	
		361 E M E V K M E E E E T E E V R E E S E K Q Q D 1081 GAAATGGAGGTTAAGATGGAGGAGGAAACTGAGGTAAGGGAAAGTGAGAAGCAGCAGGAT	
		381 S Q P E E E V M D V L E E M V E N V K H V I 1141 AGTCAGCCTGAAGAAGTTATGGATGTGCTAGAGATGGTTGAGAATGTCAAACATGTAATT	
		401 A D Q E E V M E E T N R V E E S V E E P S E N E 1201 GCTGACCAGGAGGAGGTAATGGAAACTAATCGAGTTGAAAGTGTAGAACCTTCAGAAAATGAA	
		421 A S K E E L E E P E E M E E F E E I E E P D K E E C K 1261 GCTAGCAAAGAAGAATTGGAACCAGAAGAAATGGAATTTGAAATTGAGCCAGATAAAGAATGTAAA	
		441 S L S P G K E E N V S S A L D M E E K E E S E E E 1321 TCCCTTTCTCCTGGGAAAGAGAATGTCAGTGCTTTAGACATGGAAAAGGAGTCTGAGGAA	
		461 K E E E K E S E E P Q P E E P P V A Q P P Q P Q S 1381 AAAGAAGAAAAAGAATCTGAGCCCCAACCTGAGCCTGTGGCTCAACCTCAGCCTCAGTCT	
		481 Q P Q L Q L Q S Q S Q P P V L Q S Q P P P S 1441 CAGCCCCAGCTTCAGCTTCAATCCCAGTCCCAACCAGTACTCCAGTCCCAGCCTCCCTCT	
		501 Q P E E D L S S L A A V L Q P P T P Q V T Q E Q 1501 CAGCCTGAGGATTTGTCATTAGCTGTTTTACAGCCAACACCCCAAGTTACTCAGGAGCAA	
		521 G H L L P E E R K D F P P V E S V K K L L T E E V	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		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	
WBC013A09.bFSP_20010810.abd	Homo sapiens sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase), transcript variant 2.	1 GAGGAGGTTCCTGTAGGGCGGCACAACCAGGGAGGGCGTGGAAGCTCTGCATCCCTTCTC 61 CCATACCTTGCTCTACACATCTCTTCATCTGTATCCTCTGCAGCATCCTTGATGATAAAC 121 CAGTAAATATGAGTTTTGATCATCCTGAGAAAAATGGGCCTTGGCCTGCAGACCCAATAA 181 ACCTTCCCTCCCATGGATAATAGTGCTAATTCCTGAGGACCTGAAGGGCCTGCCGCCCCT 241 GGGGGATTAGCCAGAAGCAGGCTTGTTTTCCTGCTCAGAACAAAGTGACTTCCCTGAACA 301 CATCTTCATTATGATTCACACCAACCTGAAGAAAAAGTTCAGCTGCTGCGTCCTGGTCTT 361 TCTTCTGTTTGCAGTCATCTGTGTGTGGAAGGAAAAGAAGAAAGGGAGTTACTATGATTC 421 CTTTAAATTGCAAACCAAGGAATTCCAGGTGTTAAAGAGTCTGGGGAAATTGGCCATGGG 481 GTCTGATTCCCAGTCTGTATCCTCAAGCAGCACCCAGGACCCCCACAGGGGCCGCCAGAC 541 CCTCGGCAGTCTCAGAGGCCTAGCCAAGGCCAAACCAGAGGCCTCCTTCCAGGTGTGGAA 601 CAAGGACAGCTCTTCCAAAAACCTTATCCCTAGGCTGCAAAAGATCTGGAAGAATTACCT 661 AAGCATGAACAAGTACAAAGTGTCCTACAAGGGGCCAGGACCAGGCATCAAGTTCAGTGC 721 AGAGGCCCTGCGCTGCCACCTCCGGGACCATGTGAATGTATCCATGGTAGAGGTCACAGA	SEQ ID NO:52

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		781 TTTTCCCTTCAATACCTCTGAATGGGAGGGTTATCTGCCCAAGGAGAGCATTAGGACCAA	
		841 GGCTGGGCCTTGGGGCAGGTGTGCTGTTGTGTCGTCAGCGGGATCTCTGAAGTCCTCCCA	
		901 ACTAGGCAGAGAAATCGATGATCATGACGCAGTCCTGAGGTTTAATGGGGCACCCACAGC	
		961 CAACTTCCAACACAAGATGTGGGCACAAAAACTACCATTCGCCTGATGAACTCTCAGTTGGT	
		1021 TACCACAGAGAAGCGCTTCCTCAAAGACAGTTTGTACAATGAAGGAATCCTAATTGTATG	
		1081 GGACCCATCTGTATACCACTCAGATATCCCAAGTGGTACCAGAATCCGGATTATAATTT	
		1141 CTTTAACAACTACAAGACTTATCGTAAGCTGCACCCCAATCAGCCCTTTTACATCCTCAA	
		1201 GCCCCAGATGCCTTGGGAGCTATGGGACATTCTTCAAGAAATCTCCCCAGAAGATTCA	
		1261 GCCAAACCCCCCATCCTCTGGGATGCTTGGTATCATCATCATGATGACGCTGTGTGACCA	
		1321 GGTGGATATTTATGAGTTCCTCCCATCCAAGCGCAAGACTGACGTGTGCTACTACTACCA	
		1381 GAAGTTCTTCGATAGTGCCTGCACGATGGGTGCCTACACCCGCTGCTCTATGAGAAGAA	
		1441 TTTGGTGAAGCATCTCAACCAGGGCACAGATGAGAGACATCTACCTGCTTGGAAAAGCCAC	
		1501 ACTGCCTGGCTTCCGGACCATTCACTGCTAAGCACAGGCTCCTCACTCTTCTCCATCAGG	
		1561 CATTAAATGAATGGTCTCTTGGCCACCCCAGCCTGGGAAGAACATTTTCCTGAACAATTC	
		1621 CAGCCTGCTCCTTTTACTCTAGGGGCCTCTGTCAGCAAGACCATGGGGGCTTCAAGAGCC	
		1681 TGTGGTCAGGAAATCAGGTCCAGCCTTCCCTGTAGCCAGACAGTTTATGAGCCCAGAGCC	
		1741 TCCTGCCACACACATGCACACATATCTAGCATTCTTTCCAGACAGCATCCTCCCCGCCTT	
		1801 CCACCTTGGTAGATGCAAGGTCTATCTCTCCCATCAGGGCTGCCAAAGCTGGGCTTTGTT	
		1861 TTTCCCAGCAGAATGATGCCATTCTCACAAACCAATGCTCTATATTGCTTGAAGTCTGCA	
		1921 TCTAAATATTGATTTCACGTTTTAAAGAAATTCTCTTAAATTACAATTGTGCCCAATGCA	
		1981 GGGTGGCTCTGGGGGGCAAGTAGGTGGTACAGGGGATTGGAAACATGCTCCGCGCCTCCA	
		2041 GAGAAAAGTTGCTCCCGAGGTCCATGCCCCTGGAACGTGTTCCTATCACTCTGGCTGGTT	
		2101 GGGCTGGTCCTTAGACTGGGTGCTTATGATTAAAGGGTCTTGGTTAGCCCACTTTCCCTC	
		2161 TCCATGTGGAGATGGAAGGTAGAGAAGGATACAGTGTCTATCCTCAAGTTGCTACGGTTC	
		2221 AGTGAGAGAGGCAGACATCTGAACAGGCAGGTAGGATTCAGTGTGCTCAGTGCACTGGGG	
		2281 ATTTGGAGAGAGATGGGCTTGCTCTCTCTCTGTGCACCCAGGAGGGCCACGCACTTAAAACT	
		2341 GTGTTTGTGGATCAGAGAAGGCTTTATAGCACAGGGGGCATTCAGATGAGTCTTAGAGGA	
		2401 AGAGAGAAACATGGCAAGCAGATTACATCTGAGCCGTTTGAATTGTGTTTTTCTTTCTT	
		2461 CCCATGTTTATTTTCTAAGATCTACCTGAACTTAGAGACTCAAGATATTTTTTAGGAAA	
		2521 CCTCCTACCCATGTCTGAGGTAGCAAGTGCAGCCTCACGACAGATACCAGGCAATCCAGA	
		2581 GCCACAAAACGTGATTCCTCCAGGCTCTGCCTGGCCTGACCCTGTCCTGTCAGCTGGGTT	
		2641 TACATACCAGTCCCCATTCTTCCTTTTCAATACCTACCCCCAAATCTTCTCCTAACCACCA	
		2701 TCTGTTTTTTTTTTTTTAAAGCATTTTTTGCTTTAAAAGCATCCTGACCCCAATTTCTTTG	
		2761 AGCTCACGGGCCTTTTGCTGAAGGTCTCTCAGGGTGTAGTGGTGTGGCTCTCTGGACTTA	
		2821 ACGTCACTCTCAGAGGTCAGAACCTTGGAGATCAGAACTGATTCTCACCAGGTGTGAGAG	
		2881 GTGTGGTAGCAGATTGCAATGCTCTGCACCTCTTCCTTGCAAGTGAGCAACTTCAGGCTC	
		2941 TCTGGGCAGAGGCTGGCCCACTGTAGTTTGCAGACATGCTCTCCAGATGGTTTTACTAAG	
		3001 TCCCCTCTCCCTGATAGGGAATCCTGCTGGACCAGCGCAGCCCTGGTGTGGAGAGGGTAA	
		3061 AGGACTTGCACAGGATCACCAAGTCATGCTGTAGAGCCAGGATTCCTAGACCCAGGGCTC	
		3121 TGCACTCTCAAGGCTGGCCCCATGTGCTCAAGGGCCTCCAATGTTTGCGCTCCAGACCAG	
		3181 CCGTCTGCAAGCTGGACTTCTCATTTGCTGCCAAACCCTTGGCTTACATATGCAGTAGAA	
		3241 AGAGCCCTGGAGTTAGAAGCCCTGGGTTTTCAAGTTGATGTTCCTCTACTTACTAGCTGT	
		3301 GCCACTCTGGGCAAATGCTCTTCCTTGAGCCTGTTTCCACACCTGTAAAGTGGGGATGAT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		3361 GATCCTATCTCACTGCTTTGTGAGGATTACAGGAAAGCACCTGTCCTGGTTCTGCACCT	
		3421 GGCTCATGGCAGGTGCTCAGTACATGGTGGTGTCCTTCCTTCCTTCGTTCACTAAGGACCTGCT	
		3481 CTGAGCTCACACCTCGGCTGCATGCACCCTGCTGTGACGGAGGCTAGTGTGGAAGAGGTC	
		3541 CTGTCCTCAGGGAATTAACTGTCTTATTGGAGACAACAACTACCCTGCCTGGGGCACCC	
		3601 AGGAAACCATCCGAGGCAGTGGACAACACAGAACACGCCCCTCCTCCTCGCTGCCTGCAGC	
		3661 TCCAATCTGATTCTGCTTGGGAATGGGCTGAGCACGTGGGCTGCTTAACTGCTGTATAGG	
		3721 ACAAGCCCCTTACCCCTCTCTGGGCCCATGAATTCCTGGCTCTCTTTATGTTCTGATTTG	
		3781 ACACATTCATTGCAATCTTTGAATCATGAACATGAGTGCAGAGGAAGGTGGCATTCCATC	
		3841 AGCAGAAGAGATGTTGGTGTGGGACCCTGAGACTACACTGGGTAGATGCTAGCTTTTA	
		3901 ATTATGATTAAATATAAGGGATCAAATTAATTTAAATATGATTCTGAAGTCTACAGAACTT	
		3961 TTAGTTCTGTGCTGTCTATGTGGACACTTTGGTAAAATGCAAATTATGATATGGACGTTA	
		4021 TCATTGGTCTGGTGAGCTGTTTTAATATTTGTGACAGATAATTTAAAATTATGACTTAAT	
		4081 GCTGCCTGTGTCTATGGGGTTCTGTCTTCTTTGATAGCCATCTATTCATCTGGATCATGG	
		4141 GACCCTCTCTAATCCTTCCAACAATCAAATAAGCTATCGATATTGTTTTGGAGTTGAGAT	
		4201 ATCAGTCTCGGAAACTTCTGAAAAATGCTAATTAATTACCCAAGGATTATGTCAAATTTTA	
		4261 AAATAAATGTGTGTGTTCTTTAAAAAAAAAAAAAAA	
		1 M I H T N L K K K K F S C C V L V F L L F	SEQ ID NO:53
		1 ATGATTCACACCAACCTGAAGAAAAAGTTCAGCTGCTGCGTCCTGGTCTTTCTTCTGTTT	
		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 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 CTCAGAGGCCTAGCCAAGGCCAAACCAGAGGCCTCCTTCCAGGTGTGGAACAAGGACAGC	
		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 G I K F S A E 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 AATACCTCTGAATGGGAGGGTTATCTGCCCAAGGAGAGCATTAGGACCAAGGCTGGGCCT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		181 W G R C A V V S S A G S L K S S Q L G R 541 TGGGGCAGGTGTGCTGTTGTGTCGTCAGCGGGATCTCTGAAGTCCTCCCAACTAGGCAGA 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	
WBC013A11.bFSP_20010810.abd	Homo sapiens nucleosome assembly protein 1-like 2.	1 ATGGCAGACATTGACAACAAAGAACAGTCTGAACTTGATCAAGATTTGGATGATGTTGAA 61 GAAGTAGAAGAAGAAGAAACTGGTGAAGAAACAAAAATCAAAGCGCGTCAGCTGACTGTT 121 CAGATGATGCAAAATCCTCAGATTCTTGCAGCCCTTCAAGAAAGACTTGATGGTCTGGTA 181 GAAACACCAACAGGATACATTGAAAGCTTGCCTAGAGTAGTTAAAAGACGAGTGAATGCT 241 CTCAAAAACCTACAAGTTAAATGTGCACAGATAGAAGCCAAATTCTATGAGGAAGTTCAT	SEQ ID NO:54

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		301 GATCTTGAAAGAAAGTATGCTGTTCTCTATCAGCCTCTATTTGATAAGCGGTTTGAGATT 361 ATTAATGCAATTTATGAACCTACGGAAGAGAATGTGAGTGGAAACCAGATGAGGAAGAT 421 GAAATTTCGGAGGAATTGAAAGAAAAGGCCAAGATTGAAGATGAGAAAAAGGATGAAGAA 481 AAAGAAGACCCCAAGGGAATTCCTGAATTTTGGTTGACTGTTTTTAAGAATGTTGACTTG 541 CTCAGTGATATGGTTCAGGAACATGATGACCTATTCTGAAGCACTTGAAGATATTAAA 601 GTGAAGTTCTCAGATGCTGGCCAACCTATGAGCTTTGTCTTAGAATTTCACTTTGAACCC 661 AATGAATATTTCACAAATGAAGTGCTGACAAAGACATATAGGATGAGGTCAGAGCCAGAT 721 GATTCTGATCCCTTTTCTTTTGATGGACCAGAAATTATGGGTTGTACAGGGTGCCAGATA 781 GACTGGAAAAAAGGAAAGAATGTCACTTTGAAAACCATTAGAAGCAGAAACACAAG 841 GGACGTGGGACAGTTCGTACTGTGACCAAAACAGTTTCCAATGACTCTTTCTTTAATTTT 901 TTTGCCCCTCCTGAAGTTCCTGAGAGCGGAGATCTGGATGATGCTGAAGCTATCCTT 961 GCTGCAGACTTTGAAATTGGTCACTTTTTACGTGAGCGTATAAATCCCAAGATCAGTGTTA 1021 TACTTTACTGGAGAAGCTATTGAAGATGATGACGACGATTATGATGAAGAAGGTGAAGAA 1081 GCGGATGAGGAAGGGGAAGAAGAAGGAGATGAGGAAAATGATCCAGACTATGACTCAAAG 1141 AAGGATCAAAATCCAGCAGAGTGCAAGCAGCAGTAG 1 M A D I D N K E Q S E L D D Q D L D D D V E 1 ATGGCAGACATTGACAACAAGAACAGTCTGAACTTGATCAAGATTTGGATGATGTTGAA 21 E V E E E E T G E E T K I K A R Q L T V 61 GAAGTAGAAGAAGAAACTGGTGAAGAAACAAAAATCAAAGCGCGTCAGCTGACTGTT 41 Q M M Q N P Q I L A A L Q E R L D G L V 121 CAGATGATGCAAAATCCTCAGATTCTTGCAGCCCTTCAAGAAAGACTTGATGGTCTGGTA 61 E T P T G Y I E S L P R V V K R R V N A 181 GAAACACCAACAGGATACATTGAAAGCTTGCCTAGAGTAGTTAAAAGACGAGTGAATGCT 81 L K N L Q V K C A Q I E A K F Y E E V H 241 CTCAAAAACCTACAAGTTAAATGTGCACAGATAGAAGCCAAATTCTATGAGGAAGTTCAT 101 D L E R K Y A V L Y Q P L F D K R F E I 301 GATCTTGAAAGAAAGTATGCTGTTCTCTATCAGCCTCTATTTGATAAGCGGTTTGAGATT 121 I N A I Y E P T E E E C E W K P D E E D 361 ATTAATGCAATTTATGAACCTACGGAAGAAGAATGTGAGTGGAAACCAGATGAGGAAGAT 141 E I S E E L K E K A K I E D E K K D E E 421 GAAATTTCGGAGGAATTGAAAGAAAAGGCCAAGATTGAAGATGAGAAAAAGGATGAAGAA 161 K E D P K G I P E F W L T V F K N V D L 481 AAAGAAGACCCCAAGGGAATTCCTGAATTTTGGTTGACTGTTTTTTAAGAATGTTGACTTG	SEQ ID NO:55

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		181 L S D M V Q E H D E P I L K H L K D I K 541 CTCAGTGATATGGTTCAGGAACATGATGAACCTATTCTGAAGCACTTGAAAGATATTAAA 201 V K F S D A G Q P M S F V L E F H F E P 601 GTGAAGTTCTCAGATGCTGGCCAACCTATGAGCTTTGTCTTAGAATTTCACTTTGAACCC 221 N E Y F T N E V L T K T Y R M R S E P D 661 AATGAATATTTCACAAATGAAGTGCTGACAAAGACATATAGGATGAGGTCAGAGCCAGAT 241 D S D P F S F D G P E I M G C T G C Q I 721 GATTCTGATCCCTTTTCTTTTGATGGACCAGAAATTATGGGTTGTACAGGGTGCCAGATA 261 D W K K G K N V T L K T I K K K Q K H K 781 GACTGGAAAAAAGGAAAGAATGTCACTTTGAAAACCATTAAGAAGAAGCAGAAACACAAG 281 G R G T V R T V T K T V S N D S F F N F 841 GGACGTGGGACAGTTCGTACTGTGACCAAAACAGTTTCCAATGACTCTTTCTTTAATTTT 301 F A P P E V P E S G D L D D D A E A I L 901 TTTGCCCCTCCTGAAGTTCCTGAGAGCGGAGATCTGGATGATGATGCTGAAGCTATCCTT 321 A A D F E I G H F L R E R I I P R S V L 961 GCTGCAGACTTTGAAATTGGTCACTTTTTACGTGAGCGTATAATCCCAAGATCAGTGTTA 341 Y F T G E A I E D D D D D Y D E E G E E 1021 TACTTTACTGGAGAAGCTATTGAAGATGATGACGACGATTATGATGAAGAAGGTGAAGAA 361 A D E E G E E E G D E E N D P D Y D S K 1081 GCGGATGAGGAAGGGGAAGAAGAAGGAGATGAGGAAAATGATCCAGACTATGACTCAAAG 381 K D Q N P A E C K Q Q - 1141 AAGGATCAAAATCCAGCAGAGTGCAAGCAGCAGTAG	
WBC013C09.bFSP_20010810.abd	Human lymphoid-restricted membrane protein (Jaw1).	1 TATATTGGCAGTTATTGAGGGTAAAGCAATATATTGTAACAGAATGTATAAATATTTTTG 61 ATAAAACAGTCTATATTTTATTAAAAAATGAATTATAACCCATTTTCAGTTTTGCCTGCA 121 TCATAAGAGTGAGCACTCCATTGCTTTCTTTCCTGGCCACACTGCTACAATCCAGCACTA 181 ACTATCCATGTCCAGGTTGAGGATCGAGATCGGGCAGCCCACGGTGCCAGTGAAAAAGCT 241 AAGTCTTTGCTGCATAAATTAGAGGAAGCAATTTCGGAACAACGGACTCTGCAGGCTATA 301 AATACTGAGTTAGTGAACACTTGCCAGACACTTGAGCAGAAGACAAGAAAACTGAAGAAG 361 CTTTTTAGATGAGGAATTTCCTCACTATGATTCCCTGTCCTGCGCAGATGCAATTCAACA 421 ACCTCTTCAAGAAAAATTGAAGCAGTGTTGCCATAAACTATATAGTGGTCAAGACGCCAG 481 AATACATCAGACGCCCCTGACCTTCAAACATACATGCTGGTACACACCTCTGCTGGATGC	SEQ ID NO:56

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		541 CTTGCATCTGGATAGTCTTACAACGATTCCAAGGCTGGAATTGACACCTTTCTCATGTTT 601 GGCCAACCGAATCCATGCTTCATGTGAAAGACCTAAATATGGAGAAATAGAGGATGGTGC 661 TTTGGATGTAAAAAGACAACACAAGTGCCCAGGCCCCACAGTGGCCCCAGCCCAGGAAC 721 GAATCTTTCAGGTTGCATCAGGATGAGTGATGACCTAAGTATGAACGAGAATGGTGTTGA 781 ACGCGTGTGTCCTGAGAGCCTGCTGCAGTCCAGGGGATATTCCTCACTACCATTACCCAG 841 ACACACTTCATCGACAGACGGTACTATAACTTCAAGTGATCCTGGATTAGAAATTCTGAA 901 TATGGCTTCTTGTGACCTTGACAGAAACTCGCTCTGTAAGAAAGAGGAGGATACAAGATC 961 AGCTTCTCCCACGATAGAGGCCCAAGGCACAAGTCCAGCTCATGATAATATTGCATTCCA 1021 AGACTCTACGAGTAAGGATAAAACCATATTAAATCTGGAAGCCAAAGAGGAACCAGAAAC 1081 AATAGAAGAACATAAAAAAGAACATGCTTCAGGAGACTCTGTGGTTTCCCCTCTTCCTGT 1141 AACCACTGTGAAAATCGGTTAACGTTAGACAAAGTGAGAACACTTCTGCTAATGAGAAGA 1201 GGTGGAGGCAGAATTTCTCAGATTATCTTTGGGATTTAAGTGTGACTGGTTTACCTTGGA 1261 GAAGAGAGTGAAGCTTGAAGAGAGGTCCCGTGACTGGGCAGAAGAAAATTTGAAGAAAGA 1321 AATCACTATACTCTTTAAAACTATTAGAGTCTTTAACACCTCTGTGTGAAGATGACACCA 1381 GGCACAGGAAATCATTAAGAAGCTGGAGAAGAGTATATAAAGTTTCTTAGCCAGTGTGCAGC 1441 ACGAGTGGCCAGTAGGGCTGAGATGTTGGGAGCCATCAATCAGGAAAGCCGGGTTAGTAA 1501 AGCAGTTGAAGTGATGATTCAGCACGTAGAAAACTTGAAGAGGATGTATGCCAAAGAGCA 1561 CGCTGAATTAGAAGAACTGAAACAGGTTCTTCTGCAGAATGAAAGGTCTTTCAATCCTCT 1621 TGAAGATGATGATGACTGCCAAATTAAAAAACGTTCAGCTTCTCTAAACTCCAAGCCATC 1681 TTCTCTACGAAGAGTGACTATTGCCTCTTTACCCAGAAATATTGGAAATGCAGGAATGGT 1741 GGCTGGGATGGAAAATAATGATCGATTCAGTAGAAGGTCAAGCAGTTGGCGTATTTTGGG 1801 GTCAAAGCAGAGTGAACACCGTCCCTCATTACCTCGATTTATTAGCACCTATTCCTGGGC 1861 AGATGCTGAAGAAGAAAAATGTGAACTAAAAACTAAAGATGACTCAGAACCACCTGAAGA 1921 AGAAATAGTAGAAAGAACAGAAAGCCAAGTCTTTCTGAAAAGAGAAATAATCCATCGAA 1981 ATGGGATGTCTCTTCAGCTTATATGACACAATAGCTTCCTGGACAACAAATCTCAAGACTTC 2041 CATCGGAAAGGCTAACAAGGCACTCTGTTTGTCTGTTGCCTTCATTGTACTGTTTGCAGC 2101 TTTGATGAGCTTCCTCACAGGCCTGTTTTTCCAAAAGTCCGTGGATGCCGCTCCCACACA 2161 GGATGGGGACTCCTGGATGTCTCTAGAACATATCTTGTGGCCATTTACCAGACTTAGACA 2221 CAATGGGCCACCACCAGTGTGACTGCAGCACATCCCAATGTGTGCATCTTGATTTTTAAG 2281 GTTTCAGTATCTGAACTTTGTAAATTAGTAAATTTTAGCTGGAAAATTATAGCATGGAAC 2341 CAAAGGTTCTCAGGATGCCTGTAAGATATTTTACATTCCCTCTTTTTGTGATTATCTCCC 2401 CAACTGAAATACAGTGGG 1 L E L T P F S C L A N N R I H A S C E R P 1 CTGGAATTGACACCTTTCTCATGTTTGGCCAACCGAATCCATGCTTCATGTGAAAGACCT 21 K Y G E I E D G A L D D V K K R Q H K C P G 61 AAATATGGAGAAATAGAGGATGGTGCTTTGGATGTAAAAAGACAACACAAGTGCCCAGGC 41 P T S G P S P G T N L S G C I R M S D D 121 CCCACAAGTGGCCCCAGCCCAGGAACGAATCTTTCAGGTTGCATCAGGATGAGTGATGAC 61 L S M N E N G V E R V C P E S L L Q S R	SEQ ID NO:57

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		181 CTAAGTATGAACGAGAATGGTGTTGAACGCGTGTGTCCTGAGAGCCTGCTGCAGTCCAGG 81 G Y S S L P L P R H T S S T D G T I T S 241 GGATATTCCTCACTACCATTACCCAGACACACTTCATCGACAGACGGTACTATAACTTCA 101 S D P G L E I L N M A S C D L D R N S L 301 AGTGATCCTGGATTAGAAATTCTGAATATGGCTTCTTGTGACCTTGACAGAAACTCGCTC 121 C K K E E D T R S A S P T I E A Q G T S 361 TGTAAGAAAGAGGAGGATACAAGATCAGCTTCTCCCACGATAGAGGCCCAAGGCACAAGT 141 P A H D N I A F Q D S T S K D K T I L N 421 CCAGCTCATGATAATATTGCATTCCAAGACTCTACGAGTAAGGATAAAACCATATTAAAT 161 L E A K E E P E T I E E H K K E H A S G 481 CTGGAAGCCAAAGAGGAACCAGAAACAATAGAAGAACATAAAAAAGAACATGCTTCAGGA 181 D S V V S P L P V T T V K S V N V R Q S 541 GACTCTGTGGTTTCCCCTCTTCCTGTAACCACTGTGAAATCGGTTAACGTTAGACAAAGT 201 E N T S A N E K E V E A E F L R L S L G 601 GAGAACACTTCTGCTAATGAGAAGGAGGTGGAGGCAGAATTTCTCAGATTATCTTTGGGA 221 F K C D W F T L E K R V K L E E R S R D 661 TTTAAGTGTGACTGGTTTACCTTGGAGAAGAGAGTGAAGCTTGAAGAGAGGTCCCGTGAC 241 W A E E N L K K E I T N S L K L L E S L 721 TGGGCAGAAGAAAATTTGAAGAAAGAAATCACTAACTCTTTAAAACTATTAGAGTCTTTA 261 T P L C E D D N Q A Q E I I K K L E K S 781 ACACCTCTGTGTGAAGATGACAACCAGGCACAGGAAATCATTAAGAAGCTGGAGAAGAGT 281 I K F L S Q C A A R V A S R A E M L G A 841 ATAAAGTTTCTTAGCCAGTGTGCAGCACGAGTGGCCAGTAGGGCTGAGATGTTGGGAGCC 301 I N Q E S R V S K A V E V M I Q H V E N 901 ATCAATCAGGAAAGCCGGGTTAGTAAAGCAGTTGAAGTGATGATTCAGCACGTAGAAAAC 321 L K R M Y A K E H A E L E E L K Q V L L 961 TTGAAGAGGATGTATGCCAAAGAGCACGCTGAATTAGAAGAACTGAAACAGGTTCTTCTG 341 Q N E R S F N P L E D D D D C Q I K K R 1021 CAGAATGAAAGGTCTTTCAATCCTCTTGAAGATGATGATGACTGCCAAATTAAAAAACGT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		361 S A S L N S K P S S L R R V T I A S L P 1081 TCAGCTTCTCTAAACTCCAAGCCATCTTCTCTACGAAGAGTGACTATTGCCTCTTTACCC 381 R N I G N A G M V A G M E N N D R F S R 1141 AGAAATATTGGAAATGCAGGAATGGTGCTGGGATGGAAAATAATGATCGATTCAGTAGA 401 R S S S W R I L G S K Q S E H R P S L P 1201 AGGTCAAGCAGTTGGCGTATTTTGGGTCAAAGCAGAGTGAACACCGTCCCTCATTACCT 421 R F I S T Y S W A D A E E E K C E L K T 1261 CGATTTATTAGCACCTATTCCTGGGCAGATGCTGAAGAAGAAAAATGTGAACTAAAAACT 441 K D D S E P P E E E I V E R T R K P S L 1321 AAAGATGACTCAGAACCACCTGAAGAAGAAATAGTAGAAAGACAGAAAGCCAAGTCTT 461 S E K R N N P S K W D V S S A Y D T I A 1381 TCTGAAAAGAGAAATAATCCATCGAAATGGGATGTCTCTTCAGCTTATGACACAATAGCT 481 S W T T N L K T S I G K A N K A L C L S 1441 TCCTGGACAACAAATCTCAAGACTTCCATCGGAAAGGCTAACAAGGCACTCTGTTTGTCT 501 V A F I V L F A A L M S F L T G L F F Q 1501 GTTGCCTTCATTGTACTGTTTGCAGCTTTGATGAGCTTCCTCACAGGCCTGTTTTTCCAA 521 K S V D A A P T Q D G D S W M S L E H I 1561 AAGTCCGTGGATGCCGCTCCCACACAGGATGGGGACTCCTGGATGTCTCTAGAACATATC 541 L W P F T R L R H N G P P P V - 1621 TTGTGGCCATTTACCAGACTTAGACACAATGGGCCACCACCAGTGTGA	
WBC013E05.bFSP_20010810.abd	Equus caballus MHC class II DQ-alpha chain (DQalpha).	1 AAAGCTGAGAAGACAATGATCCTAAACAGAGCTCTGATTCTGGGGGCCCTCACCCTGACC 61 ACCATGATGAGTGCCTGCGGAGGTGAACACATTGTGGCTGATCACTTTGCCTCCTACGGC 121 ACAAACGTCTACCAGTCTTATGGTGATTTTGGTCAGTACACACCCACGAATTTGATGGAGAT 181 GAGAAGTTCCATGTGGACCTGGAAGAAGGAGACTGTGTGGCGGCTGCCTGTGTTTAGC 241 GAGTTTACAAGTTTTGACCCACAGGGCGCGCTGCAAAACATTGCTACGGCAAAATACAAC 301 TTGGACATCTTGATTAAACGTTCCAACTCTACTGCTGCTACCAATGAGGTTCCTGAGGTG 361 ACTGTGTTTCCCAAGTCTCCTGTGGTGCTGGGTCAGCCCAACACCCTCATCTGTCTTGTG 421 GACAACATCTTCCCTCCTGTGATCAATGTCACATGGTTGAGGAATGGGCACTCAGTCAGT 481 GAAGGTGTTTTTGAGATGATTTTCCTCCCCAAGACTGATGATTCCTTCCTGAAGATCAGT 541 TACCTCACCTTCCTCCCCTTCTGCTGATGATATTTATGATTGCAAGGTGGAGCACTGGGGG 601 CTGGATGAGCCACTTCTGAAACACTGGGAACCTGAGATTCCAACCCCAATGTCAGAGCTG	SEQ ID NO:58

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		661 ACAGAGACTGTGGTCTGTGCCCTGGGGTTGGCTGTTGGCTTTGTGGGCATCGTGGTGGGC 721 ACCTTCCTCATCATCCGAGCCCTACGCTCAGGTGGTGCCTTAAGACGCCAAGGATGCTTG 781 TGAGTTGCATCATAGAAGGGAAGGCACATTGCCCATCTACAAGAGCAGAAGAGTGGATGT 841 GCTAGATGACCTCGCACTATTTACTGGCCCAGTTCATCATACTCCTTCTCTTCTTCATCG 901 TTTTTCCTCTAACCTTTTCCCTAGGACTTAAGGTGCTGTATCTCCTAAGAGCTCTCATAC 961 TCTTCAGAATTCTCCCCCTGACTGCCGGATTATTTTTTCTCTTCTCACTTGTTACCTACT 1021 ATGGGATCCNTGGGACATTCCACCTAGTTACCTAATCTCTAGGGACCTGATCCATGTCTC 1081 CATGGAAGCAATAATTCTCCTTTATGAGATCTTTTATT	
		1 M I L N R A L I L G A L T L T T M M S A 1 ATGATCCTAAACAGAGCTCTGATTCTGGGGGCCCTCACCCTGACCACCATGATGAGTGCC	SEQ ID NO:59
		21 C G G E D I V A D H F A S Y G T N V Y Q 61 TGCGGAGGTGAAGACATTGTGGCTGATCACTTTGCCTCCTACGGCACAAACGTCTACCAG	
		41 S Y G D F G Q Y T H E F D G D E K F H V 121 TCTTATGGTGATTTTGGTCAGTACACCCACGAATTTGATGGAGATGAGAAGTTCCATGTG	
		61 D L E K K E T V W R L P V F S E F T S F 181 GACCTGGAGAAGAAGGAGACTGTGTGGCGGCTGCCTGTGTTTAGCGAGTTTACAAGTTTT	
		81 D P Q G A L Q N I A T A K Y N L D I L I 241 GACCCACAGGGCGCGCTGCAAAACATTGCTACGGCAAAATACAACTTGGACATCTTGATT	
		101 K R S N S T A A T N E V P E V T V F P K 301 AAACGTTCCAACTCTACTGCTGCTACCAATGAGGTTCCTGAGGTGACTGTGTTTCCCAAG	
		121 S P V V L G Q P N T L I C L V D N I F P 361 TCTCCTGTGGTGCTGGGTCAGCCCAACACCCTCATCTGTCTTGTGGACAACATCTTCCCT	
		141 P V I N V T W L R N G H S V S E G V F E 421 CCTGTGATCAATGTCACATGGTTGAGGAATGGGCACTCAGTCAGTGAAGGTGTTTTTGAG	
		161 M I F L P K T D D S F L K I S Y L T F L 481 ATGATTTTCCTCCCCAAGACTGATGATTCCTTCCTGAAGATCAGTTACCTCACCTTCCTC	
		181 P S A D D I Y D C K V E H W G L D E P L 541 CCTTCTGCTGATGATATTTATGATTGCAAGGTGGAGCACTGGGGGCTGGATGAGCCACTT	
		201 L K H W E P E I P T P M S E L T E T V V 601 CTGAAACACTGGGAACCTGAGATTCCAACCCCAATGTCAGAGCTGACAGAGACTGTGGTC	
		221 C A L G L A V G F V G I V V G T F L I I	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		661 TGTGCCCTGGGGTTGGCTGTTGGCTTTGTGGGCATCGTGGTGGGCACCTTCCTCATCATC 241 R A L R S G G G A L R R Q G G C L - 721 CGAGCCCTACGCTCAGGTGGTGCCTTAAGACGCCAAGGATGCTTGTGA	
WBC013E10.bFSP_20010810.abd	Homo sapiens cDNA FLJ45679 fis, clone ERLTF2001835	1 aaaaacccca gcaggttagc ttctcattaa atagcttctc ctgagggcag acttgttaa 61 gaagaacaaa atgctctggc gtatttcaaa atggctcctt ttccccaccc actaccagag 121 gcatggataa tcaccctgag gacctgtgag agatccagga gcttaaaaaa aattgggggag 181 cgggggaagag ggaatggcta ggtcccctctg acttgtccac actgatcctt caggtttacc 241 tatcctggta cttgttccat tggaggcttc agcggctagt ttctgctctg tggttaccaa 301 tgacacagga gctgagcttc caaaaattta ttgaacaatc tgacttacta ggagaactta 361 aatatgactt caatgaaaaa gatgaattca gacatactga gacacaaagg cctttgtct 421 ttaactatta tgaaaatgtc cttgagaaaa atagcaagcg ctaccaggcc cttggccatt 481 tgcttgaaca atacatttat gagcttttgg agaaagtgtg caaattagaa aaagtatata 541 tcccacctga ggctgataaa gaagaaccaa gaagcttctt ttcatgagc gagaaagcat 601 taacaaatca ccattctgct cttcttatcc ttcttcaaga ccatgggctc tttcgagctg 661 gtcagtggag tcaacaggca ataatacatc atggtctcca acatggaagt cagataccat 721 gtattcaaat ggcattgcag gcacactatg atgtaattgt gctaaacccc aatgataatt 781 ttgtggaacc aaaggtggaa aaagagtgga aaggccttt aacacaaaat attgagtcat 841 cttctctaaa aatggttcaa ggtgggagct ttttctctct ccagcatcct cccaaatgca 901 ttccaaaaag atgcagcaac acccccgaag aacacacggc ttacatatgg gattacttca 961 ttcaaagac 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 ttcctatggg tttctgctgg cacagaaaag tacatcttag 1261 ccccttcctc tagccttcag tcaatttttа agtacttaaa aaaagcttta aaagccagaa 1321 caaccattaa tttctctcga atgccaatag tgactagaag ctccacaaaa agaaagcaaa 1381 gtgcttaaac tacttttgtc atctaagatt tttttgtcct tctgcaactt tgctaataca 1441 gattcttggaa 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 tatttataag tgttagttaa gtgtgaagat ctttctttta aaaagctgtg gtttgatata 2101 atgacaacaa aatggcaatt gataaaaatt agatattgaa tcaatctttg atttctataa 2161 taataccata gtaaaattac aagtgaacat aaaaattaaa catcataagc aaactgcatt	SEQ ID NO:60

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2221 ctttgtgtgt ttatgttttt tgttaagatt tgttgtactc cctgttcacc aggtctgaag 2281 aaaaataaat tttaaat	
WBC014B05.bFSP_20010910.abd	Homo sapiens neuronal apoptosis inhibitory protein mRNA	1 ACAAAAGGTCCTGTGCTCACCTGGGACCCTTCTGGACGTTGCCCTGTGTACCTCTTCGAC 61 TGCCTGTTCATCTACGACGAACCCCGGGTATTGACCCCAGACAACAATGCCACTTCATAT 121 TGGGGACTTCGTCTGGGATTCCAAGGTGCATTCATTGCAAAGTTCCTTAAATATTTTCTC 181 ACTGCTTCCTACTAAAGGACGGACAGAGCATTTGTTCTTCAGCCACATACTTCCTTCCA 241 CTGGCCAGCATTCTCCTCTATTAGACTAGAACTGTGGATAAACCTCAGAAAATGGCCACC 301 CAGCAGAAAGCCTCTGACGAGAGGATCTCCCAGTTTGATCACAATTTGCTGCCAGAGCTG 361 TCTGCTCTTCTGGGCCTAGATGCAGTTCAGTTGGCAAAGGAACTAGAAGAAGAGGAGCAG 421 AAGGAGCGAGCAAAAATGCAGAAAGGCTACAACTCTCAAATGCGCAGTGAAGCAAAAGG 481 TTAAAGACTTTTGTGACTTATGAGCCGTACAGCTCATGGATACCACAGGAGATGGCGGCC 541 GCTGGGTTTTACTTCACTGGGGTAAAATCTGGGATTCAGTGCTTCTGCTGTAGCCTAATC 601 CTCTTTGGTGCCGGCCTCACGAGACTCCCCATAGAAGACCACAAGAGGTTTCATCCAGAT 661 TGTGGGTTCCTTTTGAACAAGGATGTTGGTAACATTGCCAAGTACGACATAAGGGTGAAG 721 AATCTGAAGAGCAGGCTGAGAGGAGGTAAAATGAGGTACCAACAAGAGGAGGCTAGACTT 781 GCGTCCTTCAGGAACTGGCCATTTTATGTCCAAGGGATATCCCCTTGTGTGCTCTCAGAG 841 GCTGGCTTTGTCTTTACAGGTAAACAGGACACGGTACAGTGTTTTTCCTGTGGTGGATGT 901 TTAGGAAATTGGGAAGAAGGAGATGATCCTTGGAAGGAACATGCCAAATGGTTCCCCAAA 961 TGTGAATTTCTTCGGAGTAAGAAATCCTCAGAGGAAATTACCCAGTATATTCAAAGCTAC 1021 AAGGGATTTGTTGACATAACGGGAGAACATTTTGTGAATTCCTGGGTCCAGAGAGAATTA 1081 CCTATGGCATCAGCTTATTGCAATGACAGCATCTTTGCTTACGAAGAACTACGGCTGGAC 1141 TCTTTTAAGGACTGGCCCCGGAATCAGCTGTGGGAGTTGCAGCACTGGCCAAAGCAGGT 1201 CTTTTCTACACAGGTATAAAGGACATCGTCCAGTGCTTTTCCTGTGGAGGGTGTTTAGAG 1261 AAATGGCAGGAAGGTGATGACCCATTAGACGATCACACACCAGATGTTTTCCCAATTGTCCA 1321 TTTCTCCAAAATATGAAGTCCTCTGCGGAAGTGACTCCAGACCTTCAGAGCCGTGGTGAA 1381 CTTTGTGAATTACTGGAAACCACAAGTGAAAGCAATCTTGAAGATTCAATAGCAGTTGGT 1441 CCTATAGTGCCAGAAATGGCACAGGGTGAAGCCCAGTGGTTTCAAGAGGCAAAGAATCTG 1501 AATGAGCAGCTGAGAGCAGCTTATACCAGCGCCAGTTTCCGCCACATGTCTTTGCTTGAT 1561 ATCTCTTCCGATCTGGCCACGGACCACTTGCTGGGCTGTGATCTGTCTATTGCTTCAAAA 1621 CACATCAGCAAACCTGTGCAAGAACCTCTGGTGCTGCCTGAGGTCTTTGGCAACTTGAAC 1681 TCTGTCATGTGTGTGGAGGGTGAAGCTGGAAGTGGAAAGACGGTCCTCCTGAAGAAAATA 1741 GCTTTTCTGTGGGCATCTGGATGCTGTCCCCTGTTAAACAGGTTCCAGCTGGTTTTCTAC 1801 CTCTCCCTTAGTTCCACCAGACCAGACGAGGGGCTGGCCAGTATCATCTGTGACCAGCTC 1861 CTAGAGAAAGAAGGATCTGTTACTGAAATGTGCATGAGGAACATTATCCAGCAGTTAAAG 1921 AATCAGGTCTTATTCCTTTTAGATGACTACAAAGAAATATGTTCAATCCCTCAAGTCATA 1981 GGAAAACTGATTCAAAAAAACCACTTATCCCGGACCTGCCTATTGATTGCTGTCCGTACA 2041 AACAGGGCCAGGGACATCCGCCGATACCTAGAGACCATTCTAGAGATCAAAGCATTTCCC 2101 TTTTATAATACTGTCTGTATATTACGGAAGCTCTTTTTCACATAATATGACTCGTCTGCGA 2161 AAGTTTATGGTTTACTTTGGAAAGAACCAAAGTTTGCAGAAGATACAGAAAACTCCTCTC 2221 TTTGTGGCGGCGATCTGTGCTCATTGGTTTCAGTATCCTTTGACCCATCTTTGATGAT 2281 GTGGCTGTTTTCAAGTCCTATATGGAACGCCTTTCCTTCAAGGAACAAGCGACAGCTGAA	SEQ ID NO:61

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2341 ATTCTCAAAGCAACTGTGTCCTCCTGTGGTGAGCTGGCCTTGAAAGGGTTTTTTTCATGT	
		2401 TGCTTTGAGTTTAATGATGATGATCTCGCAGAAGCAGGGGTTGATGAAGATGAAGATCTA	
		2461 ACCATGTGCTTGATGAGCAAATTTACAGCCCAGAGACTAAGACCATTCTACCGGTTTTTA	
		2521 AGTCCTGCCTTCCAAGAATTTCTTGCGGGATGAGGCTGATTGAACTCCTGGATTCAGAT	
		2581 AGGCAGGAACATCAAGATTTGGGACTGTATCATTTGAAACAAATCAACTCACCCATGATG	
		2641 ACTGTAAGCGCCTACAACACAATTTTTTCAACTATGTCTCCTGTCACGCTTCAACAAAGGCA	
		2701 GGGCCAAAAGTTGTCTCTCATTTGCTTCGTTTGGTGGATAAGAAAGAGTCCTTGGAGAAT	
		2761 ATACTTGAATCTGATGACTACCTGAAACACCGTCCAGAAATTCAGTGCACATGGAATAT	
		2821 TTTAGGGTGTTGTGGCAATTATCTCCAAAATATTACTTTTCCCAGGTTTCAGAACATTTA	
		2881 CTTGCTCTTGCCATAAAAATCGCTTATCAAAGCAATGCTCTTGCTGCATGTTCTCCATTT	
		2941 ATTTTGAGATTCCTTCAAGGGAGAACCCTGACTTTCAATATGCTTAAGTCACAGTACTTT	
		3001 TTTGACCACCCCGAAAGCCTATTGTTGTTGAGAAGCATCCAGTTCTCGATAAAAGGAAGG	
		3061 AAGTCAAGCAGACTAGATCTTTCAGTCCTGGAAACGTGTTTGGACAAATCACAGGCACCG	
		3121 ACTATCGATCAGGACTATGCTTCTGCCTTTGAACCGGCGAAAGAATGGGAGCAGAATTTA	
		3181 GCAGAAAAAGAGGAAAACGTGAAGAGTTTTCTGGATATGCAACTCAATGCACCACCAGAC	
		3241 ATCAGCACTGGCTATTGGAAACTTTCTCCAAAGCCATACAAGATTCCCCTTCTGGAAGTC	
		3301 CACGTGACTGATATCGACGCTGTGGACCAGGAGATGCTCAGGGTTCTAACGGCAGTTTTC	
		3361 TCAGCTTCACAGCACATCGAACTCCACCTAAACGACTGCAGGGGCTTTCCGGAAAGCGTC	
		3421 CGCCCAGCTCTTGAGCTGTCTAAGGCCTCTGTCACCAAGTGCTCCATAAGCAAGTTGGAA	
		3481 CTCAGCGCAGCCGAACAGGAACTGCTTCTCACCCTGCCTTCCCTGGAATCTCTTGAAGTC	
		3541 TCAGGGACAATCCAGTCACAAGACCAAATCTTTCCTAATCTGGATAAGTTCCTGTGCCTG	
		3601 AAAGAACTGTCTGTGGATCTGGAGGGCAATATATAAATGTTTTTTCAGTCATTCCTGAAGAA	
		3661 TTTCCAAACTTCCACCATATGGAGAAATTATTGATCCAAATTTCAGCTGAGTATGATCCT	
		3721 TCCAAACTAGTAAAATTAATTCAAAATTCTCCCAAACCTTCATGTTTTCCATCTGAAGTGT	
		3781 AACTTCTTTCGGATTTTGGGTCTCTCATGACTATGCTTGTTTCCTGTAAGAAACTCACA	
		3841 GAAATTAAGTTTTCGGATTCATTTTTTCAAGCCGTCCCATTTGTTGCCAGTTTGCCAAAT	
		3901 TTTATTTCTCTGAAGATATTAAATCTTGAAGGCCAGCAATTTCCTGATGAGGAAACATCA	
		3961 GAAAAATTTGCCTACATTTTAGGTTCTCTTAGTAACCTGGAAGAATTGATCCTTCCTACT	
		4021 GGGGATGGAATTTATCGAGTGGCCAAACTGATCATCCAGCAGTGTCAGCAGCTTCATTGT	
		4081 CTCCGAGTCCTCTCATTTTTCAAGACTTTGAATGATGACAGCGTGGTGGAAATTGCCAAA	
		4141 GTAGCAATCAGTGGAGGTTTCCAGAAACTTGAGAACCTAAAGCTTTCAATCAATCACAAG	
		4201 ATTACAGAGGAAGGATACAGAAATTTCTTTCAAGCACTGGACAACATGCCAAACTTGCAG	
		4261 GAGTTGGACATCTCCAGGCATTTCACAGAGTGTATCAAAGCTCAGGCCACAACAGTCAAG	
		4321 TCTTTGAGTCAATGTGTGTTACGACTACCAAGGCTCATTAGACTGAACATGTTAAGTTGG	
		4381 CTCTTGGATGCAGATGATAATTGCATTGCTTAATGTCATGAAAGAAAGACATCCTCAATCT	
		4441 AAGTACTTAACTATTCTCCAGAAATGGATACTGCCGTTCTCTCCAATCATTCAGAAATAA	
		4501 AAGATTCAGCTAAAAACTGCTGAATCAATAAATTTGTCTTGGGGCATATTGAGGATGTAAA	
		4561 AAAAGTTGTTGATTAATGCTAAAAACCAAATTATCCAAAATTATTTATTAAATATTGCA	
		4621 TACAAAAGAAAAATGTGTAAGGCTTGCTAAAAAACAAAACAAAACACAGTCCTGCA	
		4681 TACTCACCACCAAGCTCAAGAAATAAATCATCACCAATACCTTTGAGGTCCCTGAGTAAT	
		4741 CCACCCCAGCTAAAGGCAAACCCTTCAATCAAGTTTATACAGCAAACCCTCCATTGTCCA	
		4801 TGGTCAACAGGGAAGGGGTTGGGGACAGGTCTGCCAATCTATCTAAAAGCCACAATATGG	
		4861 AAGAAGTATTCAATTTATATATAATGGCTAACTTAACGGTTGAATCACTTTCATACAT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		4921 GGATGAAACGGGTTTAACACAGGATCCACATGAATCTTCTGTGGGCCAAGAGATGTTCCT 4981 TAATCCTTGTAGAACCTGTTTTCTATATTGAACTAGCTTTGGTACAGTAGAGTTAACTTA 5041 CTTTCCATTTATCCACTGCCAATATAAAGAGGAAACAGGGGTTAGGGAAAAATGACTTCA 5101 TTCCAGAGGCTTCTCAGAGTTCAACATATGCTATAATTTAGAATTTTCTTATGAATCCAC 5161 TCTACTTGGGTAGAAAATATTTTATCTCTAGTGATTGCATATTATTTCCATATCATAGTA 5221 TTTCATAGTATTATATTTGATATGAGTGTCTATATCAATGTCAGTGTCCAGAATTTCGTT 5281 CCTACCAGTTAAGTAGTTTTCTGAACGGCCAGAAGACCATTCGAAATTCATGATACTACT 5341 ATAAGTTGGTAAACAACCATACTTTTATCCTCATTTTTATTCTCACTAAGAAAAAAGTCA 5401 ACTCCCCTCCCCCTTGCCCAAGTATGAAATATAGGGACAGTATGTATGGTGTGGTCTCATT 5461 TGTTTAGAAAACCACTTATGACTGGGTGCGGTGGCTCACACCTGTAATCCCAGCACTTTG 5521 GGAGGCTGAGGCGGGCGAATCATTTGAGGTGAGGAATTCGAGACCAGCCTGGCCAGCATG 5581 GTGAAACCCCATCTCTACTAAAAATACAAAAATTAGCCAGGTGTGGTGGCACATGCCTGT 5641 AGTCCCAGCCACTAGGGCGGCTGAGACGCAAGACTTGCTTGAACCCGGGAGGCAGAGGTT 5701 GCAGTGAGCCAAGATGGCGCCACTGCATTCCAGCCTGGGCAACAGAGCAAGACCCTGTCT 5761 GTCTCAAAACACAAAAACACAAAACCACTTATATTGCTAGCTACATTAAGAATTTCTGAATAT 5821 GTTACTGAGCTTGCTTGTGGTAACCATTTATAATATCAGAAAGTATATGTACACCAAAAC 5881 ATGTTGAACATCCATGTTGTACAACTGAAATATAAATAAATTTTGTCAATTATACCTAAAT 5941 AAAACTGGAAAAAAAATTTCTGGAAGTTTATATCTAAAAATGTTAATAGTGCGTACCTCTA 6001 GGAAGTGGGCCTGGAAGCCATTCTTACTTTTCAGTCTCTCCCATTCTGTACTGTTTTTTG 6061 TTTTACTTTCGTGCCTGCATTATTTTTCTATTTAAAACAAAAATAAATCTAGTTTAGCAC 6121 T 1 M A T Q Q K A S D E R R I S Q F D H N L L 1 ATGGCCACCCAGCAGAAAGCCTCTGACGAGAGGATCTCCCAGTTTGATCACAATTTGCTG 21 P E L S A L L G L D A V Q L A K E L E E 61 CCAGAGCTGTCTGCTCTTCTGGGCCTAGATGCAGTTCAGTTGGCAAAGGAACTAGAAGAA 41 E E Q K E E R A K K M Q K G Y N S Q M R S E 121 GAGGAGCAGAAGGAGCGAGCAAAAATGCAGAAAGGCTACAACTCTCAAATGCGCAGTGAA 61 A K R L K T F V T Y E P Y S S W I P Q E 181 GCAAAAAGGTTAAAGACTTTTGTGACTTATGAGCCGTACAGCTCATGGATACCACAGGAG 81 M A A A G F Y F T G V K S G I Q C F C C 241 ATGGCGGCCGCTGGTTTTACTTCACTGGGGTAAAATCTGGGATTCAGTGCTTCTGCTGT 101 S L I L F G A G L T R L P I E D H K R F 301 AGCCTAATCCTCTTTGGTGCCGGCCTCACGAGACTCCCCATAGAAGACCACAAGAGGTTT 121 H P D C G F L L N K D V G N I A K Y D I 361 CATCCAGATTGTGGGTTCCTTTTGAACAAGGATGTTGGTAACATTGCCAAGTACGACATA	SEQ ID NO:62

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		141 R V K N L K S R L R G G K M R Y Q E E E 421 AGGGTGAAGAATCTGAAGAGCAGGCTGAGAGGAGGTAAAATGAGGTACCAAGAAGAGGAG	
		161 A R L A S F R N W P F Y V Q G I S P C V 481 GCTAGACTTGCGTCCTTCAGGAACTGGCCATTTTATGTCCAAGGGATATCCCCTTGTGTG	
		181 L S E A G F V F T G K Q D T V Q C F S C 541 CTCTCAGAGGCTGGCTTTGTCTTTACAGGTAAACAGGACACGGTACAGTGTTTTTCCTGT	
		201 G G C L G N W E E G G D D P W K E H A K W 601 GGTGGATGTTTAGGAAATTGGGAAGAAGGAGATGATCCTTGGAAGGAACATGCCAAATGG	
		221 F P K C E F L R S K K S S E E I T Q Y I 661 TTCCCCAAATGTGAATTTCTTCGGAGTAAGAAATCCTCAGAGGAAATTACCCAGTATATT	
		241 Q S Y K G F V D I T G E H F V N S W V Q 721 CAAAGCTACAAGGGATTTGTTGACATAACGGGAGAACATTTTGTGAATTCCTGGGTCCAG	
		261 R E L P M A S A Y C N D S I F A Y E E L 781 AGAGAATTACCTATGGCATCAGCTTATTGCAATGACAGCATCTTTGCTTACGAAGAACTA	
		281 R L D S F K D W P R E S A V G V A A L A 841 CGGCTGGACTCTTTTAAGGACTGGCCCCGGGAATCAGCTGTGGGAGTTGCAGCACTGGCC	
		301 K A G L F Y T G I K D I V Q C F S C G G 901 AAAGCAGGTCTTTTCTACACAGGTATAAAGGACATCGTCCAGTGCTTTTCCTGTGGAGGG	
		321 C L E K W Q E G D D P L D D H T R C F P 961 TGTTTAGAGAAATGGCAGGAAGGTGATGACCCATTAGACGATCACACCAGATGTTTCCC	
		341 N C P F L Q N M K S S A E V T P D L Q S 1021 AATTGTCCATTTCTCCAAAATATGAAGTCCTCTGCGGAAGTGACTCCAGACCTTCAGAGC	
		361 R G E L C E L L E T T S E S N L E D S I 1081 CGTGGTGAACTTTGTGAATTACTGGAAACCACAAGTGAAAGCAATCTTGAAGATTCAATA	
		381 A V G P I V P E M A Q G E A Q W F Q E A 1141 GCAGTTGGTCCTATAGTGCCAGAAATGGCACAGGGTGAAGCCCAGTGGTTTCAAGAGGCA	
		401 K N L N E Q L R A A Y T S A S F R H M S 1201 AAGAATCTGAATGAGCAGCTGAGAGCAGCTTATACCAGCGCCAGTTTCCGCCACATGTCT	
		421 L L D I S S D L A T D H L L G C D L S I	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1261 TTGCTTGATATCTCTTCCGATCTGGCCACGGACCACTTGCTGGGCTGTGATCTGTCTATT	
		441 A S K H I S K P V Q E P L V L P E V F G 1321 GCTTCAAACACATCAGCAAACCTGTGCAAGAACCTCTGGTGCTGCCTGAGGTCTTTGGC	
		461 N L N S V M C V E G E A G S G K T V L L 1381 AACTTGAACTCTGTCATGTGTGTGGAGGGTGAAGCTGGAAGTGGAAAGACGGTCCTCCTG	
		481 K K I A F L W A S G C C P L L N R F Q L 1441 AAGAAAATAGCTTTTCTGTGGCATCTGGATGCTGTCCCCTGTTAAACAGGTTCCAGCTG	
		501 V F Y L S L S S T R P D E G L A S I I C 1501 GTTTTCTACCTCTCCCTTAGTTCCACCAGACCAGACGAGGGCTGGCCAGTATCATCTGT	
		521 D Q L L E K E G S V T E M C M R N I I Q 1561 GACCAGCTCCTAGAGAAGAAGGATCTGTTACTGAAATGTGCATGAGGAACATTATCCAG	
		541 Q L K N Q V L F L L D D Y K E I C S I P 1621 CAGTTAAAGAATCAGGTCTTATTCCTTTTAGATGACTACAAAGAAATATGTTCAATCCCT	
		561 Q V I G K L I Q K N H L S R T C L L I A 1681 CAAGTCATAGGAAAACTGATTCAAAAAACCACTTATCCCGACCTGCCTATTGATTGCT	
		581 V R T N R A R D I R R Y L E T I L E I K 1741 GTCCGTACAAACAGGGCCAGGACATCCGCCGATACCTAGAGACCATTCTAGAGATCAAA	
		601 A F P F Y N T V C I L R K L F S H N M T 1801 GCATTTCCCTTTTATAATACTGTCTGTATATTACGGAAGCTCTTTTCACATAATATGACT	
		621 R L R K F M V Y F G K N Q S L Q K I Q K 1861 CGTCTGCGAAAGTTTATGGTTTACTTTGGAAAGAACCAAAGTTTGCAGAAGATACAGAAA	
		641 T P L F V A A I C A H W F Q Y P F D P S 1921 ACTCCTCTCTTTGTGGCGGCGATCTGTGCTCATTGGTTTCAGTATCCTTTTGACCCATCC	
		661 F D D V A V F K S Y M E R L S L R N K A 1981 TTTGATGATGTGGCTGTTTTCAAGTCCTATATGGAACGCCTTTCCTTAAGGAACAAGCG	
		681 T A E I L K A T V S S C G E L A L K G F 2041 ACAGCTGAAATTCTCAAAGCAACTGTGTCCTCCTGTGGTGAGCTGGCCTTGAAAGGGTTT	
		701 F S C C F E F N D D D L A E A G V D E D 2101 TTTTCATGTTGCTTTGAGTTTAATGATGATCTCGCAGAAGCAGGGGTTGATGAAGAT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		721 E D L T M C L M S K F T A Q R L R P F Y 2161 GAAGATCTAACCATGTGCTTGATGAGCAAATTTACAGCCCAGACTAAGACCATTCTAC	
		741 R F L S P A F Q E F L A G M R L I E L L 2221 CGGTTTTTAAGTCCTGCCTTCCAAGAATTTCTTGCGGGATGAGGCTGATTGAACTCCTG	
		761 D S D R Q E H Q D L G L Y H L K Q I N S 2281 GATTCAGATAGGCAGGAACATCAAGATTTGGGACTGTATCATTTGAAACAAATCAACTCA	
		781 P M M T V S A Y N N F F N Y V S C H A S 2341 CCCATGATGACTGTAAGCGCCTACAACAATTTTTTCAACTATGTCTCCTGTCACGCTTCA	
		801 T K A G P K V V S H L L R L V D K K E S 2401 ACAAAGGCAGGGCCAAAAGTTGTCTCTCATTTGCTTCGTTTGGTGGATAAGAAAGAGTCC	
		821 L E N I L E S D D Y L K H R P E I S V H 2461 TTGGAGAATATACTTGAATCTGATGACTACCTGAAACACCGTCCAGAAATTTCAGTGCAC	
		841 M E Y F R V L W Q L S P K Y Y F S Q V S 2521 ATGGAATATTTTAGGGTGTTGTGGCAATTATCTCCAAAATATTACTTTCTCCAGGTTTCA	
		861 E H L L A L A I K I A Y Q S N A L A A C 2581 GAACATTTACTTGCTCTTGCCATAAAAATCGCTTATCAAGCAATGCTCTTGCTGCATGT	
		881 S P F I L R F L Q G R T L T F N M L K S 2641 TCTCCATTTATTTTGAGATTCCTTCAAGGGAGAACCCTGACTTTCAATATGCTTAAGTCA	
		901 Q Y F F D H P E S L L L L R S I Q F S I 2701 CAGTACTTTTTTGACCACCCCGAAAGCCTATTGTTGTTGAGAAGCATCCAGTTCTCGATA	
		921 K G R K S S R L D D L S V L E T C L D K S 2761 AAAGGAAGGAAGTCAAGCAGACTAGATCTTTCAGTCCTGGAAACGTGTTTTGGACAAATCA	
		941 Q A P T I D Q D Y A S A F E P A K E W E 2821 CAGGCACCGACTATCGATCAGGACTATGCTTCTGCCTTTGAACCGGCGAAAGAATGGGAG	
		961 Q N L A E E K E E N V K S F L D M Q L N A 2881 CAGAATTTAGCAGAAAAAGAGGAAAACGTGAAGAGTTTTCTGGATATGCAACTCAATGCA	
		981 P P D I S T G Y W K L S P K P Y K I P L 2941 CCACCAGACATCAGCACTGGCTATTGGAAACTTTCTCCAAAGCCATACAAGATTCCCCTT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1001 L E V H V T D I D A V D Q E M L R V L T 3001 CTGGAAGTCCACGTGACTGATATCGACGCTGTGGACCAGGAGATGCTCAGGGTTCTAACG	
		1021 A V F S A S Q H I E L H L N D C R G F P 3061 GCAGTTTTCTCAGCTTCACAGCACATCGAACTCCACCTAAACGACTGCAGGGGCTTTCCG	
		1041 E S V R P A L E L S K A S V T K C S I S 3121 GAAAGCGTCCGCCCAGCTCTTGAGCTGTCTAAGGCCTCTGTCACCAAGTGCTCCATAAGC	
		1061 K L E L S A A E Q E L L L T L P S L E S 3181 AAGTTGGAACTCAGCGCAGCCGAACAGGAACTGCTTCTCACCCTGCCTTCCCTGGAATCT	
		1081 L E V S G T I Q S Q D Q I F P N L D K F 3241 CTTGAAGTCTCAGGGACAATCCAGTCACAAGACCAAATCTTTCCTAATCTGGATAAGTTC	
		1101 L C L K E L S V D L E G N I N V F S V I 3301 CTGTGCCTGAAAGAACTGTCTGTGGATCTGGAGGGCAATATAAATGTTTTTTCAGTCATT	
		1121 P E E F P N F H H M E K L L I Q I S A E 3361 CCTGAAGAATTTCCAAACTTCCACCATATGGAGAAATTATTGATCCAAATTTCAGCTGAG	
		1141 Y D P S K L V K L I Q N S P N L H V F H 3421 TATGATCCTTCCAAACTAGTAAAATTAATTCAAAATTCTCCAAACCTTCATGTTTTCCAT	
		1161 L K C N F F S D F G S L M T M L V S C K 3481 CTGAAGTGTAACTTCTTTTCGGATTTTGGGTCTCTCATGACTATGCTTGTTTCCTGTAAG	
		1181 K L T E I K F S D S F F Q A V P F V A S 3541 AAACTCACAGAAATTAAGTTTTCGGATTCATTTTTTCAAGCCGTCCCATTTGTTGCCAGT	
		1201 L P N F I S L K I L N L E G Q Q F P D E 3601 TTGCCAAATTTTATTTCTCTGAAGATATTAAATCTTGAAGGCCAGCAATTTCCTGATGAG	
		1221 E T S E K F A Y I L G S L S N L E E L I 3661 GAAACATCAGAAAAATTTGCCTACATTTTAGGTTCTCTTAGTAACCTGGAAGAATTGATC	
		1241 L P T G D G I Y R V A K L I I Q Q C Q Q 3721 CTTCCTACTGGGGATGGAATTTATCGAGTGGCCAAACTGATCATCCAGCAGTGTCAGCAG	
		1261 L H C L R V L S F F K T L N D S V V E 3781 CTTCATTGTCTCCGAGTCCTCTCATTTTTCAAGACTTTGAATGATGACAGCGTGGTGGAA	
		1281 I A K V A I S G G F Q K L E N L K L S I	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		3841 AITGCCAAAGTAGCAATCAGTGGAGGTTTCCAGAAACTTGAGAACCTAAAGCTTTCAATC 1301 N H K I T E E G Y R N F F Q A L D N M P 3901 AATCACAAGATTACAGAGGAAGGATACAGAAATTTCTTTCAAGCACTGGACAACATGCCA 1321 N L Q E L D I S R H F T E C I K A Q A T 3961 AACTTGCAGGAGTTGGACATCTCCAGGCATTTCACAGAGTGTATCAAAGCTCAGGCCACA 1341 T V K S L S Q C V L R L P R L I R L N M 4021 ACAGTCAAGTCTTTGAGTCAATGTGTGTTACGACTACCAAGGCTCATTAGACTGAACATG 1361 L S W L L D A D D I A L L N V M K E R H 4081 TTAAGTTGGCTCTTGGATGCAGATGATATTGCATTGCTTAATGTCATGAAAGAAAGACAT 1381 P Q S K Y L T I L Q K W I L P F S P I I 4141 CCTCAATCTAAGTACTTAACTATTCTCCAGAAATGGATACTGCCGTTCTCTCCAATCATT 1401 Q K - 4201 CAGAAATAA	
WBC014E06.bFSP_20 010910.abd	No Homology	1 TTAAAGAATGAAAGAAAGCCGTTTCACAAAGAAGTAGTGGTGCTTGGAGTCACATTGGGA 61 TAGATTTTCTGGTGATTCCCAGTCTGTAAACATCACAGATGTTAGTTTAATGGAATAGGA 121 TACATACTGCATTGGCTCCTGTTGAAATTTGAGGAGGAGAATTGGCTTGAAGCTTAGGTT 181 TCCTTACCGAAAGCGGCTACTCACTTTCTTAAGTGAGGGTCCTTTCATTCAAGACAAAAA 241 TTTTCCTGCCCCTTCTGTTTGTAGTCTCCAAAATTGGAAGGAGAGCTTTATCAACTGCAA 301 AGTACAAATTAAGTGCCCTTGCCAAGCTGACTTCTCTTAATTACACTATTGTTCACACTG 361 ATTGCCGTCCTTTAGTTCTTTCCTGCTAAACAATGGACTAGTTTCCTCCTCAGTCACTTA 421 GAGCTGATTAATATCAGCCTTGGTAAACCAAAAATGTGAGGCTACACCTAATCCAGATTG 481 TCTGCAGGACTTTTCTCCTGCATCCCTGCTTGAGGAAGCTTTCTCTAGATAGCAGGTGGC 541 CATCGTTACTTTATTGGTTCAGATAACGTTTTATACCGTCTTAGGGGCGCTGATCTGCTA 601 TTCTGGAAAGGTTTTATCTTAATAAAGGTGAACTAACAGTGCAGCCAACTACTCTCTACCT 661 GGATACTTTTCTTCCATCCTACCTCTGGATCTCATACTTCTTCATCACTCAAGACCTGGA 721 TGCCACCTCTGTGAAACGCTCCCCAACTCACCGTTAGTAGGAGAAGGGCCGTTATTTTGG 781 TTTCCGTGGTCCTTTCCAGAGAGCTGTGCTGTTCATACTAACTGTTGTAATGGAATGATT 841 TGATAGCATGTCTCCATTTTCTCTTTCAAACTGAAAATCTGTGTATCTCCTTGCGTATGCTC 901 AGCACCTAATGCACATAGAACTTTACAGGTGCTTGGTAAATTAACCACACTTCTGTTGTC 961 TTTTCAAAGACTTTCAAAAGTAATACCAGTTTACAAAGAGTTAATTCTCTAGGGTTCTAG 1021 AAGCACAAATCAGGAACGGTACTATTTATTTTGGTTCTCTGCTGTAAAAAATATCAGGT 1081 TACCTGCCTCCAGAGTTCTAAAAAGAGTTGTGTATTTTCAAACAGCTTTTCAGGATGTAA 1141 ATACTCACAAAGCAACATATGTATATAGGAATAGATTTAAAATGGAATTTAAAATCACCT 1201 TTACTGACGGTTGTTGGTTGTTTTTTGTTTTGTTTTTTTTTTACTGTTTCTCTGA 1261 GTAACTTTGTATCTAAATGTTTGTTTTGATTGTGGAAGAAAAGACGTGGTGGTACAAAT	SEQ ID NO:63

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE		SEQUENCE IDENTIFIER:
		1321	TACAGATGTATGCGTGAGAAGGCCCCGTGATATAATAGTGCTTAGCATTCTCTGTTGTAA	
		1381	TTGCGTGTCTGTCCTTTCCTCTTGTCCTTAAACTCCATAGGGCAGGGGTCAGCTCTGTAT	
		1441	TATTGACCATTTTATTCCTTATGTATAACATAATACATGATAAATAATAGGCCTTCAATA	
		1501	AATATTT	
WBC014G03.bFSP_20010910.abd	Homo sapiens non-POU domain containing, octamer-binding, mRNA	1	GAGAGGCCGTGTAGCGTCGCCGTTACTCCGAGGAGATACCAGTCGGTAGAGGGGTGCAAA	SEQ ID NO:64
		61	AATGCAGAGTAATAAACTTTAACTTGGAGAAGCAAACCATACTCCAAGAAAGCATCA	
		121	TCAACATCACCACCAGCAGCACCACCAGCAGCAACAGCAGCCGCCACCACCGCC	
		181	AATACCTGCAAATGGGCAACAGCCAGCAGCCAAAATGAAGGCTTGACTATTGACCTGAA	
		241	GAATTTTAGAAAACCAGGAGAGAAGACCTTCACCCAACGAAGCCGTCTTTTTGTGGGAAA	
		301	TCTTCCTCCCGACATCACTGAGGAAGAAATGAGGAAACTATTTGAGAAATATGGAAAGGC	
		361	AGGCGAAGTCTTCATTCATAAGGATAAAGGATTTGGCTTTATCCGCTTGGAAACCCGAAC	
		421	CCTAGCGGAGATTGCCAAAGTGGAGCTGGACAATATGCCACTCCGTGGAAAGCAGCTGCG	
		481	TGTGCGCTTTGCCTGCCATAGTGCATCCCTTACAGTTCGAAACCTTCCTCAGTATGTGTC	
		541	CAACGAACTGCTGGAAGAAGCTTTTCTGTGTTTGGCCAGGTAGAGAGGGCTGTAGTCAT	
		601	TGTGGATGATCGAGGAAGGCCCTCAGGAAAAGGCATTGTTGAGTTCTCAGGGAAGCCAGC	
		661	TGCTCGGAAAGCTCTGGACAGATGCAGTGAAGGCTCCTTCCTGCTAACCACATTTCCTCG	
		721	TCCTGTGACTGTGGAGCCCATGGACCAGTTAGATGATGAAGAGGCACTTCCAGAGAAGCT	
		781	GGTTATAAAAACCAGCAATTTCACAAGGAACGAGAGCAGCCACCCAGATTTGCACAGCC	
		841	TGGCTCCTTTGAGTATGAATATGCCATGCGCTGGAAGGCACTCATTGAGATGGAGAAGCA	
		901	GCAGCAGGACCAAGTGGACCGCAACATCAAGGAGGCTCGTGAGAAGCTGGAGATGGAGAT	
		961	GGAAGCTGCACGCCATGAGCACCAGGTCATGCTAATGAGACAGGATTTGATGAGGCGCCA	
		1021	AGAAGAACTTCGGAGGATGGAAGAGCTGCACAACCAAGAGGTGCAAAAACGAAAGCAACT	
		1081	GGAGCTCAGGCAGGAGGAAGAGCGCAGGCGCCGTGAAGAAGAGATGCGGCGGCAGCAAGA	
		1141	AGAAATGATGCGGCGACAGGAAGGATTCAAGGGAACCTTCCCTGATGCGAGAGAGCA	
		1201	GGAGATACGGATGGGCCAGATGGCTATGGGAGGTGCTATGGCATAAACAACAGAGGCGC	
		1261	CATGCCCCCTGCTCCCTGTGCCAGCTGGTACCCCAGCTCCTCCAGGACCTGCTACTATGAT	
		1321	GCCAGATGGAACCTTGGGATTGACCCCACCAACACAACTGAACGCTTTGGTCAAGCTGCTAC	
		1381	AATGGAAGGAATTGGGGCAATTGGTGGAACCCCTCCTGCGTTCAACCGTGCAGCTCCTGG	
		1441	AGCTGAATTTGCTCCGAACAAACGTCGCCGATACTAATAAAATTGCAGTGTCTAGTTTCC	
		1501	CAAAACCCCTAAAAGAAGGACCCTTTTTGGACTAGCCAGAATTCTACCCTGGAAAAGTGT	
		1561	TAGGGATTCCTCCCCAATAGTTAGGTCTTCCCTGCCTGTACAACTTACTCTAGGGAGTATG	
		1621	CTGGAGGCAGAGGGCAAGGGAGGGGCGATATGTAACAAATCAGTTCTGTGTGGTATTTCG	
		1681	TTTAATCAATTCTGTGTGGTGCATTCCTGAAGTCTCATGTGATTGTTGAGGGCCTGGGGG	
		1741	GGAACCATGGCAAAATGGATCCAGTTAGAGCCCCCATTAATCTTAATCATTCCGGTTTTT	
		1801	TTTTTTTTTGTCCATCTTGTTTCATTTGCTTGCCCCGCCCCCGAGACGGAGTCTTACTCT	
		1861	GTCGCCCAGGCTGGAGTGTAGTGGCATGATCTCGGCTCACTGCAATCTCTGCCTCCCGGG	
		1921	TTCAAGCTTGTCCAGGTTGATCTTGAACTCCTGACCTCGTGATCTACCCACCTCGGCCTC	
		1981	CCAAAATGCTGGGATTACAGGGGTGAGCCACCGTGCCCCAACCTCACTTGCTTCTTATCCT	
		2041	TACACTCCCCCAGCCCCAGAGACACTGCCACATATACCACAAAAACCAAATGTCCCCCA	
		2101	ATGACCTTAGCCCCATTGCTCCATTCACTCCCAGGTGGGAATTCAGGCAAATGTCCGCAG	
		2161	AGGTCACAGACAACGTGCATACGGTTCTGTTATATCCCATATATTACCCCTTCATGTCCT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2221 AAGGAAGACGTTTTCTCTTAGTGATTTTCATTTTAGTATATCTTTTAAAAAATCTTGTGT 2281 TAACTTGCCTCCCATCTTTTTCTTGGGTGAAGACAACCCAGGAATGGCCCTTTGTGTCTA 2341 TGATGTTGCTGTTCACAGCTTTTCTTGGTAGGCTTAGTACAATCTTGGGAACAGGGTTGC 2401 TGTGTGCTGAAGGTGGGACAGTAACTCTTAGCCTTGCCTATCTTAGGTAGTTACGCTGTG 2461 CATTTTTATTGGTGTACCATGTTTGATTTGTCCCTGATACCTTTGGAGTTTTTCTGAAA 2521 AATGGAGCAGTAATGCAGCATCAACTTATTAAAATACAGTTTTAAGCCTTTTAAAAAAAA 2581 AAAAAAAAAAAAAAAAAAA	
		1 M Q S N K T F N L E K Q N H T P R K H H 1 ATGCAGAGTAATAAAACTTTTAACTTGGAGAAGCAAAACCATACTCCAAGAAAGCATCAT 21 Q H H H Q Q Q Q H H Q Q Q Q Q P P P P P P 61 CAACATCACCACCAGCAGCAGCACCACCAGCAGCAACAGCAGCCGCCACCACCGCCA 41 I P A N G Q Q Q A S S Q N E G L T T I D L K 121 ATACCTGCAAATGGGCAACAGGCCAGCAGCCAAAATGAAGGCTTGACTATTGACCTGAAG 61 N F R K P G E E K T F F T Q R S R L F V G N 181 AATTTTAGAAAACCAGGAGAGAAGACCTTCACCCAACGAAGCCGTCTTTTTGTGGGAAAT 81 L P P D I T E E E M R K K L F E K Y G K A 241 CTTCCTCCCGACATCACTGAGGAAGAAATGAGGAAACTATTTGAGAAATATGGAAAGGCA 101 G E V F I H K D K G G F G F I R L E T R T 301 GGCGAAGTCTTCATTCATAAGGATAAAGGATTTGGCTTTATCCGCTTGGAAACCCGAACC 121 L A E I A K V E L D N M P L R G K Q L R 361 CTAGCGGAGATTGCCAAAGTGGAGCTGGACAATATGCCACTCCGTGGAAAGCAGCTGCGT 141 V R F A C H S A S L T V R N L P Q Y V S 421 GTGCGCTTTGCCTGCCATAGTGCATCCCTTACAGTTCGAAACCTTCCTCAGTATGTGTCC 161 N E L L E E A F S V F G Q V E R A V V I 481 AACGAACTGCTGGAAGAAGCCTTTCTGTGTTTGGCCAGGTAGAGAGGCTGTAGTCATT 181 V D D R G R P S G K G I V E F S G K P A 541 GTGGATGATCGAGGAAGGCCCTCAGGAAAAGGCATTGTTGAGTTCTCAGGGAAGCCAGCT 201 A R K A L D R C S E G S F L L T T F P R 601 GCTCGAAAGCTCTGGACAGATGCAGTGAAGGCTCCTTCCTGCTAACCACATTTCCTCGT 221 P V T V E P M D Q L D D E E G L P E K L 661 CCTGTGACTGTGGAGCCCATGGACCAGTTAGATGATGAAGAGGGACTTCCAGAGAAGCTG	SEQ ID NO:65

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		241 V I K N Q Q F H K E R E Q P P R F A Q P 721 GTTATAAAAAACCAGCAATTTCACAAGGAACGAGCAGCCACCCAGATTTGCACAGCCT	
		261 G S F E Y E Y A M R W K A L I E M E K Q 781 GGCTCCTTTGAGTATGAATATGCCATGCGCTGGAAGGCACTCATTGAGATGGAGAAGCAG	
		281 Q Q D Q V D R N I K E A R E K L E M E M 841 CAGCAGGACCAAGTGGACCGCAACATCAAGGAGGCTCGTGAGAAGCTGGAGATGGAGATG	
		301 E A A R H E H Q V M L M R Q D L M R R Q 901 GAAGCTGCACGCCATGAGCACCAGGTCATGCTAATGAGACAGGATTTGATGAGGCGCCAA	
		321 E E L R R M E E L H N Q E V Q K R K Q L 961 GAAGAACTTCGGAGGATGGAAGAGCTGCACACCAAGAGGTGCAAAAACGAAAGCAACTG	
		341 E L R Q E E E E R R R R E E E E M R R Q Q E 1021 GAGCTCAGGCAGGAGGAAGAGCGCAGGCGCCGTGAAGAAGAGATGCGGCGGCAGCAAGAA	
		361 E M M R R Q Q E G F K G G T F P D A R E E Q 1081 GAAATGATGCGGCGCACAGCAGGAAGGATTCAAGGGAACCTTCCCTGATGCGAGAGAGCAG	
		381 E I R M G Q M A M G G A M G I N N R G A 1141 GAGATACGGATGGCCAGATGGCTATGGGAGGTGCTATGGGCATAAACACAGAGGCGCC	
		401 M P P A P V P A G T P P A P P G P A T M M 1201 ATGCCCCCTGCTCCTGTGCCAGCTGGTACCCCAGCTCCTCCAGGACCTGCTACTATGATG	
		421 P D G T L G L T P P T T E R F G Q A A T 1261 CCAGATGGAACCTTGGGATTGACCCCACCAACAACTGAACGCTTTGGTCAAGCTGCTACA	
		441 M E G I G A I G G T P P A F N R A A P G 1321 ATGGAAGGAATTGGGGCAATTGGTGGAACCCCTCCTGCGTTCAACCGTGCAGCTCCTGGA	
		461 A E F A P N K R R R Y - 1381 GCTGAATTTGCTCCGAACAAACGTCGCCGATACTAA	
WBC014H06.bFSP_20010910.abd	No Homology	1 TTAAATTCTGACTCTGTAAATGCATAAGAGATGTTAAAAATAACAATGCACTTTGAGGAA 61 TGTTTGCATATGCCTCTGATTAGGAAGAAAACATTTGTCTATGCTCTGCAGTGGCCAATG 121 AAGAATTACTAATGCCTTATTTTCTAGGCATAGATTAGAGAATGTAGACCAGACAATTTG 181 TTTACTATTACAAGAAGACTACCAGTTTGCTTACAGGAGATTATTTTTTGTGAACAGTAG 241 GTTTGAGTCCAAGACCATTTGAAGAATTACAAACTCTTTCTTAAAAAAGGAAGAAGTCT	SEQ ID NO:66

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		301 GCTTGAAATGAATGCAAAATTCCTTTTAGTCCATCACATTCAAATGTCTTGGTTGTGAC 361 CTGTTACCAGTATAGGAGAGAAGCCCAAATCACTGTTTAGATCAAACATTCTTCATGTA 421 GGTAACTATAAGAGGCTAGTGCCTACAAATTACTTCTTCATGCATTGTTGGGAGTCTCTG 481 AAAGCACTGGCAATTTTAAGAGTCTTTCTCAGGGTAACTTAATGTTTCTTAATGAACAA 541 TGTTTTCAGCTAAAAAGTCCTTCCAAGTATATTATCTGCCCTTCAAAAAGTAATCTTAT 601 AAAAGAACTTTAGCACTTTCTCAATTGATTTAGGCTATTTTCAGTATTCAGAAATGATTT 661 TGATCTCTGTAGAATTAATTGTCTGCTTGAAAATTATTTTTCAAATCCCTTTTAGTGGCA 721 ACATTTTTTTTCTATTGAAGGTCAAAGGATTGGAAACTGGTTCTTGTATCCATGTAACGTG 781 TTATGTGAAAAAGTATTCATGTTGGCAATTTTAGTTAAGCATTATGGTGTGGGTGTAATT 841 TTTAAAACTTAATTCAGTGTCTCGTCTGATTAAAGCAGGCACTGATCAGTGTATCTCCTA 901 AGAGGTAGTTTACCTCCTATTCCCTTCCTATAATCCTTACATTCTAAATTT 1 GCTTTTGCAAAAACGGTCTCGACCCTGGTCTGGCTCCTTTGTACCTCACCTCTCTGCCA 61 AACGTGATCTTAAGCAACAAGGAAGCCACACCGTCGTCTGTGAGAAAGTGCGCCTCCTTA 121 AAGGGTCCTCTGGGGCTCAAATGGCACCAAGTGGTGAATAACATATCCCAGTTCATTTTC 181 TGGACCGTTTTTGTCCTAAATGCTTCTGTTTTATGTGGTGATCGCAAAACAAGTATATAAT 241 TCTTACAGAAAGTCCAAAAGCAAGGAGAGCGGAAACAACAAAAAGCTGGGAGGTAAAGTG 301 TTCGTTGTGGTGGCCGTCTTCTTTGTGTGCTTTGCTCCATTTCATTTTGCCAGAGTGCCA 361 TATACACAGAGCCAGACCAACAGCAGGACTGATTGCCGGGTGCAAAACCACCTGTTTATT 421 GCTAAGGAAACAACTCTCTTTTTGGCAGCAACTAACATTTGTATGGACCCCTTCATATAT 481 ATATTCTTATGTAAAAATTCACAGAAAGGCTACCATGCATGAGAGGCAGAAAGATGGCA 541 ACATCAACCCAAGAAAATCACACCATCCAGACTGACACAATAACATACCCTAGGCTGATAA 601 CTTTATTATGGTTAGCTTCTATTTATCAACAAGACTTTAAGAGACAATTTATTTGGAAAT 661 AAAATTAAGCATGAAA	SEQ ID NO:67
WBC015B08.bFSP_20010910.abd	No Homology	1 TGGAGCCTTTGCTGTCTCAGGTGTCCTGATCTCACTTCTCTGTGTGTTTGCAACAGC 61 AATTTTATGTCGCTGTGGTTTTGAGAATTTTCTTTTTTAAAAACATGAAGCCTTTAAAAA 121 AAAAATGATTTGCGCCTGTCCTCACTGTCTGGTGAAGCAGACAGAGGAGAGCCCGCCTG 181 AAGCGTGTGCAGGGCTCCTGCTCTCCGTGACCAGCCCAGCTGCTCGCAGCACCCACGTCA 241 CCTCTCAGGGCTTGGGGACCCCTGGCCACGAGCATTCACTGTTTTCACGGCCAAATAACA 301 GGACTTCTGTCACCACTGTCAGACTGATTTAGTCTTCATAATTTTATGTGCTAGTTTTAA 361 TCGGAATTGTTCCCTTTTTAAAATTAATTTTTTATTATTCATTCTTGATCATGTTCATCA 421 GTAGAGGCTGTTCATAAGAACTCTGATTCTAGCGAATTAGGGTAATTGATACCTTTCTGC 481 AGTTTTGAATAAAAGCATTTACAATTCTAAATTATTGTTTTATAAAATTCTTACATTTCA 541 GCATTCCCCTCATCACATGCTGATGTAATATTGTTTTATATTAAAATCGTCCTTTTTGCT 601 GTTGTGCCACCATTCACGCAAGTACCGTTAGTTCTTAAAATGCGTTTAAAGAAAAAGTGA 661 CCAAGTCAACTTTCACACCTCCAGTAATCAGGTAGATTACAAACCCATCCTGGGGGACAG 721 TGCCTGGGCAGATGTAGTTTCTCCCCGCTGCCTGTACTGAATAGTGTGCAGTTAGCGTGG 781 TCCCCTCACCTCGTGCTTGGAGTGGAAGTCGTCACGATCCGCGAGAGTTGACACTCAGATC 841 AGGGGTTCGCCGCTGCTCGCTGTGGCCGTGCCAGAGGCAGCCTTTCCAGAGCAAATCCAG 901 GGCCCCACGGCGCTCATGCCTTCTCTGACTGCTTTGCCTTTTTCGTTCTGTAAATTGACT 961 GGAAAGCCATCTTTAATAAACTCCTCCTGTCTCTTTATGTGTGCGGTTTATGGCCATGGA	SEQ ID NO:68

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1021 AGTGACACTTGAGGGAAGCCAGAAGTTTGGTTGAGATTGTGAGAGGCTCTTCTGTGCTTC 1081 TATGATATCATACCCGATAACACGTGTGTAAGTTACTAATATGTGAATTGTGTTAAATGT 1141 ATCTTCCGTTTGAATTCCCTTTGGATGAAATTATTTCTTGATGTGATACNATAGTGCCTT 1201 GTTCTGATTTTTGTTCTTTCCCTAAATGTTATCAAATCAGTAGAAAGTTAGAAATAAAG 1261 TGAATATAGCATTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAA	
WBC016A12.bFSP_20011010.abd	No Homology	1 AAGGGACGAAGCCCCTGTAGCCAACCCTGGCCACCGGTGTATTTGAGCCATGAGTTAAGA 61 GAACAACCTTCTATGCATGTAGAGACTGCCCCCAACCCATGTTCATCCACAACTGTCCAGA 121 GTTCCACAGCCATGGATGTGCCCACAGACTGCAGGGAGAAGGAGTCATAGCACATACAGT 181 GAGTGAACAGACATGATACAGAGAAGACATGTTATGCACACATTTGACACGAGTCCTCTT 241 GCGTTTCTTGGTCTAGATGAATTGCTAATGGCTATCACGATCTGCGTCCAGGCAGCTGAG 301 CTCAGGGGAAGGCAGCTGACCCCTCTCCCACAGGCCCCCAGACCCGGTGTACCCAGAATC 361 AGGCAGGGCAGAGGCAGGACACAAAGGTAATGAAGGACATAGGTTCAGGGATTTGTTTTC 421 AGGCTGTTGTTGTTGTTTACATTTTGCATTTTTAAATTTGCTCTCTTTTTAATTTGTTTA 481 GAGGGAAAGCTATGTGTTTTTTAATTTTTTAATTTTTCTTGTTTGTTTTGGTTTGTGATATC 541 TGTGGAGGGAGTTTTAAGTAGTGAGCTAATGGACCTTATCTGTTGGCTTAGAGGCCTAAT 601 AATAATCAGACCATTTTATTCCTTGTTTGGGTGTTATACTTTCCAAGTCCTTTCCTCTGA 661 ATCAGTGGTAATGAATATATTTACATAATCCCTTAGATTTGCTTAGTGCTTTTGTGATTT 721 TCAAAGCACTTCCATGAGCATTATCCCTTGCATTCCCTTGACAAGTATTTATGGAAAGTC 781 TGCTGTGTGCCAACCATAGTGTTAGGCATGGGGCATCTAAAACAAGTAAGCCTGGGACCC 841 TGCCCTCACAAAACGAAAAAATCTAACCAAAGAGGCAGGTTTGTAAACAAATGATTATAA 901 TAAACACAA	SEQ ID NO:69
		1 GAGGCATTTAAAATTCATGTATGATACTCTTATAATCATAACTGCTGCTAATGCTTGATT 61 ATATACTCAGGGACAATGTATAACGTAAGATTACAAATTTGTTCTCACCAACTCCCTTTT 121 GGATTTCATTAGAAAGAAAAACTCCTGGTCAGAGATAATGTATAAATCAGAGATGTAAA 181 TGGCTAGTTGTCTATATAGCATTAAATGAAGGGAAAACTGATAATTAGGCAGTTAATTTGGT 241 CAATTAAACAACCATGTCTGCATCTAGGGGAGCCTGGCTTATTTGATTGATTTCCTACTA 301 GTCTTTGACTCTCCCTTCATTCTGGTTTCCATGTGAATTTGCTTTAGAAAAGCCAGTAT 361 GGGCTGTTTCACGTGTTCAGACTTGTGTTTTCATAGCATTCATGGCGGGGCTGCAAGGCT 421 TGGAAGTGACCAGGAAGACAGTGAGAACGCGTGGTTGACACAACTGAAATGATGCAGATCA 481 GATGGCGTTTCTCCCAGCTCAGTGGATTTTCTTTGGGGTTATTCTTAAAAATATCCATCA 541 CTACACTGGAAGTCCCTGTTCTGACTATGTACTGTCCACCTGCATTACANACATTCTGCA 601 GAGCTGCTAAGTATATACATATCCGATGTGTGTTACATCTTGTATTTAATTAAATGCTAT 661 GAAACTGAAAAAAAAAAAAAAA	SEQ ID NO:70
WBC016G11.bFSP_20011010.abd	Homo sapiens mRNA for HsMcm6.	1 GGAAAAAAGCGACTTGTGGCGGTCGAGCGTGGCGCAGGCGAATCCTCGGCACTAAGCAAA 61 TATGGACCTCGCGGCGGCAGCGGAGCCGGGCGCCGGCAGCCAGCACCTGGAGGTCCGCGA 121 CGAGGTGGCCGAGAAGTGCCAGAAACTGTTCCTGGACTTCTTGGAGGAGTTTCAGAGCAG 181 CGATGGAGAAATTAAATACTTGCAATTAGCAGAGGAACTGATTCGTCCTGAGAGAAACAC 241 ATTGGTTGTGAGTTTTGTGGACCTGGAACAATTTAACCAGCAACTTTCCACCACCATTCA	SEQ ID NO:71

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		301 AGAGGAGTTCTATAGAGTTTACCCTTACCTGTGTCGGCCTTGAAAACATTCGTCAAAGA	
		361 CCGTAAAGAGATCCCTCTTGCCAAGGATTTTTATGTTGCATTCCAAGACCTGCCTACCAG	
		421 ACACAAGATTCGAGAGCTCACCTCATCCAGAATTGGTTTGCTCACTCGCATCAGTGGGCA	
		481 GGTGGTGCGGACTCACCCAGTTCACCCAGAGCTTGTGAGCGGAACTTTTCTGTGCTTGGA	
		541 CTGTCAGACAGTGATCAGGGATGTAGAACAGCAGTTCAAATACACACAGCCCAAACATCTG	
		601 CCGAAATCCAGTTTGTGCCCAACAGGAGGAGATTCTTACTGGATACAAATAAATCAAGATT	
		661 TGTTGATTTTCAAAAGGTTCGTATTCAAGAGACCCAAGCTGAGCTTCCTCGAGGGAGTAT	
		721 CCCCCGCAGTTTAGAAGTAATTTTAAGGGCTGAAGCTGTGGAATCAGCTCAAGCTGGTGA	
		781 CAAGTGTGACTTTACAGGGACACTGATTGTTGTGCCTGACGTCTCCAAGCTTAGCACACC	
		841 AGGAGCACGTGCAGAAACTAATTCCCGTGTCAGTGGTGTTGATGGATATGAGACAGAAGG	
		901 CATTCGAGGACTCCGGGCCCTTGGTGTTAGGGACCTTTCTTATAGGCTGGTCTTTCTTGC	
		961 CTGCTGTGTTGCGCCAACCAACCCAAGTTTGGGGGAAAGAGCTCAGAGATGAGGAACA	
		1021 GACAGCTGAGAGCATTAAGAACCAAATGACTGTGAAAGAATGGGAGAAAGTGTTTGAGAT	
		1081 GAGTCAAGATAAAAATCTATACCACAATCTTTGTACCAGCCTGTTCCCTACTATACATGG	
		1141 CAATGATGAAGTAAAACGGGGTGTCCTGCTGATGCTCTTTGGTGGCGTTCCAAAGACAAC	
		1201 AGGAGAAGGGACCTCTCTTCGAGGGGACATAAATGTTTGCATTGTTGGTGACCCAAGTAC	
		1261 AGCTAAGAGCCAATTTCTCAAGCACGTGGAGGAGTTCAGCCCCAGAGCTGTCTACACCAG	
		1321 TGGTAAAGCGTCCAGTGCTGCTGGCTTAACAGCAGCTGTTGTGAGATGAAGAATCTCA	
		1381 TGAGTTTGTCATTGAGGCTGGAGCTTTGATGTTGGCTGATAATGGTGTGTTGTATTGA	
		1441 TGAATTTGATAAGATGGACGTGCGGATCAAGTTGCTATTCATGAAGCTATGGAACAGCA	
		1501 GACCATATCCATCACTAAAGCAGGAGTGAAGGCTACTCTGAACGCCCGGACGTCCATTTT	
		1561 GGCAGCAGCAAACCCAATCAGTGGACACTATGACAGATCAAAATCATTGAAACAGAATAT	
		1621 AAATTTGTCAGCTCCCATCATGTCCCGATTCGATTCCTCTTCTTTATCCTTGTGGATGAATG	
		1681 TAATGAGGTTACAGATTATGCCATTGCCAGGCGCATAGTAGATTTGCATTCAAGAATTGA	
		1741 GGAATCAATTGATCGTGTCTATTCCTCGATGATATCAGAAGATATCTTCTCTTTGCAAG	
		1801 ACAGTTTAAACCCAAGATTTCCAAAGAGTCAGAGGACTTCATTGTGGAGCAATATAAACA	
		1861 TCTCCGCCAGAGAGATGGTTCTGGAGTGACCAAGTCTTCATGGAGGATTACAGTGCGACA	
		1921 GCTTGAGAGCATGATTCGTCTCTCGAAGCTATGGCTCGGATGCACTGCTGTGATGAGGT	
		1981 CCAACCTAAACATGTGAAGGAAGCTTTCCGGTTACTGAATAAATCAATCATCCGTGTGGA	
		2041 AACACCTGATGTCAATCTAGATCAAGAGGAAGAGATCCAGATGGAGGTAGATGAGGGTGC	
		2101 TGGTGGCATCAATGGTCATGCTGACAGCCCTGCTCCTGTGAACGGGATCAATGGCTACAA	
		2161 TGAAGACATAAATCAAGAGTCTGCTCCCAAAGCCTCCTTAAGGCTGGCTTCTCTGAGTA	
		2221 CTGCCGAATCTCTAACCTTATTGTGCTTCACCTCAGAAAGGTGGAAGAAGAGGACGA	
		2281 GTCAGCATTAAAGAGGAGCGAGCTTGTTAACTGGTACTTGAAGGAAATCGAATCAGAAAT	
		2341 AGATTCTGAAGAGGAACTTATAAATAAAAAGAGAATCATAGAGAAAGTCATTCATCGACT	
		2401 CACCCACTACGATCATGTTCTAATTGAGCTCACACAAGCTGGATTGAAAGGCTCGACAGA	
		2461 AGGAAGTGAGAGCTATGAAGAAGATCCCTACCTGGTGGTTAACCCTAACTACCTGCTTGA	
		2521 AGATTGAGGTATTCAAAGTAACTGACCAGAGCTGAGGAACTGTGGCACAGCACCTCGTGG	
		2581 CCTGGAGCCTGGCTGGAGCTCTGCTAGGGACAGAAGTGTTTCTGGAAGTGATGCTTCCAG	
		2641 GATTTGTTTTCAGAAACAAGAATTGAGTTGATGGTCCTATGTGTCATTCATTCACACAGGT	
		2701 TTCATACCAACACAGGCTTCAGCACTTCCTTTGGTGTTTCCTGTCCCAGTGAAGTTGG	
		2761 AACCAAATAATGTGTAGTCTCTATAACCAATACCTTTGTTTTCATGTGTAAGAAAAGGCC	
		2821 CATTACTTTTAAGGTATGTGCTGTCCTATTGAGCAAATAACTTTTTTTCAATTGCCAGCT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2881 ACTGCTTTTATTCATCAAAATAAAATAACTTGTTCTG	
		1 M D L A A A A E P G A G S Q H L E V R D	SEQ ID NO:72
		1 ATGGACCTCGCGGCGGCAGCGGAGCCGGGCGCCGGCAGCCACGCACCTGGAGGTCCGCGAC	
		21 E V A E E K C Q K L F L D F L E E F Q S S	
		61 GAGGTGGCCGAGAAGTGCCAGAAACTGTTCCTGGACTTCTTGGAGGAGTTTCAGAGCAGC	
		41 D G E I K Y L Q L A E E L I R P E E R N T	
		121 GATGGAGAAATTAAATACTTGCAATTAGCAGAGGAACTGATTCGTCCTGAGAAACACA	
		61 L V V S F V D L E Q F N Q Q L S T T I Q	
		181 TTGGTTGTGAGTTTTGTGGACCTGGAACAATTTAACCAGCAACTTTCCACCACCATTCAA	
		81 E E F Y R V Y P Y L C R A L K T F V K D	
		241 GAGGAGTTCTATAGAGTTTACCCTTACCTGTGTCGGGCCTTGAAAACATTCGTCAAAGAC	
		101 R K E I P L A K D F Y V A F Q D L P T R	
		301 CGTAAAGAGATCCCTCTTGCCAAGGATTTTTATGTTGCATTCCAAGACCTGCCTACCAGA	
		121 H K I R E L T S S R I G L L T R I S G Q	
		361 CACAAGATTCGAGAGCTCACCTCATCCAGAATTGGTTTGCTCACTCGCATCAGTGGGCAG	
		141 V V R T H P V H P E L V S G T F L C L D	
		421 GTGGTGCGGACTCACCCAGTTCACCCAGAGCTTGTGAGCGGAACTTTCTGTGCTTGGAC	
		161 C Q T V I R D V E Q Q F K Y T Q P N I C	
		481 TGTCAGACAGTGATCAGGGATGTAGAACAGCAGTTCAAATACACACAGCCAAACATCTGC	
		181 R N P V C A N R R R F L L D T N K S R F	
		541 CGAAATCCAGTTTGTGCCAACAGGAGGAGATTCTTACTGGATACAAATAAATCAAGATTT	
		201 V D F Q K V R I Q E T Q A E L P R G S I	
		601 GTTGATTTTCAAAAGGTTCGTATTCAAGAGACCCAAGCTGAGCTTCCTCGAGGGAGTATC	
		221 P R S L E V I L R A E A V E S A Q A G D	
		661 CCCCGCAGTTTAGAAGTAATTTTAAGGGCTGAAGCTGTGGAATCAGCTCAAGCTGGTGAC	
		241 K C D F T G T L I V V P D V S K L S T P	
		721 AAGTGTGACTTTACAGGGACACTGATTGTTGTGCCTGACGTCTCCAAGCTTAGCACACCA	
		261 G A R A E E T N S R V S G V D G Y E T E G	
		781 GGAGCACGTGCAGAAACTAATTCCCGTGTCAGTGGTGTTGATGGATATGAGACAGAAGGC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		281 I R G L R A L G V R D L S Y R L V F L A 841 ATTCGAGGACTCCGGGCCCTTGGTGTTAGGGACCTTTCTTATAGGCTGGTCTTTCTTGCC	
		301 C C V A P T N P R F G G K E L R D E E Q 901 TGCTGTGTTGCGCCAACCAACCCAAGGTTTGGGGGGAAAGAGCTCAGAGATGAGGAACAG	
		321 T A E S I K N Q M T V K E W E K V F E M 961 ACAGCTGAGAGCATTAAGAACCAAATGACTGTGAAAGAATGGGAGAAAGTGTTTGAGATG	
		341 S Q D K N L Y H N L C T S L F P T T I H G 1021 AGTCAAGATAAAAATCTATACCACAATCTTTGTACCAGCCTGTTCCCTACTATACATGGC	
		361 N D E V K R G V L L M L F G G V P K T T 1081 AATGATGAAGTAAAACGGGGTGTCCTGCTGATGCTCTTTGGTGGCGTTCCAAAGACAACA	
		381 G E G T S L R G D I N V C I V G D P S T 1141 GGAGAAGGGACCTCTCTTCGAGGGACATAAATGTTTGCATTGTTGGTGACCCAAGTACA	
		401 A K S Q F L K H V E E F S P R A V Y T S 1201 GCTAAGAGCCAATTTCTCAAGCACGTGGAGGAGTTCAGCCCCAGAGCTGTCTACACCAGT	
		421 G K A S S A A G L T A A V V R D E E S H 1261 GGTAAAGCGTCCAGTGCTGCTTAACAGCAGCTGTTGTGAGAGATGAAGAATCTCAT	
		441 E F V I E A G A L M L A D N G V C C I D 1321 GAGTTTGTCATTGAGGCTGGAGCTTTGATGTTGGCTGATAATGGTGTGTGTTGTATTGAT	
		461 E F D K M D V R D Q V A I H E A M E Q Q 1381 GAATTTGATAAGATGGACGTGCGGGATCAAGTTGCTATTCATGAAGCTATGGAACAGCAG	
		481 T I S I T K A G V K A T L N A R T S I L 1441 ACCATATCCATCACTAAAGCAGGAGTGAAGGCTACTCTGAACGCCCGGACGTCCATTTTG	
		501 A A A N P I S G H Y D R S K S L K Q N I 1501 GCAGCAGCAAACCCAATCAGTGGACACTATGACAGATCAAAATCATTGAAACAGAATATA	
		521 N L S A P I M S R F D L F F I L V D E C 1561 AATTTGTCAGCTCCCATCATGTCCCGATTCGATCTCTTCTTTATCCTTGTGGATGAATGT	
		541 N E V T D Y A I A R R I V D L H S R I E 1621 AATGAGGTTACAGATTATGCCATTGCCAGGCGCATAGTAGATTTGCATTCAAGAATTGAG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		561 E S I D R V Y S L D D I R R Y L L F A R 1681 GAATCAATTGATCGTGTCTATTCCCTCGATGATATCAGAAGATATCTTCTCTTTGCAAGA	
		581 Q F K P K I S K E S E D F I V E Q Y K H 1741 CAGTTTAAACCCAAGATTTCCAAGAGTCAGAGGACTTCATTGTGGAGCAATATAAACAT	
		601 L R Q R D G S G V T K S S W R I T V R Q 1801 CTCCGCCAGAGAGATGGTTCTGGAGTGACCAAGTCTTCATGGAGGATTACAGTGCGACAG	
		621 L E S M I R L S E A M A R M H C C D E V 1861 CTTGAGAGCATGATTCGTCTCTCTGAAGCTATGGCTCGGATGCACTGCTGTGATGAGGTC	
		641 Q P K H V K E A F R L L N K S I I R V E 1921 CAACCTAAACATGTGAAGGAAGCTTTCCGGTTACTGAATAAATCAATCATCCGTGTGGAA	
		661 T P D V N L D Q E E E I Q M E V D E G A 1981 ACACCTGATGTCAATCTAGATCAAGAGGAAGAGATCCAGATGGAGGTAGATGAGGGTGCT	
		681 G G I N G H A D S P A P V N G I N G Y N 2041 GGTGGCATCAATGGTCATGCTGACAGCCCTGCTCCTGTGAACGGGATCAATGGCTACAAT	
		701 E D I N Q E S A P K A S L R L G F S E Y 2101 GAAGACATAAATCAAGAGTCTGCTCCCAAAGCCTCCTTAAGGCTGGGCTTCTCTGAGTAC	
		721 C R I S N L I V L H L R K V E E E E E D E 2161 TGCCGAATCTCTAACCTTATTGTGCTTCACCTCAGAAAGGTGGAAGAAGAAGAGGACGAG	
		741 S A L K R S E L V N W Y L K E I E S E I 2221 TCAGCATTAAAGAGGAGCGAGCTTGTTAACTGGTACTTGAAGGAAATCGAATCAGAAATA	
		761 D S E E E L I N K K R I I E K V I H R L 2281 GATTCTGAAGAGGAACTTATAAATAAAAAGAGAATCATAGAGAAAGTCATTCATCGACTC	
		781 T H Y D H V L I E L T Q A G L K G S T E 2341 ACCCACTACGATCATGTTCTAATTGAGCTCACACAAGCTGGATTGAAAGGCTCGACAGAA	
		801 G S E S Y E E D P Y L V V N P N Y L L E 2401 GGAAGTGAGAGCTATGAAGAAGATCCCTACCTGGTGGTTAACCCTAACTACCTGCTTGAA	
		821 D - 2461 GATTGA	
WBC017B09.bFSP_20	Homo sapiens G		

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
011010.abd	protein-coupled receptor 155, mRNA (cDNA clone MGC:33390 IMAGE:4813561)	1 agcggacttt atcggaacgt gcctaagctg ctgcagctgg cacccggttg cgctcggcga 61 agagggctgg gggcgggaga tgacggtggt cttctccctg cttggcaccc tgcgagcacc 121 agctcccttc tcctcgccac tccaaggttg cagacgaagc aggtactgtc ctagatgtta 181 aggacacaac attgagcaaa aacatgcata gtccctgctt ccgtgacact tgagtgaact 241 gaatgtgcaa agtccctgtg gcacaaagtc cctgggggcca gtgtgtgtgg cgggtgtaga 301 aggagctaaa gagatctggt tggagttgga gggtgagaga aaatgaattc taatttacct 361 gcagagaact taaccattgc agtcaatatg accaagactt tgcctacagc agtaacgcat 421 ggatttaatt ccactaatga cccacctcca atgtcaatta caaggcttct tccagcctta 481 ctggaatgct ttggcattgt cctttgtggc tacatagcag gaagggccaa tgtcataaca 541 tcaacccagg ccaaaggact aggaaatttt gtctccagat ttgcacttcc agctttatta 601 ttcaaaaaca tggttgtact taatttttcc aatgtggact ggtccttcct atatagtatc 661 ttaattgcca aagcttctgt attttcatt gtatgtgtat taacttatt ggttgccagt 721 cctgatagtc gatttagcaa agctggacta ttccctattt ttgctacaca aagtaatgac 781 ttgcattggg gataccctat agttgaagct ttatatcaaa ctacataccc agaatatctc 841 cagtacattt atttggtggc accaatatct cttatgatgt taaaccctat aggtttatt 901 ttctgtgaaa tccaaaagtg ggaagacact caaaatgctt ctcaaaataa aataaaaatt 961 gtgggactcg gactcctgcg tgtattacag aaccaatag tatttatggt cttcattggc 1021 atcgccttca atttattct tgatcgaaag gtacctgtat atgtcgaaaa ttttcttgat 1081 ggacttggaa attcttttttc tggatcagcc ctatttatc ttggttccac gatggtggga 1141 aaaataaaga gactgaagaa gtcggcattt gtagtactaa ttcttcttcat cacagctaaa 1201 cttctggtgc tgccacttct gtgcagagaa atggtggaac tcttggacaa gggcgacagt 1261 gtggtgaacc atacaagttt atcaaattat gcatttctgt atggtgtatt tcctgtagca 1321 ccaggagtgg ctatcttgc aacacaattc aacatggaag tagaaattat aacctaggg 1381 atggtgataa gcacatttgt gtctgctccc atcatgtacg tttctgcctg gttactgacc 1441 tttcccacta tggaccctaa gccattggca tatgccatcc agaatgttag ttttgatata 1501 agtattgtca gcctgatctc cttgatctgg tctctggcta ttcttctttt gagtaagaaa 1561 tataaacagc ttcctcatat gcttacaact aatttactca ttgctcagtc tattgtctgt 1621 gctggaatga tgatatggaa ttttgttaaa gaaaaaatt ttgttggaca aattttggtg 1681 tttgttctat tgtacagctc cctctatagc acctacctgt ggacaggcct tctagcaatt 1741 tctttgtttc ttttgaaaaa gcgagagagg gtacaaattc ctgttggaat aatcataata 1801 tctggctggg gaattcctgc tctccttgtt ggtgttcttt tgataactgg aaaacacaat 1861 ggagatagca ttgactcagc cttcttttat ggaaaagaac agatgatcac cacagcagtc 1921 accctgttct gcagcatcct gatagctggc atatccctca tgtgcatgaa ccagactgcc 1981 caagcaggag gctatgaagg tttcgatcag tctcagagcc acaaagtggt ggagcctgga 2041 aatactgctt ttgaggagag tccagcacca gtaaatgaac cagaacttt tacaagctct 2101 attccagaaa caagttgctg ctcctgctcc atgggaaatg gtgaattaca ctgcccatca 2161 atagagccaa tagcaaacac aagcaccagt gagcctgtga ttcctcgtt tgagaaaaac 2221 aatcatgtg tgagtcgctg taacttccag agctgcatat tagccagga agaagaacag 2281 tatctacaga gtggagacca gcaactgacc cgacatgtgt tgctgtgttt actctcatc 2341 attggcctgt tcgctaatct ttacagttgt ttatggtggc tattcaacca agagcctgga 2401 agactttatg ttgagttaca gttttctgt gccgtgttta actttggtca gggatttatt 2461 tcatttggaa tcttttggatt agataaacat ttaatcatcc tgccttccaa aagaagactt 2521 gaattcctat ggaacaataa agacacagca gaaaacaggg attctcctgt ttcagaggaa	SEQ ID NO:73

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2581 ataaaaatga cctgtcaaca atttatccat tatcaccgtg acttctgtat ccgaaacatt 2641 gtcaaagaaa gaaggtgtgg tgcaaagact tctgctggaa ctttctgtgg ctgtgacctg 2701 gtgagctggc taattgaagt cggccttgcc tccgaccgtg gtgaagctgt gatatacgga 2761 gacaggctgg tacaaggggg agtcatccaa catattacca atgagtatga attccgggat 2821 gagtacttgt tttacagatt tcttcaaaag agtcctgaac agagtcctcc tgctattaat 2881 gcaaacactc tccaacagga aagatataaa gaaattgagc attcatcccc accctcacat 2941 tcccctaaga cctaaattat gcaggggaga accctacatg gaatcatatt ctagccgcgt 3001 attcattagt ttttagctgg gtgaccttgg gcaagttaac agaggcaacc tctctgagcc 3061 tcagttgtct cttctgtaaa atgtgaaaag atgtgctccc accacatgcg cagggtctgt 3121 gattttacat gtatgtaaaa cacataggaa gctgacttag gaaaaagaga aaaccaaatt 3181 aaagttctga taatgaatat aatatagtca tcctttagta cccaagggga ttggttccag 3241 gactcctgaa gatcccaaaa tctgaggata ctcaagtccc ttatataaaa tggtgtaggc 3301 cgggcatggt ggctcacgcc tgtaatccca gtactttggg aggccgagtc aggtggatca 3361 cctgaggtca ggagttcaag accagcctgg ccaacatggc gaaaccccgt ctctactata 3421 aaatacaaaa aattagttgg gtgtggtggc gggtgcctgt aatcccagct actcaggagg 3481 ctgaggcagg agaatcgctt gaatctggga ggcagaggtt gctgtgagcc gagatcgtgc 3541 cactgcactc cagcctgagc aacagagcaa gactctatct caaaaataaa ataaaataaa 3601 ataaaataaa ataattaata aaatggtgta gtatttgcat ataacctatg cacattctcc 3661 catatagttt aatcatcttt agatacttat aatgcctaat acaatgtaaa tgctatgtaa 3721 atagttgttg ttatactgta ttgtttaggg aataacaata agaaaaacag tctgtacatg 3781 ttcactacag atgcaaccat tgttaagcct gactacatct ttttatctgc agttgattga 3841 atctatggat gtggaacctg tgcatatgga gggtcaactg tactataaat aatacgaata 3901 tgccaacatt atataatcat tgctttctgc aaaaaaaaaa aaaaa 1 M N S N L P A E N L T I A V N M T K T L 1 ATGAATTCTAATTTACCTGCAGAGAACTTAACCATTGCAGTCAATATGACCAAGACTTTG 21 P T A V T H G F N S T N D P P S M S I T 61 CCTACAGCAGTAACGCATGGATTTAATTCCACTAATGACCCACCTTCAATGTCAATTACA 41 R L F P A L L E C F G I V L C G Y I A G 121 AGGCTTTTTCCAGCCTTACTGGAATGCTTTGGCATTGTCCTTTGTGGCTACATAGCAGGA 61 R A N V I T S T Q A K G L G N F V S R F 181 AGGGCCAATGTCATAACATCAACCCAGGCCAAAGGACTAGGAAATTTTGTCTCCAGATTT 81 A L P A L L F K N M V V L N F S N V D W 241 GCACTTCCAGCTTTATTATTCAAAACATGGTTGTACTTAATTTTTCCAATGTGGACTGG 101 S F L Y S I L I A K A S V F F I V C V L 301 TCCTTCCTATATAGTATCTTAATTGCCAAAGCTTCTGTATTTTTCATTGTATGTGTATTA 121 T L L V A S P D S R F S K A G L F P I F	SEQ ID NO:74

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		361 ACCTTATTGGTTGCCAGTCCTGATAGTCGATTTAGCAAAGCTGGACTATTCCCTATTTTT	
		141 A T Q S N D F A L G Y P I V E A L Y Q T	
		421 GCTACACAAAGTAATGACTTTGCATTGGGATACCCTATAGTTGAAGCTTTATATCAAACT	
		161 T Y P E Y L Q Y I Y L V A P I S L M M L	
		481 ACATACCCAGAATATCTCCAGTACATTTATTTGGTGGCACCAATATCTCTTATGATGTTA	
		181 N P I G F I F C E I Q K W E D T Q N A S	
		541 AACCCTATAGGGTTTATTTTCTGTGAAATCCAAAAGTGGGAAGACACTCAAAATGCTTCT	
		201 Q N K I K I V G L G L L R V L Q N P I V	
		601 CAAAATAAAATATAAAAATTGTGGGACTCGGACTCCTGCGTGTATTACAGAACCCAATAGTA	
		221 F M V F I G I A F N F I L D R K V P V Y	
		661 TTTATGGTCTTCATTGGCATCGCCTTCAATTTTATTCTTGATCGAAAGGTACCTGTATAT	
		241 V E N F L D G L G N S F S G S A L F Y L	
		721 GTCGAAAATTTTCTTGATGGACTTGGAAATTCTTTTTCTGGATCAGCCCTATTTTATCTT	
		261 G L T M V G K I K R L K K S A F V V L I	
		781 GGTCTCACGATGGTGGGAAAATAAGACTGAAGAAGTCGGCATTTGTAGTACTAATT	
		281 L L I T A K L L V L P L L C R E M V E L	
		841 CTTCTCATCACAGCTAAACTTCTGGTGCTGCCACTTCTGTGCAGAGAAATGGTGGAACTC	
		301 L D K G D S V V N H T S L S N Y A F L Y	
		901 TTGGACAAGGGCGACAGTGTGGTGAACCATACAAGTTTATCAAATTATGCATTTCTGTAT	
		321 G V F P V A P G V A I F A T Q F N M E V	
		961 GGTGTATTTCCTGTAGCACCAGGAGTGGCTATCTTTGCAACACAATTCAACATGGAAGTA	
		341 E I I T S G M V I S T F V S A P I M Y V	
		1021 GAAATTATAACCTCAGGGATGGTGATAAGCACATTTGTGTCTGCTCCCATCATGTACGTT	
		361 S A W L L T F P T M D P K P L A Y A I Q	
		1081 TCTGCCTGGTTACTGACCTTTCCCACTATGGACCCTAAGCCATTGGCATATGCCATCCAG	
		381 N V S F D I S I V S L I S L I W S L A I	
		1141 AATGTTAGTTTTGATATAAGTATTGTCAGCCTGATCTCCTTGATCTGGTCTCTGGCTATT	
		401 L L L S K K Y K Q L P H M L T T N L L I	
		1201 CTTCTTTTGAGTAAGAAATATAAACAGCTTCCTCATATGCTTACAACTAATTTACTCATT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		421 A Q S I V C A G M M I W N F V K E K N F 1261 GCTCAGTCTATTGTCTGTGCTGGAATGATGATATGGAATTTGTTAAAGAAAAAAATTTT	
		441 V G Q I L V F V L L Y S S L Y S T Y L W 1321 GTTGGACAAATTTTGGTGTTTGTTCTATTGTACAGCTCCCTCTATAGCACCTACCTGTGG	
		461 T G L L A I S L F L L K K R E R V Q I P 1381 ACAGGCCTTCTAGCAATTTCTTTGTTTCTTTGAAAAAGCGAGAGAGGGTACAAATTCCT	
		481 V G I I I I S G W G I P A L L V G V L L 1441 GTTGGAATAATCATAATATCTGGCTGGGGAATTCCTGCTCTCCTTGTTGGTGTTCTTTTG	
		501 I T G K H N G D S I D S A F F Y G K E Q 1501 ATAACTGGAAAACACAATGGAGATAGCATTGACTCAGCCTTCTTTTATGGAAAGAACAG	
		521 M I T T A V T L F C S I L I A G I S L M 1561 ATGATCACCACAGCAGTCACCCTGTTCTGCAGCATCCTGATAGCTGGCATATCCCTCATG	
		541 C M N Q T A Q A G G Y E G F D Q S Q S H 1621 TGCATGAACCAGACTGCCCAAGCAGGAGGCTATGAAGGTTTCGATCAGTCTCAGAGCCAC	
		561 K V V E P G N T A F E E S P A P V N E P 1681 AAAGTGGTGGAGCCTGGAAATACTGCTTTTGAGGAGAGTCCAGCACCAGTAAATGAACCA	
		581 E L F T S S I P E T S C C S C S M G N G 1741 GAACTTTTTACAAGCTCTATTCCAGAAACAAGTTGCTGCTCCTGCTCCATGGGAAATGGT	
		601 E L H C P S I E P I A N T S T S E P V I 1801 GAATTACACTGCCCATCAATAGAGCCAATAGCAAACACAAGCACCAGTGAGCCTGTGATT	
		621 P S F E K N N H C V S R C N S Q S C I L 1861 CCTTCGTTTGAGAAAAACAATCATTGTGTGAGTCGCTGTAACTCCCAGAGCTGCATATTA	
		641 A Q E E E Q Y L Q S G D Q Q L T R H V L 1921 GCCCAGGAAGAAGAACAGTATCTACAGAGTGGAGACCAGCAACTGACCCGACATGTGTTG	
		661 L C L L L I I G L F A N L Y S C L W W L 1981 CTGTGTTTACTTCTCATCATTGGCCTGTTCGCTAATCTTTACAGTTGTTTATGGTGGCTA	
		681 F N Q E P G R L Y V E L Q F F C A V F N 2041 TTCAACCAAGAGCCTGGAAGACTTTATGTTGAGTTACAGTTTTTCTGTGCCGTGTTTAAC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		701 F G Q G F I S F G G I F G L D K H L I I L 2101 TTTGGTCAGGGATTTATTTCATTTGGAATCTTTGGATTAGATAAACATTTAATCATCCTG 721 P F K R R L E F L W N N K D T A E N R D 2161 CCTTTCAAAAGAAGACTTGAATTCCTATGGAACAATAAAGACACAGCAGAAACAGGGAT 741 S P V S E E I K M T C Q Q F I H Y H R D 2221 TCTCCTGTTTCAGAGGAAATAAAAATGACCTGTCAACAATTTATCCATTATCACCGTGAC 761 L C I R N I V K E R R C G A K T S A G T 2281 CTCTGTATCCGAAACATTGTCAAAGAAAGAAGGTGTGGTGCAAAGACTTCTGCTGGAACT 781 F C G C D L V S W L I E V G L A S D R G 2341 TTCTGTGGCTGTGACCTGGTGAGCTGGCTAATTGAAGTCGGCCTTGCCTCCGACCGTGGT 801 E A V I Y G D R L V Q G G V I Q H I T N 2401 GAAGCTGTGATATACGGAGACAGGCTGGTACAAGGGGGAGTCATCCAACATATTACCAAT 821 E Y E F R D E Y L F Y R F L Q K S P E Q 2461 GAGTATGAATTCCGGGATGAGTACTTGTTTTACAGATTTCTTCAAAGAGTCCTGAACAG 841 S P P A I N A N T L Q Q E R Y K E I E H 2521 AGTCCTCCTGCTATTAATGCAAACACTCTCCAACAGGAAAGATATAAAGAAATTGAGCAT 861 S S P P S H S P K T - 2581 TCATCCCCACCCTCACATTCCCCTAAGACCTAA	SEQ ID NO:75
WBC017C08.bFSP_20011010.abd	No homology	1 TTACAGTGTGAAGCCAGCTTCTGTTTCTGGGTCAGTTACCAGCAGCCACACAAGGTCTG 61 AAAGGTGTGAGGTGGATCAGTGATGCTGTGACCACCTTCTGAATGAATCTGTCCAGCAGAG 121 TAATGTCTTTTTTGTCTTATTCTTTGAGAATTTTTTTTCTTTTTCCCTTTGATTTTGGTAT 181 TTTCGTTTGAAGTCTGAATGCTTTTTCAAAGTTCAAGGTTCTAAATCAATACTTGAGGATT 241 TGTAGAATAAAGTAACGGAACTGTGTTTGGCTCCCTAGATTTTCTGTTTATAAAAATAGA 301 TCTCAAAGATCAATAAAGATGAATGCCAGCATTTGCATAGTACTTTACGTGTGAAAGATA 361 AGTCACTGTGCTGCATCTTTAGTTATTTAAGGCAGAGGATTCCTTTTTTAGTTTAATAA 421 TGAAAGTTTGAGTTAATTGGATATGGAAAACAGGAATCATTTCAGCAAAAATTTTTCCTG 481 TGGGAACACTATCATTTTAAGAAGATTAGTGATTTAATGTGTATTCTCTTACTCTTGAGC 541 TTTAAAAAAAGTCAAAAACATTTTCTGTATGGGGAGGATATTAATACCCGTATTTTAGTT 601 GTCATAGAGTAATTTATACATACTGTACAAAGATATAGTTACACTCCCATATGAAGATAT 661 AGTTAATGCCATCTTTGGCCAAGTGTTAGGAGTTTTGGCTTTGTAGTCAGGCAAGCCTAT 721 GTTGGGTCCTGGCTGTTGCCACTTAATAGCGGTGTGACTTTGCTTAGGTTTCTCAACTTC 781 GCTGAGCCTCATTATCCACATCTGTAAATATAAGAATGCTACCTTTTTAGGTTGTCCTGA 841 AGATTTAAATGAATAAATGTGAGTATCTAACCTCAAATAATAATAGCAGTTACTTAACA	SEQ ID NO:75

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		901 TAGCTTATA	
		1 TTCCTTTTTTAGTTTAATAATGAAAGTTTGAGTTAATTGGATATGGAAAACAGGAATCAT	SEQ ID NO:76
		61 TTCAGCGAAAATTTTTCCTGTGGGAACACTATCATTTTAAGAAGATTAGTGATTTTAATGT	
		121 GTATTCTCTTACTCTTGAGCTTTAAAAAAAGTCAAAAACATTTTCTGTATGGGGAGGATA	
		181 TTAATACCCGTATTTTAGTTGTCATAGAGTAATTTATACATACTGTACAAAGATATAGTT	
		241 ACACTCCCATATGAAGATATAGTTAATGCCATCTTTGGCCAAGTGTTAGGAGTTTTGGCT	
		301 TTGTAGTCAGGCAAGCCTATGTTGGGTCCTGGCTGTTGCCACTTAATAGCGGTGTGACTT	
		361 TGCTTAGGTTTCTCAACTTCGCTGAGCCTCATTATCCACATCTGTAAATATAAGAATGCCT	
		421 ACCTTTTTAGGTTGTCCTGAGGATTTAAATGAATAAATGTGAAGTATCTAACTCAAATAA	
		481 TAATAGCAGTTACTTAACATAGCTTATATGCCAGACAATTTTATTAATTTATTTAATCCT	
		541 TATAACAATCCTGTGAAGTTGGTACAGTTATTTTCCTCATTTTTACAGATGAAGAAACTG	
		601 AGGCTAATGAAAGGTTATATAAACTTATGCAAGCTCGTACAGCTAATAAGTACATAACACT	
		661 CGACAAATGCTGACTGTTGTCATAAAAAAAAAA	
WBC018B05.bFSP_20011110.abd	Human transcriptional repressor (CTCF) mRNA.	1 TGTGTCTGAGCCTGTGGAGCGATTAAACCGTGCGCGGAGCTGCTTCTTTGGCGGCAGCGG	SEQ ID NO:77
		61 CGGCGGCGGTGGCCGGTGCGGACGCGCGGAGCTCGCCGGAGACGCCGGGTGGCCGGAGCC	
		121 GTGGAGCGGCGGCGAGCGGGCGCCGCGGGGGGTGTGGCGCGGAGAATGATTACGGACCT	
		181 GAAGCCAAAGAACAAGATGCGCTAGTGGACAGATTGCTGACCAGGGGCTTGAGAGCTGGG	
		241 TTCTATTTTCCCTCCTCCAACTGACTTTGCAGCCACGGAGAGGCAGGGGAAATGGAAGGT	
		301 GATGCAGTCGAAGCCATTGTGGAGGAGTCCGAAACTTTATTAAAGGAAAGGAGAGAAAG	
		361 ACTTACCAGAGACGCCGGGAAGGGGGCCAGGAAGAGATGCCTGCCACTTACCCCAGAAC	
		421 CAGACGGATGGGGGTGAGGTGGTCCAGGATGTCAACAGCAGTGTACAGATGGTGATGATG	
		481 GAACAGCTGGACCCCACCCTTCTTCAGATGAAGACTGAAGTAATGGAGGGCACAGTGGCT	
		541 CCAGAAGCAGAGGCTGCTGTGGACGATACCCAGATTATAACTTTACAGGTTGTAAATATG	
		601 GAGGAACAGCCCATAAACATAGGAGAACTTCAGCTTGTTCAAGTACCTGTTCCTGTGACT	
		661 GTACCTGTTGCTACCACTTCAGTAGAAGAACTTCAGGGGCTTATGAAAATGAAGTGTCT	
		721 AAAGAGGGCCTTGCGGAAAGTGAACCCATGATATGCCACACCTACCTTTGCCTGAAGGG	
		781 TTTCAGGTGGTTAAAGTGGGGGCCAATGGAGAGGTGGACACACTAGAACAAGGGGAACTT	
		841 CCACCCCAGGAAGATCCTAGTTGGCAAAAAGACCCAGACTATCAGCCACCAGCCAAAAAA	
		901 ACAAAGAAAACCAAAAAGAGCAAACTGCGTTATACAGAGGAGGGCAAAGATGTAGATGTG	
		961 TCTGTCTACGATTTTGAGGAAGAACAGCAGGAGGGTCTCTATCAGAGGTTAATGCGGAG	
		1021 AAAGTGGTTGGTAATATGAAGCCTCCAAAGCCAACATAAAAATTAAAAGAAAGGTGTAAAG	
		1081 AAGACATTCCAGTGTGAGCTTTGCAGTTACACGTGTCCACGGCGTTCAAATTTGGATCGT	
		1141 CACATGAAAAGCCACACTGATGAGAGACCACACACAAGTGCCATCTCTGTGGCAGGGCATTC	
		1201 AGAACAGTCACCCTCCTGAGGAATCACCTTAACACACACACAGGTACTCGTCCTCACAAG	
		1261 TGCCCAGACTGCGCACATGGCCTTTGTGACCAGTGGAGAATTGGTTCGGCATCGTCGTTAC	
		1321 AAACACACCCACGAGAAGCCATTCAAGTGTTCCATGTGCGATTACGCCAGTGTAGAAGTC	
		1381 AGCAAATTAAAACGTCACATTCGCTCTCATACTGGAGAGGCGTCCGTTTCAGTGCAGTTTG	
		1441 TGCAGTTATGCCAGCAGGGACACATACAAGCTGAAAAGGCACATGAGAACCCATTCAGGG	
		1501 GAAAAGCCTTATGAATGTTATATTTGTCATGCTCGGTTTACCCAAAGTGGTACCATGAAG	
		1561 ATGCACATTTTACAGAAGCACACAGAAAATGTGGCCAAATTTCACTGTCCCCACTGTGAC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1621 ACAGTCATAGCCCGAAAAAGTGATTTGGGTGTCCACTTGAGAAAGCAGCATTCCTATATT	
		1681 GAGCAAGGCAAGAAATGCCGATACTGCGATGCTGTTTTTCATGAGCGTTATGCCCTCATC	
		1741 CAGCATCAGAAGTCACACAAGAACGAGAAGCGCTTTAAGTGTGACCAGTGTGATTATGCT	
		1801 TGCAGACAGGAGAGGCACATGATAATGCACAAGCGCACTCACACTGGGAGAAGCCTTAT	
		1861 GCCTGCAGCCACTGCGACAAGACCTTCCGCCAGAAACAGCTCCTCGACATGCACTTCAAA	
		1921 CGCTATCATGACCCCAACTTTGTTCCTGCGGCCTTCGTCTGTTCTAAGTGTGGGAAAACA	
		1981 TTTACACGCCGGAATACCATGGCAAGACATGCTGATAATTGTGCTGGTCCAGATGGCGTA	
		2041 GAGGGGGAAAATGGAGGAGAAACGAAGAAGAGTAAACGTGGAAGAAAAGAAAGATGCGA	
		2101 TCTAAAAAAGAAGATTCCTCTGACAGTGAAAATGCTGAGCCAGACCTGGATGACAATGAG	
		2161 GATGAGGAGGAGCCTGCCGTGGAAATTGAACCTGAGCCAGAGCCTCAGCCTGTTACCCCA	
		2221 GCCCCACCACCCGCCAAGAAGCGGAGAGGACGCCCCCCTGGCAGAACCAACCAGCCCAAA	
		2281 CAGACCCAGCCCATCATTCAGGTTGAAGACCAGAGTACAGGTGCAATTGAGAACATTATA	
		2341 GTTGAAGTCAAAAAAGAGCCAGATGCAGAGCCCGTGGAGGGGGAAGAAGAGGAGGCCCAG	
		2401 CCAGCTGCCACAGACGCCCCCAATGGGAGACCTCACATCCAAGATGATCCTCACCATGAT	
		2461 GGACCGGTGATGGCGGAGCCTTGTGCGTCGCCAGGACTTCTCTGGGCTGTGTTTAAACGG	
		2521 CCCGCATCTTAATTTTTCTCCCTTCTTTCTTTTTGGCTTTGGGAAAAGCATCATTTTA	
		2581 CCAAACATACCGAGAACGAAAACTTCAAGGATGATGTTAGAAAAAAATGTGATTTAACTA	
		2641 GAACTTGCTGTCTGATGTTAGCAAATCATGGAATGTTCTGAGTCCCTGAGGGTTTACTGT	
		2701 GAAGTGCTGAGGACAGTGTTGACAACTAACTCGTTTTCCTAGATGGAAACGGAGACATTG	
		2761 ACCCCTCCCTCCATGTGGTAAACCACTCCAGAATGGCCACCAGGCTTCCCAGAGTTCTAT	
		2821 GGTCTTCTTCCCAAGAGAGTTTTTAATTGTAAATGCATACTTGGGAAGGACTTAGAGTTT	
		2881 TAAACTGTTTTTTGCTTTTGCTTTTCCCTGACTCCCTTTGCTTGGAGTCAGCTGCACACC	
		2941 AGTAGTATGGCATGCTACGATCAGGTTCTGTCCTGAAAGCTTTGCCTCTTCTTGGCAAA	
		3001 GTTTCTGGTATGGTCAAGCTTGTAAATAACTTTTTTTACATTTTAATCTTTTCCATTAAT	
		3061 TAAGAGGTTGAAAAGAAGTGCAGTGTAAGAAAAACCCAGCATTTTAATTACTTGCAAATTA	
		3121 AGTTACCACAGACTCTGTAGTGTGTCAGTGTTGACAAGAAATTGGATCACAATCATGTAG	
		3181 CAGAACGGCACCCAGACCACTGCCCACCAGTGACGGACATGCACGTGGCAGATCGTGAAT	
		3241 TCCAGCCCGCGGAGCCAGCATTTGAACCTTGTACAATTAACTTTCAGTTATGATTTCCCA	
		3301 TCGACATTTCTTTGCTCTGTTTGTAGCTGAATTGTTTGTGTTCTGTAAATCCTCTGTTA	
		3361 AAGCAGAAGGGTGATTATGAGCGGGTCACAGCAGCCCTTAAAAGCTGGGCCAGGAAATTC	
		3421 ACTAGGTCAGTAATTTAAACTTTGGATCTTCAAAAAAAAATATAATGTGAAGCAAAACC	
		3481 AACTAAAAAGTGATTCTTGCACATGAACTGTCACACGTTTAAAATGTGTTTTTTAGAGAG	
		3541 CCTCAGTCTTGCTGATTTCAAACACTTTTTTCTTCTGTGTATTGCTTTTAAGAGAGCCAT	
		3601 CAGTTAGCTATCAGACTCTAGGTTGATGCATTTTGTACTTAGCTGTACTGTGTGATATTT	
		3661 TTCATTATTTTAGGATGCCAACAAGAGACCTGTAATAAAATATGTGATGGGGTTGAGAGC	
		3721 TGGGGAGGAGGATCTACTGCTGTACAGCTAATAAATCATACGGATTAACAAGTGA	
		SEQ ID NO:78	
		1 M E G D A V E A I V E E S E T F I K G K	
		1 ATGGAAGGTGATGCAGTCGAAGCCATTGTGGAGGAGTCCGAAACTTTATTAAAGGAAAG	
		21 E R K T Y Q R R R E G G Q E E D A C H L	
		61 GAGAGAAAGACTTACCAGAGACGCCGGGAAGGGGGCCAGGAAGAAGATGCCTGCCACTTA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		41 P Q N Q T D G G E V V Q D V N S S V Q M 121 CCCCAGAACCAGACGGATGGGGGTGAGGTGGTCCAGGATGTCAACAGCAGTGTACAGATG	
		61 V M M E Q L D P T L L Q M K T E V M E G 181 GTGATGATGGAACAGCTGGACCCCACCCTTCTTCAGATGAAGACTGAAGTAATGGAGGGC	
		81 T V A P E A E A A V D D T Q I I T L Q V 241 ACAGTGGCTCCAGAAGCAGAGGCTGCTGTGGACGATACCCAGATTATAACTTTACAGGTT	
		101 V N M E E Q P I N I G E L Q L V Q V P V 301 GTAAATATGGAGGAACAGCCCATAAACATAGGAGAACTTCAGCTTGTTCAAGTACCTGTT	
		121 P V T V P V A T T S V E E L Q G A Y E N 361 CCTGTGACTGTACCTGTTGCTACCACTTCAGTAGAAGAACTTCAGGGGGCTTATGAAAAT	
		141 E V S K E G L A E S E P M I C H T L P L 421 GAAGTGTCTAAAGAGGGCCTTGCGGAAAGTGAACCCATGATATGCCACACCCTACCTTTG	
		161 P E G F Q V V K V G A N G E V E T L E Q 481 CCTGAAGGGTTTCAGGTGGTTAAAGTGGGGGCCAATGGAGAGGTGGAGACACTAGAACAA	
		181 G E L P P Q E D P S W Q K D P D Y Q P P 541 GGGGAACTTCCACCCCAGGAAGATCCTAGTTGGCAAAAAGACCCAGACTATCAGCCACCA	
		201 A K K T K K T K K S K L R Y T E E G K D 601 GCCAAAAAAACAAAGAAAACCAAAAAGAGCAAACTGCGTTATACAGAGGAGGGCAAGAT	
		221 V D V S V Y D F E E E Q Q E G L L S E V 661 GTAGATGTGTCTGTCTACGATTTTGAGGAAGAACAGCAGGAGGGTCTGCTATCAGAGGTT	
		241 N A E K V V G N M K P P K P T K I K K K 721 AATGCGGAGAAAGTGGTTGGTAATATGAAGCCTCCAAAGCCAACAAAAATTAAAAAGAAA	
		261 G V K K T F Q C E L C S Y T C P R R S N 781 GGTGTAAAGAAGACATTCCAGTGTGAGCTTTGCAGTTACACGTGTCCACGGCGTTCAAAT	
		281 L D R H M K S H T D E R P H K C H L C G 841 TTGGATCGTCACATGAAAAGCCACACTGATGAGAGACCACACAAGTGCCATCTCTGTGGC	
		301 R A F R T V T L L R N H L N T H T G T R 901 AGGGCATTCAGAACAGTCACCCTCCTGAGGAATCACCTTAACACACACACAGGTACTCGT	
		321 P H K C P D C D M A F V T S G E L V R H	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		961 CCTCACAAGTGCCCAGACTGCGACATGGCCTTTGTGACCAGTGGAGAATTGGTTCGGCAT	
		341 R R Y K H T H E K P F K C S M C D Y A S	
		1021 CGTCGTTACAAACACACCCACGAGAAGGCCATTCAAGTGTTCCATGTGCGATTACGCCAGT	
		361 V E V S K L K R H I R S H T G E R P F Q	
		1081 GTAGAAGTCAGCAAATTAAAACGTCACATTCGCTCTCATACTGGAGAGCGTCCGTTTCAG	
		381 C S L C S Y A S R D T Y K L K R H M R T	
		1141 TGCAGTTTGTGCAGTTATGCCAGCAGGGACACATACAAGCTGAAAAGGCACATGAGAACC	
		401 H S G E K P Y E C Y I C H A R F T Q S G	
		1201 CATTCAGGGGAAAAGCCTTATGAATGTTATATTTGTCATGCTCGGTTTACCCAAAGTGGT	
		421 T M K M H H I L Q K H T E N V A K F H C P	
		1261 ACCATGAAGATGCACATTTTACAGAAGCACACAGAAAATGTGGCCAAATTTCACTGTCCC	
		441 H C D T V I A R K S D L G V H L R K Q H	
		1321 CACTGTGACACAGTCATAGCCCGAAAAAGTGATTTGGGTGTCCACTTGAGAAAGCAGCAT	
		461 S Y I E Q G K K K C R Y C D A V F H E R Y	
		1381 TCCTATATTGAGCAAGGCAAGAAATGCCGATACTGCGATGCTGTTTTTCATGAGCGTTAT	
		481 A L I Q H Q K S H K N E K R F K C D Q C	
		1441 GCCCTCATCCAGCATCAGAAGTCACACAAGAACGAGAAGCGCTTTAAGTGTGACCAGTGT	
		501 D Y A C R Q E R H M I M H K R T H T G E	
		1501 GATTATGCTTGCAGACAGGAGAGGCACATGATAATGCACAAGCGCACTCACACTGGGGAG	
		521 K P Y A C S H C D K T F R Q K Q L L D M	
		1561 AAGCCTTATGCCTGCAGCCACTGCGACAAGACCTTCCGCCAGAAACAGCTCCTCGACATG	
		541 H F K R Y H D P N F V P A A F V C S K C	
		1621 CACTTCAAACGCTATCATGACCCCAACTTTGTTCCTGCGGCCTTCGTCTGTTCTAAGTGT	
		561 G K T F T R R N T M A R H A D N C A G P	
		1681 GGGAAAACATTTACACGCCGGAATACCATGGCAAGACATGCTGATAATTGTGCTGGTCCA	
		581 D G V E G E N G G G E T K K S K R G R K R	
		1741 GATGGCGTAGAGGGGGAAAATGGAGGAGAAACGAAGAAGAGTAAACGTGGAAGAAAAGA	
		601 K M R S K K K E D S S D S E N A E E P D D L D	
		1801 AAGATGCGATCTAAAAAAGAAGATTCCTCTGACAGTGAAAATGCTGAGCCAGACCTGGAT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		621 D N E D E E E P A V E I E P E P E P Q P 1861 GACAATGAGGATGAGGAGGAGCCTGCCGTGGAAATTGAACCTGAGCCAGAGCCTCAGCCT 641 V T P A P P P A K K R R G R P P G R T N 1921 GTTACCCCAGCCCCACCACCCGCCAAGAAGCGGAGAGGACGCCCCCCTGGCAGAACCAAC 661 Q P K Q T Q P I I Q V E D Q S T G A I E 1981 CAGCCCAAACAGACCCAGCCCATCATTCAGGTTGAAGACCAGAGTACAGGTGCAATTGAG 681 N I I V E V K K E P D A E P V E G E E E 2041 AACATTATAGTTGAAGTCAAAAAAGAGCCAGATGCAGAGCCCGTGGAGGGGGAAGAAGAG 701 E A Q P A A T D A P N G R P H I Q D D P 2101 GAGGCCCAGCCAGCTGCCACAGACGCCCCCAATGGGAGACCTCACATCCAAGATGATCCT 721 H H D G P V M A E P C A S P G L L W A V 2161 CACCATGATGGACCGGTGATGGCGGAGCCTTGTGCGTCGCCAGGACTTCTCTGGGCTGTG 741 F K R P A S - 2221 TTTAAACGGCCCGCATCTTAA	
WBC018D03.bFSP_20011110.abd	No homology	1 ATCTGTATTAGCCAGAGCATTGGGCTTCCAAAATACAGCCTTCTGTTCATTAGATCTTGA 61 GGATTTTAATAGATTGACACCCCATACCTTATAGAATTGGAGTTGGAATATGATTTCTCA 121 AAAATGAATTTGATAATTTCAAGTATAATATGCATATGTGCCAAAAGAATGCTGCAAATA 181 TAATTATGGGTAGCCAAATTTGGGGTTATGTGAACATTTTATATTGCTCATTTTGTTTAT 241 GTAATTTTTTTTCTCGGAAAAACAGTTGTTTTTCCTCTCAGAAGTGTTTAGGCATTATTG 301 CACGTGAGTTTCAGTTCTGCTACATGAACTGTTAGCTGTTTTGTTTGAAGCAACACAGCA 361 CTAAAGAACCAGTATTGTTGACTAATATGCTTCATCTTTCAGTTTGTATGGTTGTAATTC 421 AGTTTACCACATCTAGTTTGGTGTTTGATGATCTGAAAAATATTTCACAGTGAGGGCAAT 481 GCTCAGTGCCTGGAAGAAGCAGACAGTCTTTATTGGTCTGACAATATTTGATGCAACTAC 541 AAGAGCTCCATGGACATGACCCTTGCACATTTGTCTGTAATACACAATGCTGTAATTGAA 601 TTGTTTCCTATGTTGATTCTCTCATGTACCCAAGTATAAAAAATTGGTAAGTTTCTCTTG 661 TCTTCAAAGTACCATTAGGATTTTATTTCCTGAATTTAAAATGAATATTAAAATTTTTGT 721 AATGGCGTTCTTTAACCTGCCCTAAATTTTTATAGAAAAGCCTTGCCAAATATTGTTGTC 781 CTCATACTTAAAAGTTTCCACA 1 CCCATTCTAATTAAGAAAGAGCTTTCCCAAAATAGTCTCTAATTTCCAGTTTTTGTAAAA 61 GAAGTTCGTTTTTGGAGTAAAAAGTATTTTCATATCTGTTTGGGGGAAGTTAACGCATCA 121 GGAAAGAATATTATTAGGTGTTTAAACCCTGAAACAAACATATACTGATGCATAACTTAG 181 TAGATCACCGAAACTAACTTGCTGAAATCTTTGGTTTTGTCCTGTGAGACCAGTGCTTGA 241 CATCGTCTGTTCGCCTGAGCCCAGTTGGTGGCTCCAGTTTGCTTTTCTCTTCGGTCTCGT	SEQ ID NO:79 SEQ ID NO:80

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		301 GGTAGCAGCCTTGGTCGTTTTCGTTGGAGGTTGGAGAGGAGCTGAGGAGAAAGTGCTCTT 361 CGGGGTTTTGATTCCTCTGCTAGGACGCTGCCTAAACCAGCTCATCTCAATGTCCTGTTG 421 ACTTTATTATTATTCCGGGTAGTTGAAGAAAAAGAAAATGGATGACGTCATTAAAACCA 481 GCTCAAAAATATATTCTTGTCAGTAAAGATTTCTTGTCGAGATGTCTTGGATTGCACTTT 541 CGTGGAGGGAAAACAGTGTAAATAGTTAAAGAATGTTGATAAAATTGAAACATTTGGTTA 601 TGGAATTGTGTGTGGTGTTAGAAGGTTTCTGTTTGTGAAATGTCTGTATTAAAATAATAA 661 ATTTCAGAAACT	
WBC018F03.bFSP_20011110.abd	Human mRNA for integrin alpha-4 subunit	1 GATTGTTGAAGCTTCTTTAAACCATCCTGAGTCAGTTAATAGAACGAATTTTGACTGTAT 61 TGAAAATGGATTGCCTTCTGTGTGCATGGATCTGAAACTCTGTTTCTCATACAAGGGCAA 121 AGAGGTTCCAGGTTATATTGTTTTGTTTTATAACATGAGTCTGGATGTGAACCGAAAGGC 181 GGAGTCTCCATCGAGATTTTACTTTTCTTCAAATGGAACCTCTGATGTGATTACAGGAAG 241 CATGAAAGTATCAAGCAGAGCGGCTAACTGCAGAACCCATCAAGCATTTATGCGGAAAGA 301 TGTGCGGGACATCCTCACCCCAATTCAGATCAAAGCTGCTTACCACCTTGGGCATCACGT 361 CATCAGTAAACGAAGCACAGAGGAATTCCCGCCCCTTCAGCCAATTCTTCAGCAGAAGAG 421 AGAAAAGGATGTGATTGAAAAAACAATAAACTTTGCAAGGTTTTGTGCCCATGAAAATTG 481 TTCTGCAGATTTACAGCTTTCTGCAAAAATTGGATTTTTGAAGCCACATGAAAATAAAAC 541 CTATCTTGCTGTTGGAAATATGAAGACGTTAATGTTGAATGTGTCCTTGTTTAATGCTGG 601 AGACGATGCATTATGAAACGACTCTGCATATCAAACTACCCACTGGTCTTTATTTCATTA 661 AGATTTTAGATCTGGAAGAGAAACAAATAAACTGTGAAGTCACAGACAGCTCTTGCATAG 721 TAAAACTTGACTGCAATGTTGGTTATATATATGTAGATCATCTCTCAAGGATAGACGTTA 781 GCTTTCTCCT 1 GTAGGATCCATGGTAGAAAATCAAACCCAAATTCAGAATCGCTTTCTCAAGATGATCCC 61 TGAGGAACATTAGTTCTTTCTTATTCAGAAATGATGGCATTTCAGATTGCTGGATAACAT 121 GACTTTCAGGAGCAAGAGGAACACAGCTCCCAATTAGGCCAGATTCTGCCCAGTTAGATA 181 TTTTGCACAGTTTAAAATAAAATTTGTTATAAAGTCTTAAATTACCTGTATTATGAATTT 241 TAAAACCCTACCACTTTAAGAAAATCAACTTTCAGAGAAGATTCACAAAATTGGAACCAT 301 AACTTTTAAAAAAAAAAGATTGGGTTTCTTTTTGGGCAAGTAGTCTAGGTATTGGAGAG 361 ATTTGAAAAAAAAAAATAGTTCTATTTCTGGTTATATCATTAACTAGCTGTGTAATTTTG 421 AAATTTAACCTCACTGGATTGGCACCTCCCCAGGAAAATCAGGGCATTCTTATGTGAACT 481 TGTGGTTTGTCTGTACCAGGCCATAGGAAACTTAACATTAGAATTGAAGACTCAAATCC 541 TGAAAAATCAAAAAATCCAAATTATTTCACTTTGGAATCATCTAGTTAAAATTGATATAC 601 TGATGTTTAAATTTTAAGTACCTGCAATGTTTACTTTCAGTTCTAATAAATACCTTCTAA 661 AAACCAAAAAAAAAAAAAAAAA	SEQ ID NO:81 SEQ ID NO:82
WBC019B05.bFSP_20011110.abd	No Homology	1 TCCTTCCCCTCCTACCTGAGCCATGAAAGTACGGAGACGTCCACTGTCATGGCAGAACA 61 TGGGCCATAAAGCAAATTCAACAAGGGGTGTTCTGTTTTAATAGGACCTCAACCAGTTCC 121 ATGAACTGAGTGAAGGACGTTCATTTTAAAGTCATTTAATAATAAGCTTAGTTAAACTC 181 TTTCACCTATTCTCCCAAGACCTATTGGCATTGTTAAAAACCAAGTATATCAAATATCTA 241 ACTAAGGATGTAGTTAACCTTATTAAATATTGATTAGAATTGTTCTGTAATATTACTGAA	SEQ ID NO:83

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		301 TTTGTAAGATCTTTAGCAAAGATTTTTGAGCAATTTATAAATATAGAGCAAATGTTTCTG 361 TTTACTGCACTTTTTTGTAATTGAAGGTGATAAATTCTCAAGCCATGGTTATTGGCTTCCA 421 TGCACTGCATATTTACCCACAATTCTAGACAGTTTCCATTTTTATGGAAGAGTTGCTATT 481 ACCTTAATCATAAATGCAATCATGTGGTTAATGAGAGCTAATGCTAATAGTTAACCTTTT 541 AAAGTGAATTGGCCACAGTTTAGGAAGAAATCTCTTTTAATACAGAGTATGTCATTCCTT 601 ATTGCTTCACTTAGAAGGAGACTGAAAGCTTTGTTTTTTTTAAGCACTATTTAGTATCCT 661 AAGCTTCCTGAGGGTAGAGATTGTATCTCTTTTTGTCTGCACAATGGCCAGCACATGTCA 721 GCATTTGATCATTGTTAAATGACAACAAGTGTTCCCCAATTCCAACTTTTTTCCTGGATT 781 CTTTTGGTAAATTTATATAAATATGGCAAGCTGTATGGTTAACACTTTCTTCTACAACCAA 841 GTATTAAAGCCACATTTGAAAAGACCACATGAAATGCTGATTCCTAATTGTGTGTAGGTC 901 TTGAGGATTAAGCACACAAATTTCACCAAACTCTGTGAGTAACAAACTCAGCCTTCTGTA 961 AATATACATGCAAGTCTGGAAACGATAATACTGTACCTATAAATATATGCTGTCTGTTTT 1021 GTGTACAGTATGTAAAAACTCCTTTTCTGCCACACTAAAAATGCAAGCCATTTGTGGGAA 1081 TCCTAAAAATAGTATTATACTAAAACTTTGCTAATGATCTTTACTAGAGGATCATCTGAC 1141 TTTTCACTTACATTGGGTTTTCTTTTCAACTCACTCTTACAGTAGTCTGCTTATTTCCAG 1201 CTGTTTATTTTTATTGAGTCCTGAATTTAAAAAAAAAATATTTTGATTCATTTTGTAAATA 1261 CAAGCTGTAAAAAAAGAGAGATTTAATGTTGTCTTTTTAAATACTCCGATTTTCATTCTAA 1321 TATGAATGTTGTTATATTGTACTTAGAAACTGTACCTTTAATATTACATTACCTTTATTA 1381 AAAGTGCATTGAACACATCAATTTTAGATGTGCTTTATGTACTGTTATCCTATAATAAAA 1441 CTTCAGCTTCTAATGGAAAAAAAAAAAAAAAAAA	
WBC019C11.bFSP_20011110.abd	Human proline-rich protein (PRP) mRNA.	1 AAAACTCTGATCTGGGGAGGAACCAGGACTACATAGATCAAGGCAGTTTTCTTCTTGAG 61 AAACTATCCCAGATATCATCATAGAGTCTTCTGCTCTTCCTCAACTACCAACAGAAAAACA 121 TCAGCGAAGCAGCAGGCCATGCACCCCCCAAAAACTCCATCTGGGGCTCTTCATAGAAAA 181 AGGAAAATGGCAGCCTGGCCCTTCTCCAGGCTGTGGAAAGTCTCTGATCCAATTCTCTTC 241 CAAATGACCTTGATCGCTGCTCTGTTGCCTGCTGTTCTTGGCAATTGTGGTCCTCCACCC 301 ACTTTATCATTTGCTGCCCCGATGGATATTACGTTGACTGAGACACGCTTCAAAACTGGA 361 ACTACTCTGAAATACACCTGCCTCCCTGGCTACGTCAGATCCCATTCAACTCAGACGCTT 421 ACCTGTAATTCTGATGGCGAATGGGTGTATAACACCTTCTGTATCTACAAACGATGCAGA 481 CACCCAGGAGAGTTACGTAATGGGCAAGTAGAGATTAAGACAGATTTATCTTTTGGATCA 541 CAAATAGAATTCAGCTGTTCAGAAGGATTTTTCTTAATTGGCTCAACCACTAGTCGTTGT 601 GAAGTCCAAGATAGAGGAGTTGACTGGAGTGATCCTCTCCCAGTATGTGTAATTGCCAAG 661 TGTGAGGCCCCTCCAGCCATCAGCAATGGGAAGCACAGTGGTGGAGATGAAGACGTCTAC 721 ACATATGGCTCTTCTGTCACCTACAGCTGTGACCCTCACTTCTCAATGATAGGCAAAGCC 781 TCCATTTCCTGCACAGTGGAGAATAAAACGATAGGTGTCTGGAGCCCAAGCCCTCCTACC 841 TGTGAAAAAATCACCTGTCGCAAGCCAGATGTTTCACATGGGGAAATGGTCTCTGGATTT 901 GGACCCCTCTATACTTACAAAGACGCTATTGTGTTGGACTGCAAGAAGGGTTATGTCCTC 961 ACAGGCAGCAGTTTAATCCACTGTGAAGCTGATAACAACTGGGACCCTCCTCCTCCTGTT 1021 TGTGAGCTCAATGGTTGTACCAACTTACCAGACATCCCAAATGCCTTCTGGGAACGATAC 1081 AGGTATCAGAGGCCAACAAAAGAGGACGTGTATAATGTTGGGACTGTGTTGAAGTACCAT 1141 TGCCTGACTGGCTATAAACCTGCTTCAGATAAACCCACGGCTGTGATTTGTCAGGAAGAT 1201 TTCAGGTGGACTCCATACACGGAATGTGAGGAGGTATGTTGCCCAGTACCAGAGCTGAAG	SEQ ID NO:84

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1261 AACGGTGAAATCACTCAACACAGGAAAAGTCGTCCTGCCAATCACTGTGTTTATTTCTAT 1321 GGAGATGAGATTTCATTTTCATGTCATGAGACCAGTAGGTTTTCAGCTATATATGCCAAGGA 1381 GATGGCACGTGGAGTCCCCGAACACCATCATGTGGAGACATTTGCAATTTTCCTCCTAAA 1441 ATTGCCCATGGGCATTATAAACAATCTAGTTCATACAGCTTTTTCAAAGAAGAGATTATA 1501 TATGAATGTGATAAAGGCTACATTCTGGTCGACAGGCGAAACTCTCCTGCAGTTATTCA 1561 CACTGGTCATCTCCAGCTCCTCAATGTAAAGCTCTGTGTCCGAAACCACAGATAGAGCAT 1621 GGACGGCTGTCTGTGGTTAAGGATCAGTATATTACACCTGAAAATGTCACCATCCAGTGT 1681 GACCCTCACTATCGTTTGGTTGGTCTCCAAAGTATCACTTGCTCAGAGAACAGCACCTGG 1741 TACCCCGAGGTGCCCATGTGTGAGTGGGAGATCGCTGAAGGCTGTGAGCAAGTGCTCGCA 1801 GGCAGAAAAATCATGCAGTGTCTCCCCAAAGCCGGAGGATGTGAGAACGGCCCTGGAGCTG 1861 TATAAGCTGTCTCTGGAAATTGAACAACTGGAACTACAGAGAGACAGCGCAAGACAATCC 1921 ACTTTGGATAAAGAACTATATAATTTTTCTCAAAAGAAGGAGGAAAAGGTGTCTTGCTGGCT 1981 TGCCTCTTGCAATTCAATACAGATCAGTTTTAGCAAATCTACTGTCAATTTGGCAGTGATA 2041 TTCATCATAATAAATATCTAGAAAGGATAATTGGTTAATGTTTAATGCTTTGAGATTGTG 2101 AAATTATTAATCATCCTCTGTGTGGCTCATGTTTTTGCTTTTCAACACACAAAGCACAAA 2161 TTTTTTTTCGATTAAAAATGTATGTAT	SEQ ID NO:85
		1 M H P P K T P S S G A L H R K K M A A W 1 ATGCACCCCCCAAAAACTCCATCTGGGGCTCTTCATAGAAAAAGGAAAATGGCAGCCTGG	
		21 P F S R L W K V S D P I L F Q M T L I A 61 CCCTTCTCCAGGCTGTGGAAAGTCTCTGATCCAATTCTCTTCCAAATGACCTTGATCGCT	
		41 A L L P A V L G N C G P P P T L S F A A 121 GCTCTGTTGCCTGCTGTTCTTGGCAATTGTGGTCCTCCACCCACTTTATCATTTGCTGCC	
		61 P M D I T L T E T R F K T G T T L K Y T 181 CCGATGGATATTACGTTGACTGAGACACGCTTCAAAACTGGAACTACTCTGAAATACACC	
		81 C L P G Y V R S H S T Q T L T C N S D G 241 TGCCTCCCTGGCTACGTCAGATCCCATTCAACTCAGACGCTTACCTGTAATTCTGATGGC	
		101 E W V Y N T F C I Y K R C R H P G E L R 301 GAATGGGTGTATAACACCTTCTGTATCTACAAACGATGCAGACACCCAGGAGAGTTACGT	
		121 N G Q V E I K T D L S F G S Q I E F S C 361 AATGGGCAAGTAGAGATTAAGACAGATTTATCTTTTGGATCACAAATAGAATTCAGCTGT	
		141 S E G F F L I G S T T S R C E V Q D R G 421 TCAGAAGGATTTTTCTTAATTGGCTCAACCACTAGTCGTTGTGAAGTCCAAGATAGAGGA	
		161 V D W S D P L P V C V I A K C E A P P A 481 GTTGACTGGAGTGATCCTCTCCCAGTATGTGTAATTGCCAAGTGTGAGGCCCCTCCAGCC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		181 I S N G K H S G G D E D V Y T Y G S S V 541 ATCAGCAATGGGAAGCACAGTGGTGGAGATGAAGACGTCTACACATATGGCTCTTCTGTC	
		201 T Y S C D P H F S M I G K A S I S C T V 601 ACCTACAGCTGTGACCCTCACTTCTCAATGATAGGCAAAGCCTCCATTTCCTGCACAGTG	
		221 E N K T I G V W S P S P P T C E K I T C 661 GAGAATAAAACGATAGGTGTCTGGAGCCCAAGCCCTCCTACCTGTGAAAAAATCACCTGT	
		241 R K P D V S H G E M V S G F G P L Y T Y 721 CGCAAGCCAGATGTTTCACATGGGGAAATGGTCTCTGGATTTGGACCCCTCTATACTTAC	
		261 K D A I V L D C K K G Y V L T G S S L I 781 AAAGACGCTATTGTGTTGGACTGCAAGAAGGGTTATGTCCTCACAGGCAGCAGTTTAATC	
		281 H C E A D N N W D P P P P V C E L N G C 841 CACTGTGAAGCTGATAACAACTGGGACCCTCCTCCTCCTGTTTGTGAGCTCAATGGTTGT	
		301 T N L P D I P N A F W E R Y R Y Q R P T 901 ACCAACTTACCAGACATCCCAAATGCCTTCTGGGAACGATACAGGTATCAGAGGCCAACA	
		321 K E D V Y N V G T V L K Y H C L T G Y K 961 AAAGAGGACGTGTATAATGTTGGGACTGTGTTGAAGTACCATTGCCTGACTGGCTATAAA	
		341 P A S D K P T A V I C Q E D F R W T P Y 1021 CCTGCTTCAGATAAACCCACGGCTGTGATTTGTCAGGAAGATTTCAGGTGGACTCCATAC	
		361 T E C E E V C C P V P E L K N G E I T Q 1081 ACGGAATGTGAGGAGGTATGTTGCCCAGTACCAGAGCTGAAGAACGGTGAAATCACTCAA	
		381 H R K S R P A N H C V Y F Y G D E I S F 1141 CACAGGAAAAGTCGTCCTGCCAATCACTGTGTTTATTCTATGGAGATGAGATTTCATTT	
		401 S C H E T S R F S A I C Q G D G T W S P 1201 TCATGTCATGAGACCAGTAGGTTTTCAGCTATATGCCAAGGAGATGGCACGTGGAGTCCC	
		421 R T P S C G D I C N F P P P K I A H G H Y 1261 CGAACACCATCATGTGGAGACATTTGCAATTTTCCTCCTAAAATTGCCCATGGGCATTAT	
		441 K Q S S S Y S F F K E E I I Y E C D K G 1321 AAACAATCTAGTTCATACAGCTTTTTCAAAGAAGAGATTATATATGAATGTGATAAAGGC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		461 Y I L V G Q A K L S C S Y S H W S S P A 1381 TACATTCTGGTCGGACAGGCGAAACTCTCCTGCAGTTATTCACACTGGTCATCTCCAGCT 481 P Q C K A L C P K P Q I E H G R L S V V 1441 CCTCAATGTAAAGCTCTGTGTCCGAACCACAGATAGAGCATGGACGGCTGTCTGTGTT 501 K D Q Y I T P E N V T I Q C D P H Y R L 1501 AAGGATCAGTATATTACACCTGAAAATGTCACCATCCAGTGTGACCCTCACTATCGTTTG 521 V G L Q S I T C S E N S T W Y P E V P M 1561 GTTGGTCTCCAAAGTATCACTTGCTCAGAGAACAGCACCTGGTACCCCGAGGTGCCCATG 541 C E W E I A E G C E Q V L A G R K I M Q 1621 TGTGAGTGGGAGATCGCTGAAGGCTGTGAGCAAGTGCTCGCAGGCAGAAAAATCATGCAG 561 C L P K P E D V R T A L E L Y K L S L E 1681 TGTCTCCCAAAGCCGGAGGATGTGAGAACGGCCCTGGAGCTGTATAAGCTGTCTCTGGAA 581 I E Q L E L Q R D S A R Q S T L D K E L 1741 ATTGAACAACTGGAACTACAGAGAGACAGCGCAAGACAATCCACTTTGGATAAAGAACTA 601 - 1801 TAA	
WBC020F05.bFSP_20011110.abd	Human translation initiation factor 3 large subunit mRNA.	1 GGCGACTGCTGGCGAGGCGCGTGGGACCTTACGCTGGTTCCCTTCGTCTCCTCTCCCGG 61 CCCGGGCCACTAGAGAGTTCGCTGACGCCGGGTGAGCTGAGCCTGCCGCCAACGATGCCGG 121 CCTATTTTCAGAGGCCGGAAAATGCCCCTCAAACGCGCCCAACGAATTTCTTGAGGTTGGCA 181 AAAAGCAGCCTGCTCTGGATGTTCTTTATGATGTTATGAAAAGTAAAAAACATAGAACAT 241 GGCAAAAGATACACGAACCAATTATGTTGAAATACTTGGAACTTTGCGTGGATCTTCGCA 301 AGAGCCACTTGGCAAAGGAGGGGTTATACCAGTATAAGACATTTGTCAACAGGTGAACA 361 TAAAATCTCTGGAGGATGTTGTTAGGGCATATTTGAAAATGGCAGAGGAAAAACTGAAG 421 CTGCTAAAGAAGAATCTCAGCAGATGGTCTTAGATATAGAGGATCTAGATAATATTCAAA 481 CTCCTGAGAGTGTTCTCCTAAGTGCTGTAAGTGGTGAAGACACTCAGGATCGTACTGACA 541 GATTACTTTTAACTCCATGGGTTAAATTCCTGTGGGAGTCTTACAGGCAGTGTTTGGACC 601 TTCTTAGAAACAATTCTAGAGTAGAGCGCCTGTACCATGATATTGCCCAGCAAGCTTTCA 661 AATTCTGCCTCCAATACACGCGTAAGGCTGAATTCCGTAAACTGTGTGACAATTTGAGAA 721 TGCACTTATCGCAGATTCAGCGCCACCATAACCAAAGTACGGCAATCAATCTTAATAATC 781 CAGAGAGCCAGTCCATGCATTTGGAAACCAGACTTGTTCAGCTGGACAGTGCTATCAGCA 841 TGGAATTGTGGCAGGAAGCATTCAAAGCTGTGGAAGATATTCACGGGCTATTCTCCTTGT 901 CTAAAAAACCACCTAAACCTCAGTTGATGGCAAATTACTATAACAAAGTCTCAACTGTGT 961 TTTGGAAATCTGGAAATGCTCTTTTTCATGCATCTACACTCCATCGTCTTTACCATCTCT 1021 CTAGAGAAATGAGAAAGAATCTCACACAAGACGAGATGCAAAGAATGTCTACTAGAGTCC	SEQ ID NO:86

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1081 TTTTAGCCACTCTTTCCATCCCTATTACTCCTGAGCGTACGGATATTGCTCGACTTCTGG	
		1141 ATATGGATGGCATTATAGTTGAAAAACAGCGTCGCCTTGCAACACTACTAGGTCTTCAAG	
		1201 CCCCACCGACACGAATTGGCCTTATTAATGATATGGTCAGATTTAATGTACTACAATATG	
		1261 TTGTCCCAGAAGTGAAAGACCTTTACAATTGGCTTGAAGTAGAATTTAACCCATTAAAAC	
		1321 TCTGTGAGAGACGTCACAAAGGTTCTAAATTGGGTTAGAGAACAACCTGAAAAGGAACCAG	
		1381 AGTTGCAGCAGTATGTCCCACAGCTGCAAAACAACACCATACTCCGTCTTCTGCAGCAGG	
		1441 TGGCACAAATTTATCAGAGCATTGAGTTTTCTCGTTTGACTTCTCTGGTTCCTTTTGTTG	
		1501 ATGCTTTCCAACTGGAACGGGCCATAGTAGATGCAGCCAGGCACTGTGACCTGCAGGTTC	
		1561 GTATTGACCACACTTCTCGGACCCTTAGTTTTGGATCCGATTTGAATTATGCTACTCGAG	
		1621 AAGATGCTCCAATTGGTCCTCATTTGCAAAGCATGCCTTCAGAACAGATAAGAAATCAGC	
		1681 TGACAGCCATGTCCTCAGTACTTGCAAAAGCACTTGAAGTCATTAAGCCAGCTCATATAC	
		1741 TGCAAGAGAAAGAAGAACAGCATCAGTTGGCTGTTACCGCGTACCTTAAAAATTCACGAA	
		1801 AAGAGCATCAGCGCATCCTGGCTCGCCGTCAGACCATTGAGGAAAGGAAGAGAGCGGCTTG	
		1861 AGAGTCTGAATATCCAGCGGGAGAAAGAAGAATTGGAGCAGAGGCAAGCTGAACTCCAGA	
		1921 AAGTACGGAAGGCTGAAGAAGAGAGGCTGCGACAGGAGGCAAAGGAGAGAGAAGGAGC	
		1981 GTATCTTACAGGAACATGAACAAATCAAAAAGAAAACTGTTCGTGATCGTTTGGAGCAGA	
		2041 TCAAGAAAACGGAACTGGGTGCCAAAGCATTCAAAGATATCGATTGAAGACCTTGAAG	
		2101 AATTGGATCCAGATTTCATCATGGCTAAACAGGTTGAACAACTGGAGAAAAAAAAGAAGG	
		2161 AACTTCAGGAACGCCTAAAGAATCAAGAAAAGAAGATTGACTATTTTGAAAGAGCTAAGC	
		2221 GTTTGGAAGAAATTCCTTTGATAAAGAGCGCTTACGAGGAACAGAGAATTAAAGACATGG	
		2281 ATCTGTGGGAGCAACAAGAGGAAGAAAGAATTACTACAATGCAGCTAGAACGTGAAAAGG	
		2341 CTCTTGAACATAAGAATCGAATGTCACGAATGCTTGAAGACAGAGATTTATTCGTAATGC	
		2401 GACTCAAAGCTGCACGGCAGTCTGTTTATGAGGAAAAACTTAAACAGTTTGAAGAGCGAT	
		2461 TAGCAGAAGAAAGGCATAATCGATTGGAAGAACGGAAAAGGCAGCGTAAAGAAGAACGCA	
		2521 GGATAACATACTATAGAGAAAAAGAAGAGGAGGAGCAGAGAAGGGCAGAAGAACTAAATGC	
		2581 TAAAAGAGCGGGAAGAGAGAGCGCCGCCGAACGAGCAAAACGCGAGGAAGAGCTACGAG	
		2641 AGTATCAGGAGCGGGTGAAGAAATTAGAAGAAGTGGAAAGGAAAAAAACGCCAAAGGGAGT	
		2701 TGGAAATTGAAGAACGAGAACGGCGTAGAGAGGAAGAGAGAAGACTTGGCGATAGTTCCC	
		2761 TTTCTAGAAAGGACTCTCGTTGGGGAGATAGAGATTCAGAAGGCACCTGGAGAAAAGGAC	
		2821 CTGAAGCAGATTCTGAGTGGAGAAGAGGCCCGCCAGAGAAGGAGTGGAGACGTGGAGAAG	
		2881 GGCGAGATGAGGACAGGTCTCATAGAAGAGATGAAGAGCGGCCCCGGCGTCTGGGGGATG	
		2941 ATGAAGATAGAGAGCCCTCTCTTAGACCAGACGATGATCGGGTTCCCCGGCGTGGCATGG	
		3001 ATGATGACAGAGGCCCTAGACGTGGTCCTGAGGAAGATAGTTCTCTCGTCGTGGGGCAG	
		3061 ACGATGACCGGCCTTCCTGGCGTAACACAGATGATGACAGGCCTCCCAGACGAATTGCCG	
		3121 ATGAAGACAGGGGAAACTGGCGTCATGCGGATGATGACACGACCACCTAGACGAGGACTGG	
		3181 ATGAGGACAGAGGAAGCTGGCGAACAGCTGATGAGGACAGAGGACCAGACGTGGGATGG	
		3241 ATGATGACCGGGGGGCCGAGGCGAGGAGGCGCTGATGATGAGCGATCATCCTGCGCGTAATG	
		3301 CTGATGATGACCGGGGTCCCAGGCGAGGGTTGGATGATGATCGGGGTCCCAGGCGAGGCA	
		3361 TGGATGATGACCGGGGTCCCAGGCGAGGCATGGATGATGACCGGGGTCCCAGGCGAGGCA	
		3421 TGGATGATGACCGGGGTCCCAGGCGAGGGTTGGATGATGATCGAGGACCTTGGAGGAACG	
		3481 CCGATGATGACACGAGAATTCCCAGGCGTGGTGCAGAGGATGACAGGGGGCCCTTGGAGAAACA	
		3541 TGGATGATGATCGCCTTTCAAGACGTGCTGATGATGATCGGTTTCCCAGACGGGGTGATG	
		3601 ACTCAAGACCTGGTCCTTGGAGACCATTAGTCAAGCCAGGTGGATGGAGAGAGAAAGAAA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		3661 AAGCCAGAGAGGAGAGCTGGGTCCACCTCGAGAATCAAGGCCATCAGAAGAACGTGAAT 3721 GGGACAGAGAAAAAGAAAGGACAGAGATAATCAAGATCGGGAGGAGAATGACAAGGACC 3781 CTGAGAGAGAAAGGGACAGAGAGAGATGTGGATCGAGAGGATCGCTTCAGACGACCCA 3841 GGGATGAAGGTGGCTGGAGAAGAGGACCAGCTGAAGAATCTTCTAGCTGGAGAGATTCGA 3901 GTCGCCGTGACGATAGGGATCGGGATGACCGTCGTGAGCGAGATGATCGCCGTGATC 3961 TGAGAGAAAGACGAGATGACAGAGACCGAAGAGGACCTCCTTTGAGATCAGAACGTGAAG 4021 AAGCAAGTTCTTGGAGACGTGCTGATGACAGGAAAGATGAGCGGCGGAAGAGCGGGACG 4081 CCCCTCGTCGTGTTCCTCCCCAGCTCTTTCAAGAGACCGAGAAAGAGACCGAGACCGAG 4141 AAAGAGAAGGTGAAAAAGAGAAGGCCTCATGGAGAGCTGAGAAAGATAGGGAATCTCTTC 4201 GTCGTACTAAAAATGAGACTGATGAAGATGGATGGACCACGGTACGACGTTAAGTCTCAA 4261 GATAATGGGTTCGAACTCATGTGTCACATAGGTTTGATCACATTCGCGGATTATTAGACT 4321 TGTGCTTCAACCAGTCTAAATTGGATTCTTTAATGTTGTCTCACCATAACACACAAAAGCA 4381 TGAACTTGTATTTAATCCTATATAATAGATTGATCATGCACCGTATCCACAGAAAGCTGGA 4441 AAACCATGCCATTTTCTGGAATTTAAGGTGTTGCATTATTTCATCAATCATTTGTTGACA 4501 AAAAAGAAAAACTAAAAAATAAATTTAAAATGTGAACCTTCAGGTATTGAGTAACACCTT 4561 TATCTTGGTATAGAACTGATACCATTTTTTGATTTTGAAATATCTGATAATAATTTGGAA 4621 TGAAGTAAGGTTCTGTTAAAATATATTTGAAGACCCTTTAAAGCAGTGAATCTGAAACAA 4681 TTTTCACACCCTTAAGTGGTTGATACGTACCTATTTTAGGTATTTTGAGGTATTTACCAT 4741 AAACTAAATTTAGAAATTTTTAGATTCACTTGAAGTAAACATTACAAACATTGGATACG 4801 GTGGGGTTTCTTTAGATTTTACTTGAGAGAAGGTGAGTACAAAGCAATTTGCAGTTGTT 4861 GTAATGACAAGATTACTGCGCAAGTGTGAATCCAAACAGTATAGCTTTTAAATTTTAAAG 4921 CATTTGGTAAATTATCGCTGAGTTTTTTTCTGTTGCCAATAGCAAACTGCTTTTCCATTA 4981 ATGGAGAATTCATGCCTTTCAAGCATTTTAAATATGACAATATTTATAAATGTATGGTTT 5041 GGAGGAATCGTTTAAATTCTCTTTCCTAATTTTCTTTCTTTTGAAGATAGATTCTTTCAA 5101 CAAGTAATTTGTAGTAATGACTGTGTTGACTTCAATTTTGGAGCGCAGTAGCTATGTTAA 5161 AGATGAACTATTTGGTCTCATTGAAGCCAACACAGAACTTGCTGCTGTGTTTTTTCTTCA 5221 GTGATAAATAAAATACTTACAGAAA 1 M P A Y F Q R P E N A L K R A N E F L E 1 ATGCCGGCCTATTTTCAGAGGCCGGAAAATGCCCTCAACGCGCCAACGAATTTCTTGAG 21 V G K K Q P A L D V L Y D V M K S K K H 61 GTTGGCAAAAAGCAGCCTGCTCTGGATGTTCTTTATGATGTTATGAAAAGTAAAAAACAT 41 R T W Q K I H E P I M L K Y L E L C V D 121 AGAACATGGCAAAAGATACACGAACCAATTATGTTGAAATACTTGGAACTTTGCGTGGAT 61 L R K S H L A K K E G L Y Q Y K N I C Q Q 181 CTTCGCAAGAGCCACTTGGCAAAGGAGGGGTTATACCAGTATAGAACATTTGTCAACAG 81 V N I K S L E D V V R A Y L K M A E E K 241 GTGAACATAAAATCTCTGGAGGATGTTGTTAGGGCATATTTGAAAATGGCAGAGGAAAAA	SEQ ID NO:87

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		101 T E A A K E E S Q Q M V L D I E D L D N 301 ACTGAAGCTGCTAAAGAAGAATCTCAGCAGATGGTCTTAGATATAGAGGATCTAGATAAT	
		121 I Q T P E S V L L S A V S G E D T Q D R 361 ATTCAAACTCCTGAGAGTGTTCTCCTAAGTGCTGTAAGTGGTGAAGACACTCAGGATCGT	
		141 T D R L L L T P W V K F L W E S Y R Q C 421 ACTGACAGATTACTTTTAACTCCATGGGTTAAATTCCTGTGGAGTCTTACAGGCAGTGT	
		161 L D L L R N N S R V E R L Y H D I A Q Q 481 TTGGACCTTCTTAGAAACAATTCTAGAGTAGAGCGCCTGTACCATGATATTGCCCAGCAA	
		181 A F K F C L Q Y T R K A E F R K L C D N 541 GCTTTCAAATTCTGCCTCCAATACACGCGTAAGGCTGAATTCCGTAAACTGTGTGACAAT	
		201 L R M H L S Q I Q R H H N Q S T A I N L 601 TTGAGAATGCACTTATCGCAGATTCAGCGCCACCATAACCAAAGTACGGCAATCAATCTT	
		221 N N P E S Q S M H L E T R L V Q L D S A 661 AATAATCCAGAGAGCCAGTCCATGCATTTGGAAACCAGACTTGTTCAGCTGGACAGTGCT	
		241 I S M E L W Q E A F K A V E D I H G L F 721 ATCAGCATGGAATTGTGGCAGGAAGCATTCAAAGCTGTGGAAGATATTCACGGGCTATTC	
		261 S L S K K P P K P Q L M A N Y Y N K V S 781 TCCTTGTCTAAAAAACCACCTAAACCTCAGTTGATGGCAAATTACTATACAAAGTCTCA	
		281 T V F W K S G N A L F H A S T L H R L Y 841 ACTGTGTTTTGGAAATCTGGAAATGCTCTTTTTCATGCATCTACACTCCATCGTCTTTAC	
		301 H L S R E M R K N L T Q D E M Q R M S T 901 CATCTCTCTAGAGAAATGAGAAGAATCTCACACAAGACGAGATGCAAAGAATGTCTACT	
		321 R V L L A T L S I P I T P E R T D I A R 961 AGAGTCCTTTTAGCCACTCTTTCCATCCCTATTACTCCTGAGCGTACGGATATTGCTCGA	
		341 L L D M D G I I V E K Q R R L A T L L G 1021 CTTCTGGATATGGATGGCATTATAGTTGAAAAACAGCGTCGCCTTGCAACACTACTAGGT	
		361 L Q A P P T R I G L I N D M V R F N V L 1081 CTTCAAGCCCCACCGACACGAATTGGCCTTATTAATGATATGGTCAGATTTAATGTACTA	
		381 Q Y V V P E V K D L Y N W L E V E F N P	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1141 CAATATGTTGTCCCAGAAGTGAAAGACCTTTACAATTGGCTTGAAGTAGAATTTAACCCA	
		401 L K L C E R V T K V L N W V R E Q P E K	
		1201 TTAAAACTCTGTGAGAGAGTCACAAAGGTTCTAAATTGGGTTAGAGAACAACCTGAAAAG	
		421 E P E L Q Q Y V P Q L Q N N T I L R L L	
		1261 GAACCAGAGTTGCAGCAGTATGTCCCACAGCTGCAAAACAACACCATACTCCGTCTTCTG	
		441 Q Q V A Q I Y Q S I E F S R L T S L V P	
		1321 CAGCAGGTGGCACAAATTTATCAGAGCATTGAGTTTTCTCGTTTGACTTCTCTGGTTCCT	
		461 F V D A F Q L E E R A I V D A A R H C D L	
		1381 TTTGTTGATGCTTTCCAACTGGAACGGGCCATAGTAGATGCAGCCAGGCACTGTGACCTG	
		481 Q V R I D H T S R T L S F G S D L N Y A	
		1441 CAGGTTCGTATTGACCACACTTCTCGGACCCTTAGTTTTGGATCCGATTTGAATTATGCT	
		501 T R E D A P I G P H L Q S M P S E Q I R	
		1501 ACTCGAGAAGATGCTCCAATTGGTCCTCATTTGCAAAGCATGCCTTCAGAACAGATAAGA	
		521 N Q L T A M S S V L A K A L E V I K P A	
		1561 AATCAGCTGACAGCCATGTCCTCAGTACTTGCAAAAGCACTTGAAGTCATTAAGCCAGCT	
		541 H I L Q E K E E Q H Q L A V T A Y L K N	
		1621 CATATACTGCAAGAGAAAGAAGAACAGCATCAGTTGGCTGTTACCGCGTACCTTAAAAAT	
		561 S R K E H Q R I L A R R R Q T I E E R K E	
		1681 TCACGAAAAGAGCATCAGCGCATCCTGGCTCGCCGTCAGACCATTGAGGAAAGGAAAGAG	
		581 R L E S L N I Q R E E K E E L E Q R E A E	
		1741 CGGCTTGAGAGTCTGAATATCCAGCGGGAGAAAGAAGAATTGGAGCAGAGGGAAGCTGAA	
		601 L Q K V R R K A E E E E R L R Q E E A K E R E	
		1801 CTCCAGAAAGTACGGAAGGCTGAAGAAGAGAGGCTGCGACAGGAGGCAAAGGAGAGAG	
		621 K E R I L Q E H E Q I K K K K T V R D R L	
		1861 AAGGAGCGTATCTTCACAGGAACATGAACAAATCAAAAAGAAAACTGTTCGTGATCGTTTG	
		641 E Q I K K T E L G A K A F K D I D I E D	
		1921 GAGCAGATCAAGAAAACGGAACTGGGTGCCAAAGCATTCAAAGATATCGATATTGAGAC	
		661 L E E L D P D F I M A K K Q V E Q L E K K K	
		1981 CTTGAAGAATTGGATCCAGATTTCATCATGGCTAAACAGGTTGAACAACTGGAGAAAAAA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		681 K K E L Q E R L K N Q E K K I D Y F E R 2041 AAGAAGGAACTTCAGGAACGCCTAAAGAATCAAGAAAAGAAGATTGACTATTTTGAAAGA	
		701 A K R L E E I P L I K S A Y E E Q R I K 2101 GCTAAGCGTTTGGAAGAAATTCCTTTGATAAAGAGCGCTTACGAGGAACAGAGAATTAAA	
		721 D M D L W E Q Q E E E R I T T M Q L E R 2161 GACATGGATCTGTGGGAGCAACAAGAGGAAGAAATTACTACAATGCAGCTAGAACGT	
		741 E K A L E H K N R M S R M L E D R D L F 2221 GAAAAGGCTCTTGAACATAAGAATCGAATGTCACGAATGCTTGAAGACAGAGATTTATTC	
		761 V M R L K A A R Q S V Y E E K L K Q F E 2281 GTAATGCGACTCAAAGCTGCACGGCAGTCTGTTTATGAGGAAAAACTTAAACAGTTTGAA	
		781 E R L A E E R H N R L E E E R K R Q R K E 2341 GAGCGATTAGCAGAAGAAAGGCATAATCGATTGGAAGAACGGAAAAGGCAGCGTAAAGAA	
		801 E R R I T Y Y R E K E E E E Q R R A E E 2401 GAACGCAGGATAACATACTATAGAGAAAAAGAAGAGGAGGCAGAGAAGGGCAGAAGAA	
		821 Q M L K E R E E E R E E R A E E R A K R E E E E 2461 CAAATGCTAAAAGAGCGGGAAGAGAGAGAGCGCCGCCGAACGAGCAAAACGCGAGGAAGAG	
		841 L R E E Y Q E R R V K K K L E E E V E E R K K K R Q 2521 CTACGAGAGTATCAGGAGCGGGTGAAGAAATTAGAAGAAGTGGAAAGGAAAAAACGCCAA	
		861 R E E L E I E E E R R R R E E E E R R R L G D 2581 AGGGAGTTGGAAATTGAAGAACGAGAACGGCGTAGAGAGGAAGAGAGAAGACTTGGCGAT	
		881 S S L S R K K D S R R W G G D R R D D S E E G T W R 2641 AGTTCCCTTTCTAGAAAGGACTCTCGTTGGGGAGATAGAGATTCAGAAGGCACCTGGAGA	
		901 K G P E E A D S E E W R R R G P P P E K E E W R R R 2701 AAAGGACCTGAAGCAGATTCTGAGTGGAGAAGAGGCCCGCCAGAGAAGGAGTGGAGACGT	
		921 G E G G R D D E D D R S H R R R D D E E E R P R R R L 2761 GGAGAAGGGGCGAGATGAGGACAGGTCTCATAGAAGAGATGAAGAGCGGCCCCGGCGTCTG	
		941 G D D E D D R E E P S L R R P D D D D R R V P R R R 2821 GGGGATGATGAAGATAGAGAGCCCTCTCTTAGACCAGACGATGATCGGGTTCCCCGGCGT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		961 G M D D D R G P R R G P E E D R F S R R 2881 GGCATGGATGATGACAGAGGCCCTAGACGTGGTCCTGAGGAAGATAGGTTCTCTCGTCGT	
		981 G A D D D R P S W R N T D D D R P P P R R 2941 GGGGCAGACGATGACCGGCCTTCCTGGCGTAACACAGATGATGACAGGCCTCCCAGACGA	
		1001 I A D E D R G N W R H A D D D R P P P R R 3001 ATTGCCGATGAAGACAGGGGAAACTGGCGTCATGCGGATGATGACAGACCACCTAGACGA	
		1021 G L D E D R G S W R T A D E D R G P P R R 3061 GGACTGGATGAGGACAGAGGAAGCTGGCGAACAGCTGATGAGGACAGAGGACCAAGACGT	
		1041 G M D D D R G P P R R G G A D D E R R S S W 3121 GGGATGGATGATGACCGGGGCCGAGGCGAGGCGCTGATGATGAGCGATCATCCTGG	
		1061 R N A D D D R G P R R R G L D D D R G P R 3181 CGTAATGCTGATGATGACCGGGGTCCCAGGCGAGGGTTGGATGATGATCGGGGTCCCAGG	
		1081 R G M D D D R G P R R R G M D D D R G P R 3241 CGAGGCATGGATGATGACCGGGGTCCCAGGCGAGGCATGGATGATGACCGGGGTCCCAGG	
		1101 R G M D D D R G P R R R G L D D D R G P W 3301 CGAGGCATGGATGATGACCGGGGTCCCAGGCGAGGGTTGGATGATGATCGAGGACCTTGG	
		1121 R N A D D D R I P R R R G A E D D R G P W 3361 AGGAACGCCGATGATGACAGAATTCCCAGGCGTGGTGCAGAGGATGACAGGGGCCCTTGG	
		1141 R N M D D D R L S R R R A D D D R F P R R 3421 AGAAACATGGATGATGATCGCCTTTCAAGACGTGCTGATGATCGGTTTCCCAGACGG	
		1161 G D D S R P G P W R P P L V K P G G W R E 3481 GGTGATGACTCAAGACCTGGTCCTTGGAGACCATTAGTCAAGCCAGGTGGATGGAGAGAG	
		1181 K E K A R E E S W G P P R R E S R P S E E 3541 AAAGAAAAAGCCAGAGAGGAGAGCTGGGGTCCACCTCGAGAATCAAGGCCATCAGAAGAA	
		1201 R E W D R E E K E E R D R D N Q D R E E E N D 3601 CGTGAATGGGACAGAGAAAAAGAAAAGGGACAGAGATAATCAAGATCGGGAGGAGAATGAC	
		1221 K D P E E R R E E R R D R E E R D V D R E E D R F R 3661 AAGGACCCTGAGAGAGAAAGGGACAGAGAGAGATGTGGATCGAGAGGATCGCTTCAGA	
		1241 R P R D E G G W R R R G P A E E S S S W R	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		3721 CGACCCAGGGATGAAGGTGGCTGGAGAAGAGGACCAGCTGAAGAATCTTCTAGCTGGAGA	
		1261 D S S R R D D D R D D R R R E R D D R 3781 GATTCGAGTCGCCGTGACGATAGGGATCGGGATGACCGTCGTCGTGAGCGAGATGATCGC	
		1281 R D L R E R R D D D R D R R G P P P L R S E 3841 CGTGATCTGAGAGAAAGACGAGATGACACAGAGACCGAAGAGGACCTCCTTTGAGATCAGAA	
		1301 R E E E A S S W R R R A D D D R K D D E R A E E 3901 CGTGAAGAAGCAAGTTCTTGGAGACGTGCTGATGACAGGAAGATGAGCGGGCGGAAGAG	
		1321 R D D A P P R R R V P P P A L S S R D D R E E R D D R 3961 CGGGACGCCCCTCGTCGTGTTCCTCCCCCAGCTCTTTCAAGAGACCGAGAAAGAGACCGA	
		1341 D R E E R E G E E K E E K K A S W R R A E E K K D D R R E 4021 GACCGAGAAAGAGAAGGTGAAAAAGAGAAGGCCTCATGGAGAGCTGAGAAAGATAGGGAA	
		1361 S L R R T T K N E E T D D E D G W T T T V R R R - 4081 TCTCTTCGTCGTACTAAAAATGAGACTGATGAAGATGGATGGACCACGGTACGACGTTAA	
WBC020H01.bFSP_20011110.abd	Human CSaids binding protein (CSBP1) mRNA	1 GGAACCGCGACCACTGGAGCCTTAGCGGGCGCAGCTGGAACGGGAGTACTGCGACGC 61 AGCCCGGAGTCGCCTTGTAGGGGCGAAGGTGCAGGAGATCGCGGCGGGCGCAGTCTTG 121 AGCGCCGGAGCGCGTCCCTGCCCTTAGCGGGGCTTGCCCCAGTCGCAGGGGCACATCCAG 181 CCGCTGCGGCTGACAGCAGCCGCGCGCGCGGGAGTCTGCGGGGTCGCGGCAGCCGCACCT 241 GCGCGGGCGACCAGCGCAAGGTCCCCGCCCGGCTGGGCGGGCAGCAAGGGCCGGGAGAG 301 GGTGCGGGTGCAGGCGGGGGCCCCACAGGGCCACCTTCTTGCCCGGCGGCTGCCGCTGGA 361 AAATGTCTCAGGAGAGGCCCACGTTCTACCGGCAGGAGCTGAACAAGACAATCTGGGAGG 421 TGCCCGAGCGTTACCAGAACCTGTCTCCAGTGGGCTCTGGCGCTATGGCTCTGTGTGTG 481 CTGCTTTTGACACAAAAACGGGGTTACGTGTGGCAGTGAAGAAGCTCTCCAGACCATTTC 541 AGTCCATCATTCATGCGAAAGAACCTACAGAGAACTGCGGTTACTTAAACATATGAAAC 601 ATGAAAATGTGATTGGTCTGTTGGACGTTTTTACACCTGCAAGGTCTCTGGAGGAATTCA 661 ATGATGTGTATCTGGTGACCCATCTCATGGGGCAGATCTGAACACAACATTGTGAAATGTC 721 AGAAGCTTACAGATGACCATGTTCAGTTCCTTATCTACCAAATTCTCCGAGGTCTAAAGT 781 ATATACATTCAGCTGACATAATTCACAGGGACCTAAAACCTAGTAATCTAGCTGTGAATG 841 AAGACTGTGAGCTGAAGATTCTGGATTTTGGACTGGCTCGGCACACAGATGATGAAATGA 901 CAGGCTACGTGGCCACTAGGTGGTACAGGGCTCCTGAGATCATGCTGAACTGGATGCATT 961 ACAACCAGACAGTTGATATTTGGTCAGTGGGATGCATAATGGCCGAGCTGTTGACTGGAA 1021 GAACATTGTTTCCTGGTACAGACCATATTAACCAGCTTCAGCAGATTATGCGTCTGACAG 1081 GAACACCCCCCGCTTATCTCATTAACAGGATGCCAAGCCATGAGGCAAGAAACTATATTC 1141 AGTCTTTGACTCAGATGCCGAAGATGAACTTTGCGAATGTATTTATTGGTGCCAATCCCC 1201 TGGCTGTCGACTTGCTGGAGAAGATGCTTGTATTGGACTCAGATAAGAGAATTACAGCGG	SEQ ID NO:88

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1261 CCCAAGCCCTTGCACATGCCTACTTTGCTCAGTACCACGATCCTGATGATGAACCAGTGG 1321 CCGATCCTTATGATCAGTCCTTTGAAAGCAGGGACCTCCTTATAGATGAGTGGAAAAGCC 1381 TGACCTATGATGAAGTCATCAGCTTTGTGCCACCACCCTTGACCAAGAAGAGATGGAGT 1441 CCTGAGCACCTGGTTTCTGTTGTTGATCCCACTTCACTGTGAGGGGAAGGCCTTTTCA 1501 CGGGAACTCTCCAAATATTATTCAAGTGCCTCTTGTTGCAGAGATTTCCTCCATGGTGGA 1561 AGGGGGTGTGCGTGCGTGTGTAGTGTGTGTGCATGTGTGTCTGTTGCTCTTTG 1621 TGGGAGGGTAAGACAATATGAACAAACTATGATCACAGTGACTTTACAGGAGGTTGTGGA 1681 TGCTCCAGGGCAGCCTCCACCTTGCTCTTCTTCTTCTGAGAGTTGGCTCAGGCAGACAAGAG 1741 CTGCTGTCCTTTTAGGAATATGTTCAATGCAAAGTAAAAAAATATGAATTGTCCCCAATC 1801 CCGGTCATGCTTTGCCACTTTGCTTCTCCTGTGACCCCACCTTGATGGTGGGAGGTAG 1861 AATTGACCATATCCCCCAGCGGCACAGAGAGAAGGCGCACACCTTCTGGCTGCTTCAGAT 1921 CTGAAGCCGTCCATCAGCGATGCATACATACAGCCAAAAAGGACCAACTGGCTTCTGTGCTCTA 1981 GTCTATGATTAACTTGCTTAATATGATTCTCAGAACTCAACAGGTGTATCTGAAACTGTA 2041 AATATGTTTGTGCCTTAAAGGAGAAGGGAGTGTAGAGAGTTAAGAGAGTGCAGCAGA 2101 TGAAGTTCTGAGCCAGGCGCGTCGTCAGGTTGTCGGACGGCTACTTGTGAAGCTGAAGTA 2161 ACCAGGGAGCCTTCAGAGGCGCCGTGTATGCATGTGTGAGCATGCGTATATGTGCTTCTC 2221 TCTCTTTCTTCCTCGCCCCCCAGGTGGTTGTCCGTTTCTCTGCTTACCCCCACCTTCAG 2281 TGCAGAGGTTTCTTGAGTATTGGCCCCGGTAGTCAGAAGCCGGTTCTTGCTGTCAGTGTA 2341 CTTCCTGTGTGCTCTTTATTCCTAGCAGAGTGACATGTGTTTGCACGTCTTGCTATTTG 2401 AGCATGCACAGCTGCTGTCCTGTTCTCTTCGGGAGGCCCTGGTGCCAGGCAGGTTTGCCA 2461 GTGAAGACTTTTTGGGTAGTTCGGAACCCATGTCACCTTGGCTCATGCTTTGGGCAGGTG 2521 ACATCATCCTCTCTTCAGCCCCCAGTGCTATTTTGTGTTGAACACAATTAATACTCCCAGG 2581 TGCTTTTGATGTGAAAACTATGAAAAAATGGAACAGATGGACATATAGCATTTTCATTCT 2641 TGCCATCTGGTTTTTCAACAAACTATTTTTGGGGAGCTGTCATGGGAAAGATCAGGGCTT 2701 TTCCTAGGAATATCTCAAATTTTGGAAAACAAATTGTTCTCTTCCCTCCCAATAACTAAT 2761 GCTAAGAAATGCTGAAAATCAAAGTAAAAAATTAAAGCCCATAAGGCCAGAAACTCCTTT 2821 TGCTGTCTTTCTCTAAATATGATTACTTTAAAATATAAAAAAGTAACAAGGTGTCTTTTCCA 2881 CTCCTATGGAAAAAGGGTCTTCTTGGCAGCTTAACATTGACTTCTTGGTTTGGGGAGAAAT 2941 AAATTTTGTTTCAGAATTTTGTATATTGTAGGAATCCCTTTGAGAATGTGATTCCTTTTG 3001 ATGGGGAGAAAGGGCAAATTATTTTAATATTTTGTATTTTCAACTTTATAAAGATAAAAT 3061 ATCCTCAGGGGTGGAGAGATGTGTCGTTTTCATAACTTGCTGAATTTCAGGCATTTTGTTCT 3121 ACATGAGGACTCATATATTTAAGCCTTTTGTGTAATAAGAAAGTATAAAGCTACTTCCAG 3181 TGTTGGCTATGTGACAGAATCTTGTATTTGGGCCAAGGTGTTTCCATTTCTCCATCACAG 3241 TGCGGTGATGCATGCGCTCCAGAGGGGCAGGTAGGACCCTGGGTCAACTGGAGTGAGAAG 3301 GAACAGGCAGACTGATGGCGATTCCCTCTCACCCGGGACTCTCCCCCTTTCAAGGAAAGT 3361 GAACCTTTAAAGTAAAGGCCTCATCTCCTTTATATGCAGGTCAAATCCTCACGATGCACA 3421 GCAAGATGAATTTTATCGGCCATGTTTGGTTGTAAATGCTAGTGTGATTTCCTACAGAAA 3481 TACTGCTCTGACTATTTTCATAAAGGTCTTTGCACATGTGACCATATCTGTGTTAGGAGG 3541 CTGAATGCTCCGGGAGCCTGAACTCAGCTGGAGCCTGTGGAAGAGCTCCTTGGTTTCTGA 3601 GCATCACGCTCCCATCTCCTGATTTCTCTGAACGGAAAACAGAAGAGAGAGAATGAGGGATA 3661 CTGCTATGTTATTTGTACTCATGAACTTGGCTGTAATCAGT 1 M S Q E R P T F Y R Q E L N K T I W E V SEQ ID NO:89	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1 ATGTCTCAGGAGAGGCCCACGTTCTACCGGCAGGAGCTGAACAAGACAATCTGGGAGGTG	
		21 P E R Y Q N L S P V G S G A Y G S V C A	
		61 CCCGAGCGTTACCAGAACCTGTCTCCAGTGGGCTCTGGCGCCTATGGCTCTGTGTGTGCT	
		41 A F D T K T G L R V A V K K L S R P F Q	
		121 GCTTTTGACACAAAAACGGGGTTACGTGTGGCAGTGAAGAAGCTCTCCAGACCATTTCAG	
		61 S I I H A K R T Y R E L R L L K H M K H	
		181 TCCATCATTCATGCGAAAGAACCTACAGAGAACTGCGGTTACTTAACATATGAACAT	
		81 E N V I G L L D V F T P A R S L E E F N	
		241 GAAAATGTGATTGGTCTGTTGGACGTTTTTACACCTGCAAGGTCTCTGGAGGAATTCAAT	
		101 D V Y L V T H L M G A D L N N I V K C Q	
		301 GATGTGTATCTGGTGACCCATCTCATGGGGGCAGATCTGAACAACATTGTGAAATGTCAG	
		121 K L T D D H V Q F L I Y Q I L R G L K Y	
		361 AAGCTTACAGATGACCATGTTCAGTTCCTTATCTACCAAATTCTCCGAGGTCTAAAGTAT	
		141 I H S A D I I H R D L K P S N L A V N E	
		421 ATACATTCAGCTGACATAATTCACAGGGACCTAAAACCTAGTAATCTAGCTGTGAATGAA	
		161 D C E L K I L D F G L A R H T D D E M T	
		481 GACTGTGAGCTGAAGATTCTGGATTTTGGACTGGCTCGGCACACAGATGAAATGACA	
		181 G Y V A T R W Y R A P E I M L N W M H Y	
		541 GGCTACGTGGCCACTAGGTGGTACAGGGCTCCTGAGATCATGCTGAACTGGATGCATTAC	
		201 N Q T V D I W S V G C I M A E L L T G R	
		601 AACCAGACAGTTGATATTTGGTCAGTGGGATGCATAATGGCCGAGCTGTTGACTGGAAGA	
		221 T L F P G T D H I N Q L Q Q I M R L T G	
		661 ACATTGTTTCCTGGTACAGACCATATTAACCAGCTTCAGCAGATTATGCGTCTGACAGGA	
		241 T P P A Y L I N R M P S H E A R N Y I Q	
		721 ACACCCCCCGCTTATCTCATTAACAGGATGCCAAGCCATGAGGCAAGAAACTATATTCAG	
		261 S L T Q M P K M N F A N V F I G A N P L	
		781 TCTTTGACTCAGATGCCGAAGATGAACTTTGCGAATGTATTTATTGGTGCCAATCCCCTG	
		281 A V D L L E K M L V L D S D K R I T A A	
		841 GCTGTCGACTTGCTGGAGAAGATGCTTGTATTGGACTCAGATAAGAGAATTACAGCGGCC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		301 Q A L A H A Y F A Q Y H D P D D E P V A 901 CAAGCCCTTGCACATGCCTACTTTGCTCAGTACCACGATCCTGATGATGAACCAGTGGCC 321 D P Y D Q S F E S R D D L L I D E W K S L 961 GATCCTTATGATCAGTCCTTTGAAAGCAGGGACCTCCTTATAGATGAGTGGAAAAGCCTG 341 T Y D E V I S F V P P P L D D Q E E M E S 1021 ACCTATGATGAAGTCATCAGCTTTGTGCCACCACCCCTTGACCAAGAAGAGATGGAGTCC 361 - 1081 TGA	
WBC020H11.bFSP_20011110.abd	Homo sapiens nuclear factor (erythroid-derived 2)-like 2, mRNA	1 GCAGCCGCCACCGCCGCCGCCGCCGCCACCAGAGCCGCCCTGTCCGCGCCGCCGCCTCGGC 61 AGCCGGAACAGGGCCGCCGTCGGGGAGCCCCAGAGCACGGTCCCCACCTCAGTATGATGG 121 ACTTGGAGGTGCCGCCGCCCGCACAGCCGTCCCAGCAGGACATGGATTTGATTGACATAC 181 TATGGAGGCAAGATATAGATCTTGGTGTAAGTCGAGAAGTATTTGACTTCACTCAACGAC 241 TACAGCATGAGCTGGAAAAACAGAAAAACACTTGAAAGACAAGAAAGACAAGAACAACTCC 301 AAAAGGAGCAAGAGAAAGCCTTTTTCGCTCAGTTGCAACTAGATGAAGAGACAGGTGAAT 361 TCCTCCCGATTCAGCCAGCCCAACATCTCATCAGAAACCAGTGGGTCTGCCAACTTCT 421 CCCAGGTTTCCCACATTCCCAAACCAGATGCTCTGAACTTCGATGACTGCATGCAGCTTT 481 TGGCAGAGACATTCCCGTTTGTAGATGACAATGAGGTTTCTCCAGCTACGTTTCAATCAC 541 TTGTTCCTGATAGTCCCAGCAACATCGAGAGCCCAGACTTCATTGCTCCTAACCAGGCCC 601 AGTCACCTGAAACTCTTGTCCTTCAGCCAGCCGTTGCTGATTCAGACAATATGCAGCAGG 661 ACCTTGAGCAAGTTTGGGAGGAGCTATTATCCATTCCAGAATTACAGTGTCTTAACATTC 721 AAAACGACAAGCTGGTTGAGACTAGCACGGTTCCAAGTTCAGAAACCAAGTGACAGAAA 781 TTGACAACAATTACCATTTCTACTCATCGATCCCCCTCACTGGAAAAAGAAGTAGGTAACT 841 GCAGTCCACAGCTTCTCAATGCTTTTGACGATTCCTTCAGCAGCATCCTCTCCACAGAAG 901 ACACCACCCAGTTGACAATGAACTCATTAAATTCAGATGCCACAGTCAACACAGATTTTG 961 GTGATGAATTTTATTCTGCTTTCATAGCTGAGCCCAGTATCAGCAACAGCATGCCCTCAC 1021 CTGCTACTTTAAGCCATTCACTCTCTGAACTTCTTAAATGGGCCCATTGATGTTTCTGATC 1081 TATCACTTTGCAAAGCTTTCAACCAAAACCACCCTGAAAGCACAGCAGAATTCAATGATT 1141 CTGACTCCGGCATTTCACTAAACACAAGTCCCAGTGTGGCATCACCAGAACACTCAGTGG 1201 AATCTTCCAGCTATGGAGACACACTACTTGGCCTCAGTGATTCTGAAGTGGAAGAGCTAG 1261 ATAGTGCCCCTGGAAGTGTCAAACAGAATGGTCCTAAAACACCAGTACATTCTTCTGGGG 1321 ATATGGTACAACCCTTGTCACCATCTCAGGGCAGAGCACTCACGTGCATGATGCCCAAT 1381 GTGAGAACACACCAGAGAAAGAATTGCCTGTAAGTCCTGGTCATCGGAAAACCCCATTCA 1441 CAAAAGACAAACATTCAAGCCGCTTGGAGGCTCATCTCACAAGAGATGAACTTAGGGCAA 1501 AAGCTCTCCATATCCCATTCCCTGTAGAAAAAATCATTAACCTCCCTGTTGTGACTTCA 1561 ACGAAATGATGTCCAAAGAGCAGTTCAATGAAGCTCAACTTGCATTAATTCGGGATATAC 1621 GTAGGAGGGGTAAGAATAAAGTGGCTGCTCAGAATTGCAGAAAAGAAAACTGGAAAATA 1681 TAGTAGAACTAGAGCCAAGATTTAGATCATTTGAAAGATGAAAAAGAAAAATTGCTCAAAG	SEQ ID NO:90

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1741 AAAAAGGAGAAAATGACAAAAGCCTTCACCTATTGAAAAACGACTCAGCACCTTGTATC 1801 TCGAAGTCTTCAGCATGCTACGTGACGAAGATGGAAGACCTTACTCCCCCAGCGAATACT 1861 CCCTGCAGCAGACGAGACGGCAGCGTGTTCCTTGTTCCCAAAAGTAAGAAGCCAGATG 1921 TTAAGAAAAACTAGATTTAGGAGGATTTGACCTTTCTGAGCTAGTTTTTTTGTACTGTT 1981 ATACTAAAAGCTCCTACTGTGATGTGAAATGCAGAAATATACTTTATAAGTAATTCTATG 2041 CAAATTTATAGTCAAAACTAGTGTAGAAAATATAAAACTTTAAAAAGCATTGGAGTGTCA 2101 GTATGCTGAATCAGTAGTTTCACTTTAACTGCAAACTTAATTTCTTAGAACACCATTTGG 2161 GCTAGTTTCTGTGTAAGTGTAAATACTACAAAAACTTTATTTATACTGTTCTTATCTCAT 2221 TTGTTACGTTCCTAGATTTATATGATACATCTGGCTAAAAAGCAAATTGTTGCAAAACTA 2281 ACCACTATGTACTTTTTTATAAATACTGTATGGACAAAAAATGGCATTTTTTATATTAAA 2341 TTGTTTAGCTCTGGCAAAAAAAAAAAATTTTAAGAGCTGGTACTAATAAAGGATTATTAT 2401 GACTGTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA SEQ ID NO:91 1 M M D L E V P P P A Q P S Q Q D M D L I 1 ATGATGGACTTGGAGGTGCCGCCGCCCGCACAGCCGTCCCAGCAGGACATGGATTTGATT 21 D I L W R Q D I D L G V S R E E V F D F T 61 GACATACTATGGAGGCAAGATATAGATCTTGGTGTAAGTCGAGAAGTATTTGACTTCACT 41 Q R L Q H E L E K Q K T L E R Q E R Q E 121 CAACGACTACAGCATGAGCTGGAAAAACAGAAAACACTTGAAAGACAAGAAAGACAAGAA 61 Q L Q K E Q E K A F F A Q L Q L D E E T 181 CAACTCCAAAAGGAGCAAGAGAAAGCCTTTTTCGCTCAGTTGCAACTAGATGAAGAGACA 81 G E F L P I Q P P A Q H I S S E T S G S A 241 GGTGAATTCCTCCCGATTCAGCCAGCCCAACACATCTCATCAGAAACCAGTGGGTCTGCC 101 N F S Q V S H I P K P D D A L N F D D C M 301 AACTTCTCCCAGGTTTCCCACATTCCCAAACCAGATGCTCTGAACTTCGATGACTGCATG 121 Q L L A E T F P F V D D N E V S P A T F 361 CAGCTTTTGGCAGAGACATTCCCGTTTGTAGATGACAATGAGGTTTCTCCAGCTACGTTT 141 Q S L V P D S P S N I E S P D D F I A P N 421 CAATCACTTGTTCCTGATAGTCCCAGCAACATCGAGAGCCCAGACTTCATTGCTCCTAAC 161 Q A Q S P E T L V L Q P A V A D S D N M 481 CAGGCCCAGTCACCTGAAACTCTTGTCCTTCAGCCAGCCGTTGCTGATTCAGACAATATG 181 Q Q D L E Q V W E E L L S I P E L Q C L 541 CAGCAGGACCTTGAGCAAGTTTGGGAGGAGCTATTATCCATTCCAGAATTACAGTGTCTT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		201 N I Q N D K L V E T S T V P S S E T K V 601 AACATTCAAAACGACAAGCTGGTTGAGACTAGCACGGTTCCAAGTTCAGAAACCAAAGTG	
		221 T E I D N N Y H F Y S S I P S L E K E V 661 ACAGAAATTGACAACAATTACCATTTCTACTCATCGATCCCCTCACTGGAAAAGAAGTA	
		241 G N C S P Q L L N A F D D S F S S I L S 721 GGTAACTGCAGTCCACAGCTTCTCAATGCTTTTGACGATTCCTTCAGCAGCATCCTCTCC	
		261 T E D T T Q L T M N S L N S D A T V N T 781 ACAGAAGACACCACCCAGTTGACAATGAACTCATTAAATTCAGATGCCACAGTCAACACA	
		281 D F G D E F F Y S S A F I A E P S I S N S M 841 GATTTTGGTGATGAATTTTATTCTGCTTTCATAGCTGAGCCCAGTATCAGCAACAGCATG	
		301 P S P A T L S H S L S E L L N G P I D V 901 CCCTCACCTGCTACTTTAAGCCATTCACTCTCTGAACTTCTAAATGGGCCCATTGATGTT	
		321 S D L S L C K A F N Q N H P E S T T A E F 961 TCTGATCTATCACTTTGCAAAGCTTTCAACCAAAACCACCCTGAAAGCACAGCAGAATTC	
		341 N D S D S G I S L N N T S P S V A S P E H 1021 AATGATTCTGACTCCGGCATTTCACTAAACACAAGTCCCAGTGTGGCATCACCAGAACAC	
		361 S V E S S S Y G D T L L G L S D S E V E 1081 TCAGTGGAATCTTCCAGCTATGGAGACACACTACTTGGCCTCAGTGATTCTGAAGTGGAA	
		381 E L D S A P G S V K Q N G P K T P V H S 1141 GAGCTAGATAGTGCCCCTGGAAGTGTCAAACAGAATGGTCCTAAAACACCAGTACATTCT	
		401 S G D M V Q P L S P S Q G Q S T H V H D 1201 TCTGGGGATATGGTACAACCCTTGTCACCATCTCAGGGGCAGAGCACTCACGTGCATGAT	
		421 A Q C E N T P E K E L P V S P G H R K T 1261 GCCCAATGTGAGAACACACCAGAGAAAGAATTGCCTGTAAGTCCTGGTCATCGGAAAACC	
		441 P F T K D K H S S R L E A H L T R D E L 1321 CCATTCACAAAGACAAACATTCAAGCCGCTTGGAGGCTCATCTCACAAGAGATGAACTT	
		461 R A K A L H I P F P V E K I I N L P V V 1381 AGGGCAAAAGCTCTCCATATCCCATTCCCTGTAGAAAAATCATTAACCTCCCTGTTGTT	
		481 D F N E M M S K E Q F N E A Q L A L I R	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1441 GACTTCAACGAAATGATGTCCAAAGAGCAGTTCAATGAAGCTCAACTTGCATTAATTCGG 501 D I R R R G K N N K V A A Q N C R K R K L 1501 GATATACGTAGGAGGGGTAAGAATAAAGTGGCTGCTCAGAATTGCAGAAAAAGAAAACTG 521 E N I V E L E Q D L D H L K D E E K K L 1561 GAAAATATAGTAGAACTAGAGCAAGATTTAGATCATTTGAAAGATGAAAAAGAAAAATTG 541 L K E K G E N D K S L H L L K K R L S T 1621 CTCAAAGAAAAAGGAGAAAATGACAAAAGCCTTCACCTATTGAAAAAACGACTCAGCACC 561 L Y L E V F S M L R D E D G R P Y S P S 1681 TTGTATCTCGAAGTCTTCAGCATGCTACGTGACGAAGATGGAAGACCTTACTCCCCCAGC 581 E Y S L Q Q T R D G S V F L V P K S K K 1741 GAATACTCCCTGCAGCAGACGAGAGACGGCAGCGTGTTCCTTGTTCCCAAAGTAAGAAG 601 P D V K K N - 1801 CCAGATGTTAAGAAAAACTAG	
WBC021E02.bFSP_20011210.abd	No homology.	1 GGACCTTACCTTCAAGCACCAATGAGAGCTCAGAATGAGAGGAAAAAACTATGAACGGAAG 61 GAATGTTCAAGATCTTTTATTTCATTCCGCAAGCCTCGGTGCGCATGTACAAACTCACACT 121 GCTACAACCATTACAAATGTAAGGAATGCAGAAAATCCTTTAAACGATCTGCATACCTT 181 AACGCTCATGTTCGAATTCACACTGGAAGAAAACCCTTTAAATGTAAGGAATGCAGGAAA 241 GGCTTTAAACGTTCTATGCACCTTAAGGTTCACATGCGAACCCACACTGGAGAGAAATCC 301 TATGAATGTAAGGAATGTGGGAAAACCTTCACTCAATCCTCAGGCCTCATTTACCACAAT 361 AAGATTCACACTGGAGAGAAGCCTTTTAAATGTGACACATGTGGGAAAGCCTATGCTAGT 421 TTCTCAAATCTTACTGCCCATTTTAGAACTCACACTGGAGAGAAGCGTTTTGAGTGTAAT 481 GTATGCAGGAAAAGATTTAGCAGTTCCTCATACTTAGTCGTTCACAACCGCACTCACACT 541 GGAGAGAAACCCTATAAATGTGAGGAATGTGGGAAGGGCTTTAAATGTTCTGTGTCCCTT 601 AAAGTTCACATGCGGTTTCACACTGGAGAGAAACCCTATGAATGCAAGAAATGTGGGAGA 661 GCCTTCACTCAGTCCTCAAGCCTTACTGACCATAGGAAAACTCATACTGGAGAGAATCCT 721 TTTAAATGTGACGCATGTGGGAAAGCCTTTGCTCTTTCCTCACATCTTAACAGACAT 1 GCCTATTGAGTGTAATGTATGTGGGAAGACATTTAGCAGTTTTTTGTACTTGATCGTTCA 61 CAAGCGTACTCACGCTGGAGAGAAACCTTAGAAACGTAAAGAATGTAGGGAAAGCCTTCA 121 GTTTTCCCATTTCCTTTTGGTACCATGAAAGCACTTACCTGCAGAGAATCCTGTCAGTG 181 TAAGAATGTGGTAAAGCCCTCAGTTGTCCCAATTCACTTTGAAGACGTGAAAGAACCAC 241 ACTGGAGAGATGCTCTAGAAATGTAAGGAATGAGGGAAAGCCATGAGAATCTCATCACAA 301 CCTGGCATGTATGGACTAACAGTGAAAGCATACCATTAAGAAACATGGGAAGCCCCTTCAC 361 TGTTTCCTCAGTGAAATATATTATTTTTATAAATGAGACACCTTGTAATGGAGAGAAAT 421 CCAAGTGGTGTAATGTGGGAAAATTGTTCTAGTAATGTTCACTTGTTTTTTGTGTGGAGA	SEQ ID NO:92 SEQ ID NO:93

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		481 AAAACTTTATGAATGTAAGAAATGTTGTATAGTCATTATCATTTTTCGTAAGATTGTTTC 541 TCTTCCTTAATAAACGTATGGTAATTCAAATTAAAAAAAAAAAAAAAAA	
WBC021E07.bFSP_20011210.abd	Homo sapiens vav 1 oncogene, mRNA (cDNA clone MGC:15356 IMAGE:3842829)	1 gtggtgcacg cctatagtct cagctactca ggaagttgag gcaggaggat cgcttgagcc 61 caggagtttg atgctgcagt gagctatgat tgtgctacca ctgtactcca gactggacaa 121 aagattcctg tgccttaaga acattagaac cttcctgtcc acctgctgtg agaagttcgg 181 cctcaagcgg agcgagctct tcgaagcctt tgacctcttc gatgtgcagg atttggcaa 241 ggtcatctac acctgtcctg ctctgtcctg gacccgatc gcccagaaca ggggatcat 301 gccctcccc accgaggagg agagtgtagg tgatgaagac atctacagtg gcctgtccga 361 ccagatcgac gacacggtgg aggaggatga ggacctgtat gactgcgtgg agaatgagga 421 ggcggaaggc gacgagatct atgaggacct catgcgctcg gagcccgtgt ccatgccgcc 481 caagatgaca gagtatgaca agcgctgctg ctgcctgcgg gagatccagc agacggagga 541 gaagtacact gacacgctgg gctccatcca gcagcatttc ttgaagcccc tgcaacggtt 601 cctgaaacct caagacattg agatcatctt tatcaacatt gaggacctgc ttcgtgttca 661 tactcactic ctaaaggaga tgaaggaagc cctgggcacc cctggcgcag ccaatctcta 721 ccaggtcttc atcaaataca aggagaggtt cctcgtctat ggccgctact gcagccaggt 781 ggagtcagcc agcaaacacc tggaccgtgt ggccgcagcc cgggaggacg tgcagatgaa 841 gctggaggaa tgttctcaga gagccaacaa cgggaggttc accctgcggg acctgctgat 901 ggtgcctatg cagcgagttc tcaaatatca cctcctttctc caggagctgg tgaaacacac 961 gcaggaggcg atggagaagg agaacctgcg gctggccctg gatgccatga gggacctggc 1021 tcagtgcgtg aacgaggtca agcgagacaa cgagacactg cgacagatca ccaatttcca 1081 gctgtccatt gagaacctgg accagtctct ggctcactat ggccggccca agatcgacgg 1141 ggaactcaag atcacctcgg tggaacggcg ctccaagatg gacaggtatg ccttcctgct 1201 cgacaaagct ctactcatct gtaagcgcag gggagactcc tatgacctca aggactttgt 1261 aaacctgcac agcttccagg ttcgggatga ctcttcagga gaccgagaca acaagaagtg 1321 gagccacatg ttcctcctga tcgaggacca aggtgcccag ggctatgagc tgttcttcaa 1381 gacaagagaa ttgaagaaga agtggatgga gcagtttgag atggccatct ccaacatcta 1441 tcggagaatt gccaccgcca acgggcatga cttccagatg ttctcctttg aggaccac 1501 atcctgcaag gcctgtcaga tgctgcttag aggtaccttc tatcagggct accgctgcca 1561 tcggtgccgg gcatctgcac acaaggagtg tctgggggag gtccctccat gtggccgaca 1621 tggcaagat ttcccaggaa ctatgaagaa ggacaaacta catcgcaggg ctcaggacaa 1681 aaagaggaat gagctgggtc tgcccaagat ggaggtgttt caggaatact acgggcttcc 1741 tccacccct ggagccattg gacccttct acggctcaac cctggagaca ttgtggagct 1801 cacgaaggct gaggctgaac agaactggtg ggagggcaga aatacatcta ctaatgaaat 1861 tggctggttt ccttgtaaca gggtgaagcc ctatgtccat ggccctcctc aggacctgtc 1921 tgttcatctc tggtacgcag gcccatggga gcgggcaggg gcagagagca tcctggccaa 1981 ccgctcggac gggactttct tggtgcggca gaggtgaag gatgcagcag aatttgccat 2041 cagcattaaa tataacgtcg aggtcaagca cattaaaatc atgacagcag aaggactgta 2101 ccggatcaca gagaaaagg ctttccgggg gcttacggag ctggtggagt tttaccagca 2161 gaactctcta aaggattgct tcaagtctct ggacaccacc ttgcagttcc ccttcaagga 2221 gcctgaaaag agaaccatca gcaggccagc agtgggaagc acaaagtatt ttggcacagc 2281 caaagcccgc tatgacttct gcgcccgaga ccgatcagag ctgtcgctca aggagggtga	SEQ ID NO:94

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2341 catcatcaag atcctaaca agaagggaca gcaaggctgg tggcgagggg agatctatgg 2401 ccggttggc tggttccctg ccaactacgt ggaggaagat tatcctgaat actgctgagc 2461 cctggtgcct tggcagagag acgagaaact ccaggctctg agcccggcgt gggcaggcag 2521 cggagccagg ggctgtgaca gctcccggcg ggtggagact ttgggatgga ctggaggagg 2581 ccagcgtcca gctggcggtg ctcccgggat gtgccctgac atggttaatt tataacaccc 2641 cgatttcctc ttgggtcccc tcaagcagac ggggctcaag ggggttacat ttaataaaag 2701 gatgaagatg gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2761 aaaaaaaaaa aaaaaa	
		1 M I V L P L Y S R L D K R F L C L K N I 1 ATGATTGTGCTACCACTGTACTCCAGACTGGACAAAAGATTCCTGTGCCTTAAGAACATT	SEQ ID NO:95
		21 R T F L S T C C E K F G L K R S E L F E 61 AGAACCTTCCTGTCCACCTGCTGTGAGAAGTTCGGCCTCAAGCGGAGCGAGCTCTTCGAA	
		41 A F D L F D V Q D F G K V I Y T L S A L 121 GCCTTTGACCTCTTCGATGTGCAGGATTTTGGCAAGGTCATCTACACCCTGTCTGCTCTG	
		61 S W T P I A Q N R G I M P F P T E E E S 181 TCCTGGACCCCGATCGCCCAGAACAGGGGGATCATGCCCTTCCCCACCGAGGAGGAGAGT	
		81 V G D E D I Y S G L S D Q I D D T V E E 241 GTAGGTGATGAAGACATCTACAGTGGCCTGTCCGACCAGATCGACGACACGGTGGAGGAG	
		101 D E D L Y D C V E N E E A E G D E I Y E 301 GATGAGGACCTGTATGACTGCGTGGAGAATGAGGAGGCGGAAGGCGACGAGATCTATGAG	
		121 D L M R S E P V S M P P K M T E Y D K R 361 GACCTCATGCGCTCGGAGCCCGTGTCCATGCCGCCCCAAGATGACACAGAGTATGACAAGCGC	
		141 C C C L R E I Q Q T E E K Y T D T L G S 421 TGCTGCTGCCTGCGGGAGATCCAGCAGACGGAGGAGAAGTACACTGACACGCTGGGCTCC	
		161 I Q Q H F L K P L Q R F L K P Q D I E I 481 ATCCAGCAGCATTTCTTGAAGCCCCTGCAACGGTTCCTGAAACCTCAAGACATTGAGATC	
		181 I F I N I E D L L R V H T H F L K E M K 541 ATCTTTATCAACATTGAGGACCTGCTTCGTGTTCATACTCACTTCCTAAGGAGATGAAG	
		201 E A L G T P G A A N L Y Q V F I K Y K E 601 GAAGCCCTGGGCACCCCTGGCGCAGCCAATCTCTACCAGGTCTTCATCAAATACAAGGAG	
		221 R F L V Y G R Y C S Q V E S A S K H L D	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		661 AGGTTCCTCGTCTATGGCCGCTACTGCAGCCAGGTGGAGTCAGCCAGCAAACACCTGGAC	
		241 R V A A A R E D V Q M K L E E C S Q R A 721 CGTGTGGCCGCAGCCCGGAGGACGTGCAGATGAAGCTGGAGGAATGTTCTCAGAGAGCC	
		261 N N G R F T L R D L L M V P M Q R V L K 781 AACAACGGAGGTTCACCCTGCGGACCTGCTGATGGTGCCTATGCAGCGAGTTCTCAAA	
		281 Y H L L L Q E L V K H T Q E A M E K E N 841 TATCACCTCCTTCTCCAGGAGCTGGTGAAACACACGCAGGAGGCGATGGAGAAGGAGAAC	
		301 L R L A L D A M R D L A Q C V N E V K R 901 CTGCGGCTGGCCCTGGATGCCATGAGGGACCTGGCTCAGTGCGTGAACGAGGTCAAGCGA	
		321 D N E T L R Q I T N F Q L S I E N L D Q 961 GACAACGAGACACTGCGACAGATCACCAATTTCCAGCTGTCCATTGAGAACCTGGACCAG	
		341 S L A H Y G R P K I D G E L K I T S V E 1021 TCTCTGGCTCACTATGGCCGCCCAAGATCGACGGGGAACTCAAGATCACCTCGGTGGAA	
		361 R R S K M D R Y A F L L D K A L L I C K 1081 CGGCGCTCCAAGATGGACAGGTATGCCTTCCTGCTCGACAAAGCTCTACTCATCTGTAAG	
		381 R R G D S Y D L K D F V N L H S F Q V R 1141 CGCAGGGGAGACTCCTATGACCTCAAGGACTTTGTAAACCTGCACAGCTTCCAGGTTCGG	
		401 D D S S G D D R D N K K W S H M F L L I E 1201 GATGACTCTTCAGGAGACCGAGACAACAAGAAGTGGAGCCACATGTTCCTCCTGATCGAG	
		421 D Q G A Q G Y E L F F K T T R E L K K K W 1261 GACCAAGGTGCCCAGGGCTATGAGCTGTTCTTCAAGACAAGAGAATTGAAGAAGAAGTGG	
		441 M E Q F E M A I S N I Y P E N A T A N G 1321 ATGGAGCAGTTTGAGATGGCCATCTCCAACATCTATCCGGAGAATGCCACCGCCAACGGG	
		461 H D F Q M F S F E E T T S C K A C Q M L 1381 CATGACTTCCAGATGTTCTCCTTTGAGGAGACCACATCCTGCAAGGCCTGTCAGATGCTG	
		481 L R G T F Y Q G Y R C H R C R A S A H K 1441 CTTAGAGGTACCTTCTATCAGGGCTACCGCTGCCATCGGTGCCGGCATCTGCACACAAG	
		501 E C L G R V P P C G R H G Q D F P G T M 1501 GAGTGTCTGGGGAGGGTCCCTCCATGTGGCCGACATGGGCAAGATTTCCCAGGAACTATG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		521 K K D K L H R R A Q D K K R N E L G L P 1561 AAGAAGGACAAACTACATCGCAGGCTCAGGACAAAAAGAGGAATGAGCTGGGTCTGCCC	
		541 K M E V F Q E Y Y G L P P P P G A I G P 1621 AAGATGGAGGTGTTTCAGGAATACTACGGGCTTCCTCCACCCCCTGGAGCCATTGGACCC	
		561 F L R L N P G D I V E L T K A E A E Q N 1681 TTTCTACGGCTCAACCCTGGAGACATTGTGGAGCTCACGAAGGCTGAGGCTGAACAGAAC	
		581 W W E G R N T S T N E I G W F P C N R V 1741 TGGTGGGAGGGCAGAAATACATCTACTAATGAAATTGGCTGGTTTCCTTGTAACAGGGTG	
		601 K P Y V H G P P Q D L S V H L W Y A G P 1801 AAGCCCTATGTCCATGGCCCTCCTCAGGACCTGTCTGTTCATCTCTGGTACGCAGGCCCC	
		621 M E R A G A E S I L L A N R S D G T F L V 1861 ATGGAGCGGGCAGGGGCAGAGCATCCTGGCCAACCGCTCGGACGGGACTTTCTTGGTG	
		641 R Q R V K D A A E F A I S I K Y N V E V 1921 CGGCAGAGGGTGAAGGATGCAGCAGAATTTGCCATCAGCATTAAATATAACGTCGAGGTC	
		661 K H I K I M T A E G L Y R I T E K K A F 1981 AAGCACATTAAAATCATGACAGCAGAAGGACTGTACCGGATCACACAGAGAAAAAGGCTTTC	
		681 R G L T E L V E F Y Q Q N S L K D C F K 2041 CGGGGCTTACGGAGCTGGTGGAGTTTTACCAGCAGAACTCTCTAAGGATTGCTTCAAG	
		701 S L D T T L Q F P F K E P E K R T I S R 2101 TCTCTGGACACCACCTTGCAGTTCCCCTTCAAGGAGCCTGAAAAGAGAACCATCAGCAGG	
		721 P A V G S T K Y F G T A K A R Y D F C A 2161 CCAGCAGTGGGAAGCACAAAGTATTTTGGCACAGCCAAAGCCCGCTATGACTTCTGCGCC	
		741 R D R S E L S L K E G D I I K I L N K K 2221 CGAGACCGATCAGAGCTGTCGCTCAAGGAGGGTGACATCATCAAGATCCTTAACAAGAAG	
		761 G Q Q G W W R G E I Y G R V G W F P A N 2281 GGACAGCAAGGCTGGTGGCGAGGGGAGATCTATGGCCGGGTTGGCTGGTTCCCTGCCAAC	
		781 Y V E E D Y S E Y C - 2341 TACGTGGAGGAAGATTATTCTGAATACTGCTGA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
WBC022B03.bFSP_20011210.abd	Homo sapiens T-cell receptor interacting molecule, mRNA (cDNA clone MGC:34314 IMAGE:5227396).	1 GATAAAGATAAGTTTTACTGTCATGCTGCTTTTAACATAACAGAGCAACATCACCTAGGA 61 AAAAAGTTTGTAGGAGGATTTTTAATCCATACACTTGCCTTATGATTACATTAAGATTTC 121 TTTGAGAAAAGAAGCATGTCAGGAAGCTCTGGATGCCCTTTTTCTGTCTGGGCAATTCTG 181 GCCTTCTTGGGTTTAGCTCTTGTTGTATCGCTGATCTTCAATATTTCCTGCTATGTGGAA 241 AAGCAGCGACAAGGTATAACATACAGGTTCTCTGATGACTACATTTCCCGGGAGGATGAG 301 TATTACATTGAAGACACACCCATTTATGGTAACTTAGATAATGTGATCCCAGAACCAATG 361 GATGAAAACTGCTATGAGCAAATGAAAGCCCGACCAGAGAGATCTGTGAATCAACTGCGA 421 GCAGCTCCCACACCTGCACAGGCAACCAATGAAGCACAGATGTTCTACTCCTCCCTGGAG 481 CACAGCCTTGAGGGGAAGCGCAGAAAGCCCAGGAAACACGATCCTTATTTGCCAGACAAG 541 GTTGAAGATGAGCAGTTACACGCGACGGATGCCAGCCTTTCTATGACTGCTTTGGTTGAT 601 AGTTTTGCACCTGAGGACCAGGAAGAAGAGGAAAACATCCATGATGATCCCATCAGGCTG 661 TTCGGATTGATTCGTGCGAAGAAAGAACCTATGAACTAGCTGGACTCTGATCTAGCTCAA 721 TGATTCAGCTCTTATTGGAGATGGCTTCTAAGAAAACAAGATGCACAGAGGACACAGAAG 781 GACTTGGCAGCAGGGTGATGACCTGATCATTTGTTGATGGGATGGTGGCTTACCTCTTAT 841 TCACAGCTTACACTTATGCATGCCAAATGTAAGGCCATGAAAATCAGTATTTCAAATAAC 901 TTAAAAAATGCTTTACTACTAAAATGTAAAAAATTAATGTGCTCACCTCGGCAGCACATA 961 TACTAAAAATTAATAAGACCCAGCTTGAAAATTGAGCCTGATAACAAGATTACAAATTCA 1021 CAATACCTAATACTTAGGGAAATATAAAAATTTAAGCATGAATGTGTTCTGGAACACGTT 1081 AGAAGAAAAATAAAAGCCAATGAGTTTTTTTTTAATTCTCCTTTCTCACCAATGGGCAAT 1141 AGCCCATAATTGAAATAAATTTCTGATTGAAAGGTATAGGAAACATTAAAATGCATTACT 1201 AAGAGAAGTAATATAATTTTCTTACAAAGTATTTTTCCCAAAGATAGCTTTACTATTTCA 1261 AAAATTGTCAAATTAATGCATGCTCCTTACAACAAACAAATATCAAAAAGAGTTTAGGAA 1321 TTCTACTAGCCAGAGATAGTCACTTGGAGAAACTTTCTATATATCCTTCTAAATATTTTT 1381 CTGGGCATGCTTATGTATGTACATCAGTTGTTTCTTTTTATTTTGAACCAAAAATGTGGT 1441 TTCTTTTGTACACATTACTTAAACTTTCTTTCCAGTCAACAATATATTGTGGATTTATTT 1501 TCACTGTTATATTTAACTATATATAAATACGCATATATTGTAATTTTAATGTCTGCTTAG 1561 CACCCCACTGATAACCAAATCACAGTTTATTTAAATAATTTTAATGACTTTTCAAAAACA 1621 ATTTATTGATGCAAAAAGCAAGGTTGAGATGACAATGTTTCTTTCAATAATTAAAAAATA 1681 CTGCTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1 M S G S S G C P F S V W A I L A F L G L 1 ATGTCAGGAAGCTCTGGATGCCCTTTTTCTGTCTGGGCAATTCTGGCCTTCTTGGGTTTA 21 A L V V S L I F N I S C Y V E K Q R Q G 61 GCTCTTGTTGTATCGCTGATCTTCAATATTTCCTGCTATGTGGAAAAGCAGCGACAAGGT 41 I T Y R F S D D Y I S R E D E Y Y I E D 121 ATAACATACAGGTTCTCTGATGACTACATTTCCCGGGAGGATGAGTATTACATTGAAGAC 61 T P I Y G N L D N V I P E P M D E N C Y 181 ACACCCATTTATGGTAACTTAGATAATGTGATCCCAGAACCAATGGATGAAAACTGCTAT	SEQ ID NO:96 SEQ ID NO:97

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		81 E Q M K A R P E R S V N Q L R A A P T P 241 GAGCAAATGAAAGCCCGACCAGAGAGATCTGTGAATCAACTGCGAGCAGCTCCCACACCT 101 A Q A T N E E A Q M F Y S S L E H S L E G 301 GCACAGGCAACCAATGAAGCACAGATGTTCTACTCCTCCCTGGAGCACAGCCTTGAGGGG 121 K R R K P R K H D P Y L P D K V E D E Q 361 AAGCGCAGAAAGCCCAGGAAACACGATCCTTATTTGCCAGACAAGGTTGAAGATGAGCAG 141 L H A T D A S L S M T A L V D S F A P E 421 TTACACGCGACGGATGCCAGCCTTTCTATGACTGCTTTGGTTGATAGTTTTGCACCTGAG 161 D Q E E E E N I H D D P I R L F G L I R 481 GACCAGGAAGAGAGGAAAACATCCATGATGATCCCATCAGGCTGTTCGGATTGATTCGT 181 A K K E P M N - 541 GCGAAGAAAGAACCTATGAACTAG	
WBC022C04.bFSP_20011210.abd	PREDICTED: Bos taurus similar to Caspase recruitment domain protein 8 (Apoptotic protein NDPP1) (DACAR) (CARD-inhibitor of NF-kappaB activating ligand) (CARDINAL) (Tumor-upregulated CARD-containing antagonist of CASP9) (TUCAN) (LOC511229), partial mRNA	< 1 gtgaggacag cagctttgag agcggttctg aagctgaatc tgcccatgtc actgatattg 61 ctcgaggaca tagtaattac aagtgtcctt ttggtgaagt accgaagagt acttatatgg 121 atagcggctg tggaataagg ttgaaagatt ttctggtgca ggacttggat cggtgtttca 181 gaaccttcag atctatgggg tccccaaccc ctgggccact gtctggtacc attaggagcc 241 gggccacaca gcaggagctg agcggtgagc tagcgagcaa agcctcatct gtatttacag 301 ccacttcccg ttgcttgcgt taccgcctga gtgccacctc ctgtcagagc agcggtggga 361 caagattgtc atgggaatac agaccctact gtgaactgcc catggaacta ggttgcccac 421 tcgggaaaca caatgaactg gtgaccccca ggcttctttc cgaggacag ttttgctga 481 aggtggatgg agagggaact taccagtgca cggagactgg tctgatattt gaggttaacg 541 ggaaagttga tatcaagtat tgcgtcttgt cctggagcaa atattcagac ctcattgtga 601 agccctgggc cgtcggtgga ccctgtttg atgttaaatg tgacccgctc tgtcttacct 661 ccattcagtt tccacattcc ctctgcttgg gtcaccgaga tgccaacatg acgttcaaag 721 tcttccatgt taaaagtact gggcctcat tagaatatac tgtggaccat tctgcaaccc 781 acgtcaaatg gcgtgtgagc tctctttctc ctgtgggacc cgttgttcaa agcgaagaga 841 cggtattcca ccacgggcca gtgattctgt acaaagccat cgaccataac ccgtccttgt 901 cttttcgagt gtatgtagca accaataatg aatccttcat caaggatatt tccaagtctg 961 taaagcactc ctctaagaaa ttcatgaaaa tcgacaagcc tccggtttgc cagaagttgc 1021 tgcagaatgg gaagaagtac aggctgatca gtgagccaga agctgagatc accccagagg 1081 aaattgaatt tgtggatggt tcacttttaa aattgaaaag ttatattgaa gtgtatctgg 1141 agcaaccagt ggagtttaaa ttacttcttgg ttgaaatgga ttctgaggaa attgtatgga 1201 aagcaaaact gagagagtgt gactgggttc agcatcatca gaaccagaac atttcaaaaa 1261 gcagcacaag tggtaacagg cgacgaaaaa tgagtagcag cttacctgat gagatggtct 1321 atgataaaag aatgaagcag attgacagtt caggtttgta aacatgtcct ctgtggctct	SEQ ID NO:98

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1 E D S S F E S G S E E A E S A H V T D I A	SEQ ID NO:99
		3 GAGGACAGCAGCTTTGAGAGCGGTTCTGAAGCTGAATCTGCCCATGTCACTGATATTGCT	
		21 R G H S N Y K C P F G E V P K S T Y M D	
		63 CGAGGACATAGTAATTACAAGTGTCCTTTTGGTGAAGTACCGAAGAGTACTTATATGGAT	
		41 S G C G I R L K D F L V Q D L D R C F R	
		123 AGCGGCTGTGGAATAAGGTTGAAAGATTTTCTGGTGCAGGACTTGGATCGGTGTTTCAGA	
		61 T F R S M G S P T P G P L S G T I R S R	
		183 ACCTTCAGATCTATGGGGTCCCCAACCCCTGGGCCACTGTCTGGTACCATTAGGAGCCGG	
		81 A T Q Q E V S G E L A S K A S S V F T A	
		243 GCCACACAGCAGGAGGTGAGCGGTGAGCTAGCGAGCAAAGCCTCATCTGTATTTACAGCC	
		101 T S R C L R Y R L S A T S C Q S S G G T	
		303 ACTTCCCGTTGCTTGCGTTACCGCCTGAGTGCCACCTCCTGTCAGAGCAGCGGTGGGACA	
		121 R L S W E Y R P Y C E L P M E L G C P L	
		363 AGATTGTCATGGGAATACAGACCCTACTGTGAACTGCCCATGGAACTAGGTTGCCCACTC	
		141 G K H N E L V T P R L L S R G Q F L L L K	
		423 GGGAAACACAATGAACTGGTGACCCCCAGGCTTCTTTCCCGAGGACAGTTTTTGCTGAAG	
		161 V D G E G T Y Q C T E T G L I F E V N G	
		483 GTGGATGGAGAGGGAACTTACCAGTGCACGGAGACTGGTCTGATATTTGAGGTTAACGGG	
		181 K V D I K Y C V L S W S K Y S D L I V K	
		543 AAAGTTGATATCAAGTATTGCGTCTTGTCCTGGAGCAAATATTCAGACCTCATTGTGAAG	
		201 P W A V G G P L F D V K C D P L C L T S	
		603 CCCTGGGCCGTCGGTGGACCCTTGTTTGATGTTAAATGTGACCCGCTCTGTCTTACCTCC	
		221 I Q F P H S L C L G H R D A N M T F K V	
		663 ATTCAGTTTCCACATTCCCTCTGCTTGGGTCACCGAGATGCCAACATGACGTTCAAAGTC	
		241 F H V K S T G A S L E Y T V D H S A T H	
		723 TTCCATGTTAAAGTACTGGGGCCTCATTAGAATATACTGTGGACCATTCTGCAACCCAC	
		261 V K W R V S S L S P V G P V V Q S E E T	
		783 GTCAAATGGCGTGTGAGCTCTCTTTCTCCTGTGGGACCCGTTGTTCAAAGCGAAGAGACG	
		281 V F H H G A V I L Y K A I D H N P S L S	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		843 GTATTCCACCACGGGGCAGTGATTCTGTACAAAGCCATCGACCATAACCCGTCCTTGTCT 301 F R V Y V A T N N E S F I K D I S K S V 903 TTTCGAGTGTATGTAGCAACCAATAATGAATCCTTCATCAAGGATATTTCCAAGTCTGTA 321 K H S S K K F M K I D K P P V C Q K L L 963 AAGCACTCCTCTAAGAAATTCATGAAAATCGACAAGCCTCCGGTTTGCCAGAAGTTGCTG 341 Q N G K K Y R L I S E P E A E I T P E E 1023 CAGAATGGGAAGAAGTACAGGCTGATCAGTGAGCCAGAAGCTGAGATCACCCCAGAGGAA 361 I E F V D G S L L K L K S Y I E V Y L E 1083 ATTGAATTTGTGGATGGTTCACTTTTAAAATTGAAAAGTTATATTGAAGTGTATCTGGAG 381 Q P V E F K L L L V E M D S E E I V W K 1143 CAACCAGTGGAGTTTAAATTACTCTTGGTTGAAATGGATTCTGAGGAAATTGTATGGAAA 401 A K L R E C D W V Q H H Q N Q N I S K S 1203 GCAAAACTGAGAGAGTGTGACTGGGTTCAGCATCATCAGAACCAGAACATTTCAAAAAGC 421 S T S G N R R R K M S S S L P D E M V Y 1263 AGCACAAGTGGTAACAGGCGACGAAAAATGAGTAGCAGCTTACCTGATGAGATGGTCTAT 441 D K R M K Q I D S S G L - 1323 GATAAAAGAATGAAGCAGATTGACAGTTCAGGTTTGTAA	
WBC022D03.bFSP_20011210.abd	No homology	1 GCTGCGAAGCTCCTTTACATTGGGTCTGTAAGAAGGTCAGACTTTGACAGATGGTCAGAT 61 CTGTCATATGACTCCCTTAAAAGGGGGAGCTGGCCTCTGGGTGTTGGGATAGCCATGAGT 121 ATATATATATATATATATAGTGAATGCTGAACCTTTGAGGATATGGCATTAGATGCAAGA 181 TTAAATGCAGCTTCCCCAGGGTTGATGGTTTATTGGTGGACTTTGAGAGTATTTAGATAT 241 TATCTTAACAATTTAAAAACCAGATCTAGGCAAATTTGTGAAATAGATAAAGTTTTTTTT 301 AGTATTTTTCACTCTAGTGACTAATGCTGCTTCCTTCATCCTCACCCCCACCATCTCAGT 361 CAAAAATATACCTTTTATATGCTATATTCTGAGCTGATCTAATGAAATCTGTGCAAATAT 421 ATACTATTGCTAATGTAGCAGAGGGTTTTTATGTGCATTAATGGGTTGACATGTTACTTT 481 TCTCTGATAATATATTTTTATCCTAACAGTGGCCCTTTGCAGATAAAGCATTATTCTAAA 541 GAATAATGCTAATGGTGAGAAAATAAATTATGAAAGTAGATGAGAGCAGGGTGATGCTGT 601 CTGGTCTTCAGCTCTTCACACTTACTTAAGACCTGGCCTTGACTGAATTTAGTTTTTCTG 661 AATATGCGTAGATGTGGTTGAATGAAACAATGTGTGACTATATTTTTTCCATGTTGTGAA 721 CATGTGATTTGCATGTTGATTTTACAACAGTGGTCTCTTTGACAAGGCATTTTTGTAGAG 781 GAAAATTTACGGAAGCAGTTTATGTGGTTCATTCTCAAATTATTTTAGGCACTAATGCCC 841 TCAAAAATGAGAAAAACTTATTAATTTTTCTTTA	SEQ ID NO:100

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1 GGGTTTTTATGTGCATTAATGGGTTGACATGTTACTTTTCTCTGATAATATTTTTATC 61 CTAACAGTGGCCCTTTGCAGATAAAGCATTATTCTAAAGAATAATGCTAATGGTGAGAAA 121 ATAAATTATGAAAGTAGATGAGAGCAGGGTGATGCTGTCTGGTCTTCAGCTCTTCACACT 181 TACTTAAGACCTGGCCTTGACTGAATTTAGTTTTTCTCTGAATATGCGTAGATGTGGTTGAA 241 TGAAACAATGTGTGACTATATTTTTTCCATGTTGTGAACATGTGATTTGCATGTTGATTT 301 TACAACAGTGGTCTCTTTGACAAGGCATTTTTGTAGAGGAAAATTTACGGAAGCAGTTTA 361 TGTGGTTGATTCTCAAATTATTTTAGGCACTAATGCCTCAAAAATGAGAAAAACTTATTA 421 TTTTTCTTTAGTAGGATTTGGACATAGATAAGGAGAGGGAAGATGTTGTTTAACATATTGG 481 AGGGAGTAATGAAAGGGACGATACTTCTTACTGTTGTTGACGCTGGATTGTAGTCTGTTT 541 ACTTGTCTTTCTCTTTCGTAGTTTTTAAGGACGTGGACTGTATCTTATCCACCATTGTAT 601 CTCAGACACCTAAAATAGTGTTTGTATCAATGAATATTAAATAAATGAATGGATTAATAA 661 AAAAAAAAGGGGGGGCCCGTACCCAT	SEQ ID NO:101
WBC023F12.bFSP_20011510.abd	No signficant homology	1 GTTAAACATTATTTCCTTAAAAAAATTATTTTTACATGAAACAAATATATTTGGAGT 61 GTACTTCCATCAAAAATTTCACTTCTATATCTGAGGTCTACTTATTTCAAAGTAAAAATT 121 TTCACTTGTCAGCTGAAATTTCTGATTAGAACTAATATTTGTGTATTTTTGTGCTTAGTC 181 AGAATGTAAATTTCACAGTGGATTTAAATTTATCCTTAATTTGGATAAAAGCAAGGGATA 241 TATTTAAAAGTTATTATAGGGATGAAAGTGGAAATTCTGTTTTTGGTTTTTTTTAACT 301 ACTAATGAGATCACGTTTGTAGTTCTTTTTACATGTGTTTAGCACAGGCTCTAAATTAAA 361 AAATACAGTATAGTCTGTGTTTGACCTTAAAAATATTCCATAAATTAATAAATATATGGCA 421 AGTTTTTCATAGCTAAATCTAACTCTTGTAGAAGGAAGCTGTGCCTTCTGTTTAATTACA 481 TTAATTGAAATGTGTTTAAGAGAAATGTTTTTCAGCATATTTTGTATACTAAAAAACAAAA 541 AGGATTAGTATTGGGCCAATGGCCAAGAGGTAATATTACTACCATGTAGACTGTTACAGT 601 TCAAATTGTCCCACTTCCCCCAGAGTTTTAGAAGCTAGAAGTCTGGGAGATACTGTATCA 661 GCTGTAGTTGGGTGATTCTAAGTGCTATAAGTACTATTCATCTTTTAATTGTGTGAGATG 721 GAACAAATGCCAGTTGCACACAAGATGCATACTTTGAATATGTAATGGTTTGTTTCAGGTG 781 AAAAATACCAGCAAGTCATGTCTTGTGTATTTTACTTATATATTTCCTTGTAAAACTAAATT 841 AAGTAAGATTTTGGAAAATGATTTGAATTGATTGCTGACTTGACCTGCCTGGTCAAATAT 901 CTGAATGATGGCCTTACTGGGTAAAT	SEQ ID NO:102
		1 AATATTACTACCATGTAGACTGTTACAGTTCAAATTGTCCCACTTCCCCCAGAGTTTTAG 61 AAGCTAGAAGTCTGGGAGATACTGTATCAGCTGTAGTTGGGTGATTCTAAGTGCTATAAG 121 TACTATTCATCTTTTAATTGTGTGAGATGGAACAAATGCCAAGTTGCACAAGATGCATAC 181 TTTGAATATGTAATGGTTTGTTTCAGGTGAAAAATACCAGCAAGTCATGTCTTGTGTATT 241 TTACTTATATTTCCTTGTAGAACTAAATTAAGTAGATTTTGGAAAATGATTTGAATTGA 301 TTGCTGACTTGACCTGCCTGGTCAAATATCTGAATGATGGCATTACTGGGTAGATTCTAA 361 CCCATGATTCTAACTGTGGAATAAAGAGTAGTATAGACCGTAAAACTATGTTCAGGCACT 421 TACTCTTCGTTTATAATTATGTATTACCCTCTATCATAACACACTTATTGAATTTCCAAGT 481 TGAACAGTTCTGTAACTATTGTTGCTATTCATGTAATAAAACATGCTTATGATAGTAAAA 541 TGAATAGAAGTGCCCCCAAATGCTATTTTTTTTAATTCACTTGTAACTGTTACTCTTGTA 601 ATTGTGTATGACATAAAATTTGTAAAAATTTTAGCATGAAAAAAAAAAA	SEQ ID NO:103

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
WBC024B05.bFSP_20011510.abd	Adducin 3 (gamma) (ADD3), transcript variant 2	1 GAGAGAAGCTGCTGCTGCTAATGCTGCTGCTGCCGCCGCCGCTGCTGCTGC 61 TGCTGTTGGTCTGAGGCTGCAGTAGGTTTCTGTGCAGCATTGCAGAATCCACACCTAGAG 121 AACAGAAGACACAGACACGTACGTCTACTACCCTTGTTAGAAGGAAGCTTTGGATCTTCG 181 GTGGATAACAAGAGTAATCCACAGACTTAAACATGAGCTCAGATGCCAGCCAAGGCGTG 241 ATTACCACTCCTCCTCCTCCCAGCATGCCTCACAAAGAGAGATATTTTGACCGCATCAAT 301 GAAAATGACCCAGAATACATTAGGGAGAGGAACATGTCTCCTGATCTACGACAAGACTTC 361 AACATGATGGAGCAGAGGAAACGAGTTACTCAGATCCTGCAAAGTCCTGCCTTTCGGGAA 421 GACTTGGAATGCCTTATTCAAGAACAGATGAAGAAGGCCACAACCCAACTGGATTACTA 481 GCATTACAGCAGATTGCAGATTACATCATGGCCAATTCTTTCTCGGGTTTTTCTTCACCT 541 CCTCTCAGTCTTGGCATGGTCACACCTATCAATGACCTTCCTGGTGCAGATACATCCTCA 601 TATGTGAAGGGAGAAAAACTTACTCGCTGTAAACTTGCCAGCCTGTACAGACTTGTAGAC 661 TTGTTTGGATGGGCACACCTGGCAAATACCTATATCTCAGTAAGAATAAGTAAGGAGCAA 721 GACCACATTATAATAATTCCCAGAGGCCTATCTTTTTCTGAAGCTACAGCCTCCAATTTG 781 GTGAAAGTCAATATAATAGGAGAAGTGGTTGACCAGGGAAGTACCAATTTGAAAATTGAC 841 CATACAGGATTCAGTCCCCATGCTGCAATCTATTCAACACGTCCTGATGTTAAGTGTGTG 901 ATACACATCCATACCCTTGCAACAGCAGCTGTATACCTCCATGAAATGTGGGATCCTTCCA 961 ATTTCTCAAGAGTCTCTTCTTCTTGGGAGATGTTGCCTATTATGACTACCAAGGGTCACTT 1021 GAAGAACAGGAGGAGAGAATTCAACTGCAGAAGGTTCTGGGACCAAGTTGTAAGGTGCTG 1081 GTACTCAGGAATCATGGTGTGGTTGCACTTGGAGAAACATTAGAGGAGGCTTTTCATTAT 1141 ATTTTTAATGTGCAACTAGCCTGTGAGATTCAGGTGCAGGCCCTAGCAGGTGCAGGTGGA 1201 GTAGACAATCTCCATGTACTGGACTTTCAGAAGTATAAAGCTTTCACTTACACTGTAGCA 1261 GCGTCTGGTGGAGGAGGTGTGAATATGGGTTCCCATCAAAAATGGAAGGTTGGCGAAATT 1321 GAGTTTGAAGGGCTTATGAGGACTCTGGACAACTTGGGTATAGAACAGGCTATGCTTAC 1381 AGGCATCCTCTCATTCGAGAGAAGCCTAGGCACAAGAGTGATGTGGAAATCCCAGCAACT 1441 GTGACTGCTTTTTCCTTTGAAGACGATACAGTGCCACTCTCCTCCTCTCAAATACATGGCA 1501 CAGAGGCAACAGCGTGAAAAAACAAGATGGCTGAACTCACCAAATACTTACATGAAAGTG 1561 AATGTGCCTGAGGAGTCTCGGAACGGAGAAACCAGTCCCCGAACCAAAATCACGTGGATG 1621 AAAGCAGAAGACTCATCTAAAGTTAGTGGTGGAACACCTATCAAAATTGAAGATCCAAAT 1681 CAGTTTGTTCCTTTAAACACAAACCCGAATGAGGTACTAGAAAAGAGAAATAAGATTCGG 1741 GAACAAAATCGATATGACTTGAAAACAGCAGGACCACAATCTCAGTTGCTTGCTGGAATT 1801 GTTGTGGATAAGCCACCTTCTACTATGCAATTTGAAGATGATGATCATGGCCCACCAGCT 1861 CCTCCTAACCCATTTAGTCATCTCACAGAAGGAGAACTTGAAGAGTATAAGAGGACAATC 1921 GAACGTAAACAACAAGGCCTAGAAGAAAACCATGAGCTGTTTTCCAAGAGCTTCATCTCC 1981 ATGGAAGTGCCTGTCATGGTAGTAAATGGCAAGGATGATATGCATGATTGAAGATGAG 2041 CTTGCTAAGCGAGTGAGTAGGTTAAGCACAAGTACAACCATAGAAAACATCGAGATTACT 2101 ATTAAGTCTCCAGAGAAAATCGAAGAAGTCCTGTCACCTGAAGGCTCCCCTTCAAAATCG 2161 CCATCCAGAAAAAGAAGAGAAATTCCGCACTCCTTCTTTCTGAAAAAGAACAAAAAAAAG 2221 GAGAAAGTTGAGGCCTAAATAAAGTCTTTTTATAATTATTATATTACAATGTGACATTG 2281 CACATCTAAATACCACATTTAAGTTGATCATTAATATGCAATGGTAGATCAGATTGGGGG 2341 ATGTAGCAAACTGGACTTTAAGAACTGGAAAGAGGTTTTACAAAGAAAAACTTTCAGAT 2401 TCATCTCTCATTTTTATATGTCCAGAAATGGCTTTGAATTTTAAGCAATTACTAGTTTTAA 2461 TTAGCTCTGCCCTCATGAAGTATTATTATAATTCACCATAAACAGCTATCTGTCTGAATT	SEQ ID NO:104

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2521 ACTTCAGGCCTTCTCCATAATATCTGTTAGAAAGAAATTGCCAGTGAGCAAGTGAGAATT 2581 TTTATTTCTCAATACCTGCTTCACTTGATAATCATATTATAATTTTTTATCATGATTATT 2641 GACTATATTTTTGGAGTCCCATTGTTTCAGTGGGCATTAACAGAATGCTTTAAAAACTTC 2701 TAAGACAAGAATCTATAGCATTAGTATACACTGGCACATAATTTTTTAAAAGTTTAAG 2761 AAAAGATTCATTTGGAATTTTATTCACAGTATATAAATTTCCTCACCTGAAGTAACTTTGT 2821 TTGCCAAAAAAGTTGTTTTAATAAACTATAATTTTTGAAAACTTCCTTTTTTATTAGTTT 2881 AGAAAGCCCCTTATTTTTTCAACAAAGGGATTTTGTACACATAACATGGGTTATTTAGTT 2941 TAACTCTGGCAAAAAAAAAAAAAAAATTTTGTATGTTGATGTTTGTATACCGTTCAGTA 3001 TAAAAGTGTCCTAAGCATATTAGCCAATCTTTTCACAGTAGAGCATACTTAAGGCTGCTT 3061 GGTACTGAGTATACTTAAATATAACTCCAGAATCCAGGGACTTGGTGTTAAAACAGGATT 3121 AGAGCATGTAAAGGTACATCTAGATTCATATTTGAATCTTAAACTGTATTTTTCTCTTAG 3181 TATTGCTAATGAGTAAAGAAAAGTCTCATAAGGTAGCCAAATGAAAAAGAATGAAAGGA 3241 AAGTGAAAAATTAAGGGACAAAAGATGGGATGTGTGAAAAGAAGAATTCTAGTTTGATGGT 3301 GACTCATATTCACGATAGGATACAAAGTGTGATTTGTTGGAAACATGTCCCAAATTTCTA 3361 AAATTCTGCTTCTCTGCCAAAAGCAATGTCTTTCTTGGTTGATATTTGAGTTTTAAAAGG 3421 GTCAAATCTTTCTAATTTTTTTGTATCTTTAGAGGGCAGCACTAGAAGAAATCAGCAGGTC 3481 TAATCCCACCAGTAAGAAAACTACCACTTCTTGATTTTTACAGATTTAAAAAAATCTTTT 3541 CAGTGACCTTTCTTTTTTAATGTAAATACAAATTTAAACCTAGGCTTAATATAGGCGTTTC 3601 CCCTTTCACCCAAGTGATGTCACAGTTCGATGCAAAATCAATGATCCAGAATGATCGTGG 3661 GTAAAAATAACTCAAAGTGTTTCTTTAAGGGTGAGTTGGCATGCAAAAAATTACATTGATT 3721 ACAGTGTGTTTTTGGAGCTGGCTCTGTTTGTGTGCATATGATAATGCAGAGTTGAGCCAGA 3781 GCCTGGAAATGTCATTCTAGATCTCACTAACTACTGGAATCAGTGTTTTTAATCTCTTGGT 3841 GGAAACTTTCAGTTGCTTAACTCTCTATTGGAAGATTTTTTTTAATGTTCTACATCATTTA 3901 TGTTGTATTACAATGTATGTAGAAATAGTAACCTGTGAACTATGCTTTTCCATAACTTTT 3961 TAAAAATATATATCTAAATGAATGCAATGTGCATAAATATTTTTTTAAACATAACAGTG 4021 AACTATTGCACCTTTTGCTAATGCCTCTATTTACTTGCTTTGGCATAAAGAATGAGCCAA 4081 TGAACCTCTGTGTCCTGTGGAAAAATGTATAAATGTTATCTGATATTGCTCTTAGATGTA 4141 ATGCTAATTAATGTTAAATCACAAATAAACAGTATTTTTAAATATAAAAAAAAAAA 1 M S S D A S Q G G V I T T P P P P S M P H 1 ATGAGCTCAGATGCCAGCCAAGGCGTGATTACCACTCCTCCTCCTCCCAGCATGCCTCAC 21 K E R Y F D R I N E E N D P P E Y I R E E R N 61 AAAGAGAGATATTTTGACCGCATCAATGAAAATGACCCAGAATACATTAGGGAGAGGAAC 41 M S P D L R Q D D F N M M E Q R K R V T Q 121 ATGTCTCCTGATCTACGACAAGACTTCAACATGATGGAGCAGAGGAAACGAGTTACTCAG 61 I L Q S P A F R E E D L E C L I Q E Q M K 181 ATCCTGCAAAGTCCTGCCTTTCGGGAAGACTTGGAATGCCTTATTCAAGAACAGATGAAG 81 K G H N P T G L L A L Q Q I A D Y I M A 241 AAAGGCCACAACCCAACTGGATTACTAGCATTACAGCAGATTGCAGATTACATCATGGCC	SEQ ID NO:105

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		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 GACCTTCCTGGTGCAGATACATCCTCATATGTGAAGGAGAAAAACTTACTCGCTGTAAA 141 L A S L Y R L V D L F G W A H L A N T Y 421 CTTGCCAGCCTGTACAGACTTGTAGACTTGTTTGGATGGGCACACCTGGCAAATACCTAT 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 I H T L A T A A V 661 TCAACACGTCCTGATGTTAAGTGTGTGATACACATCCATACCCTTGCAACAGCAGCTGTA 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 GTGCAGGCCCTAGCAGGTGCAGGTGGAGTAGACAATCTCCATGTACTGGACTTTCAGAAG 341 Y K A F T Y T V A A S G G G G V N M G S 1021 TATAAAGCTTTCACTTACACTGTAGCAGCGTCTGGTGGAGGAGGTGTGAATATGGGTTCC 361 H Q K W K V G E I E F E G L M R T L D N 1081 CATCAAAAATGGAAGGTTGGCGAAATTGAGTTTGAAGGGCTTATGAGGACTCTGGACAAC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		381 L G Y R T G Y A Y R H P L I R E K P R H 1141 TTGGGGTATAGAACAGGCTATGCTTACAGGCATCCTCTCATTCGAGAGAAGCCTAGGCAC	
		401 K S D V E I P A T V T A F S F E D D T V 1201 AAGAGTGATGTGGAAATCCCAGCAACTGTGACTGCTTTTTCCTTTGAAGACGATACAGTG	
		421 P L S P L K Y M A Q R Q Q R E K T R W L 1261 CCACTCTCTCCTCTCAAATACATGGCACAGAGGCAACAGCGTGAAAAAACAAGATGGCTG	
		441 N S P N T Y M K V N V P E E S R N G E T 1321 AACTCACCAAATACTTACATGAAAGTGAATGTGCCTGAGGAGTCTCGGAACGGAGAAACC	
		461 S P R 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 ACACCTATCAAAATTGAAGATCCAAATCAGTTTGTTCCTTTAAACACAAACCCGAATGAG	
		501 V L E K R N K I R E Q N R Y D L K T A G 1501 GTACTAGAAAAGAGAAATAAGATTCGGGAACAAAATCGATATGACTTGAAAACAGCAGGA	
		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	
		561 E L E E Y K R T T I E R K Q Q G L E E N H 1681 GAACTTGAAGAGTATAAGAGGACAATCGAACGTAAACAACAAGGCCTAGAAGAAAACCAT	
		581 E L F S K S F I S M E V P V M V V N G K 1741 GAGCTGTTTTTCCAAGAGCTTCATCTCCATGGAAGTGCCTGTCATGGTAGTAAATGGCAAG	
		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 I T T I K S P E K I E E V L 1861 ACAACCATAGAAAACATCGAGATTACTATTAAGTCTCCAGAGAAAATCGAAGAAGTCCTG	
		641 S P E G S P S K S P S K K K K K F R T P 1921 TCACCTGAAGGCTCCCCTTCAAAATCGCCATCCAAGAAAAAGAGAAATTCCGCACTCCT	
		661 S F L K K N K K K E K V E E A -	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1981 TCTTTTCTGAAAAAGAACAAAAAAAAGGAGAAAGTTGAGGCCTAA	
WBC024F08.bFSP_20011510.abd	No homology	1 GGATAGTGCAGCATCCTAGAGCTTTGGTGTCACACAGACCCAGGTTCGAGTCTTCACTTT 61 GCCACCTCTTGCCTGCCGAGGGGCTGTGAGCTGAATTCCTACCTCATAGGGTTGTAATG 121 AGCAGTGGATGCTGAAGCAGACACCTCTTGGTCAAGGTGACTGCTCATCCCAGATTCTCC 181 CTTTTCTGAGAATTTGTTCCCCTCAGTCCTCATATAGGAGCTGAATGGATGAGAGGCGA 241 GCATCTGGCTGTACTTGGGCCAGTCTGGTTCTCTCTCTCAGGAATAAGCAGCGAGACTCA 301 GGGATGCTGTTTCCAGCTCTGCAAGTCACTTACCTGAAGATATACAAACTCTGGAGCTGT 361 GAGCGTGTGTCTACATGTGTGTCTCTATGTACCCAAGCCTTGGGGGTGGTGGCGGCAGGG 421 GGTGGCCACCTGCATGAGTGTGTATTAGAGAAAATGGCTCGACTCAGAGAGAAGATGGAGAT 481 GTGCAGAGCAAATCAGAGACCAGAGGGAGACCCCAGGAGCCTGGAGAGGCCAGGGGAGG 541 CGCTTCCCGGAGCCTGCCGGCGCTCCTCCTCTGGGCCAAACCCTTCTCGAGCCTCAAAGT 601 CCGCCCTCCTTCCTTTGAGTCCTGTGAGATGCCCTTGTTAGGATGCATTCTCTTGTTTTG 661 CTTGAGCTGATTTGAAGTATTATCTATTACTTGCAACCAAAAGAGCTCTGAATAAGATAA 721 AATCTTGTTGCTAAAGCACAGTGTCTCTCGAATTTCGGTCATCCCTGTACCCTCCTCACA 781 ATTTTTGCATATCTATGTACCATCTGTATGTTTTACTAATAAATATTGTTCTTTAAATCT 841 TTAAAAAAAAAAAAAAAAAA	SEQ ID NO:106
WBC024G03.bFSP_20011510.abd	Horse serpin mRNA.	1 CCCCCGCCGCCGGGACCGTCAGCCGCGCGCCTTCGCCATGGAGCAGCTGAGCACAGC 61 CAACACCCACTTTGCGGTGGACTTGTTCCGCGCTTTGAATGAGAGCGATCCTACTGGAAA 121 CATCTTCATCTCTCCCTTAAGCATTTCCTCAGCGCTGGCCATGATCTTCTGGGGACCAG 181 AGGCAACACAGCGGCACAGGTGTCCAAGGCACTTTATTTTGATACTGTTGAGGATATTCA 241 TTCAAGATTTCAGAGTCTGAATGCTGATATCAACAAACCTGGAGCTCCCTATATTCTGAA 301 ACTCGCTAATAGATTATATGGAGAGAAAACCTATAATTTCCTCGCTGATTTCTTAGCTTC 361 AACTCAGAAAATGTATGGTGCTGAATTGGCCAGTGTGGATTTTCAGCAAGCCCCTGAAGA 421 TGCAAGAAAGGAGATAAATGAATGGGTCAAAGGACAGACAGAGGGGAAAATTCCGGAACT 481 GTTGGTCAAGGGTATGGTTGATAACATGACTAAACTTGTACTGGTGAATGCCATCTACTT 541 CAAGGGAAACTGGCAGGAGAAATTCATGAAAGAGGCCACCAGAGACGCCCCATTCCGATT 601 GAATAAGAAAGACACAAAAACCGTGAAAATGATGTATCAGAAGAAGAAATTTCCATACAA 661 CTACATCGAGGACCTCAAGTGCCGTGTGCTGGAGCTGCCTTACCAAGGCAAAGAGCTCAG 721 CATGATCATCCTGCTGCCAGACGACATTGAGGATGAGTCCACGGGCCTGGAGAAGATTGA 781 GAAACAGTTGACTTTGGAAAAACTGCGTGAGTGGACCAAACCTGAGAATCTGTATCTCGC 841 TGAAGTCAATGTCCACTTGCCCAGGTTCAAGCTGGAAGAGAGCTACGATCTCACCTCCCA 901 TCTAGCCCGCCTAGGTGTACAAGACCCTCTTTAACAGGGGCAAAGCTGATCTGTCTGGCAT 961 GTCAGGGGCCAGAGATCTTTCGTATCGAAAATTATCCACAAATCCTTGTGGACCTGAA 1021 TGAGGAGGGTACAGAGGCTGCGGCAGCCACAGCAGGCACGATCATGCTTGCCATGCTGAT 1081 GCCAGAGGAAAATTTCAATGCCGACCATCCATTCATTTTCTTCATTCGGCACAATCCCTC 1141 AGCTAACATCCTGTTCTTAGGCAGATTTTCTTCCCCTTAGAGAAGGTGGAAGTACAAGGT 1201 GAAGCTTAAGCTTAGAGCTTTATTACCTGCTAGTATTATTACCATTACTTTTAATAGTGA 1261 CAGTTTTCATATATCTTTACCAATAAAACTACTATCCAAAAACAAATCTTTAATTTCCTT	SEQ ID NO:107

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1321 TGTAAGTTCAGCTCTATTGGCTGTTGCACCCCTTAACTTTGGCGTTTTTTATGTTGAAA 1381 AAATCTAGTTTATTGCTTTTGGATGCATCAAGTTTAAAAAATAAAAAGACTAAATCAAATTT 1441 ATAGATTCTTGATAATGCAGTAAGCTATGAAACTACTATACTCTCCTGATAGTGGTGGGA 1501 AACATTATAGTACTGTAATTTATTTTACAGATAGACTTTTGGAAGCCATAATAGAGAGAC 1561 GCTCTGATTGTTGAAGGAAGGCTTAAAAACAGATATTCAATTGAAATATAGTAAAGCACC 1621 CCAATTAAGGCCTGGGTTGTGCAGACAAACTCGTCTTGACCGTTGTTTCTAACCCTTTGT 1681 TCCACAGGGTTAGTGTCCTAGGGCAGCACTCCAATTTCAAACTGTTAGCCACCTGGTGAT 1741 ACCCCGCCTTCTCTTTTTTGTTCTCCTTTATCCTACCTGACATGTATTTTGTGTAGGATC 1801 ACATGGGGTCAGAAAGTAGGTGTTCTATCATAAAAGATACCAAGAAACGACAAAAAGGAA 1861 AATGCGGTAGGAGAGACTGTTAAGCAAAGGGCACAAAGATCTCACTGTTACCCAGCTTC 1921 TTGCGTTTTCTGATGAAGGCTCTTGCCTTCCATTGTCTGGTAAGGTTGTTACACCAGTGC 1981 GATGGCTTTATGCAATGTTGTGGTGGGAGATGGGGGGGTTCTTTTATTAATATAAACCTT 2041 TGTCAAATGTTTGAATGGGGCTGAAAATGCTGCATTTTCTTGCTCCCACAAAGCTGGTAT 2101 GCTGGTTAATAAAGTTTCCTAAGATTCTGCA 1 M E Q L S T A N T H F F A V D L F R A L N 1 ATGGAGCAGCTGAGCACAGCCAACACCCACTTTGCGGTGGACTTGTTCCGCGCTTTGAAT 21 E S D P T G N I F I S P L S I S S A L A 61 GAGAGCGATCCTACTGGAAACATCTTCATCTCCCTTAAGCATTTCCTCAGCGCTGGCC 41 M I F L G T R G N T A A Q V S K A L Y F 121 ATGATCTTTCTGGGGACCAGAGGCAACACAGCGGCACAGGTGTCCAAGGCACTTTATTTT 61 D T V E D I H S R F Q S L N A D I N K P 181 GATACTGTTGAGGATATTCATTCAAGATTTCAGAGTCTGAATGCTGATATCAACAAACCT 81 G A P Y I L K L A N R L Y G E K T Y N F 241 GGAGCTCCCTATATTCTGAAACTCGCTAATAGATTATATGGAGAGAAAACCTATAATTTC 101 L A D F L A S T Q K M Y G A E L A S V D 301 CTCGCTGATTTCTTAGCTTCAACTCAGAAAATGTATGGTGCTGAATTGGCCAGTGTGGAT 121 F Q Q A P E D A R K E I N E W V K G Q T 361 TTTCAGCAAGCCCCTGAAGATGCAAGAAAGGAGATAAATGAATGGGTCAAGGACAGACA 141 E G K I P E L L V K G M V D N M T K L V 421 GAGGGGAAAATTCCGGAACTGTTGGTCAAGGGTATGGTTGATAACATGACTAAACTTGTA 161 L V N A I Y F K G N W Q E K F M K E A T 481 CTGGTGAATGCCATCTACTTCAAGGGAAACTGGCAGGAGAAATTCATGAAAGAGGCCACC 181 R D A P F R L N K K D T K T V K M M Y Q	SEQ ID NO:108

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		541 AGAGACGCCCCATTCCGATTGAATAAGAAAGACACAAAAACCGTGAAAATGATGTATCAG	
		201 K K K F P P Y Y N Y I E D L K C R V L E L P	
		601 AAGAAGAAATTTCCATACAACTACATCGAGGACCTCAAGTGCCGTGTGCTGGAGCTGCCT	
		221 Y Q G K E L S M I I L L L P D D I E E D E S	
		661 TACCAAGGCAAAGAGCTCAGCATGATCATCCTGCTGCCAGACGACATTGAGGATGAGTCC	
		241 T G L E K I E K Q L T L E K L R E W T K	
		721 ACGGGCCTGGAGAAGATTGAGAAACAGTTGACTTTGGAAAAACTGCGTGAGTGGACCAAA	
		261 P E N L Y L A E V N V H L P R F K L E E	
		781 CCTGAGAATCTGTATCTCGCTGAAGTCAATGTCCACTTGCCCAGGTTCAAGCTGGAAGAG	
		281 S Y D L T S H L A R L G V Q D L F N R G	
		841 AGCTACGATCTCACCTCCCATCTAGCCCGCCTAGGTGTACAAGACCTCTTTAACAGGGGC	
		301 K A D L S G M S G A R D L F V S K I I H	
		901 AAAGCTGATCTGTCTGGCATGTCAGGGGCCAGAGATCTTTTCGTATCGAAAATTATCCAC	
		321 K S F V D L N E E G T E A A A A T A G T	
		961 AAATCCTTTGTGGACCTGAATGAGGAGGGTACAGAGGCTGCGGCAGCCACAGCAGGCACG	
		341 I M L A M L M P E E N F N A D H P F I F	
		1021 ATCATGCTTGCCATGCTGATGCCAGAGGAAAATTTCAATGCCGACCATCCATTCATTTTC	
		361 F I R H N P S A N I L F L G R F S S P -	
		1081 TTCATTCGGCACAATCCCTCAGCTAACATCCTGTTCTTAGGCAGATTTTCTTCCCTTAG	
WBC024G08.bFSP_20011510.abd	No homology	1 CAGACCTGTCCTGGATTCCCACCCACTCTCTTCTTACACTTCTTGCAAAATGATGACGCATC	SEQ ID NO:109
		61 ACTTGGTTCTCTGCCACCCAGTTTTAGGACTGGCACTCCACACAAATGATGCTGACTTTGTA	
		121 TGGAAGGATTTAGCTGAAAAAAAGCCCAGACATTATCACTATAACTAGCCCAGCTGGTTC	
		181 TTTTCTTTCATTTTATAAAAAGAATCATTTAAAAGCATTAATTAAAATTTATTTCTATAA	
		241 TTAAATTTGTGTTGGTATTGCCAGCAAAATAATTGAAGCCCCAAGGCTCTTGTCTTTTTT	
		301 AAAAGCAAATTAAAATATTTTGAAGATGGTGTCTTTAAAAGAGAGGTTAGATCAGACAC	
		361 TAAAATAACAGTGCCTTTCACCTTGAGGCATGGCACTGGCTATGTGACCTTCACCACCTA	
		421 TATTCTGTAGCCTATCAGCAAAGCAAAGGAAACCTCTCTTTTTAAAGTGCTACAGCAATG	
		481 CATCAATATTTATGTAGCAATTCCATCCCGTAATGCATGACTGTCCTGAAAACACTGACA	
		541 GCCACCATTGGCAGACACAACTTTCCATCCTGTTCCAGCCACCTCAGGGAGTCTGAGCCA	
		601 TGTCACCATGAATATCCCAGGACGTGAGGACACGTTAAAGGTAATCAAATTAGATGTTTA	
		661 CCAGATGAGCTCATCATGATTATTCTCTTGGTAACTGGTAAGAGGAAAAATTTTAAGTGT	
		721 ATACCCAGCCCAAACTAATGAATTCACAGGGCTTTCAGCAGAAAGGCTGCTCAAAAGCA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		781 CGAAGCCAGAGTGCGGAGCACCTGTGTGTGCATTTCCGCTCATTCCAGTTGTTTCCATTT 841 TTTTCTCCTAACACCTTCTT	SEQ ID NO:110
		1 GACTTGTCACATCTCATGGAGACACTCAGAGGTGCCTGGGCTGGGTTTGGCTGTAGGATG 61 GGCTTTGGTATGACAGACAAGACCAGTGAACTTGTCCTTGCCAGATGGGTCCCTAAAAC 121 AGATTTTTATTTCCGCAATCAAGCTGGAAACAAGCTGTGCCTTCAAAAAAGTGGCTTTTC 181 TAACTTTAGTTTTATGTTAAGTATGCTACTAACTTAAAAATAAGTGCATTCTCCTCAGAG 241 GAAACTATTTCTAACATCTGGTGATGTGTAACTCAGCAGTGAGTTGCCTGTGGCTGTCTT 301 TTCTTGTATTCTGTAGGAAAGGAGACCTGAATTTAACTCAGGTGGCAAGAAAAAAAATAC 361 TAAGTGCTTTTTAATTTCTCTAACTTCTTTTTGTGAATATGTAATTTTAAGTGTACACTA 421 CACCAACTTAGTAAAAACTCTTATATTTTGCCTATGTAGGCCTTTTCTGCAGAATTTTTAA 481 AGTTACCAATGTCTTTAAGCATCTTCAGCTCTGATCAATGAAATGTCTTGCATATGGAAT 541 GATGAGCTAGTCATTGGAAGTGCTCATGGGAGGGGGCTTTTTGTTCAGTCTGTATCAGAA 601 CAGCGTTTGTGCTCCATGCCTTCAACTCAACAAATGACCATAATCCATAAAATAAAATGT 661 GAAGTTTTTAAATCAGAAAAAAAAAAAAAAAAA	
WBC024H07.bFSP_20011510.abd	Homo sapiens interferon gamma receptor 2 (interferon gamma transducer 1), mRNA	1 GCGGGCCCTGCGCGCCCTGCGCTCGCCATGGCGGTTTGGGCGGCGACGTGAGCGCTCCG 61 CGGACCCCGAGCGGGGCCCCGGCCGCGACCTGAGCCGCCGCGAGCGCCCGGGGCCATGC 121 GACCGACGCTGCTGTGGTCGCTGCTGCTGCTCGGAGTCTTCGCCGCCGCCGCCGCGG 181 CCCCGCCAGACCCTCTTTCCCAGCTGCCTGCTCCCCAAAACCCGAAGATTCGCCTCTACA 241 ACGCTGAGCAGCTTCTGAGCTGGGAGCCGGTGCCCCCTGGCAATGGCACGGGGCCGGTGG 301 TCTACCACGTGCAGTTTAAATACACCGACACAGTAAATGGTTCACGGCCGACATCATGTCCA 361 TAGGGGTGAATTGTACACAGATCACAGCAACAGAGTGTGACTTCACTGCCGCCAGTCCCT 421 CAGCAGGCTTCCCAATGGATTTCAATGTCACTCTACGCCTTCGAGCTGAGCTGGGAGCAC 481 TCCATTCTGCCTGGGTGACGGTACCTTGGTTCCAGCACTTTCGGAATGTTACCATTGGGC 541 CTCCAGAAAACATTTGGGTGACCCCAGGAGAAGGCTCCCCTTATCATCAAGTTGTCCCCTC 601 CCTTTGACATCGCTGATACCTCCACGGCCTTTTTTTGTTATTATGTCCATTACTGGGAAA 661 AAGGAGGAATCCAACAGGTCAAAGGCCCTTTCAGAAGCAACTCCATTTCATTGGATAACT 721 TAAAACCCTCCAGAGTGTACTGTTTACAAGTCAAGGCACAACTACTTTGGACAATGCTAA 781 ACATCTCTAGACCCGGGCATTTAAGCAGCATATCTTGCTACGAAACGATGGCAGATGCCT 841 CCACCAAGCTTCAGCAAGTGATTCTCATCGCCTTTGGAACCTTTCTGTTGCTGTTCGCGA 901 TGGCAGGGGCCTGTCTCTTCTTCCTGGTCCTGAAATACAGAGGCCTGGTTAAATACTGGTTTC 961 ATTCCTCCGCCAAGCATCCCATTACAGATAGAAGAGTATTTAAAGGACCCGGCTCAGCCTA 1021 TCTTAGACGCCTTGGACAAGGACAGCTCCCCACGGAAGATGCCTGGGACTCTGTGTCTG 1081 TCGTTGTGTTTCCAGAGAAGGAGTAAGAAGATGTTCTCCAAAGCACTTTGAAGCAAAGCA 1141 TTGGCCTAGCCCACTGGCTCCCTGGAAGATCAAGCCATCGGAGCTGCTAGAGTTCTGT 1201 CTGGACTTTCCAGAGACCAGTATTCCCTTTTGCTGCCTCTAAAAGGCCTGTCCCTGCAGA 1261 CATGAGAGACAGCAGGTCTCATGGGGGTGACAAGCTTTTTTTTTTTTTCTTAAAGAATTTT 1321 CAAAATCAAATTCCAGAATGATTCTACAGAGATCTCTCAGAATAATTAAGATTTCTCTTA 1381 AACACTAAACAAGCATGTAATTATTTGTTAGCAAAATGGCTCTGGCACACCTGTGATATT 1441 TTGTTCATTGTCGGTTGGGCTGAGCAGTCAGAAGACCTGGTCGTCGTCTTGACTTTGGCA 1501 AATGAGCCGGAGCCCCTTGGGCAGGTCACACAACCTGTCCCAGCGAGGACACCGAGTGG	SEQ ID NO:111

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1561 CCCTTCATGTACATCCATGGTGTGCTGGCTTAAAATGTAATTAATCTTGTAAATATACTC 1621 CTAGTAATTTAAGATTTTGTTTTTAAACTGGAAATAAAAGATTGTATAGTGCATGTTTTTT 1681 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1 M R P T L L W S L L L L L G V F A A A A 1 ATGCGACCGACGCTGCTGTGGTCGCTGCTGCTCGGAGTCTTCGCCGCCGCCGCC 21 A A P P D P L S Q L P A P Q N P K I R L 61 GCGGCCCCGCCAGACCCTCTTTCCCAGCTGCCTGCTCCCCAAACCCGAAGATTCGCCTC 41 Y N A E Q L L S W E P P V P P G N G T G P 121 TACAACGCTGAGCAGCTTCTGAGCTGGGAGCCGGTGCCCCCTGGCAATGGCACGGGGCCG 61 V V Y H V Q F K Y T D S K W F T A D I M 181 GTGGTCTACCACGTGCAGTTTAAATACACCGACAGTAAATGGTTCACGGCCGACATCATG 81 S I G V N C T Q I T A T E C D F T A A S 241 TCCATAGGGGTGAATTGTACACAGATCACAGCAACAGAGTGTGACTTCACTGCCGCCAGT 101 P S A G F P M D F N V T L R L R A E L G 301 CCCTCAGCAGGCTTCCCAATGGATTTCAATGTCACTCTACGCCTTCGAGCTGAGCTGGGA 121 A L H S A W V T V P W F Q H F R N V T I 361 GCACTCCATTCTGCCTGGGTGACGGTACCTTGGTTCCAGCACTTTCGGAATGTTACCATT 141 G P P E N I W V T P G E G S L I I K L S 421 GGGCCTCCAGAAACATTTGGGTGACCCCAGGAGAAGGCTCCCTTATCATCAAGTTGTCC 161 P P F D I A D T S T A F F C Y Y V H Y W 481 CCTCCCTTTGACATCGCTGATACCTCCACGGCCTTTTTTGTTATTATGTCCATTACTGG 181 E K G G I Q Q Q V K G P F R S N S I S L D 541 GAAAAAGGAGGAATCCAACAGGTCAAAGGCCCTTTCAGAAGCAACTCCATTTCATTGGAT 201 N L K P S R V Y C L Q V K A Q L L W T M 601 AACTTAAAACCCTCCAGAGTGTACTGTTTACAAGTCAAGGCACAACTACTTTGGACAATG 221 L N I S R P G H L S S I S C Y E T M A D 661 CTAAACATCTCTAGACCCGGGCATTTAAGCAGCATATCTTGCTACGAAACGATGGCAGAT 241 A S T K L Q Q V I L I A F G T F L L L F 721 GCCTCCACCAAGCTTCAGCAAGTGATTCTCATCGCCTTTGGAACCTTTCTGTTGCTGTTC	SEQ ID NO:112

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		261 A M A G A C L F L V L K Y R G L V K Y W 781 GCGATGGCAGGGGCCTGTCTCTTCCTGGTCCTGAAATACAGAGGCCTGGTTAAATACTGG 281 F H S P P S I P L Q I E E Y L K D P A Q 841 TTTCATTCTCCGCCAAGCATCCCATTACAGATAGAAGAGTATTTAAAGGACCCGGCTCAG 301 P I L D A L D K D S S P T E D A W D S V 901 CCTATCTTAGACGCCTTGGACAAGGACAGCTCCCCAACGGAAGATGCCTGGGACTCTGTG 321 S V V V F P E K E - 961 TCTGTCGTTGTGTTTCCAGAGAAGGAGTAA	
WBC025A06.bFSP_20011710.abd	No homology	1 TTCCTGAAGCTTTGTCTGATGAATGTCTTCCATTCTTCAAAGTTTCTCTGTTTTAACTAC 61 ACAACTTGATTTGCCACATCATCAGTGTCTTTATTTCTTTAGTTCTGTATTTCTTTGCAA 121 TGTCAGAAAGTCATACATCTGTGATTCTCTTGGTGTTTGGAACCTGCTTGGAGGTGTAGT 181 AAAAAGTCATAAAGCAGAGAATAGAGTCAGAATCACCAGTAACTTCTTTGCTGCAGTGTG 241 AACATGCCAGTGGTTTCACTCTAGCATGGAGTGTTATTTTCCTAAGATCAAGTGAATAAG 301 AGAAGTAATCATGCATGCCTCCACCTTGCCTGAAATGGGAATGCCTTAGTGAATGTAGTG 361 TTGTGTGGTGTGTGCGTTCTTTCACATATATGCGTACGCACATACGTATATATGCATATA 421 TTTCAATCACAAGCCGCTGCTGATACTGTGGTTTAGAGCAGCCAGTAGTACTGGTTTTTGA 481 ATTCTTGAGAAGAGAAATTAAGTGACACAAATCATTATATCACCTGCCTCCAGCTGTAGC 541 TGAACAGATGCCAGCATTATAAATGTCACACCTTTCTTTACCACTAAACATTTGCCTTCA 601 ACAGGGCAACAGTGAGCTTTTCCTATATATTATGGTAAGTTATCAGAAATTACAGTTTAA 661 AAATATTTTCACATTTCCTGAAGTTTGAGGCAGTCTAAACATGACATTTTAGGTCTTCAT 721 TAGCTTTGTTTAAATAACATTTTGCCCTTATCAAGCTTGCTCTTTGTCTTAGATATAAAT 781 TGGAAGTTTCCTGAATGCAAATCTAAGATGCCAAATTCTTGTTTTTCCAGAATTAAAAAA 841 ACTGTTTAAAAATTGCAGTCATTAAAATATTGATTGTTTTTTCAGCTTTATCATAATTTTT 901 ACTTCCTATAGAAAAATGTTTATTAAGAAAAATTTAATTTTTCTTTTTC 1 TTGTTACTCAAAATTGCGGTTCTGGACTTTGTTTTTATTAGTTGCTTGATTGATTTTTAG 61 TCTTCTGAATAATAGTGAAAATATCGGTAAGGTGTGAAAGACTCCTGCTATTATAAGCAC 121 TCAGTCCGCTTCCCACGGAACTGAGCAGAGAATTAGTCACTGGGCCAGGCGAGCCCGAGC 181 AGGTCCCGGGGCGCTCCAGTGTGGTGGTTAGTCTGCCTTGGTGAAGGGCAGCCCACTGGCA 241 TCGTGTCAGCACAGAAACCTTCTCAGGTACAGGCTTTGTTTTAGATTGTGAGCTCTGGAA 301 CAATTCAGAAGTGTCCAGCCCAGCCCTCCTTTCCCTGTGTCGGTTACCACTCAAGACGCA 361 CATCGTCGGGGCCGCCGGTGGCGCAGCGGTTAAGTGCGCACGTTCCACTTCTCCACGG 421 CCCGGGGTTCGCCGGTTTGGATTCCGGCTGCGGACATGGCACTGCTTGGCAAAAGCCATG 481 CTGTGGTAGGCATCCCACGTATAAAGTAGAGGAAGATGGGCACAGATGTTAGCTCAGGGC 541 CGTCTTCCTCAGCAAAAGAGGAGGACTGGCAGTAGTTAGCTCAGGGCTAATCTTCGTCAA 601 AAAAAAAAAAAAAA	SEQ ID NO:113 SEQ ID NO:114
WBC025B03.bFSP_20	Homo sapiens pro-		

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE		SEQUENCE IDENTIFIER:
011710.abd	oncosis receptor inducing membrane injury gene, mRNA	1	CCACGCGTCCGGGAAGCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCGC	SEQ ID NO:115
		61	CACCTCGGCTGGGAGCCCCACGAGGCTGCCGCATCCTGCCCTCGGAACAATGGGACTCGGC	
		121	GCGCGAGGTGCTTGGGCCGCGCTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGG	
		181	GCCGCCCATGAAAGCGCAGCCATGGCGGCATCTGCAAACATAGAGAATTCTGGGCTTCCA	
		241	CACAACTCCAGTGCTAACTCAACAGAGACTCTCCAACATGTGCCTTCTGACCATACAAAT	
		301	GAAACTTCCAACAGTACTGTGAAACCACCAACTTCAGTTGCCTCAGACTCCAGTAATACA	
		361	ACGGTCACCACCATGAAACCTACAGCGGCATCTAATACAACAACCACGGGATGGTCTCA	
		421	ACAAATATGACTTCTACCACCTTAAAGTCTACACCCAAAACAACACAAGTGTTTCACAGAAC	
		481	ACATCTCAGATATCAACATCCACAATGACCGTAACCCACATAGTTCAGTGACATCTGCT	
		541	GCTTCATCAGTAACAATCACAACAACTATGCATTCTGAAGCAAGAAAGGATCAAAATTT	
		601	GATACTGGGAGCTTTGTTGGTGGTATTGTATTAACGCTGGGAGTTTTATCTATTCTTTAC	
		661	ATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTCGGTATCGAACCATAGATGAACAT	
		721	GATGCCATCATTTAAGGAAATCCATGGACCAAGGATGGAATACAGATTGATGCTGCCCTA	
		781	TCAATTAATTTTGGTTTATTAATAGTTTATTAAACAATATTCTCTTTTTGAAAATAGTATAA	
		841	ACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTAAAGATTCTTCAAGGTAA	
		901	CAAGGGTTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGTTCATACAATGGTTTT	
		961	AGCAAGTTCATAGTAAGACAAACAAGTCCTATCTTTTTTTTTGGCTGGGGTGGGGGCA	
		1021	TTGGTCACATATGACCAGTAATTGAAAGACGTCATCACTGAAGACAGAATGCCATCTGG	
		1081	GCATACAAATAAGAAGTTTGTCACAGCACTCAGGATTTTGGGTATCTTTTGTAGCTCACA	
		1141	TAAAGAACTTCAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACACAGAAA	
		1201	TTATACAATCAAACTAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTGTGCT	
		1261	TTAAACTGTAGTAGTTGGTCTAGAAACAAAATACTCCAAGAAAAAGAAAATTTTCAAATA	
		1321	AAACCCAAAATAATAGCTTTGCTTAGCCCTGTTAGGGATCCATTGGAGCATTAAGAGCA	
		1381	CATATTTTTATTAACTTCTTTTGAGCTTTCAATGTTGATGTAATTTTTGTTCTCTGTGTA	
		1441	ATTTAGGTAAACTGCAGTGTTTAACATAATAATGTTTTAAAAACTTAGTTGTTAGTATTA	
		1501	AATAAGTTAGATTATTTGCTACTGTGAGAATATTGTCACCACTGGAAGTTACTTTAGTTC	
		1561	ATTTAATTTTAATTTTATCTTTAGTGAATATTTTTAAGAGATAGAGCTGCTTTCAATA	
		1621	TCTAGAAATGTTTAATGTAGTGTAAACATGCCTAACTTTAAAAAAAAGAGCCCCTTATAT	
		1681	GATTTCCAAAACAACATTTAGAACTGTATACACAGAACTATAGATTAATGCTCTGTTTAT	
		1741	CAAGCCAGGGATTGTGGGGGCCCCCCTCAGGCTACTAAACCCACAGGATGAAAATGCTAT	
		1801	ATTTTCTTTCATGCACTGTCGATATTACTCAGATTTGGGGAAATGACATTTTTATACTAA	
		1861	AACAAACACCAAAATATTTTAGAATAAATTCTTAGAAAGTTTTGAGAGGAATTTTTAGAG	
		1921	AGGACATTTCCTCCTTCCTGATTTGGATATTCCCTCAAATCCCTCCTCTTACTCCATGCT	
		1981	GAAGGAGAAGTACTCTCAGATGCATTATGTTAATGGAGAGAAAAGCACAGTATTTTAGG	
		2041	GATACCAATATTAGCCAAGGTATTTTGAAGTGTTTCGGTTTTAGTTCATACTGAATACTGAGATA	
		2101	TCAAAACTCAGGGTCAAGTTTTGACAAAAGATGTATTTAGTCATACTGAATACTGAGATA	
		2161	GTATTTCTATCTTAGGTGGTCAAAGTAAATCACACCAATTTCTGATAGTCCAAAAATCAG	
		2221	CTGAGAAGTCCTAATGAACATGTACCTACAATTAATAGGAGTACAATAAACTGTTGTCA	
		2281	GCTTTTGTTTTACAGAGAACGCTAGATATTAAGAATTTTGAAATGGATCATTTCTACTTG	
		2341	CTGTGCATTTTAACCAATAATCTGATGAATATAGAAAAAAATGATCCAAAATATGGATAT	
		2401	GATTGGATGTATGTAACACATACATGGAGTATGGAGGAAATTTTCTGAAAAATACATTTA	
		2461	GATTAGTTTAGTTTGAAGGAGAGGTGGGCTGATGGCTGAGTTGTATGTTATCTAACTTGGC	
		2521	CCTGACTGGTTGTGCAACCATTGCTTCATTTCTTTGCAAATGTAGTTAAGATATACTTT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2581 ATTCTAATGAAGGCCTTTTAAATTTGTCCACTGCATTCTTGGTATTTCAGTACTTCAAGT 2641 CAGTCAGAACTTTGTAGACAGGCCTGAAACTTTCTTCTATACTTGCTTCTTTTAGCACTTT 2701 GAAGATATAAACCACTTTTTAAGTACTAAATGTCGAAATTTGCCTTTCAAGTTTCCTGT 2761 GCTTTGGGTTTGAAATAATTTAGTTATGTCTTTTCTCTGTATGTAAATTGTATAATTTGT 2821 TATTTTCAAATACCCGTACTTTGAATGTAGGTTTTTTTGTTGTTATCTATAAAAATT 2881 GAGGGAACTGGTGATGCAAACCAATATTCTGCTTTGGAGCACATTTCCTAAGCATAAAA 2941 AAATGCTCAGTTTTGCTTGCATTCCTTGAGAATGTATTTATCTGAAGATCAAAACAAACA 3001 ATCCAGATGTATAAGTACTAGGCAGAAGCCAATTTTAAAATTTCTTTGGATAATCCATAA 3061 AATGAATAATTCAAATACAGATAAGAGTGGTAGCATATTACAGTGATCATTTTGTATTTT 3121 TTCACAAAAAAAAAGTTAAACTCTTCTTTTTCTTTTATTATAAGGATCAGCTTTTGGTAT 3181 TTCATTGTTACTGAGATCTATTTTTAGAATAAAATTGTTCTCCTTCCAAAAAAAAAAAA 3241 AAAA	SEQ ID NO:116
		1 M G L G A R G A W A A L L L G T L Q V L 1 ATGGGACTCGGCGCGCGAGGTGCTTGGGCCGCGCTGCTCCTGGGGACGCTGCAGGTGCTA 21 A L L G A A H E S A A M A A S A N I E N 61 GCGCTGCTGGGGGCCGCCCATGAAAGCGCAGCCATGGCGGCATCTGCAAACATAGAGAAT 41 S G L P H N S S A N S T E T L Q H V P S 121 TCTGGGCTTCCACACAACTCCAGTGCTAACTCAACAGAGACTCTCCAACATGTGCCTTCT 61 D H T N E T S N S T V K P P T S V A S D 181 GACCATACAAATGAAACTTCCAACAGTACTGTGAAACCACCAACTTCAGTTGCCTCAGAC 81 S S N T T V T T T M K P T T A A S N T T T P 241 TCCAGTAATACAACGGTCACCACCATGAAACCTACAGCGGCATCTAATACAACAACACCA 101 G M V S T N M T S T T L K S T P K T T S 301 GGGATGGTCTCAACAAATATGACTTCTACCACCTTAAGTCTACACCCAAAACAACAAGT 121 V S Q N T S Q I S T S T M T V T H N S S 361 GTTTCACAGAACACATCTCAGATATCAACATCCACAATGACCGTAACCCACAATAGTTCA 141 V T S A A S S V T I T T T T M H S E A K K 421 GTGACATCTGCTGCTTCATCAGTAACAATCACAACAACTATGCATTCTGAAGCAAAGAAA 161 G S K F D T G S F V G G I V L T L G V L 481 GGATCAAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAACGCTGGGAGTTTTA 181 S I L Y I G C K M Y Y S R R G I R Y R T 541 TCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTCGGTATCGAACC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		201 I D E H D A I I - 601 ATAGATGAACATGATGCCATCATTTAA	
WBC025C03.bFSP_20011710.abd	Homo sapiens TBP-interacting protein, mRNA	1 GGCGTCGCGCTGCGACCCTGGAAGCGGGAGCCGCCGCGAGCGAGAGGAGGAGCTCCAGTG 61 GCGGCGGCGGCGGCGGCAGCGGCAGCGGCAGCAGCTCCAGCAGCGCCAGCAGGCGGGAT 121 CGAGGCCGTCAACATGGCGAGCGCCTCGTACCACATTTCCAATTTGCTGGAAAAAATGAC 181 ATCCAGCGACAAGGACTTTAGGTTTATGGCTACAAATGATTTGATGACGGAACTGCAGAA 241 AGATTCCATCAAGTTGGATGATAGTGAAAGCAAAGTAGTGAAAATGATTTTGAAGTT 301 ATTGGAAGATAAAAATGGAGAGGTACAGAATTTAGCTGTCAAATGTCTTGGTCCTTTAGT 361 GAGTAAAGTGAAAGAATACCAAGTAGAGACAATTGTAGATACCCTCTGCACTAACATGCT 421 TTCTGATAAAGAACACAACTTCGAGACATTTCAAGTATTGGTCTTAAACAGTAATTGGAGA 481 ACTTCCTCCAGCTTCCAGTGGCTCTGCATTAGCTGCTAATGTATGTAAAAAGATTACTGG 541 ACGTCTTACAAGTGCAATAGCAAAACAGGAAGATGTCTCTGTTCAGCTAGAAGCCTTGGA 601 TATTATGGCTGATATGTTGAGCAGGCAAGGAGGACTTCTTGTTAATTTCCATCCTTCAAT 661 TCTGACCTGTCTACTTCCCCAGTTGACCAGCCCTAGACTTGCAGTGAGGAAAAGAACCAT 721 TATCGCTCTTGGCCATCTGGTTATGAGCTGTGGAAATATAGTTTTTGTAGATCTTATTGA 781 ACATCTGTTGTCAGAGTTGTCCAAAAATGATTCTATGTCAACACAAGAACCTACATACA 841 ATGTATTGCTGCTATTAGTAGGCAAGCTGGTCATAGAATAGGTGAATACCTTGAGAAGAT 901 AATTCCTTTGGTGGTAAAATTTTGCAATGTAGATGATGATGAATTAAGAGAGTACTGTAT 961 TCAAGCCTTTGAATCATTTGTAAGAAGATGTCCTAAGGAAGTATATCCTCATGTTTCTAC 1021 CATTATAAATATTTGTCTTAAATATCTTACCTATGATCCAAATTATATAATTACGATGATGA 1081 AGATGAAGATGCAAAATGCAATGGATGCTGATGGTGGTGATGATGATCAAGGAGTGA 1141 TGATGAATACAGTGATGATGATGACATGAGTTGGAAAGTGGAGACGTGCAGCTGCGAAGTG 1201 CTTGGATGCTGTAGTTAGCTACAAGGCATGAAATGCTTCCAGAATTCTACAAGACCGTCTC 1261 TCCTGCACTGATATCCAGATTTAAAGAACGAGAAGAACGTAAAGGCAGATGTTTTTCA 1321 TGCATACCTTTCTCTTTTGAAGCAAACTCGTCCTGTGCAAAGTTGGCTGTGTGACCCTGA 1381 TGCAATGGAACAAGGAGAAACACCTTTAACAATGCTTCAGAGTCAGGTTCCCAACATTGT 1441 TAAGCTCTGCACAAACAGATGAAAGAAAAAAGTGTGAAGACTCGACAGTGCTGTTTTAA 1501 CATGTTAACTGAACTGGTAAATGTGTTACCTGGGGCCCTAACACACATGTTCCTGTGCT 1561 TGTACCAGGAATCATTTTCTCACTGAATGATAAATCAAGCTCATCAAATTTGAAGATTGA 1621 TGCTCTGTCGTGTCTCTACGTAATCCTCTGTAACCACTCTCCTCAAGTCTTCCATCTTCA 1681 TGTCCAGGCTTTGGTCCCTCCAGTGGTGGCTTGTGTTGGATACCCATTTTACAAGATTAC 1741 GTCTGAAGCACTTCTTGTTACTCAACAGCTTGTGAAGTCATTCGTCCTTTAGATCAGCC 1801 TTCCTCATTTGATGCCACTCCTTACATCAAAGATTTGTTTACCTGTACCATTAAGAGGTT 1861 AAAAGCAGCTGACATTGATCAGGAAGTCAAGGAAAGGGCTATTTCCTGTATGGGACAAAT 1921 TATTCTGCACCTTGGAGACATTTTGGGTTCTGACTTGCCTAATACACTTCAGATTTTCTT 1981 GGAGAGACTAAAGAATGAAATTACCAGGTTAACTACAGTAAAGGCATTGACACTGATTGC 2041 TGGGTCACCTTTGAAGATAGATTTGAGGCCTGTTCTGGGAGAAGGGGTTCCTATCCTTGC 2101 TTCATTTCTTAGAAAAAACCAGAGAGCTTTGAAACTGGGTACTCTTTCTGCCCTTGATAT 2161 TCTAATAAAAAACTATAGTGACAGCTTGACAGCTGCCATGATTGATGCAGTTCTAGATGA 2221 GCTCCCACCTCTTATCAGCGAAAGTGATATGCATGTTTCACAAATGGCCATCAGTTTCT	SEQ ID NO:117

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2281 TACCACTTTGGCAAAAGTATATCCCTCCTCCTTTCAAGATAAGTGGATCCATTCTCAA 2341 TGAACTTATTGGACTTGTGAGATCACCCTTATTGCAGGGGGGAGCTCTTAGTGCCATGCT 2401 AGACTTTTTCCAAGCTCTGGTTGTCACTGGAACAAATAATTTAGGATACATGGATTTGTT 2461 GCGCATGCTGACTGGTCCAGTTTACTCTCAGAGCACAGCTCTTACTCATAAGCAGTCTTA 2521 TTATTCCATTGCCAAATGTGTAGCTGCCCTTACTCGAGCATGCCCTAAAGAGGGACCAGC 2581 TGTAGTAGGTCAGTTTATTCAAGATGTCAAGAACTCAAGGTCTACAGATTCCATTCGTCT 2641 CTTAGCTCTACTTTCTCTTGGAGAAGTTGGCATCATATTGACTTAAGTGGACAGTTGGA 2701 ACTAAAATCTGTAATACTAGAAGCTTTCTCATCTCCTAGTGAAGAAGTCAAATCAGCTGC 2761 ATCCTATGCATTAGGCAGCATTAGTGTGGCAACCTTCCTGAATATCTACCGTTTGTCCT 2821 GCAAGAAATAACTAGTCAACCCAAAAGGCAGTATCTTTTACTTCATTCCTTGAAGGAAAT 2881 TATTAGCTCTGCATCAGTGGTGGCCTTAAACCATATGTTGAAAACATCTGGGCCTTATT 2941 ACTAAAGCACTGTGAGTGTGCAGAGGAAGGAACCAGAAATGTTGTTGTTGAATGTCTAGG 3001 AAAACTCACTCTAATTGATCCAGAAACTCTCCTTCCACGGCTTAAGGGGTACTTGATATTC 3061 AGGCTCATCATATGCCCGAAGCTCAGTGGTTACGGCTGTGAAATTTACAATTTCTGACCA 3121 TCCACAACCTATTGATCCACTGTTAAAGAACTGCATAGGTGATTTCCTAAAAACTTTGGA 3181 AGACCCAGATTTGAATGTGAGAAGAGTAGCCTTGGTCACATTTAATTCAGCAGCACATAA 3241 CAAGCCATCATTAATAAGGGATCTATTGGATACTGTTCTTCCACATCTTTACAATGAAAC 3301 AAAAGTTAGAAAGGAGCTTATAAGAGAGGTAGAAATGGGTCCATTTAAACATACGGTTGA 3361 TGATGGTCTGGATATTAGAAAGGCAGCATTTGAGTGTATGTACACACTTCTAGACAGTTG 3421 TCTTGATAGACTTGATATCTTTGAATTTCTAAATCATGTTGAAGATGGTTTGAAGGACCA 3481 TTATGATATTAAGATGCTGACATTTTTAATGTTGGTGAGACTGTCTACCCTTTGTCCAAG 3541 TGCAGTATTGCAGAGGTTGGACCGACTTGTTGAGCCGTTACGCGCCACGTGTACAACGAA 3601 GGTGAAGGCAAACTCAGTAAAGCAGGAGTTTGAAAAGCAGGACGAACTGAAGCGATCGGC 3661 CATGAGAGCAGTCGCGGCCCTGCTGACCATTCCCGAGGCCGAGAAGAGCCCGCTGATGAG 3721 CGAGTTCCAGTCGCAGATCAGCTCCAACCCTGAGCTGGCAGCCATCTTTGAGAGGCATCCA 3781 GAAAGACTCATCGTCCACTAACTTGGAATCAATGGACACTAGTTAGATGTTTGCTCCATA 3841 CGGGACCATTACGTTGACCATACGATGCACTGAATTGACAGGTTAATCATAGACATGGA 3901 AAGAGAAGTGTCTAAAAGCTTCAAAATGTTCCACTTTTTTTTCCTTCATGGAGACAGTTT 3961 GGCTTTCTTCCATTGTTGTTTTTGTAGCATTTATTTCAGAAATGTGTATTTCCATAATCC 4021 AGAGGTTGTAAAACCACTAATGTCTTAGTGGTTGGGGCAACATTTAAAATGGAAACTAAA 4081 AGTTAGGATTTATGGAGATAGGGTCCAGTATCTATTTGCCCTGTAATGTTTAGGATTAAA 4141 ATGTTAAAATTTAAAAAAAAAAAAAAAA 1 M A S A S Y H I S N L L E K M T S S D K 1 ATGGCGAGCGCCTCGTACCACATTTCCAATTTGCTGGAAAAAATGACATCCAGCGACAAG 21 D F R F M A T N D L M T E L Q K D D S I K 61 GACTTTAGGTTTATGGCTACAAATGATTTGATGACGGAACTGCAGAAAGATTCCATCAAG 41 L D D D S E R K V V K M I L K L L E D K 121 TTGGATGATGATAGTGAAAGGAAAGTAGTGAAAATGATTTTGAAGTTATTGGAAGATAAA 61 N G E V Q N L A V K C L G P L V S K V K	SEQ ID NO:118

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		181 AATGGAGAGGTACAGAATTTAGCTGTCAAATGTCTTGGTCCTTTAGTGAGTAAAGTGAAA	
		81 E Y Q V E T I V D T L C T N M L S D K E 241 GAATACCAAGTAGAGACAATTGTAGATACCCTCTGCACTAACATGCTTTCTGATAAAGAA	
		101 Q L R D I S S I G L K T V I G E L P P A 301 CAACTTCGAGACATTTCAAGTATTGGTCTTAAACAGTAATTGAGAACTTCCTCCAGCT	
		121 S S G S A L A A N V C K K I T G R L T S 361 TCCAGTGGCTCTGCATTAGCTGCTAATGTATGTAAAAAGATTACTGGACGTCTTACAAGT	
		141 A I A K Q E D V S V Q L E A L D I M A D 421 GCAATAGCAAAACAGGAAGATGTCTCTGTTCAGCTAGAAGCCTTGGATATTATGGCTGAT	
		161 M L S R Q G G L L V N F H P S I L T C L 481 ATGTTGAGCAGGCAAGGAGGACTTCTTGTTAATTTCCATCCTTCAATTCTGACCTGTCTA	
		181 L P Q L T S P R L A V R K R T I I A L G 541 CTTCCCCAGTTGACCAGCCCTAGACTTGCAGTGAGGAAAGAACCATTATCGCTCTTGGC	
		201 H L V M S C G N I V F V D L I E H L L S 601 CATCTGGTTATGAGCTGTGGAAATATAGTTTTTGTAGATCTTATTGAACATCTGTTGTCA	
		221 E L S K N D S M S T T R T Y I Q C I A A 661 GAGTTGTCCAAAAATGATTCTATGTCAACAACACAAGAACCTACATACAATGTATTGCTGCT	
		241 I S R Q A G H R I G E Y L E K I I P L V 721 ATTAGTAGGCAAGCTGGTCATAGAATAGGTGAATACCTTGAGAAGATAATTCCTTTGGTG	
		261 V K F C N V D D D E L R E Y C I Q A F E 781 GTAAAATTTGCAATGTAGATGATGAATTAAGAGAGTACTGTATTCAAGCCTTTGAA	
		281 S F V R R C P K E V Y P H V S T I I N I 841 TCATTTGTAAGAAGATGTCCTAAGGAAGTATATCCTCATGTTTCTACCATTATAAATATT	
		301 C L K Y L T Y D P N Y N Y D D E D D E E 901 TGTCTTAAATATCTTACCTATGATCCAAATTATAATTACGATGATGAAGATGAAGATGAA	
		321 N A M D A D G G D D D D Q G S D D E Y S 961 AATGCAATGGATGCTGATGGTGGTGATGATGATGATCAAGGGAGTGATGATGAATACAGT	
		341 D D D D M S W K V R R A A A K C L D A V 1021 GATGATGATGACATGAGTTGGAAAGTGAGACGTGCAGCTGCGAAGTGCTTGGATGCTGTA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		361 V S S T R H E E M L P E E F Y K K T T V S S P A L L I 1081 GTTAGCACAAGGCATGAAATGCTTCCAGAATTCTACAAGACCGTCTCTCCTGCACTGATA	
		381 S R F K E E R E E E N V V K K A D D V F H H A Y Y L S S 1141 TCCAGATTTAAAGAACGAGAAGAACGTAAAGGCAGATGTTTTTCATGCATACCTTTCT	
		401 L L K Q T T R P P V Q Q S W L L C D D P D D A M E E Q 1201 CTTTTGAAGCAAACTCGTCCTGTGCAAAGTTGGCTGTGTGACCCTGATGCAATGGAACAA	
		421 G E E T P P L L T M M L L Q Q S Q Q V P P N N I I V V K K A L L H 1261 GGAGAAACACCTTTAACAATGCTTCAGAGTCAGGTTCCCAACATTGTTAAAGCTCTGCAC	
		441 K Q M K K E E K K S S V V K K T T R R Q Q C C C F F N N M M L L T T E E 1321 AAACAGATGAAAGAAAAAAAAGTGTGAAGACTCGACAGTGCTGTTTTTAACATGTTAACTGAA	
		461 L L V V N N V V L L P P G G A A L L T T Q Q H H V V P P V V L L V V P P G G I I 1381 CTGGTAAATGTGTTACCTGGGGCCCTAACACACAACATGTTCCTGTGCTTGTACCAGGAATC	
		481 I I F F S S L L N N D D K K S S S S S S N N L L K K I I D D A A L L S S C C 1441 ATTTTCTCACTGAATGATAAATCAAGCTCATCAAATTTGAAGATTGATGCTCTGTCGTGT	
		501 L L Y Y V V I I L L C C N N H H S S P P Q Q V V F F H H L L H H V V Q Q A A L L 1501 CTCTACGTAATCCTCTGTAACCACTCTCCTCAAGTCTTCCATCTTCATGTCCAGGCTTTG	
		521 V V P P P P V V V V A A C C V V G G Y Y P P F F Y Y K K I I T T S S E E A A L L 1561 GTCCCTCCAGTGGTGGCTTGTGTTGGATACCCATTTTACAAGATTACGTCTGAAGCACTT	
		541 L L V V T T Q Q Q Q L L V V K K V V I I R R P P L L D D Q Q P P S S S S F F D D 1621 CTTGTTACTCAACAGCTTGTGAAAGTCATTCGTCCTTTAGATCAGCCTTCCTCATTTGAT	
		561 A A T T P P Y Y I I K K D D L L F F T T C C T T I I K K R R L L K K A A A A D D 1681 GCCACTCCTTACATCAAAGATTTGTTTACCTGTACCATTAAGAGGTTAAAAGCAGCTGAC	
		581 I I D D Q Q E E V V K K E E R R A A I I S S C C M M G G Q Q I I I I L L H H L L 1741 ATTGATCAGGAAGTCAAGGAAAGGGCTATTTCCTGTATGGGACAAATTATTCTGCACCTT	
		601 G G D D I I L L G G S S D D L L P P N N T T L L Q Q I I F F L L E E R R L L K K 1801 GGAGACATTTTGGGTTCTGACTTGCCTAATACACTTCAGATTTTCTTGGAGAGACTAAAG	
		621 N N E E I I T T R R L L T T T T V V K K A A L L T T L L I I A A G G S S P P L L 1861 AATGAAATTACCAGGTTAACTACAGTAAAGGCATTGACACTGATTGCTGGGTCACCTTTG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		641 K I D L R P V L G E G V P I L A S F L R 1921 AAGATAGATTTGAGGCCTGTTCTGGGAGAAGGGGTTCCTATCCTTGCTTCATTTCTTAGA	
		661 K N Q R A L K L G T L S A L D I L I K N 1981 AAAAACCAGAGAGCTTTGAAACTGGGTACTCTTTCTGCCCTTGATATTCTAATAAAAAAC	
		681 Y S D S L T A A M I D A V L D E L P P L 2041 TATAGTGACAGCTTGACAGCTGCCATGATTGATGCAGTTCTAGATGAGCTCCCACCTCTT	
		701 I S E S D M H V S Q M A I S F L T T L A 2101 ATCAGCGAAAGTGATATGCATGTTTCACAAATGGCCATCAGTTTCTTACCACTTTGGCA	
		721 K V Y P S S L S K I S G S I L N E L I G 2161 AAAGTATATCCCTCCTCCCTTTCAAAGATAAGTGGATCCATTCTCAATGAACTTATTGGA	
		741 L V R S P L L Q G G G A L S A M L D F F Q 2221 CTTGTGAGATCACCCTTATTGCAGGGGGGAGCTCTTAGTGCCATGCTAGACTTTTTCCAA	
		761 A L V V T G T N N L G Y M D L L R M L T 2281 GCTCTGGTTGTCACTGGAACAAATAATTTAGGATACATGGATTTGTTGCGCATGCTGACT	
		781 G P V Y S Q S T A L T H K Q S Y Y S I A 2341 GGTCCAGTTTACTCTCAGAGCACAGCTCTTACTCATAAGCAGTCTTATTATTCCATTGCC	
		801 K C V A A L T R A C P K E G P A V V G Q 2401 AAATGTGTAGCTGCCCTTACTCGAGCATGCCCTAAAGAGGGACCAGCTGTAGTAGGTCAG	
		821 F I Q D V K N S R S T D S I R L L L A L L 2461 TTTATTCAAGATGTCAAGAACTCAAGGTCTACAGATTCCATTCGTCTCTTAGCTCTACTT	
		841 S L G E V G H H I D L S G Q L E L K S V 2521 TCTCTTGGAGAAGTTGGGCATCATATTGACTTAAGTGGACAGTTGGAACTAAAATCTGTA	
		861 I L E A F S S P S E E V K S A A S Y A L 2581 ATACTAGAAGCTTTCTCATCTCCTAGTGAAGAAGTCAAATCAGCTGCATCCTATGCATTA	
		881 G S I S V G N L P E Y L P F V L Q E I T 2641 GGCAGCATTAGTGTGGGCAACCTTCCTGAATATCTACCGTTTGTCCTGCAAGAAATAACT	
		901 S Q P K R Q Y L L L H S L K E I I S S A 2701 AGTCAACCCAAAGGCAGTATCTTTTACTTCATTCCTTGAAGGAAATTATTAGCTCTGCA	
		921 S V V G L K P Y Y E N I W A L L L K H C	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2761 TCAGTGGTGGGCCTTAAACCATATGTTGAAAACATCTGGGCCTTATTACTAAAGCACTGT	
		941 E C A E E G T R N V V V E C L G K L T L 2821 GAGTGTGCAGAGGAAGGAACCAGAAATGTTGTTGTTGAATGTCTAGGAAAACTCACTCTA	
		961 I D P E T L L P R L K G Y L I S G S S Y 2881 ATTGATCCAGAAACTCTCCTTCCACGGCTTAAGGGTACTTGATATCAGGCTCATCATAT	
		981 A R S S V V T A V K F T I S D H P Q P I 2941 GCCCGAAGCTCAGTGGTTACGGCTGTGAAATTTACAATTTCTGACCATCCACAACCTATT	
		1001 D P L L K N C I G D F L K T L E D P D L 3001 GATCCACTGTTAAAGAACTGCATAGGTGATTTCCTAAAAACTTTGGAAGACCCAGATTTG	
		1021 N V R R V A L V T F N S A A H N K P S L 3061 AATGTGAGAAGAGTAGCCTTGGTCACATTTAATTCAGCAGCACATAACAAGCCATCATTA	
		1041 I R D L L D T V L P H L Y N E T K V R K 3121 ATAAGGGATCTATTGGATACTGTTCTTCCACATCTTTACAATGAAACAAAAGTTAGAAAG	
		1061 E L I R E V E M G P F K H T V D D G L D 3181 GAGCTTATAAGAGAGGTAGAAATGGGTCCATTTAAACATACGGTTGATGATGGTCTGGAT	
		1081 I R K A A F E C M Y T L L D S C L D R L 3241 ATTAGAAAGGCAGCATTTGAGTGTATGTACACACTTCTAGACAGTTGTCTTGATAGACTT	
		1101 D I F E F L N H V E D G L K D H Y D I K 3301 GATATCTTTGAATTTCTAAATCATGTTGAAGATGGTTTGAAGGACCATTATGATATTAAG	
		1121 M L T F L M L V R L S T L C P S A V L Q 3361 ATGCTGACATTTTTAATGTTGGTGAGACTGTCTACCCTTTGTCCAAGTGCAGTATTGCAG	
		1141 R L D R L V E P L R A T C T T K V K A N 3421 AGGTTGGACCGACTTGTTGAGCCGTTACGCGCCACGTGTACAACGAAGGTGAAGGCAAAC	
		1161 S V K Q E F E K Q D E L K R S A M R A V 3481 TCAGTAAAGCAGGAGTTTGAAAAGCAGGACGAACTGAAGCGATCGGCCATGAGAGCAGTC	
		1181 A A L L T I P E A E K S P L M S E F Q S 3541 GCGGCCCTGCTGACCATTCCCGAGGCCGAGAAGAGCCCGCTGATGAGCGAGTTCCAGTCG	
		1201 Q I S S N P E L L A A I F E S I Q K D S S 3601 CAGATCAGCTCCAACCCTGAGCTGGCAGCCATCTTTGAGAGCATCCAGAAAGACTCATCG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1221 S T N L E S M D T S - 3661 TCCACTAACTTGGAATCAATGGACACTAGTTAG	
WBC025E03.bFSP_20011710.abd	Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog 2 (avian) (ETS2), mRNA.	1 GCCCGGTTACTTCCTCCAGAGACTGACGAGTGCGGTGTCGCTCCAGCTCAGAGCTCCCGG 61 AGCCGCCCGGCCAGCGTCCGGCCTCCCTGATCGTCTCTGGCCGGCGCCCTCGCCCTCGCC 121 CGGCGCGCACCGAGCAGCCGCGGCGCCGAGCAGCCACCGTCCCGACCAAGCGCCGGCCC 181 TGCCCGCAGCGGCAGGATGAATGATTTCGGAATCAAGAATATGGACCAGGTAGCCCCTGT 241 GGCTAACAGTTACAGAGGGACACTCAAGCGCCAGCCAGCCTTTGACACCTTTGATGGGTC 301 CCTGTTTGCTGTTTTTCCTTCTCTAAATGAAGAGCAAACACTGCAAGAAGTGCCAACAGG 361 CTTGGATTCCATTTCTCATGACTCCGCCAACTGTGAATTGCCTTTGTTAACCCCGTGCAG 421 CAAGGCTGTGATGAGTCAAGCCTTAAAAGCTACCTTCAGTGGCTTCAAAAGGAACAGCG 481 GCGCCTGGGCATTCCAAAGAACCCTGGCTGTGGAGTGAGCAACAGGTATGCCAGTGGCT 541 TCTCTGGGCCACCAATGAGTTCAGTCTGGTGAACGTGAATCTGCAGAGGTTCGGCATGAA 601 TGGCCAGATGCTGTGTAACCTTGGCAAGGAACGCTTTCTGGAGCTGGCACCTGACTTTGT 661 GGGTGACATTCTCTGGGAACATCTGGAGCAAATGATCAAAGAAAACCAAGAAAAGACAGA 721 AGATCAATATGAAGAAAATTCACACCTCACCTCCGTTCCTCATTGGATTAACAGCAATAC 781 ATTAGGTTTTGGCACAGAGCAGGCGCCCTATGGAATGCAGACACAGAATTACCCCAAAGG 841 CGGCCTCCTGGACAGCATGTGTCCGGCCTCCACACCCAGCGTACTCAGCTCTGAGCAGGA 901 GTTTCAGATGTTCCCCAAGTCTCGGCTCAGCTCCGTCAGCGTCACCTACTGCTCTGTCAG 961 TCAGGACTTCCCAGGCAGCAACTTGAATTTGCTCACCAACAATTCTGGGACTCCCAAAGA 1021 CCACGACTCCCCTGAGAACGGTGCGGACAGCTTCGAGAGCTCAGACTCCCCTCCTCAGTC 1081 CTGGAACAGCCAGTCGTCCTTGCTGGATGTGCAACGGGTTCCTTCCTTCGAGAGCTTCGA 1141 AGATGACTGCAGCCAGTCTCTCTGCCTCAATAAGCCAACCATGTCTTTCAAGGATTACAT 1201 CCAAGAGAGGAGTGACCCAGTGGAGCAAGGCAAACCAGTTATACCTGCAGCTGTGCTGGC 1261 CGGCTTCACAGGAAGTGGACCTATTCAGCTGTGGCAGTTTCTCCTGGAGCTGCTATCAGA 1321 CAAATCCTGCCAGTCATTCATCAGCTGGACTGGAGACGGATGGGAGTTTAAGCTCGCCGA 1381 CCCCGATGAGGTGGCCCGCCGGTGGGGAAAGAGGAAAAATAAGCCCAAGATGAACTACGA 1441 GAAGCTGAGCCGGGGCTTACGCTACTATTACGACAAGAACATCATCCACAAGACGTCGGG 1501 GAAGCGCTACGTGTACCGCTTCGTGTGCGACCTCCAGAACTTGCTGGGGTTCACGCCCGA 1561 GGAACTGCACGCCATCCTGGGCGTCCAGCCCGACACGGAGGACTGAGGTCGCCGGGACCA 1621 CCCTGAGCCGGCCCCAGGCTCGTGGACTGAGTGGGAAGCCCATCCTGACCAGCTGCTCCG 1681 AGGACCCAGGAAAGGCAGGATTGAAAATGTCCAGGAAAGTGGCCAAGAAGCAGTGGCCTT 1741 ATTGCATCCCAAACCACGCCTCTTGACCAGGCTGCCTCCCTTGTGGCAGCAACGGCACAG 1801 CTAATTCTACTCACAGTGCTTTTAAGTGAAAATGGTCGAGAAAGAGGCACCAGGAAGCCG 1861 TCCTGGCGCCTGGCAGTCCGTGGGACGGGATGGTTCTGGCTGTTGAGATTCTCAAAGGA 1921 GCGAGCATGTCGTGGACACACACAGACTATTTTTAGATTTTCTTTTGCCTTTTGCAACCA 1981 GGAACAGCAAATGCAAAAACTCTTTGAGAGGGTAGGAGGGTGGGAAGGAAACAACCATGT 2041 CATTTCAGAAGTTAGTTTGTATATATTATTATAATCTTATAATTGTTCTCAGAATCCCTT 2101 AACAGTTGTATTTAACAGAAATTGTATATTGTAATTTAAAATAATTATATAACTGTATTT 2161 GAAATAAGAATTCAGACATCTGAGTTTTATTTCATTTTTCAATAGCACATATGGAATTT 2221 TGCAAAGATTTAATCTGCCAAGGGCCGACTAAGAGAAGTTGTAAAGTATGTATTATTTAC	SEQ ID NO:119

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2281 ATTTAATAGACTTACAGGGATAAGGCCTGTGGGGGTAATCCCTGCTTTTTGTGTTTTTT 2341 TGTTTGTTTGTTTTTTTTGGGGGGGTTTTCTTGCCTTGGTTCTGGCAAAGACTTTG 2401 TACATTTGGGAATTTTTATAAGAAACTTAATGTTATTATCTGGGGCACATTGGCCCCTG 2461 TGCTTTCTCCTTTAATTGTAATGTAAAAGCTATAAAGCGGTATTTTTCTTGACAAATGGC 2521 ATATGTTTTTCCATTTCTATGCATGCATTTAAATCAGTTTATACAAAAACTTATTTTAITT 2581 TTTTAGTTTTAACTGTGTTTCTCCGACAGCTCACCTCTCTGACCACCCAGCCATTTCC 2641 TTCCTGTGCTCCACGTTCTTCTGTATGATGAAAATAAGAATACTATTTTTGGAAATATGC 2701 GACTCCTTTTCAGAGACCAGGAGGGATTTATGTAGCAGCTATTTTTACTGCAAAAGTAAT 2761 TCACTGGAAAAAAATGTAATTTGTAAGAAAGCTTTATTTTTATCTCAGCTCTATGTAAAG 2821 TTAAAGTTACTGTACAGAGCTGAAGGACGGGGGCGGTAGGGGTCTTGATGAAACCTCTT 2881 GAACGAAGCACAGTTTGTCCCATCTTTGTTCACTCGTGTGTCTCAACCATCTTTAATAGCA 2941 TGCTGCTCCTTTTTTGCTCAGTGTCCCACAGCAAGATGACGTGATTCTTATTTTCTTGGACA 3001 CAGACTATTCTGAGGCACAGAGCGGGGACTTAAGATGGGAAAGAGAAAGCATCGGAGCCA 3061 TTCATTCGGAGAAAACGTTTTGATCAAAATGGAGACACTTTTGTAGTCGTTTCAAAAGAGCA 3121 CCTGAGTCATGTGTATTCCCGGCCTTTATAAATGACCCGGTCAAGTTGGTTTCAAAGTCC 3181 GACAGGCTTGTCTGTTTACTAGCTGCGTGGCCTTGGACGGGTGGCTGACATCTGTAAAGA 3241 ATCCTCCTGTGATGAAACTGAGGAATCGGGTGGCCGGGCAAGCTGGGAAGAGCAAAGCCA 3301 GAGCTGCGCTGCCTCAATACCCACACGAGACGATTTCCAGTATCTCAGCACAGGATGTTT 3361 TTCTCAAGCAGGCCCTGTTTATCTCTCGGACATCTGTTTATAACATCAACAGACATGCGA 3421 CTGGGAACATCTTGTTGCTGAAAGAAGTCATGAACCATTGGCTCATTTTATATGGCTCG 3481 AGCCACATGAAATTGCCAATATTTGACTTTTTATCTACGAAGTTGGCAGTTTTGTGTGG 3541 TCCAACCTAATAGTTATGGAATCTGAAGTCCAGTATAAACCTCTGGCGTGGTAATGAACA 3601 GGACTTAAGTATATAAAAATTTTGTAATTGGGCCTCTTCTTTCTCAAATAATAAAGTATTTT 3661 GTTTATATAAAAAAAAAAAAAA 1 M N D F G I K N M D Q V A P V A N S Y R 1 ATGAATGATTTCGGAATCAAGAATATGGACCAGGTAGCCCCTGTGGCTAACAGTTACAGA 21 G T L K R Q P A F D T F D G S L F A V F 61 GGGACACTCAAGCGCCAGCCAGCCTTTGACACCTTTGATGGGTCCCTGTTTGCTGTTTTT 41 P S L N E E Q T L Q E V P P T G L D S I S 121 CCTTCTCTAAATGAAGAGCAAACACTGCAAGAAGTGCCAACAGGCTTGGATTCCATTTCT 61 H D S A N C E L P L L T P C S K A V M S 181 CATGACTCCGCCAACTGTGAATTGCCTTTGTTAACCCCGTGCAGCAAGGCTGTGATGAGT 81 Q A L K A T F S G F K K E Q R R L G I P 241 CAAGCCTTAAAAGCTACCTTCAGTGGCTTCAAAAGGAACAGCGGCCCTGGGCATTCCA 101 K N P W L W S E Q Q V C Q W L L W A T N 301 AAGAACCCCCTGGCTGTGGAGTGAGCAACAGGTATGCCAGTGGCTTCTCTGGGCCACCAAT	SEQ ID NO:120

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		121 E F S L V N V N L Q R F G M N G Q M L C 361 GAGTTCAGTCTGGTGAACGTGAATCTGCAGAGGTTCGGCATGAATGGCCAGATGCTGTGT	
		141 N L G K E R F L E L A P D F V G D I L W 421 AACCTTGGCAAGGAACGCTTTCTGGAGCTGGCACCTGACTTTGTGGGTGACATTCTCTGG	
		161 E H L E Q M I K E N Q E K T E D Q Y E E 481 GAACATCTGGAGCAAATGATCAAGAAAACCAAGAAAAGACAGAAGATCAATATGAAGAA	
		181 N S H L T S V P H W I N S N T L G F G T 541 AATTCACACCTCACCTCCGTTCCTCATTGGATTAACAGCAATACATTAGGTTTTGGCACA	
		201 E Q A P Y G M Q T Q N Y P K G G L L D S 601 GAGCAGGCGCCCTATGGAATGCAGACACAGAATTACCCCAAAGGCGGCCTCCTGGACAGC	
		221 M C P A S T P S V L S S E Q E F Q M F P 661 ATGTGTCCGGCCTCCACACCCAGCGTACTCAGCTCTGAGCAGGAGTTTCAGATGTTCCCC	
		241 K S R L S S V S V T Y C S V S Q D F P G 721 AAGTCTCGGCTCAGCTCCGTCAGCGTCACCTACTGCTCTGTCAGTCAGGACTTCCCAGGC	
		261 S N L N L L T N N S G T P K D H D S P E 781 AGCAACTTGAATTTGCTCACCAACAATTCTGGGACTCCCAAAGACCACGACTCCCCTGAG	
		281 N G A D S F E S S D S L L Q S W N S Q S 841 AACGGTGCGGACAGCTTCGAGAGCTCAGACTCCCTCCTCCAGTCCTGGAACAGCCAGTCG	
		301 S L L D V Q R V P S F E S F E D D C S Q 901 TCCTTGCTGGATGTGCAACGGGTTCCTTCCTTCGAGAGCTTCGAAGATGACTGCAGCCAG	
		321 S L C L N K P T M S F K D Y I Q E R S D 961 TCTCTCTGCCTCAATAAGCCAACCATGTCTTTCAAGGATTACATCCAGAGAGGAGTGAC	
		341 P V E Q G K P V I P A A V L A G F T G S 1021 CCAGTGGAGCAAGGCAAACCAGTTATACCTGCAGCTGTGCTGGCCGGCTTCACAGGAAGT	
		361 G P I Q L W Q F L L E L L S D K S C Q S 1081 GGACCTATTCAGCTGTGGCAGTTTCTCCTGGAGCTGCTATCAGACAAATCCTGCCAGTCA	
		381 F I S W T G D G W E F K L A D P D E V A 1141 TTCATCAGCTGGACTGGAGACGGATGGGAGTTTAAGCTCGCCGACCCCGATGAGGTGGCC	
		401 R R W G K R K N K P K M N Y E K L S R G	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1201 CGCCGGTGGGGAAAGAGGAAAAATAAGCCCAAGATGAACTACGAGAAGCTGAGCCGGGGC 421 L R Y Y Y D K N I I H K T S G K K R Y V Y 1261 TTACGCTACTATTACGACAAGAACATCATCCACAAGACGTCGGGAAGCGCTACGTGTAC 441 R F V C D L Q N L L G F T P E E L H A I 1321 CGCTTCGTGTGCGACCTCCAGAACTTGCTGGGGTTCACGCCCGAGGAACTGCACGCCATC 461 L G V Q P D T E D - 1381 CTGGGCGTCCAGCCCGACACGGAGGACTGA	
WBC027B01.bFSP_20012210.abd	No Homology.	1 CCTTATTTAACCAGTCAAGTAACCAACCAAAGTGTTAAGTTTAGGCATTTAGGAAAAGCT 61 GTAAACTCTCACATTGCTGAAATTCCCCCTCATTGTGTCCCCTGGCCAGGTGCCTCCCGA 121 GGGTTGGTCTTGTTCCATTTTGTTCTGGTCACCGGATGATTCTTCCTTCGCCATCAAAT 181 ACTTCTTCGTAATGGTCACCATCTGAGGGTTTGTCCCATTTCTGGATTCTTCCCAAGCTC 241 TAACCCAACACTCCTCCTATTTAAACATCCCACCGTGGTCAGACCTCTGTGGTGAAGCT 301 GACTCTCACCCCTCACTGTTCTGTCTACAGAGCTGCTCGCTAGAGTGGCCTGCCCTGCTG 361 CTCGAGCGCGAGGGCGGGCACCGTGGAAGAACTCTGACTGCTTGCAGACTGTCTCTGCT 421 TGGGTTCTTATTGCTTTCTGCTTTTCGAAATTATGCCAGCCTCTGCCTGGGTCTGGGTCT 481 AGATTAGGATTTAAGCTGGTAAAGGAAAATGTTGGTAAATCCTCTGCTCAGAAGTCATTT 541 ATCATGTTTCTATTTAGGATTAAAGTTATTAACTTACCCTATTTAGAAGCTGACCCATT 601 TAAATATAACTCTTCGAAGTTCTACTTCTCTTTATTCTTGATGTCTTAAGATGATTCTA 661 ACTGGCATCTGGGGCTTGGGGTCTCCCTGTCCTTCCATTATCTTTTGTTTTTCCCAAGAA 721 ATTCTGAACACATACCTCTTTGCTAAACCAGGATCCTCTGTTTTGACTCTGTTTTCGTAC 781 CAGGTAAGAGGACTTCTTTCAAAGAGCTTTTTACTGCTTGACCAAAGAACAAATCTGAAA 841 ATCACCAAGTTTAACGTTGTTACTTTTTCTGTTGACCAAAGCTTAAGTGAGGAGAATTTTT 901 GGCTT SEQ ID NO:121	SEQ ID NO:121
		1 ACTCTCAGCATCTGAGAGCCTTAAGCCCCCGAAATATTCCAAGGTTTTATTGTACTTTTT 61 TAAAGAACAGAAAAGGGTGAATAAAAGAACCAAGTAGAAATGCAGGGACTATATTTAGCA 121 TGTACAAGTTGAAGTAAAAAAGAGATTGTGGCAACTAAGTAACTAGTCCTGTAAAATAAA 181 ATACATTGCTCACCTTTCCTGTACATCTAGTTCCTCACCATAGAACCCACCTGGGCAAAC 241 CCCAACTCTAGAACTCTCAGACGCTGCGACAGCGTCCGAACAGGCAAAGAGCTAGATTTC 301 AAAGGCTCGCTTCGCAAAAATACTCCATCTTGGCACCTTGCTCTTTTAGAAAGGCCTTAA 361 TGATTGAAAAAAATTACTTGGCCCCTGAGATATAATTTTCAGCCCCTGAAGCTTGCTAA 421 TATAAAGAACAACTTTTAATTATGAGAAATAAAAACTGAGATGCTGTAAAATCCTGTCAG 481 ACCACCGATAGACTGATCGGAAAGACAGTGTCAGCTCAGAAGGGGTCAGCGGACACTGTA 541 CGGAGCGTGGGTGTTTGGATTCTCAGGGAAACTCCGACTGGATTTATTTTTCTACCTGTG 601 TATGTCTTATATAGTGCTGGTGCTCTATAGTTTTGTTCTCTATTTAATCTGTATGTATTA 661 ACGATAACACGTTTGATAGTTGTCACATAAAAAAAAAAAAAA SEQ ID NO:122	
WBC027D09.bFSP_20	No homology		

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
012210.abd		1 TGCATCCTGTCAGGATAGAATCCTATCAGACAACCAATTTGGATTTGTCCTCTTATGGAG 61 AACGTTCATTTCCGTCCCTTGATTAAGATGGTGTGTGCTATGCTTCTCCATCGCAAAGTC 121 ACTCTTTTATCCTTTGAAATTAACAAATATTTGTTTGGGGATGTGCTTGAGATGATGTAA 181 ATGTCCTATTCCTCATTAAATCTCTAATTTATCCATTATTCCTGATATAGACTTAGTGA 241 TTCTTATTTTATTCGGTGGGCTGTAATCTGTTATCATTATCATCTCATTTATCTATTCTC 301 ATGTGCCCATTTTTCTTGATTTGGCCAATAGGACACCTTCAAGCTGACTTCCGTGTCTTT 361 TTTGACTTGTCCCTACTTCCTTACTTTCTGACAGCAATATGATTTTCCTGGCTCATCTCA 421 TTCTTTCCCTTCCCCAGCCCAGGAATCTACCATTTCTCTAAGGAGCCTTGCTTTCTTTTA 481 GTGGAGAATAGTATTAAGAAAACCAAGATCTGGGTACTAAATGATCTCATTGCTATTGGA 541 GTCTTGCTACTCCTAGATCCTTTCCATGGACAGAGGTTGGGAATGTGTACACACACACAT 601 ACACATATGCACACATACACATGCAAACATAATTTGTTCATGTTCAACATCTATATTTCT 661 ATATTTATCTATTATTTAAAAATCATGATGACACACTCACATCTCTGATTTCAGTCCAACAC 721 TACAGGGTTCATTCTGGTTCTCCACTTTCATATTTTGTAATTTCCTTCCCCACCAGTGAGA 781 AACCGGGCTTCCATTATCCTCCACATATATCCTTATTTGGCCAGTTCTTCTGTATGTATC 841 CAGTATCCCAT 1 TGGTAGAAATGAGTCAAAGTTCTGAGTGTTAGGATAGTTGAGATGAACTGGAGCTACTTC 61 ACAATTTTGCCTGCACTCTTCATTCTTACCTGCACCCTAACCCCTTGCACCATGACTGAT 121 GTGTGGCAAATACTCAATGTTAGTGAATAGAACACGTTAGTTCTTGTGTTATTGCATTAG 181 CTCCCTTCGATGGGCATCTCTATGAATTAGATGGATGGAAACTATTTCCAATTAACTTTA 241 TTAGAGGATGCCACAGAGGTTTGCAAGAAACTTATGGAATGTGACCCTGATGAATTAGGA 301 TTCATTGTGATCACTCTTTTCTGACGCATAGCTTGTCAATAATGGAAGCACCAAATACTGT 361 CTTATTTGCAACAGAAATTAAATTTTTGCTGCCATACACTAACTCAAAAATTTTGATATT 421 TTCATTAACTTGACTTGATAAACTTTATGTGAATTAAACCTTGTGAATTAAACCTTGTCT 481 TTAAAAAAAAAAA	SEQ ID NO:123 SEQ ID NO:124
WBC027E07.bFSP_20 012210.abd	No Homology	1 ACTCATTTATATCTTGTAGTTTACTATTTTACCTCTAGAAATAGACTTAAAGTAGTTTG 61 TGTGTGAATATTTAACTACACGAAAGTTAGCAAAATTACACATTTGGAAACCTTCTATTCC 121 ATATGTTAGCATTTATTCCAACATCTTTTTAGCCTTATTTAGTCTAATTTAAAATTTTCA 181 AGCAACCCTATCTTATCATCTTCACATGGTGTTTACAATTTTGCAACGTGGATTATTCTC 241 TGTATAATATGTGAAATTCATTGCTTGATACTTTTGACCCAAAATTATGTTTGTTACAGT 301 TGAACTTAAATAAAGATCTTTAAACAAAAAAAAAAAAAAAAAAAACGCGAGACTAGTTCTCT 361 CGTGACACCCACTCTTCCACCTTCGATGCTGGGGCTGGCATTGCCCTCAACGACCACTTT 421 GTCAAGCTCATTTCCTGGTATGACAATGAATTTGGCTACAGCAATAGGGTGGTGGACCTT 481 ATGGCCCACATGGCCTCCAAGGAGTAAGAGCCCCCTGGACCACCAATCACCCAGCAAGAG 541 AAGGAGAAAGGCCCCTCAGCTGCTGGGAATGCTTGTCCCAACTTGACCCCCTAACATATTG 601 AGAGTCTCCTGACCTCCACAGTTTCCATCTCAGACCCCCCTGAAGAAGGGGAGGGGCTTG 661 GGGAGCCCTACCTTGTCATGTACCATCAATAAAGTACACTGTACCCAAAAAAAAAAAAAA 721 AAAAAAAAA	SEQ ID NO:125
WBC027F05.bFSP_20 012210.abd	Homo sapiens collagenase mRNA.	1 GCTCGCCAGGGAAGGGCCCTACCCAGAGGACAGAAAGAAAGCCAGGAGGGGTAGAGTTTG	SEQ ID NO:126

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		61 AAGAGAAGATCATGTTCTCCCTGAAGACGCTTCCATTTCTGCTCTTACTCCATGTGCAGA 121 TTTCCAAGGCCTTTCCTGTATCTTCTAAAGAGAAAAATACAAAAACTGTTCAGGACTACC 181 TGGAAAAGTTCTACCAATTACCAAGCAACCAGTATCAGTCTACAAGGAAGAATGGCACTA 241 ATGTGATCGTTGAAAAGCTTAAAGAAATGCAACGATTCTTTGGTTGAATGTGACAGGGA 301 AGCCAAATGAGGAAACTCTGGAAATGATGCAGAAACCTCGCTGTGGAGTGCCTGACACTG 361 GAGAGTTTATGATAACCCCAGGGAACCCCAAGTGGGAACGAAATAACCTGACCTACAGGA 421 TTATTAACTATACCCCACAGCTGTCAGAGGCTGAGGTAGAAAGAGCTATCAAGGATGCCT 481 TTGAACTCTGGAGTGTTGCATCACCTCTCATCTTCACCAGGATCTCACAGGGAGAAGCAG 541 ACATCAGGATTGCTTTTTACCAAGGAGATCATGGTGACAATTCTCCATTTGATGGACCCA 601 ATGGAATCCTTGCTCATGCCTTTCAGCCCAGGTCCCAGGTATTGGAGGAGATGCTCATTTTG 661 ATGCAGAAGAAACATGGACCGACAACAGAACAAATTACAACTTGCTTATTGTTGCTGCCC 721 ATGAATTTGGCCATTCCTTGGGGCTCGCTCACTCCACAAACCCTGCTGCCTTGATGTATC 781 CCACCTACGCTTTCAGGGACCCCAGCACCTACTTGCTCTCTCAGGATGACATCAATGGCA 841 TTCAGGCCATCTATGGACCTTCAAATGACCCTATCCAACCAACTGGATCAACCGCGCCCA 901 CCGCCTGTGACCCCAGACTGACATTTGATGCTATCGTCACACTCCGCGGAGAAACGCTTT 961 TCTTTAAGACAGGTACTTTTGGAGAAGGCATCCCCAACTGCCAACAGTCGAACTCAATT 1021 TCATTTCTCTGTTCTGGCCATCCTTGCCAAATGGTATACAGGCGGCTTATGAGGATTTTG 1081 ACAGGGACCTAATTTTCCTATTTAAAGGCAACCAATACTGGGCTCTGAATGGCTATGACA 1141 TTCAGCAAGGTTATCCCAAGGACATATCAAACTACGGCTTCCCAAGCAGTGTCCAAGCAA 1201 TTGATGCAGCTGTTTCCTATAGGAGTAAAACATACTTCTTTGTAAATGATCAATTCTGGA 1261 GATATGATAACCAAAGACGATCCATGGAAGCAGGTTATCCCCAAAGCATAGCAAGTACCT 1321 TTCCAGGAATAGGAAGCAGAATTGATGCAGTTTTCCAGCAAGATGACTTCTTTTCTTTCT 1381 TCAGCGGACCAGTTTATTATGCATTTGATCTTAATACTCAGAGAGTTACTAGGGTTGCAA 1441 GAATCAATAAATGGCTTAACTGTAGATATGGCTGAAGCAAAATCAAATGTGGCTGTATCC 1501 ACTTTCAGAATGTTGAAGGGAAGTTCAGCATGCATTTTCGTTACATTGTGTCCTGCTTAT 1561 ACTTTTCTCAATATTAAGTCATTGTTTCCCATCACTGTATCCATTCTACCTGTCCTCCGT 1621 GAAAATATGTTTGGAATATTCCACTATTTGCAGAGGCTTATTCAGTTCTTACACATTCCA 1681 TCTTACATTAGTGATTCCATCAAGAGAAGGAAAGTAAGCCTTTTTGTCACCTCAATATT 1741 TACTATTTCAATACTTACATATCTGACTTCTAGGATTTATTGTTATATTACTTGCCTATC 1801 TGACTTCATACATCCCTCAGTTTCTTAAAATGTCCTATGTATATCTCTTACATGCAATTT 1861 AGAACTAGATTTTGGTTAGAAGTAAGGATTATATAAACAACCTAGACAGTACCCTTGGCCTT 1921 TACAGAAAATATGGTGCTGTTTTCTACCCTTGGAAAGAAATGTAGATGATATGTTTTCGTG 1981 GGTTGAATTGTGTCCCCCATAAAAGATATGTTGAAGTTCTAACCCCAGGTACCCATGAAT 2041 GTGAGCTTACCAGGGTCTTTGCAGATGTAATTAGTTTAAGTTAAGGTGAGATCACACTGAA 2101 TTAGGGTGGGCTCTAAATCCATTATGACTGTTGTTCTTATAAGAAGAAGAGCATAGCC 2161 ACCTAGGGGAGGAGGCCGTGTGAAGACAGAGGCAGAGATTGGAGTGACGCATCTCCAAGC 2221 CAA 1 M F S L K T L P F L L L L H V Q I S K A SEQ ID NO:127 1 ATGTTCTCCCTGAAGACGCTTCCATTTCTGCTCTTACTCCATGTGCAGATTTCCAAGGCC 21 F P V S S K E K N T K T V Q D Y L E K F 61 TTTCCTGTATCTTCTAAAGAGAAAAATACAAAAACTGTTCAGGACTACCTGGAAAAGTTC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		41 Y Q L P S N Q Y Q S T R K N G T N V I V 121 TACCAATTACCAAGCAACCAGTATCAGTCTACAAGGAAGAATGGCACTAATGTGATCGTT	
		61 E K L K E M Q R F F G L N V T G K P N E 181 GAAAAGCTTAAAGAAATGCAACGATTCTTTGGGTTGAATGTGACAGGGAAGCCAAATGAG	
		81 E T L E M M Q K P R R C G V P D T G E F M 241 GAAACTCTGGAAATGATGCAGAAACCTCGCTGTGGAGTGCCTGACACTGGAGAGTTTATG	
		101 I T P G N P K W E R N N L T Y R I I N Y 301 ATAACCCCAGGGAACCCCAAGTGGGAACGAAATAACCTGACCTACAGGATTATTAACTAT	
		121 T P Q L S E A E V E R A I K D A F E L W 361 ACCCCACAGCTGTCAGAGGCTGAGGTAGAAAGAGCTATCAAGGATGCCTTTGAACTCTGG	
		141 S V A S P L I F T R I S Q G E A D I R I 421 AGTGTTGCATCACCTCTCATCTTCACCAGGATCTCACAGGGAGAAGCAGACATCAGGATT	
		161 A F Y Q G D H G D N S P F D G P N G I L 481 GCTTTTTACCAAGGAGATCATGGTGACAATTCTCCATTTGATGGACCCAATGGAATCCTT	
		181 A H A F Q P G P G I G G D A H F D A E E 541 GCTCATGCCTTTCAGCCAGGCCCAGGTATTGGAGGAGATGCTCATTTTGATGCAGAAGAA	
		201 T W T D N R T N Y N L L I V A A H E F G 601 ACATGGACCGACAACAGAACAAATTACAACTTGCTTATTGTTGCTGCCCATGAATTTGGC	
		221 H S L G L A H S T N P A A L M Y P T Y A 661 CATTCCTTGGGGCTCGCTCACTCCACAAACCCTGCTGCCTTGATGTATCCCACCTACGCT	
		241 F R D P S T Y L L S Q D D I N G I Q A I 721 TTCAGGGACCCCAGCACCTACTTGCTCTCTCAGGATGACATCAATGGCATTCAGGCCATC	
		261 Y G P S N D P I Q P T G S T A P T A C D 781 TATGGACCTTCAAATGACCCTATCCAACCAACTGGATCAACCGCGCCCACCGCCTGTGAC	
		281 P R L T F D A I V T L R G E T L F F K D 841 CCCAGACTGACATTTGATGCTATCGTCACACTCCGCGGAGAAACGCTTTTCTTTAAGAC	
		301 R Y F W R R H P Q L P T V E L N F I S L 901 AGGTACTTTTGGAGAAGGCATCCCCAACTGCCAACAGTCGAACTCAATTTCATTTCTCTG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		321 F W P S L P N G I Q A A Y E D F D R D L 961 TTCTGGCCATCCTTGCCAAATGGTATACAGGCGGCTTATGAGGATTTTGACAGGGACCTA 341 I F L F K G N Q Y W A L N G Y D I Q Q G 1021 ATTTTCCTATTTAAGGCAACCAATACTGGCTCTGAATGGCTATGACATTCAGCAAGGT 361 Y P K D I S N Y G F P S S V Q A I D A A 1081 TATCCCAAGGACATATCAAACTACGGCTTCCCAAGCAGTGTCCAAGCAATTGATGCAGCT 381 V S Y R S K T Y F F V N D Q F W R Y D N 1141 GTTTCCTATAGGAGTAAAACATACTTCTTTGTAAATGATCAATTCTGGAGATATGATAAC 401 Q R R S M E A G Y P Q S I A S T F P G I 1201 CAAAGACGATCCATGGAAGCAGGTTATCCCCAAAGCATAGCAAGTACCTTTCCAGGAATA 421 G S R I D A V F Q Q D D F F L F F S G P 1261 GGAAGCAGAATTGATGCAGTTTTCCAGCAAGATGACTTCTTTCTTTTCTTCAGCGGACCA 441 V Y Y A F D L N T Q R V T R V A R I N K 1321 GTTTATTATGCATTTGATCTTAATACTCAGAGAGTTACTAGGGTTGCAAGAATCAATAAA 461 W L N C R Y G - 1381 TGGCTTAACTGTAGATATGGCTGA	SEQ ID NO:128
WBC027H11.bFSP_20012210.abd	Homo sapiens ribosomal protein S8, mRNA (cDNA clone MGC:90249 IMAGE:6527505).	1 GCGCCGAGCGATGGGCATCTCTCGGGACAACTGGCACAAGCGCCGCCAAGACCGGGGGCAA 61 GAGAAAGCCCTACCACAAGAAGCGGAAGTATGAGCTGGGCCGGCCCGCGGCCAACACGAA 121 GATTGGCCCCCCGCCGCATACACACAGTCCGCGTGCGGGGAGGCAACACAAGAAGTACCGGGC 181 CTTGAGGTTGGACGTGGGGAACTTCTCCTGGGGCTCCGAGTGCTGTACGCGCAAAACAAG 241 GATTATTGATGTTGTCTACAATGCATCCAACACAACGAATTGGTCCGCACCAAGACCCTGGT 301 GAAGAACTGCATCGTGCTGGTTGACAGCACACCGTACCGACAGTGGTACGAGTCCCACTA 361 CGCACTGCCCCCTGGGCCGCAAGAGGGGGCCAAGCTGACTCCTGAGGAGGAAGAAATTTT 421 AAACAAAAAACGATCTAAAAAAAATTCAGAAGAAATATGATGAAAGGAAAAAGAATGCCAA 481 AATCAGCAGTCTCCTGGAGGAGCAGTTCCAGCAGGGCAAGCTTCTCGCATGTATCGCTTC 541 CAGACCAGGCCAGTGTGGCCGAGCAGACGGCTATGTGCTCGAGGGCAAGGAGCTGGAGTT 601 CTATCTGAGGAAAATCAAGGCCCGGAAAGGCAAATAAATCCTTGTTTTGTCTTCACCCAT 661 GTAATAAAGGTGTTTATTGTTTTGTTCCCAAAAAAAAAAAAAAA 1 M G I S R D N W H K R R K T G G K R K P 1 ATGGGCATCTCTCGGACAACTGGCACAAGCGCCGCAAGACCGGGGGCAAGAGAAAGCCC 21 Y H K K R K Y E L G R P A A N T K I G P 61 TACCACAAGAAGCGGAAGTATGAGCTGGGCCGGCCCGCGGCCAACACGAAGATTGGCCCC	SEQ ID NO:129

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		41 R R I H T V R V R G G N K K Y R A L R L 121 CGCCGCATACACACAGTCCGCGTGCGGGGAGGCAACAAGAAGTACCGGGCCTTGAGGTTG 61 D V G N F S W G S E C C T R K T R I I D 181 GACGTGGGGAACTTCTCCTGGGCTCCGAGTGCTGTACGCGCAAAACAAGGATTATTGAT 81 V V Y N A S N N E L V R T K T L V K N C 241 GTTGTCTACAATGCATCCAACAACGAATTGGTCCGCACCAAGACCCTGGTGAAGAACTGC 101 I V L V D S T P Y R Q W Y E S H Y A L P 301 ATCGTGCTGGTTGACAGCACACCGTACCGACAGTGGTACGAGTCCCACTACGCACTGCCC 121 L G R K K G A K L T P E E E E I L N K K 361 CTGGGCCGCAAGAAGGGGGCCAAGCTGACTCCTGAGGAGGAAGAAATTTTAAACAAAAAA 141 R S K K I Q K K Y D E R K K N A K I S S 421 CGATCTAAAAAAATTCAGAAGAAATATGATGAAAGGAAAAAGAATGCCAAAATCAGCAGT 161 L L E E Q F Q Q G K L L A C I A S R P G 481 CTCCTGGAGGAGCAGTTCCAGCAGGGCAAGCTTCTCGCATGTATCGCTTCCAGACCAGGC 181 Q C G R A D G Y V L E G K E L E F Y L R 541 CAGTGTGGCCGAGCAGACGGCTATGTGCTCGAGGGCAAGGAGCTGGAGTTCTATCTGAGG 201 K I K A R K G K - 601 AAAATCAAGGCCCGGAAAGGCAAATAA	SEQ ID NO:130
WBC028D04.bFSP_20012310.abd	Homo sapiens hypothetical protein FLJ25421, mRNA (cDNA clone MGC:33348 IMAGE:4831324).	1 GGGGACCGGCCTGGCCCTTGAGCCTGGCTGGAGTAGGTGGAATATCCTGGGGAGAGGAA 61 GTTTGGTCGTTGGGCAGCGGCCGACTTTCCTCTCAGGAAATTGATACTTTATCAACATAG 121 AGATTAATTATTTGTATTTGGGAGCAGCAGAACTGGGGACCAATTACCTGTCAAGAGTTT 181 TATAAACCCGTGACATAAACTGTTATTCCATTGCTTTCATCCTCCATCTCACCTTGGAAC 241 TTGTATTACTTATGGCGTTCAGGAGACAAGTGAAAAACTTTGTGAAAAATTACTCAGATG 301 CTGAAATAAAAGTCAGGGAAGCAACTTCTAACGACCCTTGGGGTCCCTCTAGTTCTCTGA 361 TGTTAGATATCAGTGACTTGACTTTCAACACAATTTCTCTCTCAGAGATTATGAATATGC 421 TGTGGCACAGACTCAATGACCATGGGAAGAACTGGCGCCACGTGTATAAATCCCCTTACCC 481 TAATGGATTATCTCATCAAGAATGGATCAAAGAAAGTTATTCAGCATTGCAGAGAGGGGT 541 TCTGTAACCTTCAAACACTAAAAGATTTTCAGCACATAGATGAAGCTGGAAAAGACCAAG 601 GTTATTATATCCGGGAAAAATCTAAGCAAGTCATCACATTGCTGATGGATGAACCATTGC 661 TGTGTAAAGAGAGGGAAGTGGCATGTCGGACTAGACAGCGTACCTCCCACTCTATATTGT 721 TTTCTAAAAGACAACTTGGTTCAAGTAACTCACTGACAGCGTGCACTTCTGCCCCCACAC 781 CGGATATTTCTGCTTCAGAGAAGAAGTATAAGCTTCCTAAGTTTGGAAGGTTACATAATA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		841 AAAGAAATGTGTGCAAGGCAGGATTGAAACAAGAGCATTGCCAAGATGTTCATTTGCCTA 901 CAGAAACTATGTTGTCCCAGGAAACACTTCCACTCAAGATTCATGGTTGGAAATCAACAG 961 AGGACCTGATGACATTTTTGGATGATGATCCAGAGCTGCCTTTACTAGCAACACCTCCTT 1021 CCATTGTCTCTCCAATCACTTGCTTGTCAGAAGCAGAAGAAGTTTGTAATCTTTCGGGTG 1081 CAGATGCTGTGCCTACTCTCTCAGAAAATAGTCCTTCTGGGCAGAGAGATGTGAGTTTGG 1141 ACAAGAGATCAGATGGTATCTTTACAAATACTGTCACAGAAAACCTCTTGGAAACACCTT 1201 TAGAAAAGCAATCAGCTGCAGAAGGTCTTAAAACATTGACAATTTTACCAGCATGTTGGT 1261 CAAGTAAAGAGGAGTTTATCAGCCCCGACTTAAGGGTATCAAAGTCAGATTCTACTTTCC 1321 ATAACCAGGCCTCTGTAGAAACACTCTGTCTCTCTCCCTCATTCAAAATATTTGACCGAG 1381 TGAAGGAGATTGTAATCAACAAGGCCTACCAGAAACCAGCACAATCCAGCATTCAGATGG 1441 ATGATAAAATCCTCAAGACAACCACACGGGTTTCAACTGCTTCTGAGGGAGCATCTTCCT 1501 TTTCTCCTTTATCCATGTCATCTCCTGATTTAGCCTCTCCAGAGAAGTCAGCTCATCTCT 1561 TATCACCAATTCTGGCCGGACCTTCCTTCTGGACTCTGTCCCATCAACAGTTGTCTTCTA 1621 CCTCCTTTAAAGATGAAGATAAGACAGCCAAGCTGCATCACCCCTTTGCTCCTGGAGGCC 1681 CAGTGTCTTCTGATGAAGAGGAAAATGACAACCTCAATCTACTGGAAATTCTTCCAGATA 1741 ACTCTGATTCTGCTCAAAAGAAAAGTCACATTTCCAGCAGTAACTGGGTAGAGTTTTCCA 1801 CCCAAACTGTAGACCCCTTCACCTCTATGTCCTGTTCTGGTTTTCAGACAAGCAAAGGCC 1861 TGCCTAGGGAGCCTGAAGTGAAGAATTCCATTAAGGGTCTTCTAGGGGAGGTAAAGAATG 1921 CGATAGTCAAATTACACGAAGATCTGAGCATGGTGATCCAGGAGCTGAACGTCATCAATA 1981 ACATCTTGATGAGCATGAGTCTGAATAGTTCACAAATAAGCCAGTCTTCCCAGGTCCCCC 2041 AGTCTTCTGAGGGGGGCTCAGATCCAGTCTAATCATCACAATATCTATTTTTGATAGAAC 2101 TCGTGTGGTTCCACTTCCCCAAGACTTACGTTAGCATTGTATAAATTCATATTATTATGG 2161 CAAAAAAGGGGATGGTTTGATTTCTCTTTGTCAGGTTTGTTAACAAGTATCTTTCAAACC 2221 AGTAAATTCATTCAGGTGGTTTATTTTTTAAAGAGAAAAAGTATCCCCTTTGATAATATC 2281 ATCAGATTTAGATATTAGTTCATTTGAAACTGAAAAGAATTTTATTCTTTCATGCTCTGT 2341 ACCTCAAATGGGTTAAGCATTAGTGAAATTTGTGGTAAGACCTCAAACTGCAAGTGACTA 2401 TTGCAGAGCCTTTGGATAAGGGAGGCAGGAAGAAGCTCTTTATCTTTCAACTGTATGGAG 2461 CTTGTTAACAAGCCTCTGAGGTGACCTAGGAGGATTGAGTTTGGGGGTATACATTTCACA 2521 CATTCTTTTGCAAGTTTTAGGTTCTGCAACCAAGGGCCAGAAATCTTTTCTTTCTTCCAG 2581 ATGCTAGTGTTAGGAGTTAAATGGAAACAAGAAGGACATGGGGCAAATGTTTTTACTGTC 2641 AATGTATATTGCAAAGTGAATTCAAATGCATCCTTTTATTCTACTTCAGAAAATAAATTT 2701 GATATTTTTCAAAAAAAAAAAAAAA	
		1 M A F R R Q V K N F V K N Y S D A E I K 1 ATGGCGTTCAGGAGACAAGTGAAAAACTTTGTGAAAAATTACTCAGATGCTGAAATAAAA 21 V R E A T S N D P W G P S S S L M L D I 61 GTCAGGGAAGCAACTTCTAACGACCCTTGGGGTCCCTCTAGTTCTCTGATGTTAGATATC 41 S D L T F N T I S L S E I M N M L W H R 121 AGTGACTTGACTTTCAACACAATTTCTCTCTCAGAGATTATGAATATGCTGTGGCACAGA 61 L N D H G K N W R H V Y K S L T L M D Y	SEQ ID NO:131

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		181 CTCAATGACCATGGGAAGAACTGGCGCCACGTGTATAAATCCCTTACCCTAATGGATTAT	
		81 L I K N G S K K V I Q H C R E G F C N L	
		241 CTCATCAAGAATGGATCAAAGAAAGTTATTCAGCATTGCAGAGAGGGTTCTGTAACCTT	
		101 Q T L K D F Q H I D E A G K D Q G Y Y I	
		301 CAAACACTAAAAGATTTTCAGCACATAGATGAAGCTGGAAAAGACCAAGGTTATTATATC	
		121 R E K S K Q V I T L L M D E P L L C K E	
		361 CGGGAAAAATCTAAGCAAGTCATCACATTGCTGATGGATGAACCATTGCTGTGTAAAGAG	
		141 R E V A C R T R Q R T S H S I L F S K R	
		421 AGGGAAGTGGCATGTCGGACTAGACAGCGTACCTCCCACTCTATATTGTTTTCTAAAAGA	
		161 Q L G S S N S L T A C T S A P T T P D I S	
		481 CAACTTGGTTCAAGTAACTCACTGACAGCGTGCACTTCTGCCCCCACACCGGATATTTCT	
		181 A S E K K Y K L P K F G R L H N K R N V	
		541 GCTTCAGAGAAGAAGTATAAGCTTCCTAAGTTTGGAAGGTTACATAATAAAGAAATGTG	
		201 C K A G L K Q E H C Q D V H L P T E T M	
		601 TGCAAGGCAGGATTGAAACAAGAGCATTGCCAAGATGTTCATTTGCCTACAGAAACTATG	
		221 L S Q E T L P L K I H G W K S T E D L M	
		661 TTGTCCCAGGAAACACTTCCACTCAAGATTCATGGTTGGAAATCAACAGAGGACCTGATG	
		241 T F L D D D P E L P L L A T P P S I V S	
		721 ACATTTTTGGATGATGATCCAGAGCTGCCTTTACTAGCAACACCTCCTTCCATTGTCTCT	
		261 P I T C L S E A E E V C N L S G A D A V	
		781 CCAATCACTTGCTTGTCAGAAGCAGAAGAAGTTTGTAATCTTTCGGGTGCAGATGCTGTG	
		281 P T L S E N S P S G Q R D V S L D K R S	
		841 CCTACTCTCTCAGAAAATAGTCCTTCTGGGCAGAGAGATGTGAGTTTGGACAAGAGATCA	
		301 D G I F T N T V T E N L L E T P L E K Q	
		901 GATGGTATCTTTACAAATACTGTCACAGAAAACCTCTTGGAAACACCTTTAGAAAAGCAA	
		321 S A A E G L K T L T I L P A C W S S K E	
		961 TCAGCTGCAGAAGGTCTTAAAACATTGACAATTTTACCAGCATGTTGGTCAAGTAAAGAG	
		341 E F I S P D L R V S K S D S T F H N Q A	
		1021 GAGTTTATCAGCCCCGACTTAAGGGTATCAAAGTCAGATTCTACTTTCCATAACCAGGCC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		361 S V E T L C L S P S F K I F D R V K E I 1081 TCTGTAGAAACACTCTGTCTCTCTCCCTCATTCAAAATATTTGACCGAGTGAAGGAGATT	
		381 V I N K A Y Q K P A Q S S I Q M D D K I 1141 GTAATCAACAAGGCCTACCAGAAACCAGCACACAATCCAGCATTCAGATGGATGATAAAATC	
		401 L K T T T R V S T A S E G A S S F S P L 1201 CTCAAGACACAACCACACGGGTTTCAACTGCTTCTGAGGGAGCATCTTCCTTTTCTCCTTTA	
		421 S M S S P D L A S P E K S A H L L S P I 1261 TCCATGTCATCTCCTGATTTAGCCTCTCCAGAGAAGTCAGCTCATCTCTTATCACCAATT	
		441 L A G P S F W T L S H Q Q L S S T S F K 1321 CTGGCCGGACCTTCCTTCTGGACTCTGTCCCATCAACAGTTGTCTTCTACCTCCTTTAAA	
		461 D E D K T A K L H H P F A P G G P V S S 1381 GATGAAGATAAGACAGCCAAGCTGCATCACCCCTTTGCTCCTGGAGGCCCAGTGTCTTCT	
		481 D E E E N D N L N L L E I L P D N S D S 1441 GATGAAGAGGAAAATGACAACCTCAATCTACTGGAAATTCTTCCAGATAACTCTGATTCT	
		501 A Q K K S H I S S S N W V E F S T Q T V 1501 GCTCAAAAGAAAAGTCACATTTCCAGCAGTAACTGGGTAGAGTTTTCCACCCAAACTGTA	
		521 D P F T S M S C S G F Q T S K G L P R E 1561 GACCCCTTCACCTCTATGTCCTGTTCTGGTTTTCAGACAAGCAAAGGCCTGCCTAGGGAG	
		541 P E V K N S I K G L L G E V K N A I V K 1621 CCTGAAGTGAAGAATTCCATTAAGGGTCTTCTAGGGGAGGTAAAGAATGCGATAGTCAAA	
		561 L H E D L S M V I Q E L N V I N N I L M 1681 TTACACGAAGATCTGAGCATGGTGATCCAGGAGCTGAACGTCATCAATAACATCTTGATG	
		581 S M S L N S S Q I S Q S S Q V P Q S S E 1741 AGCATGAGTCTGAATAGTTCACAAATAAGCCAGTCTTCCCAGGTCCCCCAGTCTTCTGAG	
		601 G G S D P V - 1801 GGGGGCTCAGATCCAGTCTAA	
WBC028E11.bFSP_20012310.abd	Homo sapiens regulator of G-protein signaling	1 AAGAAACGCAGCTCTTGACTGCTTTTTTGTAACATTACTGTATTATTGTGATAACTTTT 61 TATTCTACTATGTATATGTATGGAATAGTATTAATAAATGAACTAGGGAAGGATGTAATA	SEQ ID NO:132

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
	13 mRNA.	121 AATTAGACGTCTCTTCATTTTAGAGAAAGAAGATGGAAACATCATTGGTTTTCTTTTCTC 181 AATTAAATATGTGCGAATCAAAAGAAAAAACTTTTTTCAAGTTAATACATGGTTCAGGAA 241 AAGAAGAAACAAGCAAAGAAGCCAAACTCAGAGCTAAGGAAAAAAGAAACAGGTTAAGTC 301 TGCTCTTGCAGAAACCTGAATTTCATGAAGAGACCCACTCCGGTAGATCCGGGCACTTAG 361 CCAAAGAAACGAGAATCTCCCCTGCAGAAGCCGTGATATGGGGTGAATCATTTGACAAAC 421 TGCTCTCCCATAAAGGTGGACTGGAGACTTTTACCAGATTTCTTAAAACCGAATTCAGTG 481 AGGAAAACATTGAATTTTGGGTAGCCTGTGAAGATTTCAAGAAAAGCAAAGACCCTCAAC 541 AAATTATCCTTAAAGCAAAAGCAATATATGAGAAATTTATACAGAACGATGCTCCGCAAG 601 AGGTTAACCTTGATTTCCACACCAAAGAAATCATTGCCAAGAGCATCACCAAACCCACTC 661 TCCACAGTTTTGATGCTGCACAAAGCAGAGTATATCAGCTTATGGAACAAGACAGTTACA 721 CACGTTTCTGAAATCTGACATCTATTTAGACTTGACAGAAGGAAGACCTCAGAGGCCAA 781 CAAATCTTAAAAGACGGTCACGTTCATTTACCTACAATGAATTCCAGGATGTAAAGTCAG 841 ATGTTGCCATTTGGTTATAAAGAAAATTAATTTGCTCGTTTTTATGACACAAACTTATACA 901 TCTGCTTCTAACATATCGCATGTTTATGTTTAGATTTGGTCCCCATCCTTTAAACTGAAAT 961 ATGTCATGTGAAATTATTTTTAAAAATGTAAAAACAAAACTTTCTGCTAACAAAATACATA 1021 CAGTATCTGCCAGTATATTCTGTAAAACCTTCTATTTGATGTCATTCCATTTATAATCAG 1081 AAAAAAACTTATTTCTTAATCAAAAGGCAGTACAAAAAAAGTAATAATGTTTTATAAGA 1141 TTGTAGAGTTAAGTAAAAGTTAAGCTTTTGCAAAGTTGTCAAAGTTCAAACAAAAGTCT 1201 AGTTGGGATTTTTTACCAAAGCAGCATAATATGTGTTATATAAACATAATAATACTCAGA 1261 TATCCAAATGTTCAGATAGCATTTTTCATAATGAATGTTCTCTTTTTTTGGTAATAGTG 1321 TAGAAGTGATCTGGTTCTTACAATGGGAGATGAAGACATTTATTATTGGGTTACTACTA 1381 ACCCTGTCCCAAGAATAGTAATATCACCTCTAGTTATAAGCCAGCAACAGGAACTTTTGT 1441 GAAGACACATTCATCTCTACAGAACTTCAGATTAAATATAATCTAGATTAATGACTGAGA 1501 ATAAGATCCACATTTGAACTCATTCCTAAGTGAACATGGACGTACCCAGTTATACAAAGT 1561 ACTTCTGTTGGTCACAGAAACATGACCAGATTTTGCATATCTCCAGGTAGGGAACTAAGT 1621 AGACTACCTTATCACCGCTAAGAAAACTTGCTACTAAACTATTAGGCCATCAATGGCTT 1681 GAATAAAAACCAGAGAAGGTTTTTCCCAGGACGTCTCATGTTTGGCCCTTTAGAATTGGG 1741 GTAGAAATCAGAAATGAGATGAGGGAAGAAGCAAGGAGTCTAAGGCCCTAGCGATTTGG 1801 GCATCTGCCACATTGGTTCATATTCAGAAAGTGTTATCTCATTGATTATATTCTTGTTAA 1861 GCAAATCTCCTTAAGTAATTATTATTCAAATAAGATTATACTCATACATCTATATGTCAC 1921 TGTTTTAAAGAGATATTTAATTTTTAATGTGTGTTACATGGTCTGTAAATATTTGTATTT 1981 AAAAATGCCATGCATTAGGCTTTGGAAATTTAATGTTAGTTGAAATGTAAAATGTGAAAA 2041 CTTTAGATCATTTGTAGTAATAAATATATTTTTAACTTCATTCATACAGTTAAGTTTATCTG 2101 ACAATAAAAGCTCTGACTGAAAAAAAAAAAAAAAAAAAAA 1 M E T S L V F F S Q L N M C E S K E E K T 1 ATGGAAACATCATTGGTTTTCTTTTCTCAATTAAATATGTGCGAATCAAAAGAAAAAACT 21 F F K L I H G S G K E E E T S K E A K L R 61 TTTTTCAAGTTAATACATGGTTCAGGAAAAGAAGAAACAAGCAAAGAAGCCAAACTCAGA 41 A K E K R N R L S L L L L Q K P E E F H E E 121 GCTAAGGAAAAAAGAAACAGGTTAAGTCTGCTCTTGCAGAAACCTGAATTTCATGAAGAG	SEQ ID NO:133

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		61 T H S G G R S G H L A K E T R I S P A E E A 181 ACCCACTCCGGTAGATCCGGGCACTTAGCCAAGAAACGAGAATCTCCCCTGCAGAAGCC 81 V I W G E S F D K L L S H K G G L E T F 241 GTGATATGGGGTGAATCATTTGACAAACTGCTCTCCCATAAGGTGGACTGGAGACTTTT 101 T R F L K T E F S E E N I E F W V A C E 301 ACCAGATTTCTTAAAACCGAATTCAGTGAGGAAAACATTGAATTTTGGGTAGCCTGTGAA 121 D F K K S K D P Q Q I I L K A K A I Y E 361 GATTTCAAGAAAAGCAAAGACCCTCAACAAATTATCCTTAAAGCAAAAGCAATATATGAG 141 K F I Q N D A P Q E V N L D F H T K E I 421 AAATTTATACAGAACGATGCTCCGCAAGAGGTTAACCTTGATTTCCACACCAAAGAAATC 161 I A K S I T K P T L H S F D A A Q S R V 481 ATTGCCAAGAGCATCACCAAACCCACTCTCCACAGTTTTGATGCTGCACAAAGCAGAGTA 181 Y Q L M E Q D S Y T R F L K S D I Y L D 541 TATCAGCTTATGGAACAAGACAGTTACACACGTTTTCTGAAATCTGACATCTATTTAGAC 201 L T E G R P Q R P T N L K R R S R S F T 601 TTGACAGAAGGAAGACCTCAGAGGCCAACAAATCTTAAAAGACGGTCACGTTCATTTACC 221 Y N E F Q D V K S D V A I W L - 661 TACAATGAATTCCAGGATGTAAAGTCAGATGTTGCCATTTGGTTATAA	
WBC028G09.bFSP_20012310.abd	Homo sapiens mRNA for KIAA1689 protein, partial cds	1 tgcctccgcc atgttccgca gggcacgcct tagcgtgaag ccgaatgtca ggcctggtgt 61 aggcgccagg ggctccacag cttccaatcc ccagcgtgga cgggagtctc ccaggccgcc 121 ggagcctgcc acggactctg cttccaagcc cgcggagccc acagatgtgc ccacagtcga 181 ttcggtgtgga gcggagcccc aagaaaaggc tcctaggagc agtactgaaa agactggtgg 241 tgacaatgat gttgaagaat ccagtagatc ttccttctact gtttcacaga gaagaaagcg 301 aatatcaagt acttctagcc tggttaagtc tagtgtcagt gttccttcag aatctcatcc 361 cttatctaca attaatcaag aggctccaca gccaactgcc acttcaacaa aagagaaaca 421 gccatgctca gacagatacc gaatatacaa agcccagaaa ctgagggaaa tgttaaaaga 481 agaattgaga aaagagaaga aacaatggaa aaacaaatat gctataaatg aaagtcagag 541 gccaccagat cgttcaaaaa tgactatgag agacttcata tattatctac cagataataa 601 tccaatgact tcttcactgg aacaagaaaa gaaaactgaa aagccatcga ctccagtcca 661 gacaagagag caagaaggta agagtactcc taatgctgaa gataatgaaa tggaagaaga 721 gacagatgat gggccattac tggttcctcg agtaaaagtg gcagaagatg gttccattat 781 tttggatgaa gaaagtttaa ctgtagaagt tttaagaaca aaaggccctt gtgttgttga	SEQ ID NO:134

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		841 agaaaatgac cccatatttg agcgcggttc tacaactaca tactccagct ttaggaaaaa 901 ctattactct aaaccatggt caaataaaga aacagatatg ttttttttag ccatcagcat 961 ggtaggaact gacttttcta tgatcggaca actttttcct cacagagcaa ggatagaaat 1021 taagaataaa tttaaacggg aagagaaaac aaatggatgg agaatagaca aagcattcca 1081 ggaaaagcgc cctttgact tcgatttttt tgctcatttg cttcagaaag ttcttgctga 1141 agaagagaaa agaaaacaaa aatctgttaa aaatcacagt ttaaaggaga agaaatccac 1201 caaaccacgg aaaaatgtaa aagtgaaaaa agttgcctgt gaaggagtga ataatgatcc 1261 agatgagtct atgagttcta gaatttcaga cacggaaaga tctcagaagg atgctcagac 1321 agttgaagaa gagtctctga ccttatcaag ggaggatgca gagcaggttg cattagaagt 1381 agacctaaat caaaagaaaa gaaggaggaa gaagcaagat ggagctaatg aactgggagt 1441 aaacaatctt ttagaaaatg ccactgttca ggcgggtcct tctaaaggag aaaaacacaa 1501 gaataaatgt caggctataa ggcctgagct aaaggaaggt gaatgcagta aggagcagat 1561 gctttcctgc acacaaaaca tagatggcat tgtgggtttt gcctccactg aaaaagttga 1621 gaaaagaact gaccccatcc tttcattaag taatcaacaa gatgccacat cagtagcaac 1681 tgagtcttca gaatcaagca cttcagattt gccttcattc gaagttggaa ttagagcatt 1741 gtgtgaggtg aataatgctg agggtagttg tatagaagaa agaaatgttg acctaaaaaa 1801 taattcactg gaaattgatc aaacagaaaa tgttaaacca atgttgagag gtcgcttcca 1861 aagacctaaa cccaatttgt caagggctgg gaagaaatca gttctttcac aaggcaaaac 1921 agagtcagag agcaagaatt cacattcaaa aacttcagtt gaaaagaacc acgtggaaaa 1981 agataaaatg aatacattgg acattttgag aatggagact acagagagag agaatccaga 2041 agctgaaact gtatctgttt tgggtgaaaa aaattgtctg caggaaggga gtcaactaaa 2101 ggctttaaga cctgtacaag tgaggggccg attgcaaaag ccaaagccaa atgcaggtaa 2161 agctgctgaa agaaaagaaa ttctccatatc acaggaagaa attggggcca atgtagagaa 2221 gaatgaaaat gaatcctgtg ctgatagaga tactcctcaa cacatggaag atcaatcgtg 2281 taaagatttt gaagaggaag atgtcatatt acagcctgag aaaaatgatt cttttcaaaa 2341 tgtgcagcca gatgagccca aggttcttaa tgaatgtcta agcgttcaag agaataataa 2401 ggcaaataaa cttaaccaag tcccaattct aaggactcga ttcagaaaac caaagccaaa 2461 tataggaaga ggaactggaa ggagagaaat ttcctcaaag gaagaggtac tagagaagat 2521 tcttgtctct ggggaaatgg cggcagcatt gagagaaact gtaagactag acacctcacc 2581 aaaggagatg gtaccagcag agattaatac taaagaaatg cagtcagatt taaaagaaac 2641 tggaagaaga gccatttctc ccagggagaa gattctagat gtgattgatg acaccataga 2701 aatggagaca ggtctgaaag caatgggaag agagatttgt ctaagggaga agacgccaga 2761 ggtgattgat gccactgagg aaatagacaa agatttggaa gaagctggaa gaagagaaat 2821 atccccacag aaaaatggcc cagaggaggt taagcctcta ggtgaagtgg agacagattt 2881 gaaagcaact ggaaatgaga gtcccccaag ggagaagaca ccagaggtga ctgatgccac 2941 tgaggaaata gacaaaaatt tggaagaaac tggaagagaa aaaatatccc caagggaaaa 3001 tggcccagag gaggtcaagc ctgtagatga aatggagaca gatttgaacg caactggaag 3061 agagagttct ccaagggaga agacaccaga ggtgattgat gctactgagg aaatagattt 3121 ggaagaaact gaaagagaag tatccccaca ggaaaatgga ctagaggagg tcaagcctct 3181 aggtgaaatg gagacggatt tgaaagcaac tggaagagac agtttcccaa gggggaagac 3241 accagaggtg attgatgcca ttgaggaaat agagatagat ctggaagaaa ctgaaagaga 3301 aatatcccca caggaaaatg gcctagagga ggttaagcct ctaggtgaaa tgcaaacaga 3361 ttgaaagca acgggaaggg agatttcccc aagggagaag acaccagagg tgattgatgc	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		3421 cactgaggaa atagacaaag atctggaaga aactggaaga agagaaatat ccccagagga 3481 aaatggccca gaggaggtca agcctgtaga tgaaatggag acagacttga aaacaactgg 3541 aagagagggt tcctcaaggg agaagacacg agaggtgatt gatgctgctg aggtaataga 3601 gacagatttg gaagaaactg aaagagaaat atcgccacag gaaatggccc cagaggaggt 3661 caagcctgta ggtaaaatgg agacagattt gaaagaaatt agagaagaaa tttcccaaag 3721 ggaaaaggtg ctagcagaga tcagtgctat aagggaaaag gagattgatt tgaaagaaac 3781 tggaaaaaga gacattccca tgatggagaa agtatcagga aagatggctg ttgttgaaga 3841 aatggaggca gatttgaaag aaactggaaa agaaaatttt agaggagagg gatctgaaga 3901 gatctgtgtt actgaggaaa aggtggcaga attgaaacaa actggaaaaa cagacatttc 3961 tccaagggaa aacgagctag aggagaccag tacctcaaga caaactgaca cacatttaat 4021 gcagagcggt agcaatgact tcagtgctat gccttcacta gatattcaga acattagcag 4081 tgaagtactg tcgatgatgc atacacctgt agaagaaaaa agaaattctg aaaaagaagt 4141 atcaagtcac ttcagtcatt tcaagatttc ttcacagact catgaatctg ataaaacaga 4201 agtccagggg attcaatctc cagatgttcc agagcagttt tcagatatta atttaagcaa 4261 atctcttcct caagaacaga agccacttga aattaaacca gcacctttg tgaggagccg 4321 attcaaaaga ccaaaaccaa acttagcaag agcagctttg aagagagaga ctacagaatc 4381 agaaaaatat atatatgaga agaaatcaga aaccgagaaa atggagacta ttgtgatgca 4441 agaaaataat gaacaaactg atactctccc ttctcaacat gatgaagctt ccctaatgat 4501 atcaagagaa aaagacacat taggtcacag gaatgaggag gctgtgatat tgccatgtac 4561 acagactgaa aggaaccttt cacttcaaaa ttcttgtgaa cctaaagagg agtctcagtc 4621 agcaccagtc cagaaaaatg actcagttgt ttctgtgggg actaataatg taaacacttt 4681 ccagcaagaa atgaaggaaa gtgttatcca aactgctcga caagtaaggg gccgacttca 4741 gagaccgaga ccaaatataa gaaagacagg acagaggcaa atagtagaca aaggtgaagc 4801 caaaggcata attaaggaag gaagaacgat attaccaaaa gatgaaactg aaaagaaagt 4861 cttaactgtg tcaaattctc aaattgaaac tgaaattgaa gttccatcgt ccgcagttcc 4921 agaacacaga atgtatgaaa atcaaagtca ggtggttctt gtagaaaacc ttcacgttaa 4981 caaaacaaat gaaacaatca gacatgaaaa taaaccgtat gttcctagtt cagcacaaat 5041 gacaagaagg aaattccaaa aggctaagcc aaatttggga agagcacaca gtaagaaaga 5101 ggaaccagtt ttagaaaaag tcacaacaga tcagagcaag gaaggcaagc cagaagatca 5161 tttgctgcag aaaggagctt ccaacaccca gctccttcta aaagaaaaag ctgagcttct 5221 gacatctctg gaggtttcag caagaaaaga ttgtgtaggt tccaaagagt ctgctttggc 5281 aaaaatagat gcggattag aagaagttgg accatcaaga agggttggag aggaaactgt 5341 aggagataat tcaccatctt cagttgttga agagcaatat ctcaataaac taacaagctg 5401 tccacaaccg ttaaacgaaa caagttactc taaaattgcc ctggatggga aaacaactat 5461 ctcttcttaca tctgagtatg agagaaatcg tggtgaaagg agaagtcata aaaagttcaa 5521 accaaatgtc accagaggtc gtggatcaaa acgagttcgg ggtaagacct ctaagaagga 5581 acctagagct tccaaggcca tgctggtgac tcttcgggct tccaggaag aagatgatga 5641 tgctgacgat tttgagtctg actatgagga agaaagctat catcttgctc ccgaagaagt 5701 aaacaaagct ccagtatttg tacctgttgg tctcagatct cctgaacctg ttttctgctca 5761 gattgaggaa acaatggaag agcttgaaat aactgtgaat gtcccagatg taggatgcat 5821 agctgttgtt gaacatgagc taccaaacac agatgtgact actgaagaaa tgaaacaaga 5881 agaaaatttg agtgtaccgt ttgaaatgac cacaagtgaa catatccaag atgaaccagg 5941 taccaatgat ggaagcaccg aagtgcaat aactttactt acaatgggag atctagtatt	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		6001 gcagtcagag atcagtagtg aacagggtga tgtaggagta tgtataattc ctcatgttca	
		6061 ttcaaaggat aaaagccata ttcctttctag cctagataat gtaaatcaca aaattgttca	
		6121 tgaatgtcag gaactttctt cacctgtcat tactacatct cctgcatcat ttgaagaaaa	
		6181 caagattgta ttggaggaac aaagttccag agaagaaata agtttaatgg agaaagtaaa	
		6241 ggagaatgct acaccaacca ggaatacaat ttctaaagtg accagtaatt tgagaataag	
		6301 aagtaggctt gctaagccta aaccaaatct tgagaagact ttagggacca acaggcttga	
		6361 tgattatcag gaagtttcca gtttgtgtgt aaccaaaggg gcagaaatgg aaactcaaag	
		6421 agaaacagag aaaaatgctt ccaaagcaac agaattggaa aataaaaacc tcggaccagt	
		6481 tacaacagca gagaataagg atcagagcaa attggcatgt gtacatggta tcaaagggac	
		6541 cagtatttct tcagaagtaa acctaactga aagaaacgaa aatcaagaag agagcttcta	
		6601 ggaggttcac atgttgtcag ttgctccagt tgcttcctct gagacagggc cctgcacact	
		6661 tggtttggat agggggtcttg gtgaaaattc tgttgaagag ccccagataa aggactctaa	
		6721 aggagacagt gtgcttacac ttcctgtgcc agagtataca ccaacaagta ttccagaagt	
		6781 ccaacaagag aatataatca atcctcaaga cctaacagtg aatctagttg ctaatgtacc	
		6841 tcaagatgga gaagatgaac aagccatttat tttaactctg gtggaatccc cagccaatgc	
		6901 agtagaagaa tttactgatg ccactgcaca gttcatgcca aaccctttac tgccagctcc	
		6961 catattggtc aaatcagtga ataccgaaga aaggggtgac atgagtattt gtttaccagc	
		7021 aacttcagtt ggtcaagatg ccatgggttt atcctatttct ggaagagata attctaaaaa	
		7081 gccgcctgat aatttggatc ttgtatctag gaagagattt caatgcaggc ttgataaaaa	
		7141 tgaccacatt cctcctgcca aaaaacgttc actcacttta agagatgact gtcaagaata	
		7201 taccactgag gtgcactcaa aggaattaac aaatgttttt gaggaaacag gggagtctca	
		7261 caagggacaa gatattttc ttacctcagg aagcacactg acaactccag aacctcaaag	
		7321 acagcaagtt gaagcagctt ttcagagtag aggatctaga tctcctgatg catgcatgga	
		7381 caagaatgtg cctcagttac ctcaggatga aatgattgtg tctgataagg aagaaagaac	
		7441 tgatgctgct cctaagtctc agcaaatgga tagcagaaca tcgtcttcta aagcctcact	
		7501 atccagacct ggcagaagac ccctgggatt tttatcttta atatgctcaa agaatagttt	
		7561 ggagtctgat gaacctatgc aagtccatag taagaaacgc ctaaaacctc ttatacctgg	
		7621 attaagaaag aaattgaaaa gatctaatcc attcaatgaa agccaggaaa aaaatcgaga	
		7681 gtcctctgat ctgcttccat ctccaagtgt tattactact caatctgaga atattagcag	
		7741 ctcagcaact caggtttctt gtgatcagcc cttactgaaa gaaggatata aaagtgccca	
		7801 aaagcgggcc cctcaagggg aggcaaccac agtcctctgaa tatttcttca atgatatctt	
		7861 cattgaagtg gatgaaacag aataaaacaa tctttctctct ttttctttt taaattaggt	
		7921 ctaggatttc cagagtcaat tacatcaaca aaacagtatt tagagcaaaa tatcactgtc	
		7981 ttatttttct ttaggttgat tttgaatact taatgagctt gatttgaagc tttatatatc	
		8041 agtggaaaac atttctgagg ttcctttcat tctgactgat tcagcatttt gcaaatagca	
		8101 agcaattaag actgctttct cagacagaaa taacaactct tgtttacatt ttgactcttc	
		8161 ctgtgctaag cacacatgga cattgtggaa tgttgtggat atatgtctct gtatgaattg	
		8221 cagtgcagac agatttgggg gttaattgta tcatatttaa catttagcaa cttcttttgt	
		8281 gaagattttt tatttttagg gggagatgat gaaggatgaa ggctttttca tttgcttcta	
		8341 agtacagtca tgtatcacat aatgaagttt aagtcaatga tggaccacat atattacagt	
		8401 ggtcccatgc aattaaaatg gagataaatt cctatcaact agtgacatta tagccatcat	
		8461 aacacagtgc attgctttt tatgtttaga tatgtttaga tacacaaata cttactattg	
		8521 tgttacaact gcctacagta ttcagcatag taacacattg tagaggtttg tagccgagga	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		8581 gcaataggct ataccacata gcctcagtct gtacggtgtg tagcagcctg taccatctca 8641 gtgtttgtaa gtacactctg cgttgtttca cacaagatca cctaacaagg caattcttag 8701 aacatgtagt taagggacac gtgactatat gtgaaaacaa attgtcaaac ttcactttag 8761 tatggcaaat gttaaagaac ttttctatta tcagctgttt gtctgactga aaaatacata 8821 ttttctaat tcatggtgat gtaacattag tcctaattga aaaactagta tttaaacata 8881 attatttata aagatgacac atcaaagggc ttatttattt ttaaatttct tatttaaaag 8941 gatattcagt tttagctatt tttaccctc agattgtaga taaagaaggc attaaattta 9001 tgtttgtctc cttttctgt ttaattttaa agatatttaa aatgatataa ctaaaaatgt 9061 ttagctggtg tatatgtttt gaatacottt ttcccctcag tttagtatat tgacttttgta 9121 ctgtaaattt ttctgctttt ctggataat ctcaggattt tcatgaggat aggggaact 9181 caacttttatt tatgagacaa aatttccata caaagctcaa tctcctttat acacccacag 9241 acataatatt agttttaaa aagccaattt cttcatagtt ttttcccatt aaattctcaa 9301 ggaacacttg gatctttaag cacggaacat aatcatgatg ttaaaaacag agaaaataag 9361 gctttataaa gttaatgatt atcatcagta tgaatttaag gtttgtttta atttcaagat 9421 ttgatttttt atacgtgtaa ttctattatc tacccaagca gatctgtagt ggttccaatt 9481 agacttctca aacagcaaat ttatcctgat tttatttgaa aagcctcttg gattgatagt 9541 atagtagctc aggcattgga aactttctgc aaactgtttt gggtttgcag gccagatggt 9601 ctctgtggca gctactcagc tctgcaattt cagtgtgaaa gaagccatag acagtacttg 9661 aatgaaggac tgtggctgga ttggcctttt agtttgaccc cctacattag gccccaaatt 9721 ttcttaccct gaggtgctga tatctgtatg gatgagttat ttgtcactaa agttatgagt 9781 tgtgcctaaa agttaaaact gttgactgta ttatgtaatg atcagtattt cagttgggaa 9841 gatattttag agtctagata attatgtttg tatattgaaa aaatggtggc cagttttaa 9901 gttccttaat agaagagaat tatgtctcag cacatataac agtaatgcta atttattgaa 9961 actactgctg ttagagcact tcttattcat tgtcttttag tgaaatttat ggcgtaacac 10021 tttgtcagag aggaggctat ataattcgga gcggaaattg tctataagta ggcatttatt 10081 tcatgattga tatgtcacag aaatcatggt agtaaatcac attgctattt gaataccctg 10141 ttttttgtaag ttttttaaaac tcatattctg aaaagatttc attctcttag tgttagcttg 10201 ggagttagat tgccatgatt aaactattat ttatccttgt gtaatattag tttttaactt 10261 taacatctgt ttctttttaa tctataatga gctagtttta tggaaaatgg aatttcttac 10321 tatataaaga atacagagac tcattgtatt agagaatcaa gtcagccagc taaagtatcc 10381 tactgttaaa tccttaaacc taattttgga aaagagaaag ttaatcaatg tatttacctt 10441 acatgttgga aagaactatg ttaggtctga ttcatgtgaa gaagatgttg caaaggattt 10501 atttcacaaa ttttaaagga gatatgagta aaagttttta tcttttcttg actttttctc 10561 ctgaacactt atgtcttagc aagtggtcaa catgaggatt tgaacgccta attgttggta 10621 aatggttgag gcatgacaaa aatattaata tccactgttt accatcatgt tatttgaaac 10681 aaaagtgacc atgtatacta tcttgcttga agaagtcttt gacagaaaaa gcaatatcat 10741 gtcatttata aatttcttg ttctaaagaa agcagttata tatatatata aattatgtaa 10801 ataaaagtta ttttatatc 1 A S A M F R R A R L S V K P N V R P G V 2 GCCTCCGCCATGTTCCGCAGGGCACGCCTTAGCGTGAAGCCGAATGTCAGGCCTGGTGTA 21 G A R G S T A S N P Q R G R E S P R P P	SEQ ID NO:135

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		62 GGCGCCAGGGGCTCCACAGCTTCCAATCCCCAGCGTGGACGGGAGTCTCCCAGGCCGCCG	
		41 E P A T D S A S K P A E P T D V P P T V D 122 GAGCCTGCCACGGACTCTGCTTCCAAGCCCGCGGAGCCCACAGATGTGCCCACAGTCGAT	
		61 F G G A E P Q E K A P R S S T E K T G G 182 TTCGGTGGAGCGGAGCCCCAAGAAAAGGCTCCTAGGAGCAGTACTGAAAAGACTGGTGGT	
		81 D N D V E E S S R S S S S T V S S Q R R K R 242 GACAATGATGTTGAAGAATCCAGTAGATCTTCCTCTACTGTTTCACAGAGAAGAAAGCGA	
		101 I S S T S S L V K S S S V S V P S S E S H P 302 ATATCAAGTACTTCTAGCCTGGTTAAGTCTAGTGTCAGTGTTCCTTCAGAATCTCATCCC	
		121 L S T I N Q E A P Q P P T A T S S T K E K Q 362 TTATCTACAATTAATCAAGAGGCTCCACAGCCAACTGCCACTTCAACAAAAGAGAAACAG	
		141 P C S D R Y R R I Y K A Q K K L R E E M L K E 422 CCATGCTCAGACAGATACCGAATATACAAAGCCCAGAAACTGAGGGAAATGTTAAAAGAA	
		161 E L R K E K K Q W K N K Y A I N E S Q R 482 GAATTGAGAAAAGAGAAGAAACAATGGAAAAACAAATATGCTATAAATGAAAGTCAGAGG	
		181 P P D R S K M T T M R R D F I Y Y L P D N N 542 CCACCAGATCGTTCAAAAATGACTATGAGAGACTTCATATATTATCTACCAGATAAATAAT	
		201 P M T S S S L E Q E K K K T E K P S T P V Q 602 CCAATGACTTCTTCACTGGAACAAGAAAAGAAAACTGAAAAGCCATCGACTCCAGTCCAG	
		221 T R E Q E G K S T P N A E D N E M E E E E 662 ACAAGAGAGCAAGAAGGTAAGAGTACTCCTAATGCTGAAGATAATGAAATGGAAGAAGAG	
		241 T D D G P L L V P R V K V A E D G S I I 722 ACAGATGATGGGCCATTACTGGTTCCTCGAGTAAAAGTGGCAGAAGATGGTTCCATTATT	
		261 L D E E S L T V E V L R T K G P C V V E 782 TTGGATGAAGAAAGTTTAACTGTAGAAGTTTTAAGAACAAAAGGCCCTTGTGTTGTTGAA	
		281 E N D P I F E R G S T T T Y S S F R K N 842 GAAAATGACCCCATATTTGAGCGCGGTTCTACAACTACATACTCCAGCTTTAGGAAAAAC	
		301 Y Y S K P W S N K E T D M F F L A I S M 902 TATTACTCTAAACCATGGTCAAATAAAGAAACAGATATGTTTTTTTTAGCCATCAGCATG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		321 V G T D F S M I G Q L F P H R A R I E I 962 GTAGGAACTGACTTTTCTATGATCGGACAACTTTTTCCTCACAGAGCAAGGATAGAAATT 341 K N K F K R E E K T N G W R I D K A F Q 1022 AAGAATAAATTTAAACGGGAAGAGAAAACAAATGGATGGAGAATAGACAAAGCATTCCAG 361 E K R P F D F D F F A H L L Q K V L A E 1082 GAAAAGCGCCCTTTTGACTTCGATTTTTTTGCTCATTTGCTTCAGAAAGTTCTTGCTGAA 381 E E K R K Q K S V K N H S L K E K K S T 1142 GAAGAGAAAAGAAAACAAAAATCTGTTAAAAATCACAGTTTAAAGGAGAAGAAATCCACC 401 K P R K N V K V K K V A C E G V N N D P 1202 AAACCACGGAAAAATGTAAAAGTGAAAAAAGTTGCCTGTGAAGGAGTGAATAATGATCCA 421 D E S M S S R I S D T E R S Q K D A Q T 1262 GATGAGTCTATGAGTTCTAGAATTTCAGACACGGAAAGATCTCAGAAGGATGCTCAGACA 441 V E E E S L T L S R E D A E Q V A L E V 1322 GTTGAAGAAGAGTCTCTGACCTTATCAAGGGAGGATGCAGAGCAGGTTGCATTAGAAGTA 461 D L N Q K K R R R K K Q D G A N E L G V 1382 GACCTAAATCAAAAGAAAAGAAGGAGGAAGAAGCAAGATGGAGCTAATGAACTGGGAGTA 481 N N L L E N A T V Q A G P S K G E K H K 1442 AACAATCTTTTAGAAAATGCCACTGTTCAGGCGGGTCCTTCTAAAGGAGAAAAACACAAG 501 N K C Q A I R P E L K E G E C S K E Q M 1502 AATAAATGTCAGGCTATAAGGCCTGAGCTAAAGGAAGGTGAATGCAGTAAGGAGCAGATG 521 L S C T Q N I D G I V G F A S T E K V E 1562 CTTTCCTGCACACAAAACATAGATGGCATTGTGGGTTTTGCCTCCACTGAAAAAGTTGAG 541 K R T D P I L S L S N Q Q D A T S V A T 1622 AAAAGAACTGACCCCATCCTTTCATTAAGTAATCAACAAGATGCCACATCAGTAGCAACT 561 E S S E S S T S D L P S F E V G I R A L 1682 GAGTCTTCAGAATCAAGCACTTCAGATTTGCCTTCATTCGAAGTTGGAATTAGAGCATTG 581 C E V N N A E G S C I E E R N V D L K N 1742 TGTGAGGTGAATAATGCTGAGGGTAGTTGTATAGAAGAAAGAAATGTTGACCTAAAAAAT	

Gene Name	GenBank HomoLogy	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		601 N S L E I D Q T E N V K P M L R G R F Q 1802 AATTCACTGGAAATTGATCAAACAGAAAATGTTAAACCAATGTTGAGAGGTCGCTTCCAA	
		621 R P K P N L S R A G K K S V L S Q G K T 1862 AGACCTAAACCCAATTTGTCAAGGGCTGGGAAGAAATCAGTTCTTTCACAAGGCAAAACA	
		641 E S E S K N S H S K T S V E K K N H V E K 1922 GAGTCAGAGAGCAAGAATTCACATTCAAAAACTTCAGTTGAAAGAACCACGTGGAAAAA	
		661 D K M N T L D I L R M E T T E R E N P E 1982 GATAAAATGAATACATTGGACATTTTGAGAATGGAGACTACAGAGAGAGGAATCCAGAA	
		681 A E T V S V L G E K N C L Q E G S Q L K 2042 GCTGAAACTGTATCTGTTTTGGGTGAAAAAAATTGTCTGCAGGAAGGGAGTCAACTAAAG	
		701 A L R P V Q V R G R L Q K P K P N A G K 2102 GCTTTAGACCTGTACAAGTGAGGGGCCGATTGCAAAAGCCAAAGCCAAATGCAGGTAAA	
		721 A A E E R K E E I L I S Q E E I G A N V E K 2162 GCTGCTGAAGAAAAGAAAATTCTCATATCACAGGAAGAAATTGGGGCCAATGTAGAGAAG	
		741 N E N E S C A D R D T P Q H M E D Q S C 2222 AATGAAAATGAATCCTGTGCTGATAGAGATACTCCTCAACACATGGAAGATCAATCGTGT	
		761 K D F E E E D V I L Q P E K N D S F Q N 2282 AAAGATTTTGAAGAGGAAGATGTCATATTACAGCCTGAGAAAAATGATTCTTTTCAAAAT	
		781 V Q P D E P K V L N E C L S V Q E N N K 2342 GTGCAGCCAGATGAGCCCAAGGTTCTTAATGAATGTCTAAGCGTTCAAGAGAATAATAAG	
		801 A N K L N Q V P I L R T R F Q K P K P N 2402 GCAAATAAACTTAACCAAGTCCCAATTCTAAGGACTCGATTTCAGAAACCAAAGCCAAAT	
		821 I G R G T G R R E I S S K E E V L E K I 2462 ATAGGAAGAGGAACTGGAAGGAGAGAAATTTCCTCAAAGGAAGAGGTACTAGAGAAGATT	
		841 L V S G E M A A A L R E T V R L D T S P 2522 CTTGTCTCTGGGGAAATGGCGGCAGCATTGAGAGAAACTGTAGACTAGACACCTCACCA	
		861 K E M V P A E I N T K E M Q S D L K E T 2582 AAGGAGATGGTACCAGCAGAGATTAATACTAAAGAAATGCAGTCAGATTTAAAGAAACT	
		881 G R R A I S P R E K I L D V I D D T I E	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2642 GGAAGAAGAGCCATTTCTCCCAGGGAGAAGATTCTAGATGTGATTGATGACACCATAGAA	
		901 M E T G L K A M G R E E I C L R E E K T P E 2702 ATGGAGACAGGTCTGAAAGCAATGGGAAGAGAGATTTGTCTAAGGGAGAAGACGCCAGAG	
		921 V I D A T E E E I D K D L E E A G R R E E I 2762 GTGATTGATGCCACTGAGGAAATAGACAAAGATTTGGAAGAAGCTGGAAGAAGAGAAATA	
		941 S P Q K N G P E E V K P L G E V E T D L 2822 TCCCCACAGAAAAATGGCCCAGAGGAGGTTAAGCCTCTAGGTGAAGTGGAGACAGATTTG	
		961 K A T G N E S S P R E E K T P E V T D A T 2882 AAAGCAACTGGAAATGAGAGTTCCCCAAGGAGAAGACACCAGAGGTGACTGATGCCACT	
		981 E E I D K N L E E E T G R R K I S P R E N 2942 GAGGAAATAGACAAAAATTTGGAAGAAACTGGAAGAAGAAAAATATCCCCAAGGGAAAAT	
		1001 G P E E V K P V D E M E T D L N A T G R 3002 GGCCCAGAGGAGGTCAAGCCTGTAGATGAAATGGAGACAGATTTGAACGCAACTGGAAGA	
		1021 E S S P R E E K T P E V I D A T E E E I D L 3062 GAGAGTTCTCCAAGGGAGAAGACACCAGAGGTGATTGATGCTACTGAGGAAATAGATTTG	
		1041 E E T E R E E V S P Q E N G L E E E V K P L 3122 GAAGAAACTGAAAGAGAAGTATCCCCACAGGAAAATGGACTAGAGGAGGTCAAGCCTCTA	
		1061 G E M E T D L K A T G R D S F P P R G K T 3182 GGTGAAATGGAGACGGATTTGAAAGCAACTGGAAGAGACAGTTTCCCAAGGGGGAAGACA	
		1081 P E V I D A I E E I E E I D L E E T E R E 3242 CCAGAGGTGATTGATGCCATTGAGGAAATAGAGATAGATTTGGAAGAAACTGAAAGAGAA	
		1101 I S P Q E N G L E E E V K P L G E M Q T D 3302 ATATCCCCACAGGAAAATGGCCTAGAGGAGGTTAAGCCTCTAGGTGAAATGCAAACAGAT	
		1121 L K A T G R E E I S P R E E K T P E V I D A 3362 TTGAAAGCAACCGGAAGGGAGATTTCCCCAAGGAGAAGACACCAGAGGTGATTGATGCC	
		1141 T E E E I D K D L E E E T G R R E E I S P E E E 3422 ACTGAGGAAATAGACAAAGATCTGGAAGAAACTGGAAGAAGAGAAATATCCCCAGAGGAA	
		1161 N G P E E V K P V D E M E T D L K T T G 3482 AATGGCCCAGAGGAGGTCAAGCCTGTAGATGAAATGGAGACAGACTTGAAACAACTGGA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1181 R E G G S S R E E K T R E E V I D A A E E V I E 3542 AGAGAGGGTTCCTCAAGGGAGAAGACACGAGAGGTGATTGATGCTGCTGAGGTAATAGAG	
		1201 T D L E E E T T E R E E I S P Q E E N G P E E E V 3602 ACAGATTTGGAAGAAACTGAAAGAGAAATATCGCCACAGGAAAATGGCCCAGAGGAGGTC	
		1221 K P V G G K M E E T D D L K K E E I R R E E E I S Q R 3662 AAGCCTGTAGGTAAAATGGAGACACAGATTTGAAAGAAATTAGAGAAGAAATTTCCCAAAGG	
		1241 E K K V L A E E I S S A I I R R E E K K E I D D L K K E E T 3722 GAAAAGGTGCTAGCAGAGATCAGTGCTATAAGGGAAAGGAGATTGATTTGATTTGAAAGAAACT	
		1261 G K R R D D I P P M M E E K K V V S S G G K K M M A A V V V E E E 3782 GGAAAAAGAGACATTCCCATGATGGAGAAAGTATCAGGAAAGATGGCTGTTGTTGAAGAA	
		1281 M E E A A D D L L K K E E T T G G K K E E N N F F R R E E R R G G S S E E E 3842 ATGGAGGCAGATTTGAAAGAAACTGGAAAAGAAAATTTTAGAGAGAGAGGATCTGAAGAG	
		1301 I I C C V V T T E E E K K V V A A E E L L K K Q Q T T G G K K T T D D I I S S 3902 ATCTGTGTTACTGAGGAAAAGGTGGCAGAATTGAAACAAACTGGAAAAACAGACATTTCT	
		1321 P P R R E E N N E E L L E E E E T T S S T T S S R R Q Q T T D D T T H H L L M M 3962 CCAAGGGAAAACGAGCTAGAGGAGACCAGTACCTCAAGACAAACTGACACACATTTAATG	
		1341 Q Q S S G G S S N N D D F F S S A A M M P P S S L L D D I I Q Q N N I I S S S S 4022 CAGAGCGGTAGCAATGACTTCAGTGCTATGCCTTCACTAGATATTCAGAACATTAGCAGT	
		1361 E E V V L L S S M M M H H T T P P V V E E E E K K R R N N S S E E K K E E V V 4082 GAAGTACTGTCGATGATGCATACACCTGTAGAAGAAAAAGAAATTCTGAAAAAGAAGTA	
		1381 S S S H H F F S S H F F K K I I S S S S Q Q T T H H E E S S D D K K T T E E 4142 TCAAGTCACTTCAGTCATTTCAAGATTTCTTCACAGACTCATGAATCTGATAAAACAGAA	
		1401 V V Q Q G G I I Q Q S S P P D D V V P P E E Q Q F F S S D D I I N N L L S S K K 4202 GTCCAGGGGATTCAATCTCCAGATGTTCCAGAGCAGTTTTCAGATATTAATTTAAGCAAA	
		1421 S S L L P P Q Q E E Q Q K K P P L L E E I I K K P P A A P P F F V V R R S S R R 4262 TCTCTTCCTCAAGAACAGAAGCCACTTGAAATTAAACCAGCACCTTTTGTGAGGAGCCGA	
		1441 F F K K R R P P K K P P N N L L A A R R A A A L L K K R R E E T T T T E E S S 4322 TTCAAAAGACCAAAACCAAACTTAGCAAGAGCAGCTTTGAAGAGAGACTACAGAATCA	

Gene Name	GenBank HomoLogy	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1461 E K V I Y E K K S E T E K M E T I V M Q 4382 GAAAAATATATATATGAGAAGAAATCAGAAACCGACAGAAAATGGAGACTATTGTGATGCAA	
		1481 E N N E Q T D T L P S Q H D E A S L M I 4442 GAAAATAATGAACAAACTGATACTCTCCCTTCTCAACATGATGAAGCTTCCCTAATGATA	
		1501 S R E K D T L G H R N E E A V I L P C T 4502 TCAAGAGAAAAAGACACATTAGGTCACAGGAATGAGGAGGCTGTGATATTGCCATGTACA	
		1521 Q T E R N L S P S N S C E P K E E S Q S 4562 CAGACTGAAAGGAACCTTTCACCTTCAAATTCTTGTGAACCTAAAGAGGAGTCTCAGTCA	
		1541 A P V Q K N D S V V S V G T N N V N T F 4622 GCACCAGTCCAGAAAAATGACTCAGTTGTTTCTGTGGGACTAATAATGTAAACACTTTC	
		1561 Q Q E M K E S V I Q T A R Q V R G R L Q 4682 CAGCAAGAAATGAAGGAAAGTGTTATCCAACTGCTCGACAAGTAAGGGCCGACTTCAG	
		1581 R P R P N I R K T G Q R Q I V D K G E A 4742 AGACCGAGACCAAATATAAGAAAGACAGGACAGAGGCAAATAGTAGACAAAGGTGAAGCC	
		1601 K G I I K E G R T I L P K D E T E K K V 4802 AAAGGCATAATTAAGGAAGGAAGAACGATATTACCAAAGATGAAACTGAAAAGAAAGTC	
		1621 L T V S N S Q I E E T E I E V P S S A V P 4862 TTAACTGTGTCAAATTCTCAAATTGAAACTGAAATTGAAGTTCCATCGTCCGCAGTTCCA	
		1641 E H R M Y E N Q S Q V V L V E N L H V N 4922 GAACACAGAATGTATGAAAATCAAGTCAGGTGGTTCTTGTAGAAAACCTTCACGTTAAC	
		1661 K T N E T I R H E N K P Y V P S S A Q M 4982 AAACAAATGAAACAATCAGACATGAAAATAAACCGTATGTTCCTAGTTCAGCACAAATG	
		1681 T R R K F Q K A K P N L G R A H S K K K E 5042 ACAAGAAGGAAATTCCAAAAGGCTAAGCCAAATTTGGGAAGAGCACACAGTAAGAAAGAG	
		1701 E P V L E K V T T D Q S K E G K P E D H 5102 GAACCAGTTTTAGAAAAAGTCACAACAGATCAGAGCAAGGAAGGCAAGCCAGAAGATCAT	
		1721 L L Q K G A S N T Q L L L K E K A E L L 5162 TTGCTGCAGAAAGGAGCTTCCAACACCCAGCTCCTTCTAAAAGAAAAAGCTGAGCTTCTG	
		1741 T S L E V S A R K D C V G S K E S A L A	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		5222 ACATCTCTGGAGGTTTCAGCCAAGAAAAGATTGTGTAGGTTCCAAAGAGTCTGCTTTGGCA	
		1761 K I D A E L E E V G P S R R V G E E T V 5282 AAAATAGATGCGGAATTAGAAGAAGTTGGACCATCAAGAAGGGTTGGAGAGGAAACTGTA	
		1781 G D N S P S S V V E E Q Y L N K L T S C 5342 GGAGATAATTCACCATCTTCAGTTGTTGAAGAGCAATATCTCAATAAACTAACAAGCTGT	
		1801 P Q P L N E T S Y S K I A L D G K T T I 5402 CCACAACCGTTAAACGAAACAAGTTACTCTAAAATTGCCCTGGATGGGAAAACAACTATC	
		1821 S S T S E Y E R N R G E R R S H K K F K 5462 TCTTCTACATCTGAGTATGAGAGAAATCGTGGTGAAAGGAGAAGTCATAAAAAGTTCAAA	
		1841 P N V T R G R G S K R V R G K T S K K E 5522 CCAAATGTCACCAGAGGTCGTGGATCAAAACGAGTTCGGGGTAAGACCTCTAAGAAGGAA	
		1861 P R A S K A M L V T L R A S Q E E D D D 5582 CCTAGAGCTTCCAAGGCCATGCTGGTGACTCTTCGGGCTTCCCAGGAAGAAGATGATGAT	
		1881 A D D F E S D Y E E E E S Y H L A P E E V 5642 GCTGACGATTTTGAGTCTGACTATGAGGAAGAAAGCTATCATCTTGCTCCCGAAGAAGTA	
		1901 N K A P V F V P V G L R S P E P V S A Q 5702 AACAAAGCTCCAGTATTTGTACCTGTTGGTCTCAGATCTCCTGAACCTGTTTCTGCTCAG	
		1921 I E E E T M E E L E I T V N V P D V G C I 5762 ATTGAGGAAACAATGGAAGAGCTTGAAATAACTGTGAATGTCCCAGATGTAGGATGCATA	
		1941 A V V E H E L P N T D V T T E E M K Q E 5822 GCTGTTGTTGAACATGAGCTACCAAACACAGATGTGACTACTGAAGAAATGAAACAAGAA	
		1961 E N L S V P F E M T T S E H I Q D E P G 5882 GAAAATTTGAGTGTACCGTTTGAAATGACCACAAGTGAACATATCCAAGATGAACCAGGT	
		1981 T N D G S T E A A I T L L T M G D L V L 5942 ACCAATGATGGAAGCACCGAAGCTGCAATAACTTTACTTACAATGGGAGATCTAGTATTG	
		2001 Q S E I S S E Q G D V G V C I I P H V H 6002 CAGTCAGAGATCAGTAGTGAACAGGGTGATGTAGGAGTATGTATAATTCCTCATGTTCAT	
		2021 S K D K S H I P S S L D N V N H K I V H 6062 TCAAAGGATAAAAGCCATATTCCTTCTAGCCTAGATAATGTAAATCACAAAATTGTTCAT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2041 E C Q E L S S P V I T T S P A S F E E N 6122 GAATGTCAGGAACTTTCTTCACCTGTCATTACTACATCTCCTGCATCATTTGAAGAAAC	
		2061 K I V L E E Q S S R E E I S L M E K V K 6182 AAGATTGTATTGGAGGAACAAAGTTCCAGAGAAGAAATAAGTTTAATGGAGAAAGTAAAG	
		2081 E N A T P T R N T I S K V T S N L R I R 6242 GAGAATGCTACACCAACCAGGAATACAATTTCTAAAGTGACCAGTAATTTGAGAATAAGA	
		2101 S R L A K P K P N L E K T L G T N R L D 6302 AGTAGGCTTGCTAAGCCTAAACCAAATCTTGAGAAGACTTTAGGGACCAACAGGCTTGAT	
		2121 D Y Q E V S S L C V T K G A E M E T Q R 6362 GATTATCAGGAAGTTTCCAGTTTGTGTGTAACCAAAGGGGCAGAAATGGAAACTCAAAGA	
		2141 E T E K N A S K A T E L E N K N L G P V 6422 GAAACAGAGAAAAATGCTTCCAAAGCAACACAGAATTGGAAAATAAAAACCTCGGACCAGTT	
		2161 T T A E N K D Q S K L A C V H G I K G T 6482 ACAACAGCAGAGAATAAGGATCAGAGCAAATTGGCATGTGTACATGGTATCAAAGGGACC	
		2181 S I S S E V N L T E R N E N Q E E S S Q 6542 AGTATTTCTTCAGAAGTAAACCTAACTGAAAGAAACGAAAATCAAGAAGAGAGCTCTCAG	
		2201 E V H M L S V A P V A S S E T G P C T L 6602 GAGGTTCACATGTTGTCAGTTGCTCCAGTTGCTTCCTCTGAGACAGGGCCCTGCACACTT	
		2221 G L D R G L G E N S V E E P Q I K D S K 6662 GGTTTGGATAGGGGTCTTGGTGAAAATTCTGTTGAAGAGCCCCAGATAAAGGACTCTAAA	
		2241 G D S V L T L P V P E Y T P T S I P E V 6722 GGAGACAGTGTGCTTACACTTCCTGTGCCAGAGTATACACCAACAAGTATTCCAGAAGTC	
		2261 Q Q E N I I N P P Q D L T V N L V A N V P 6782 CAACAAGAGAATATAATCAATCCTCAAGACCTAACAGTGAATCTAGTTGCTAATGTACCT	
		2281 Q D G E D E Q A F I L T L V E I P A N A 6842 CAAGATGGAGAAGATGAACAAGCCTTTATTTTAACTCTGGTGGAAATCCCAGCCAATGCA	
		2301 V E E F T D A T A Q F M P N P L L P A P 6902 GTAGAAGAATTTACTGATGCCACACAGTTCATGCCAAACCCTTTACTGCCAGCTCCC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2321 I L V K S V N T E E R G D M S I C L P A 6962 ATATTGGTCAAATCAGTGAATACCGAAGAAAGGGGTGACATGAGTATTTGTTTACCAGCA	
		2341 T S V G Q D D A M G L S S I S G R D D N S K K K 7022 ACTTCAGTTGGTCAAGATGCCATGGGTTTATCTATTTCTGGAAGAGATAATTCTAAAAAG	
		2361 P P D N L D L V S R K R F Q C R L D K N 7082 CCGCCTGATAATTTGGATCTTGTATCTAGGAAGAGATTTCAATGCAGGCTTGATAAAAAT	
		2381 D H I P P A K K R S L T L R D D C Q E Y 7142 GACCACATTCCTCCTGCCAAAAAACGTTCACTCACTTTAAGAGATGACTGTCAAGAATAT	
		2401 T T E V H S K E L T N V F E E T G E S H 7202 ACCACTGAGGTGCACTCAAAGGAATTAACAAATGTTTTTGAGGAAACAGGGAGTCTCAC	
		2421 K G Q D I F L T S G S T L T T P E P Q R 7262 AAGGGACAAGATATTTTTCTTACCTCAGGAAGCACACTGACAACTCCAGAACCTCAAAGA	
		2441 Q Q V E A A F Q S R G S R S P D A C M D 7322 CAGCAAGTTGAAGCAGCTTTTCAGAGTAGAGGATCTAGATCTCCTGATGCATGCATGGAC	
		2461 K N V P P Q L P Q D E M I V S D K E E E R T 7382 AAGAATGTGCCTCAGTTACCTCAGGATGAAATGATTGTGTCTGATAAGGAAGAAAGAACT	
		2481 D A A P K S Q Q M D S R T S S S K A S L 7442 GATGCTGCTCCTAAGTCTCAGCAAATGGATAGCAGAACATCGTCTTCTAAAGCCTCACTA	
		2501 S R P G R R P L G F L S L I C S K N S L 7502 TCCAGACCTGGCAGAAGACCCCTGGGATTTTTATCTTTAATATGCTCAAAGAATAGTTTG	
		2521 E S D E P M Q V H S K K K R L K P L I P G 7562 GAGTCTGATGAACCTATGCAGTCCATAGTAAGAAACGCCTAAAACCTCTTATACCTGGA	
		2541 L R K K L K R S N P F N E S Q E K N R E 7622 TTAAGAAAGAAATTGAAAAGATCTAATCCATTCAATGAAAGCCAGGAAAAAAATCGAGAG	
		2561 S S D L L P S P S V I T T Q S E N I S S 7682 TCCTCTGATCTGCTTCCATCTCCAAGTGTTATTACTACTCAATCTGAGAATATTAGCAGC	
		2581 S A T Q V S C D Q P L L K E G Y K S A Q 7742 TCAGCAACTCAGGTTTCTTGTGATCAGCCCTTACTGAAAGAAGGATATAAAAGTGCCCAA	
		2601 K R A P Q G E A T T V S E Y F F N D I F	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		7802 AAGCGGGCCCCTCAAGGGAGGCAACCACAGTCTCTGAATATTTCTTCAATGATATCTTC 2621 I E V D E T E - 7862 ATTGAAGTGGATGAAACAGAATAA	
WBC030C04.bFSP_20012410.abd	No Homology	1 GAAGGTTTCCCTGAGCGTCTCTAAGCTCGCCCAGCCACACCCTGTGCCCCCTCCATTTG 61 TGTCCTCTGTCCCCCTTTCCTGCTTCCCTCCTTCCCCACCGTGGCTGGTCTAGGTGTCTG 121 TAATAGTCAGAATGCAGGTTTGGCAACTTGAACAAAACTTTTAAATAACAGTGGCTTAAA 181 CCACAAAAAAAAATTGATTTCTCTGGTAATATCTAAGCACAAGCAGGCCAGGCAATATGG 241 GGACTCCCTGGTTTTGAGATCCAGGATTCCCAGGTCTTGGCGCTACGAGGTCCACATTCT 301 AGGCCTCAAGACCAGGGAAGAAGGCAGTGAAAGGGAGCATGACCCTCCCCTTCAAGGCA 361 CAGCTAGGAATCACCCACATCACCTCTAATTGGCTGGAATGTGGTCACACGGTCACACCT 421 AGCTGCAAGGAAGGCAGGGAAATGTAGTCTTTATTCTGACCACAACGTGCCCAGGTGAAA 481 TTTGTCACTAGAGAACCGGTGGGCAGATATGTGTAGATAATCAATAATCTCCACCTCAGG 541 GGCATTGAGGCAGCCTCTTACTTCCTCTGCGTGACACCAGAGTTCGATTCCCATCTGAAA 601 CGACCCCTCTTTGTACCACCAGCTCCACTAGGGCTGCGTAAGGGAGGGTGGTAGTTCTCA 661 AGAAGGGGAGATTTTGCCCCCACAGGGGACATTTGGCAAAGTCCAGAGACATTTTCCGTT 721 GTCACAACTTGGGGGGTGCTATCGCCATCTAGTGGGGAGAGGTCACCGATGCTGCTAAAC 781 ATCATATGATGCCCCCACCAACATAGAGTTGTCTGGCCCAAAGCATCAGCAGAAGCCCTG 841 ATGCAGGGAAAGCGTGCGTTCCCCGGGTCAGACACGCCTGACTTCTAACCCTGAAGCCC 901 CGCCTCCCTCCCCGTGTGGCCTTAGTGACCAATCAGTCACTTCACCCCTCGGAACATCGA 961 TGATGGTAACATGGACTTCCCTGCATTGTATGAGAACCAATTCAGGTCGTTTACTGAGGG 1021 CTTACCATGTGCTGTGTGCTCTGTGTACCCTCAGATCACGTGAACTCCCTTTCCATGCGC 1081 ACATTTACTAGCACCTACTATGCGGGGAAGTGGATTCCTCTGGATGATTTTGTTATAATA 1141 AACAGAAAAACAGCTTGAAAAAA	SEQ ID NO:136
WBC030C11.bFSP_20012410.abd	Homo sapiens protein associated with Myc mRNA.	1 TCTTGGAGCGTTCTCAGTTTCTCAACAGATCTTCACTTGCTAGGCAGCCAGAAGCCGGCG 61 GCAGTGGCGGCACCGCCTCCTCCTCACATTCCCGGGGTGGCGGGGTTAGATGAGCGGCCC 121 CAGTCGCGGCGCCGGGGGCGCTGTTCATGCCGGTTCCCGACGGCTCCGTGGCTGCTGCGG 181 GGCTGGGGCTGGGGCTACCCGCCGCGGACTCCCCGGGTCACTACCAGCTGCTGCTGTCAG 241 GCCGGGCCCTGGCCGACCGCTACCGGAGGATTTATACCGCTGCGCTCAATGACAGGACC 301 AGGGGGGCGGCAGCCGCTGGACACCCAGCCTCCAGGAATAAGAAAATTTTAAATAAGAAGA 361 AATTGAAAGAAAACAGAAGAGCAAATCAAAAGTGAAGACAAGAAGCAAGTCTGAAAACT 421 TAGAGAATACAGTAATCATACCAGATATCAAACTACATAGCAATCCTTCTGCTTTCAATA 481 TTTACTGTAATGTACGCCATTGCGTTCTGGAATGGCAGAAAAGGAAATATCATTGGCAG 541 CCGCATCTAAGAACTCTGTGCAGAGTGGAGAATCAGATAGTGATGAAGAAGAGGAATCCA 601 AAGAGCCCCCTATCAAGCTTCCAAAGATTATTGAGGTTGGCCTTTGTGAAGTTTTTGAAT 661 TGATCAAAGAGACACGATTTTCTCATCCATCCCTGTGTCTCAGGAGTCTCCAAGCCCTGC 721 TCAACGTGCTGCAGGCCAGCAGCCAGAAGTGCTCCAGTCTGAGCCACCTGAGGTCCTAG 781 AGTCTCTCTTCCAGCTTCTTTTGGAAATCACCGTTCGAAGTACTGGGATGAATGACAGCA 841 CAGGACAGTCCTTAACAGCACTTTCCTGTGCTTGCCTCTTTAGTCTGGTGGCTTCTTGGG	SEQ ID NO:137

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		901 GAGAAACAGGAAGGACACTTCAGGCCATCTCTGCTATCCTCACCAACAATGGAAGCCATG	
		961 CTTGCCAAACTATTCAGGTGCCAACAATTCTAAATTCGCTACAGAGAAGTGTACAAGCAG	
		1021 TTTTGGTGGGAAAAATTCAAATTCAGGACTGGTTTAGTAATGGCATTAAGAAAGCAGCTT	
		1081 TAATGCACAAGTGGCCATTAAAAGAAATATCTGTTGATGAAGATGACCAATGTCTACTTC	
		1141 AGAATGATGGATTTTTTCTTTATCTATTATGCAAGGATGGATTATATAAAATAGGCTCTG	
		1201 GATACAGTGGAACAGTTAGGGGCCATATATACAATTCTACATCCCGTATTAGAAACAGAA	
		1261 AAGAAAAAAAGTCTTGGTTAGGGTATGCTCAGGGTTATTTATATAGAGATGTGAATA	
		1321 ACCACAGCATGACAGCCATAAGGATAAGCCCTGAAACACTGGAGCAAGATGGTACTGTGA	
		1381 TGTTACCAGATTGCCACACTGAAGGTCAAAATATTTTATTCACTGATGGAGAATATATTA	
		1441 ATCAGATAGCTGCTTCAAGAGATGATGGCTTTGTTGTCAGAATATTTGCCACAAGCACTG	
		1501 AACCTGTTCTACAGCAAGAATTGCAACTTAAACTGGCTAGAAAATGCTTACATGCCTGTC	
		1561 GTATCTCATTATTCGATCTGGAAAAGGACTTGCATATTATAAGTACAGGATTTGATGAGG	
		1621 AGTCAGCAATTCTTGGTGCAGGACGAGAGTTTGCGCTAATGAAAACAGCAAATGGAAAGA	
		1681 TATATTACACTGGCAAATACCAGAGTCTTGGAATCAAACAAGGTGGTCCTTCAGCAGGAA	
		1741 AATGGGTTGAGCTACCAATTACAAAATCTCCAAAGATAGTACACTTCTCAGTTGGACACG	
		1801 ATGGCTCTCACGCCCTTTTAGTTGCAGAAGATGGGAGCATATTCTTTACAGGATCTGCTA	
		1861 GTAAAGGAGAAGATGGAGAATCAATTAAGAGCAGACGGCAATCCAAACCTTATAAACCTA	
		1921 AAAAGATAATTAAGATGGAAGGAAAGATTGTGGTATATACAGCCTGCAATAATGGAAGTA	
		1981 GTTCTGTTATTTCTAAAGATGGAGAACTCTACATGTTTGGAAAAGATGCCATTTACTCTG	
		2041 ATAGTTCAAGTTTGGTAACTGATTTGAAGGGCCATTTTGTAACTCAGGTAGCTATGGGCA	
		2101 AAGCTCACACTTGTGTTTTAATGAAGAATGGAGAGGTGTGGACATTTGGTGTAAATAATA	
		2161 AAGGACAGTGTGGACGAGATACTGGTGCCATGAACCAAGGTGGGAAAGGGTTTGGAGTTG	
		2221 AAAATATGGCAACAGCAATGGATGAAGACCTGGAAGAAGAACTAGATGAAAAAGATGAGA	
		2281 AGTCTATGATGTGCCCTCCAGGCATGCACAAATGGAAGCTGGAGCAGTGCATGGTTTGCA	
		2341 CTGTCTGTGGAGACTGTACAGGTTATGGAGCCAGCTGTGTCAGTAGTGGACGGCCAGACA	
		2401 GAGTCCCCGGAGGGATCTGTGGTTGTGGTTCCGGAGAATCTGGTTGTGCTGTGTGTGGAT	
		2461 GTTGCAAGGCCTGTGCAAGAGAGTTTAGATGGTCAAGAGGCAAGACAAAGAGGAATTCTTG	
		2521 ATGCAGTGAAAGAAATGATACCTTTAGATCTTCTTTTAGCTGTCCCAGTGCCCGGGTTTA	
		2581 ACATTGAAGAACACCTTCAGTTACGACAAGAAGAAAAACGGCAACGTGTAATCAGAAGGC	
		2641 ACAGATTAGAGGAAGGAAGAGGCCCCCTTGTATTTGCTGGTCCTATTTTTATGAACCATC	
		2701 GAGAACAGGCTCTAGCCAGACTCAGATCCCATCCAGCACACGTAAAGCATAAACGGGACA	
		2761 AGCACAAAGATGGAAGTGGAGAAAGAGGCGAAAAGGATGCAAGCAAAATCACACAACATACC	
		2821 CTCCAGGCTCTGTGCGATTTGACTGTGAGCTCCGGGCAGTCCAAGTCAGCTGTGGATTTC	
		2881 ACCATTCAGTGGTTTTAATGGAAAATGGAGATGTCTATACATTTGGTTATGGGCAGCATG	
		2941 GGCAGCTAGGACATGGAGATGTCAACTCCAGGGGATGTCCCACTCTTGTTCAAGCATTGC	
		3001 CAGGCCCTAGCACACAAGTCACTGCAGGCAGCAACCATACGGCAGTACTTTTAATGGATG	
		3061 GACAGGTCTTCACATTTGGAAGTTTTTCTAAGGACAACTGGGCAGACCAATTTTGGATG	
		3121 TGCCATATTGGAATGCAAGCCAGCTCCCATGCCTAACATTGGATCAAAATATGGAAGAA	
		3181 AAGCTACTTGGATAGGTGCAAGTGGGGACCAAACTTTTTTACGAATTGATGAAGCACTTA	
		3241 TTAATTCTCATGTACTTGCTACATCAGAAATTTTTGCCAGTAAACACATAATAGGCTTGG	
		3301 TACCTGCTTCTATATCAGAACCTCCTCCATTTAAATGCCTTCTGATAAATAAGTGGATG	
		3361 GGAGTTGTAAAACTTTTAATGACTCAGAACAAGAGGATCTGCAAGGATTTGGTGTGTGTC	
		3421 TTGATCCTGTATATGATGTAATTTGGAGGTTTCGACCAAATACTAGAGAGCTGTGGTGTT	

Gene Name	GenBank Homology		DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		3481	ACAATGCGGTGGTTGCTGATGCCAGGCTTCCCTCTGCAGCAGACATGCAGTCCAGATGTA	
		3541	GTATCCTAAGTCCTGAACTTGCCTTACCAACAGGATCAAGGCCCTCACTACCCGATCTC	
		3601	ATGCAGCTTTGCACATTTTAGGTTGTCTTGATACCTTGGCAGCTATGCAGGACTTAAAAA	
		3661	TGGGTGTTGCAAGTACAGAGGAAGAGACTCAAGCAGTAATGAAGGTTTATTCTAAAGAAG	
		3721	ATTATAGTGTGGTAAACAGGTTTGAAAGTCATGGAGGAGGCTGGGGTTATTCTGCCCATT	
		3781	CAGTAGAAGCTATACGTTTCAGTGCCGACACTGATATTTTACTTGTGGTCTTGGTCTGT	
		3841	TTGGAGGTAGAGGAGAATATACTGCTAAAATTAAGCTGTTTGAATTGGGTCCTGATGGAG	
		3901	GAGATCATGAAACTGATGGTGACCTTCTTTGCAGAGACTGATGTATTGGCTTATGACTGTG	
		3961	CTGCTAGAGAAAAATATGCAATGATGTTTGATGAGCCTGTTCTCCTGCAAGCTGGGTGGT	
		4021	GGTATGTGGCATGGCCCGAGTGTCAGGACCCAGCAGTGACTGTGGATCTCATGGACAGG	
		4081	CATCTATTACCACAGATGATGGGGTTGTTTTCCAGTTCAAGAGTTCAAAGAAATCAAATA	
		4141	ATGGTACAGATGTTAATGCGGGTCAGATACCTCAGTTATTATACAGACTTCCAACCAGTG	
		4201	ATGGCAGTGCTTCAAAAGGCAAACAGCAACCAGTGAACCTGTACACATTTTAAAGAGGT	
		4261	CTTTTGCAAGAACTGTCTCAGTGGAATGTTTTGAGTCATTGTTGAGTATTCTTCACTGGA	
		4321	GCTGGACCACCTTAGTCTTAGGAGTTGAAGAACTTAGAGGATTAAAGGATTCCAGTTCA	
		4381	CAGCTACACTCCTAGATTTAGAGAGACTGCGCTTTGTGGGTACCTGTTGTCTGAGGTTAT	
		4441	TGCGTGTCTATACCTGTGAAATTTACCCAGTGTCAGCTACAGGAAAAGCAGTTGTAGAAG	
		4501	AAACTAGCAAATTAGCAGAGTGTATTTGGAAAAACCAGAACTTTGTTAAGAAAAATTTAT	
		4561	CAGAACCACTTGATCACTGCATGGTGAAATTGGATAATGATCCTCAAGGATATCTCAGTC	
		4621	AACCCTTGAGTCTTCTAGAAGCTGTCCTTCAGGAATGTCATAATATCTTTCACTGCCTGCT	
		4681	TTCATTCTTTCTACCCAACTCCTGCCTTACAGTGGGCTTGCCTTTGTGATCTGCTGAATT	
		4741	GTTTGGATCAGGATATCCAAGAAGCAAACTTCAAGACATCAAGTAGCCGACTCCTTGCAG	
		4801	CTGTTATGTCAGCTCTGTGTCACACGTCTGTTAAGCTGACTTCCATCTTCCCGATTGCGT	
		4861	ATGATGGAGAAGTATTACTACGATCAATTGTTAAACAAGTTAGTACAGAGAACGACTCAA	
		4921	CACTAGTTCATCGTTTTCCCCTTTTGGTGGCACATATGGAAAAACTCAGCCAGAGTGAAG	
		4981	AGAATATCTCAGGGATGACAAGCTTCCGTGAAGTTCTGGAGAAAATGCTGGTCATTGTTG	
		5041	TGCTACCAGTCAGGAACAGCCTGAGGAGAGAAATGAACTCTTCTCCTCCCACCTCGTCT	
		5101	CTAACACCTGTGGATTACTGGCCAGCATTGTCAGTGAACTGACAGCGTCAGCCCTGGGAT	
		5161	CTGAGGTTGATGGACTTAATTCTCTTCACTCTGTAAAAGCTAGTGCTAACCGATTTACAA	
		5221	AAACAAGTCAGGGCAGAAGTTGGAACACTGGGAACCGGGTCCCCTGATGCAATCTGTTTTT	
		5281	CAGTAGACAAACCTGGAATAGTTGTGGTTGGTTTCTCTGTCTATGAGAGGAGGTGGAATTC	
		5341	ATGAATATGAATTAGAGGTGTTGGTTGATGATAGTGAACATGCAGGAGATTCAACTCATT	
		5401	CCCACAGATGGACATCTCTGGAATTAGTGAAGGAACGTACACAACGGATGACTCACCCA	
		5461	GTGATATAGCTGAGATCAGACTTGACAAAGTGGTTCCTTTAAGGAAAATGTTAAATATG	
		5521	CTGTGCGCTTGAGGAACTATGGAAGCCGTACAGCCAATGGAGATGGAGGAATGACCACAG	
		5581	TTCAGTGCCCTGATGGTGTGACATTCACATTCAGCACGTGCAGCTTGAGCAGTAACGCCA	
		5641	CAAACCAAACCAGAGGACAGATCCCACAGATACTCTTACTATAGGAGTGAATTTGATGGAG	
		5701	ATTTACAATCCCAACTTCTGAGTAAAGCCAATGAAGAAGATATAAAACTGTAGCAGAGCAT	
		5761	TGTCTGTTGTAAGCACTGTCGTTCGAGCCTCTAAGGACCTCCTGCACAGAGCTCTTGCTG	
		5821	TGGATGCTGATGACATTCCAGAACTGCTGAGTTCTTCCAGTCTGTTTTCCATGCTGCTCC	
		5881	CCCTTATTATAGCCTACATAGGACCAGTAGCTGCTGCTATTCCCAAGGTGGCTGTAGAAG	
		5941	TCTTTGGCCTTGTCCAACAATTGCTTCCGTCAGTTGCCATTTTGAATCAGAAGTATGCAC	
		6001	CGCCTGCCTTCAACCCTAATCAGTCGACAGATAGCACCACAGGAAACCAGCCTGAACAGG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE		SEQUENCE IDENTIFIER:
		6061	GCCTCTCTGCTTGTACAACCTCCAGTCACTATGCTGTCATAGAGAGTGAGCACCCGTATA	
		6121	AACCTGCCTGTGTGATGCATTACAAGGTGACATTCCCAGAATGTGTGAGGTGGATGACAA	
		6181	TCGAATTTGACCCTCAGTGTGGTACTGCACAGTCAGAAGATGTCCTTCGTTTGTTGATTC	
		6241	CTGTCAGAACTGTTCAGAATTCAGGATATGGACCAAAATTGACATCTGTTCATGAAAATC	
		6301	TTAATTCATGGATAGAATTAAAGAAATTTTCAGGATCCTCTGGGTGGCCTACTATGGTTT	
		6361	TGGTGTTGCCAGGAAATGAGGCCCTTTTTTCATTGGAGACTGCATCAGATTATGTGAAAG	
		6421	ATGACAAAGCTTCTTTCTATGGTTTTATGTGTTTTGCAATTGGATATGAATTTAGCCCTG	
		6481	GACCTGATGAGGGAGTCATCCAATTGGAAAAAGAATTAGCCAATCTTGGTGGGTTTGTG	
		6541	CAGCAGCTCTGATGAAGAAGGACCTAGCACTTCCTATTGGTAATGAATTAGAAGAAGACC	
		6601	TTGAAATTCTTGAGGAGGCTGCATTGCAGGTGTGCAAAACCCATTCTGGAATTCTTGGAA	
		6661	AGGGTCTAGCTCTTTCTCATTCACCAACTATATTAGAAGCACTTGAGGGAAATTTACCAC	
		6721	TCCAAATCCAAAGCAATGAACAGTCTTTCTGGATGATTTTATTGCCTGTGTCCCAGGAT	
		6781	CAAGTGGTGGAAGGCTTGCAAGGTGGCTTCAGCCAGATTCATATGCGGATCCTCAGAAAA	
		6841	CATCTTTGATCCTGAATAAGGATGATATTCGTTGTGGTTGGCCTACCACCATAACTGTTC	
		6901	AAACAAAAGACCAGTATGGGGATGTGGTACATGTTCCCAATATGAAGGTGGAAGTGAAAG	
		6961	CTGTCCCTGTTTCTCAGAAAAAAAATGTCTTTACAACAAGATCAAGCAAAGAAACCTCAAA	
		7021	GGATTCCTGGCAGTCCTGCAGTAACAGCTGCATCTTCTAATACTGACATGACTTATGGAG	
		7081	GGCTGGCATCACCAAAGCTAGATGTTTCATATGAACCAATGATAGTGAAGGAAGCTCGAT	
		7141	ATATTGCCATAACAATGATGAAGGTTTATGAAAATTATTCATTTGAAGAACTACGTTTTG	
		7201	CATCACCAACTCCTAAGACACCCAGTGAGAAATATGCTGATCCGTGTCAATAATGATGGGA	
		7261	CTTATTGTGCAAATTGGACTCCAGGGGCTATTGGACTCTACACTCTTCATGTTACCATTG	
		7321	ATGGCATTGAAATCGATGCTGGTCTGGAAGTAAAAGTAAAAGACCCACCAAAAGGGATGA	
		7381	TACCACCAGGAACTCAGTTGGTCAAACCAAAGTCTGAACCTCAGCCTAATAAGGTTCGAA	
		7441	AATTTGTGGCCAAGGACAGTGCGGGGCTTCGCATCCGTAGCCACCCTTCCCTTCAGAGTG	
		7501	AGCAGATAGGCATAGTGAAAGTCAATGGAACTATCACTTTTATTATGATGAGATCCATAATG	
		7561	ATGATGGTGTGTGGCTGAGGCTGAATGATGAGACAATAAAGAAGTATGTCCCTAACATGA	
		7621	ATGGTTACACTGAAGCCTGGTGCCTCTCTTTTAATCAACATCTTGGCAAGAGTCTTCTGG	
		7681	TCCCTGTTGACGAATCTAAAACTAATACTGATGACTTTTTCAAAGACATAAACTCCTGCT	
		7741	GCCCACAGGAAGCAACAATGCAAGAACAAGATATGCCATTCTTGCGAGGAGGGCCAGGCA	
		7801	TGTACAAGGTAGTGAAGACGGGGACCTTCAGGTCACAACATCAGAAGCTGCCCTAACCTTA	
		7861	GAGGTATCCCAATTGGAATGTTAGTTCTGGGAAACAAAGTCAAAGCAGTGGGAGAGGTAA	
		7921	CCAATTCTGAAGGGACATGGGTGCAACTGGATCAGAACAGCATGGTAGAGTTCTGTGAGA	
		7981	GTGATGAAGGAGAGGCATGGTCCTTAGCTAGAGACAGAGGCGGAAACCAGTACCTCCGAC	
		8041	ATGAAGATGAACAAGCTCTTCTGGATCAGAATTCTCAAACTCCTCCTCCAAGCCCTTTCT	
		8101	CAGTGCAAGCTTTTAATAAAGGGGCAAGTTGCAGTGCCCAAGGATTTGATTATGGACTCG	
		8161	GAAATAGCAAAGGTGATCGAGGAAACATCTCAACATCTTCTAAACCAGCCTCTACATCAG	
		8221	GAAAATCAGAGCTGTCCTCTAAACACAGCAGATCGCTTAAACCTGATGGACGTATGAGCC	
		8281	GGACTACTGCTGATCAGAAGAAGCCAAGGGGCACAGAAAGTTTATCTGCTAGTGAATCCC	
		8341	TCATCTTAAAATCTGATGCTGCAAAGTTGAGGTCAGATTCCCACAGTAGGTCATTATCCC	
		8401	CCAACCATAACACCTTGCAGACATTGAAATCTGATGGGAGGATGCCTTCTAGCTCCCAGAG	
		8461	CTGAATCCCCAGGACCAGGTTCTCGGTTGTCATCTCCTAAGCCAAGACTCTCCCAGCCA	
		8521	ATAGGTCTAGCCCATCGGGTGCTAGTTCTCCACGCTCCTCCTCACCACATGATAAAAATC	
		8581	TACCTCAAAAAAAGTACTGCTCCTGTTAAGACAAAGCTTGATCCTCCTCGGGAACGTTCTA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		8641 AATCAGACTCTTACACACTTGATCCAGATACCCTCCGCAAGAAGAAATGCCCCTCACAG	
		8701 AACCTTTGAGAGGACGGTCAACGTCACCAAAACCAAAATCAGTACCAAGGATTCTACAG	
		8761 ATTCCCCTGGATCTGAAAATAGAGCTCCCTCTCCCCATGTGGTACAGGAAAACCTCCACA	
		8821 GTGAGGTGGTCGAAGTCTGCACCTCAAGTACTTTAAAAACACAAATAGTCTAACAGACAGCA	
		8881 CCTGCGATGACAGCAGTGAATTTAAGAGTGTGGATGAAGGTTCAAATAAAGTTCATTTTA	
		8941 GCATTGGAAAAGCACCACTGAAAGATGAACAGGAAATGAGAGCATCTCCCAAAATAAGTC	
		9001 GAAAATGTGCTAATAGACACACCAGGCCCAAAAAAGAAAAATCGAGTTTTCTTTTCAAAG	
		9061 GAGATGGATCCAAGCCTTTAGAGCCAGCCAAGCAAGCCATGTCTCCTTCTGTGGCCGAAT	
		9121 GTGCCAGAGCTGTGTTTGCTTCCTCTCTGGCATGAAGGCATAGTACATGATGCAATGG	
		9181 CTTGTTCTTCTTTCCTAAAGTTTCATCCTGAACTTTCCAAAGAACATGCTCCTATAAGGA	
		9241 GTAGTTTAAATAGCCAACAACCTACAGAAGAAAAAGAAACCAAGTTAAAAAATAGACATT	
		9301 CATTAGAAATATCATCTGCACTGAATATGTTTAATATTTGCACCCCATGGACCAGATATAT	
		9361 CTAAGATGGGTAGCATCAACAAAAACAAGGTATTGTCTATGCTTAAGGAACCACCTCTGC	
		9421 ATGAAAAATGTGAGGATGGGAAAACCGAGACCACTTTTGAAATGTCCATGCATAACACAA	
		9481 TGAAGTCTAAGTCTCCTCTTCCCTTAACTTTACAACATTTAGTGGCTTTTTGGGAAGACA	
		9541 TCTCTTTGGCTACTATCAAAGCTGCTTCCCAGAATATGATTTTTCCAAGTCCTGGTTCCT	
		9601 GTGCAGTTCTTAAAAAGAAAAGAGTGTGAGAAAGGAAGGAATAAGAAGTCCAAAAAGGAAA	
		9661 AAAGAAAAAAGAAAAGGCAGAAGTTAGGCCCAGGGTAATTTGTTTGGAGAGATGGCCC	
		9721 AGCTGGCAGTAGGAGGACCAGAGAAAGATACCATCTGTGAACTGTGTGGGAGTCACATC	
		9781 CATACCCGGTGACCTATCACATGAGACAAGCTCACCCAGGTTGTGGCCGATATGCTGGTG	
		9841 GACAAGGTTACAATAGCATTGGGCATTTTTGTGGAGGATGGGCTGGTAACTGTGGTGATG	
		9901 GTGGCATAGGAGGAAGCACTTGGTATCTGGTATGTGATCGCTGTAGAGAAAAATACCTCC	
		9961 GCGAAAAACAGGCTGCTGCAAGGGAGAAGGTCAAACAATCTAGGAGAAAACCAATGCAAG	
		10021 TCAAGACCCCTCGTGCCTTGCCCACCATGGAAGCTCACCAGGTGATTAAAGCCAATGCAC	
		10081 TCTTCCTGCTGTCCCTGAGCAGTGCAGCAGAACCGAGCATTCTGTGTTACCATCCTGCAA	
		10141 AGCCATTCCAATCTCAGTTGCCCAGTGTAAAAGAAGGCATTTCTGAGGATCTTCCTGTGA	
		10201 AAATGCCTTGTCTGTACCTGCAGACATTAGCTAGGCATCATCATGAAAATTTTGTGGGCT	
		10261 ATCAAGATGACAATCTATTCCAGGATGAAATGAGATATCTACGTTCAACATCTGTACCTG	
		10321 CCCCGTATATATCAGTAACTCCTGATGCAAGTCCTAATGTATTTGAAGAGCCAGAGAGCA	
		10381 ATATGAAGTCTATGCCACCAAGTTTAGAAACCAGTCCCATAACTGATACTTGATCTTGCAA	
		10441 AGAGAACTGTCTTCCAAAGATCATACTCAGTTGTTGCTTCCGAATATGATAACAACACT	
		10501 CCATTTTACCTGCACGAGTTAAAGCTATTCCTAGAAGAAGAGTTAACAGTGGAGACACTG	
		10561 AAGTTGGTTCTTCCCTTTTGAGACATCCGTCTCCTGAGCTTTCTCGGCTAATCTCAGCCC	
		10621 ACAGCTCTCTTTCTAAAGGAGAACGAAATTTCCAGTGGCCAGTTTTAGCTTTTGTTATAC	
		10681 AACATCATGATCTAGAAGGTCTTGAAATAGCAATGAAACAGGCCCTAAGGAAATCTGCTT	
		10741 GTCGAGTTTTTGCTATGGAGGCTTTCAACTGGCTTCTGTGTAATGTCATCCAAACCACTT	
		10801 CTCTCCATGATATTCTGTGGCATTTTGTGGCATCACTGACTCCCTGCACCAGTGGAACCAG	
		10861 AGGAAGAAGATGAAGAAATAAACAAGCAAAGAAAATTCAGAACAAGAGAAAGATA	
		10921 CAAGAGTATGTGAACATCCACTCTCAGACATAGTGATTGCCGGGGAACGTGCTCATCCTT	
		10981 TACCACACACCTTTCACCGCTTGCTGCAGACCATCTCAGACCTTATGATGTCTCTCCCCA	
		11041 GCGGCAGTTCATTACAGCAAATGGCCCTGAGGTGCTGGAGTCTCAAATTCAAGCAATCTG	
		11101 ATCACCAGTTCCTTCATCAGAGCAACGTCTTTCATCACATTAACAATATTTGTCAAAGT	
		11161 CAGATGATGGCGATAGTGAAGAGAGTTTAGCATCAGTATACAGTCTGGCTTTGAAGCTA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		11221 TGAGTCAGGAATTATGCATAGTAATGTGCTTAAAGGACTTAACCAGCATTGTTGACATAA	
		11281 AAACTTCAAGCCGACCTGCCATGATTGGCAGTTTGACAGACGGCTCCACAGAAACCTTTT	
		11341 GGGAATCAGGAGATGAAGATAAAAACAAAACTAAGAACATCACCATCAACTGTGTAAAAG	
		11401 GAATCAATGCCCGCTATGTGTCTGTTCACGTGGACAATTCCCGAGATCTTGGGAATAAAG	
		11461 TTACCTCAATGACCTTCTTAACTGGCAAAGCAGTAGAAGATTTGTGCAGAATAAAGCAAG	
		11521 TTGATCTGGATTCCAGGCACATTGGCTGGTAACAAGTGAACTTCCAGGAGGAGATAATC	
		11581 ACATCATCAAAATTGAATTAAAGGCCCAGAAAATACACTGAGAGTTCGACAAGTTAAGG	
		11641 TTCTGGGCTGGAAGGATGGTGAAAGCACTAAAATTGCTGGCCAGATTTCAGCCAGTGTGG	
		11701 CCCAGCAAAGGAACTGTGAAGCTGAGACTCTGCGAGTGTTCAGACTTATTACATCTCAAG	
		11761 TATTTGGAAAGCTCATCTCTGGAGATGCTGAACCCACACCAGAACAAGAGGAAAAAGCAC	
		11821 TGTTGTCATCACCTGAAGGAGAGGAAAAAGTATACAATGCAACATCAGATGCTGACCTGA	
		11881 AAGAACATATGGTTGGAATCATATTCAGCAGGAGTAAACTGACTAACTTACAAAAACAGG	
		11941 TGTGTGCTCACATAGTCCAGGCTATTCGCATGGAAGCTACCAGAGTTCGTGAAGAATGGG	
		12001 AACATGCCATATCAAGCAAAGAAAATGCCAATTCTCAGCCCAATGATGAAGATGCCTCCT	
		12061 CTGATGCTTACTGCTTTGAGCTGCTCTCGATGGTTTTAGCACTGAGTGGCTCTAACGTGG	
		12121 GCCGGCAGTATCTGGCTCAGCAACTAACTCTGCTCCAGGATCTCTTTTCACTGCTCCACA	
		12181 CAGCCTCCCCTCGAGTCCAGAGACAGGTGACCTCCTTACTAAGACGAGTTTTACCTGAAG	
		12241 TGACCCCTAATCGGCTGGCCAGCATCATAGGAGTGAAATCCCTTCCCCCACCAGATATCA	
		12301 GTGATATCATTCACTCAACAGAGAAAGGAGATTGGAATAAGCTAGGTATCTTGGACATGT	
		12361 TTCTAGGATGCATTGCCAAAGCACTCACAGTACAGCTAAAAGCCAAAGGAACCACATCA	
		12421 CTGGAACAGCTGGTACCACTGTGGGCAAAGGAGTTACAACAGTTACTCTTCCGATGATTT	
		12481 TCAATTCCAGTTATCTCCGACGAGGTGAAAGTCATTGGTGGATGAAGGGCTCAACCCCTA	
		12541 CCCAGATCTCAGAGATCATCATTAAACTTATCAAGGATATGGCAGCAGGTCATCTGTCAG	
		12601 AAGCTTGGTCCCGAGTGACAAAAAATGCTATTGCAGAAACCATCATTGCCTTGACCAAGA	
		12661 TGGAAGAAGAATTTAGGTCTCCAGTGAGATGTATTGCAACAACTAGACTCTGGCTTGCTC	
		12721 TCGCATCCCTATGTGTTCTTGATCAGGACCACGTAGATCGTCTCTCCTCGGGGAGATGGA	
		12781 TGGGAAAGGATGGACACAACAAAACACAAAATGCCTATGTGTGATAACCATGATGGTGAAA	
		12841 CTGCAGCAATCATTTTATGCAATGTCTGTGGAAATTTATGTACAGACTGTGACAGATTCC	
		12901 TTCACCTTCATCGAAGAACCAAAACTCATCAAAGACAGGTCTTCAAAGAAGAAGAAGAAG	
		12961 CTATAAAGGTTGACCTTCATGAAGGTTGTGGTAGAACCAAATTGTTCTGGTTGATGGCAC	
		13021 TGGCAGATTCTAAAACAATGAAGGCAATGGTGGAATTCCGAGAACACACAGGCAAACCCA	
		13081 CCACGAGTAGCTCAGAAGCATGTCGCTTCTGTGGTTCCAGGAGTGGAACAGAGTTATCTG	
		13141 CTGTTGGCAGTGTTTGTTCTGATGCAGATTGCCAGGAATACGCTAAGATAGCCTGTAGTA	
		13201 AGACGCATCCTTGTGGCCATCCATGCGGGGGTGTTAAAAACGAAGAGCACTGTCTGCCCT	
		13261 GTCTACACGGCTGTGACAAAAGTGCCACAAGCCTGAAGCAGACGCCGATGACATGTGCA	
		13321 TGATATGTTTCACCGAAGCGCTCTCGGCAGCACCAGCCATTCAGCTGGATTGTAGTCACA	
		13381 TATTCCACTTACAGTGCTGTCGGCGAGTATTAGAAAATCGATGGCTTGGCCCAAGGATAA	
		13441 CATTTGGATTTATATCTTGTCCCATTTGCAAGAACAAAATTAATCACATAGTACTAAAAG	
		13501 ACCTACTTGATCCAATAAAAGAACTCTATGAGGATGTCAGAAGAAAAGCCTTAATGAGAT	
		13561 TGGAATATGAAGGTCTGCATAAGAGTGAAGCTATCACAACTCCTGGTGTGAGGTTTTATA	
		13621 ATGACCCAGCTGGCTATGCAATGAATAGATATGCATATTATGTGTGCTACAAATGCAGAA	
		13681 AGGCATATTTTGGTGGTGAAGCTCGCTGCGATGCTGAGGCTGGACGGGGAGATGATTATG	
		13741 ATCCCAGAGAGCTCATTTGTGGTGCCTGTTCTGATGTTTCCAGGGCTCAGATGTGTCCCA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		13801 AACATGGCACAGACTTTTTGGAATATAAATGTCGCTACTGCTGTTCAGTGGCTGTTTTTT 13861 TCTGTTTTGGAACAACACATTTTTGTAATGCTTGTCATGATGATTTTCAAAGAATGACTA 13921 GCATTCCTAAGGAAGAACTACCACACTGTCCTGCAGGTCCCAAAGGCAAGCAGTTAGAAG 13981 GAACTGAATGTCCACTCCATGTTGTTCATCCACCCACTGGGGAAGAGTTTGCTCTGGGAT 14041 GTGGAGTGTGCAGAAATGCCCCACACTTTTTAGAACACGCAGATCCTTTGTCTACAGAGAG 14101 AAAAATTGCCTTCATCCCCCAAGAGGATGCGGTGAAGTTTAAACTCTGCTCAGGATAAGG 14161 ACGGGACCATTTTGACATCCATGAAAATGAACCATTCACAGTGCAAGAAGGATGCCAAAT 14221 ACCATGTACATAATTCTTGCTATGGAAAGTTTCCCCATTATTTCGGTTTATCTCTTTTG 14281 AACCAAGACATCAAACTTGTGAGGTGTTTGCATGTGGCCATTACCGTCATTGGCCTGTGA 14341 AGCATTGGACATTTATAGATAATTGATATATAAAAGAATTGCCATACCTATGGACTAAGAAT 14401 GATGCTGGCTTTCAAGCAAAAAAGAAAAATAATCATTGTTTATTGTATACTACCTTTTTG 14461 TAATCCTGTACAATTGCATCACGGGTGGGGATATAAAAAAGGAATATTCTGGTTTATTTCC 14521 TAGACTGTTATTTAAAAAAAAAAAAACATTGTGTTTAGGACGGCATATAAATGTAATAAG 14581 TATCACACTGTATATAAAGATATCAATGTTTGTCCTGTATAAGAATTACTAAATTACAAA 14641 TGCAGTTTCATTTAAACTTCTAGGTTAAGTTTGAGCCTGAAATTTTAATGAAGTGCAATA 14701 CTGAGTGTGCCTCATTATCTTGCAGCTGTAAACATATTGGAATGACATGTCAATAAACCA 14761 CTGTACATTTTTATACAGTGATAAAGTCTAAAAAAAAAAAAAAA 1 M P V P D G S V A A A G L G L G L P A A 1 ATGCCGGTTCCCGACGGCTCCGTGGCTGCTGCGGGGCTGGGGCTGGGGCTACCCGCCGCG 21 D S P G H Y Q L L L S G G R A L A D R Y R 61 GACTCCCCGGGTCACTACCAGCTGCTGCTGTCAGGCCGGGCCCTGGCCGACCGCTACCGG 41 R I Y T A A L N D R D Q G G G G S A G H P 121 AGGATTTATACCGCTGCGCTCAATGACAGGGACCAGGGGGGCGGCAGCGCTGGACACCCA 61 A S R N K K I L N K K K L K R K Q K S K 181 GCCTCCAGGAATAAGAAAATTTTAAATAAGAAGAAATTGAAAAGAAAACAGAAGAGCAAA 81 S K V K T R S K S E N L E N T V I I P D 241 TCAAAAGTGAAGACAAGAAGCAAGTCTGAAAACTTAGAGAATACAGTAATCATACCAGAT 101 I K L H S N P S A F N I Y C N V R H C V 301 ATCAAACTACATAGCAATCCTTCTGCTTTCAATATTTACTGTAATGTACGCCATTGCGTT 121 L E W Q K K E I S L A A A S K N S V Q S 361 CTGGAATGGCAGAAAAAGGAAATATCATTGGCAGCCGCATCTAAGAACTCTGTGCAGAGT 141 G E S D S D E E E E S K E P P I K L P K 421 GGAGAATCAGATAGTGATGAAGAAGAGGAATCCAAAGAGCCCCCTATCAAGCTTCCAAAG 161 I I E V G L C E V F E L I K E T R F S H	SEQ ID NO:138

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		481 ATTATTGAGGTTGGCCTTTGTGAAGTTTTTGAATTGATCAAAGAGACACGATTTTCTCAT	
		181 P S L C L R S L Q A L L N V L Q G Q Q P 541 CCATCCCTGTGTCTCAGGAGTCTCCAAGCCCTGCTCAACGTGCTGCAGGGCCAGCAGCCA	
		201 E V L Q S E P P E V L E S L F Q L L L E 601 GAAGTGCTCCAGTCTGAGCCACCTGAGGTCCTAGAGTCTCTCTTCCAGCTTCTTTTGGAA	
		221 I T V R S T G M N D S T G Q S L T A L S 661 ATCACCGTTCGAAGTACTGGGATGAATGACAGCACAGGACACTGCCTTAACAGCACTTTCC	
		241 C A C L F S L V A S W G E T G R T L Q A 721 TGTGCTTGCCTCTTTAGTCTGGTGGCTTCTTGGGGAGAAACAGGAAGGACACTTCAGGCC	
		261 I S A I L T N N G S H A C Q T I Q V P T 781 ATCTCTGCTATCCTCACCAACAATGGAAGCCATGCTTGCCAAACTATTCAGGTGCCAACA	
		281 I L N S L Q R S V Q A V L V G K I Q I Q 841 ATTCTAAATTCGCTACAGAGAAGTGTACAAGCAGTTTTGGTGGGAAAAATTCAAATTCAG	
		301 D W F S N G I K K A A L M H K W P L K E 901 GACTGGTTTAGTAATGGCATTAAGAAAGCAGCTTTAATGCACAAGTGGCCATTAAAGAA	
		321 I S V D E D D Q C L L Q N D G F F L Y L 961 ATATCTGTTGATGAAGATGACCAATGTCTACTTCAGAATGATGGATTTTTTCTTTATCTA	
		341 L C K D G L Y K I G S G Y S G T V R G H 1021 TTATGCAAGGATGGATTATATATAAATAGGCTCTGGATACAGTGGAACAGTTAGGGCCAT	
		361 I Y N S T S R I R N R K E K K S W L G Y 1081 ATATACAATTCTACATCCCGTATTAGAAACAGAAAAGAAAAAAGTCTTGGTTAGGGTAT	
		381 A Q G Y L L Y R D V N N H S M T A I R I 1141 GCTCAGGGTTATTTATTATATAGAGATGTGAATAACCACAGCATGACAGCCATAAGGATA	
		401 S P E T L E Q D G T V M L P D C H T E G 1201 AGCCCTGAAACACTGGAGCAAGATGGTACTGTGATGTTACCAGATTGCCACACTGAAGGT	
		421 Q N I L F T D G E Y I N Q I A A S R D D 1261 CAAAATATTTTATTCACTGATGGAGAATATATTAATCAGATAGCTGCTTCAAGAGATGAT	
		441 G F V V R I F A T S T E P V L Q Q E L Q 1321 GGCTTTGTTGTCAGAATATTTGCCACAAGCACTGAACCTGTTCTACAGCAAGAATTGCAA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		461 L K L A R K C L H A C R I S L F D L E K 1381 CTTAAACTGGCTAGAAAATGCTTACATGCCTGTCGTATCTCATTATTCGATCTGGAAAAG	
		481 D L H I I S T G F D E E S A I L G A G R 1441 GACTTGCATATTATAAGTACAGGATTTGATGAGGAGTCAGCAATTCTTGGTGCAGGACGA	
		501 E F A L M K T A N G K I Y Y T G K Y Q S 1501 GAGTTTGCGCTAATGAAAACAGCAAATGGAAAGATATATTACACTGGCAAATACCAGAGT	
		521 L G I K Q G G P S A G K W V E L P I T K 1561 CTTGGAATCAAACAAGGTGGTCCTTCAGCAGGAAAATGGGTTGAGCTACCAATTACAAAA	
		541 S P K I V H F S V G H D G S H A L L V A 1621 TCTCCAAAGATAGTACACTTCTCAGTTGGACACGATGGCTCTCACGCCCTTTTAGTTGCA	
		561 E D G S I F F T G S A S K G E D G E S I 1681 GAAGATGGGAGCATATTCTTTACAGGATCTGCTAGTAAAGGAGAAGATGGAGAATCAATT	
		581 K S R R Q S K P Y K P K K I I K M E G K 1741 AAGAGCAGACGGCAATCCAAACCTTATAAACCTAAAAAGATAATTAAGATGGAAGGAAAG	
		601 I V V V T A C N N G S S S V I S K D G E 1801 ATTGTGGTATATACAGCCTGCAATAATGGAAGTAGTTCTGTTATTTCTAAAGATGGAGAA	
		621 L Y M F G K D A I Y S D S S S L V T D L 1861 CTCTACATGTTTGGAAAAGATGCCATTTACTCTGATAGTTCAAGTTTGGTAACTGATTTG	
		641 K G H F V T Q V A M G K A H T C V L M K 1921 AAGGGCCATTTTGTAACTCAGGTAGCTATGGGCAAAGCTCACACTTGTGTTTTAATGAAG	
		661 N G E V W T F G V N N K G Q C G R D T G 1981 AATGGAGAGGTGTGGACATTTGGTGTAAATAATAAGGACAGTGTGGACGAGATACTGGT	
		681 A M N Q G G K G F G V E N M A T A M D E 2041 GCCATGAACCAAGGTGGGAAAGGGTTTGGAGTTGAAAATATGGCAACAGCAATGGATGAA	
		701 D L E E E L D E K D E K S M M C P P G M 2101 GACCTGGAAGAAGAACTAGATGAAAAAGATGAGAAGTCTATGATGTGCCCTCCAGGCATG	
		721 H K W K L E Q C M V C T V C G D C T G Y 2161 CACAAATGGAAGCTGGAGCAGTGCATGGTTTGCACTGTCTGTGGAGACTGTACAGGTTAT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		741 G A S C V S S G R P D R V P G G I C G C 2221 GGAGCCAGCTGTGTCAGTAGTGGACGGCCAGACAGAGTCCCCGGAGGGATCTGTGGTTGT	
		761 G S G E S G C A V C G G C C K A C A R E L 2281 GGTTCCGGAGAATCTGGTTGTGCTGTGTGGATGTTGCAAGGCCTGTGCAAGAGAGTTA	
		781 D G Q E A R Q R G I L D A V K E M I P L 2341 GATGGTCAAGAGGCAAGACAAAGAGGAATTCTTGATGCAGTGAAAGAAATGATACCTTTA	
		801 D L L L A V P V P G V N I E E H L Q L R 2401 GATCTTCTTTTAGCTGTCCCAGTGCCCGGGTTAACATTGAAGAACACCTTCAGTTACGA	
		821 Q E E K R Q R V I R R H R L E E G R G P 2461 CAAGAGAAAAACGGCAACGTGTAATCAGAAGGCACAGATTAGAGGAAGGAAGAGGCCCC	
		841 L V F A G P I F M N H R E Q A L A R L R 2521 CTTGTATTTGCTGGTCCTATTTTTATGAACCATCGAGAACAGGCTCTAGCCAGACTCAGA	
		861 S H P A H V K H K R D K H K D G S G E R 2581 TCCCATCCAGCACACGTAAAGCATAAACGGGACAAGCACAAAGATGGAAGTGGAGAAAGA	
		881 G E K D A S K I T T Y P P G S V R F D C 2641 GGCGAAAAGGATGCAAGCAAAATCACAACATACCCTCCAGGCTCTGTGCGATTTGACTGT	
		901 E L R A V Q V S C G F H H S V V L M E N 2701 GAGCTCCGGGCAGTCCAAGTCAGCTGTGGATTTCACCATTCAGTGGTTTTAATGGAAAAT	
		921 G D V Y T F G Y G Q H G Q L G H G D V N 2761 GGAGATGTCTATACATTTGGTTATGGGCAGCATGGGCAGCTAGGACATGGAGATGTCAAC	
		941 S R G C P T L V Q A L P G P S T Q V T A 2821 TCCAGGGGATGTCCCACTCTTGTTCAAGCATTGCCAGGCCCTAGCACACAAGTCACTGCA	
		961 G S N H T A V L L M D G Q V F T F G S F 2881 GGCAGCAACCATACGGCAGTACTTTTAATGGATGGACAGGTCTTCACATTTGGAAGTTTT	
		981 S K G Q L G R P I L D V P Y W N A K P A 2941 TCTAAAGGACAACTGGGCAGACCAATTTTGGATGTGCCATATTGGAATGCAAAGCCAGCT	
		1001 P M P N I G S K Y G R K A T W I G A S G 3001 CCCATGCCTAACATTGGATCAAAATATGGAAGAAAAGCTACTTGGATAGGTGCAAGTGGG	
		1021 D Q T F L R I D E A L I N S H V L A T S	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		3061 GACCAAACTTTTTTTACGAATTGATGAAGCACTTATTAATTCTCATGTACTTGCTACATCA	
		1041 E I F A S K H I I G L V P A S I S E P P 3121 GAAATTTTTGCCAGTAAACACATAATAGGCTTGGTACCTGCTTCTATATCAGAACCTCCT	
		1061 P F K C L L I N K V D G S C K T F N D S 3181 CCATTTAAATGCCTTCTGATAAATAAAGTGGGAGTTGTAAAACTTTTAATGACTCA	
		1081 E Q E D L Q G F G V C L D P V Y D V I W 3241 GAACAAGAGGATCTGCAAGGATTTGGTGTGTCTTGATCCTGTATATGATGTAATTTGG	
		1101 R F R P N T R E L W C Y N A V V A D A R 3301 AGGTTTCGACCAAATACTAGAGAGCTGTGGTGTTACAATGCGGTGGTTGCTGATGCCAGG	
		1121 L P S A A D M Q S R C S I L S P E L A L 3361 CTTCCCTCTGCAGCAGACATGCAGTCCAGATGTAGTATCCTAAGTCCTGAACTTGCCTTA	
		1141 P T G S R A L T T R S H A A L H I L G C 3421 CCAACAGGATCAAGGGCCCTCACTACCCGATCTCATGCAGCTTTGCACATTTTAGGTTGT	
		1161 L D T L A A M Q D L K M G V A S T E E E 3481 CTTGATACCTTGGCAGCTATGCAGGACTTAAAAATGGGTGTTGCAAGTACAGAGGAAGAG	
		1181 T Q A V M K V Y S K E D Y S V V N R F E 3541 ACTCAAGCAGTAATGAAGGTTTATTCTAAAGAAGATTATAGTGTGGTAAACAGGTTTGAA	
		1201 S H G G G W G Y S A H S V E A I R F S A 3601 AGTCATGGAGGAGGCTGGGGTTATTCTGCCCATTCAGTAGAAGCTATACGTTTCAGTGCC	
		1221 D T D I L L G G L F G G R G E Y T A 3661 GACACTGATATTTTACTTGGTGGTCTTGGTCTGTTTGGAGGTAGAGGAGAATATACTGCT	
		1241 K I K L F E L G P D G G D H E T D G D L 3721 AAAATTAAGCTGTTTGAATTGGGTCCTGATGGAGGAGATCATGAAACTGATGGTGACCTT	
		1261 L A E T D V L A Y D C A A R E K Y A M M 3781 CTTGCAGAGACTGATGTATTGGCTTATGACTGTGCTGCTAGAGAAAAATATGCAATGATG	
		1281 F D E P V L L Q A G W W Y V A W A R V S 3841 TTTGATGAGCCTGTTCTCCTGCAAGCTGGGTGGTGGTATGTGGCATGGGCCCGAGTGTCA	
		1301 G P S S D C G S H G Q A S I T T D D G V 3901 GGACCCAGCAGTGACTGTGGATCTCATGGACAGGCATCTATTACCACAGATGATGGGTT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1321 V F Q F K S S K K S N N G T D V N A G Q 3961 GTTTTCCAGTTCAAGAGTTCAAAGAAATCAAATAATGGTACAGATGTTAATGCGGGTCAG	
		1341 I P Q L L Y R L P T S D G S A S K G K Q 4021 ATACCTCAGTTATTATACAGACTTCCAACCAGTGATGGCAGTGCTTCAAAAGGCAAACAG	
		1361 Q T S E P V H I L K R S F A R T V S V E 4081 CAAACCAGTGAACCTGTACACATTTTAAAGAGGTCTTTTGCAAGAACTGTCTCAGTGGAA	
		1381 C F E S L L S I L H W S W T T L V L G V 4141 TGTTTTGAGTCATTGTTGAGTATTCTTCACTGGAGCTGGACCACCTTAGTCTTAGGAGTT	
		1401 E E L R G L K G F Q F T A T L L D L E R 4201 GAAGAACTTAGAGGATTAAAAGGATTCCAGTTCACAGCTACACTCCTAGATTTAGAGAGA	
		1421 L R F V G T C C L R L L R V Y T C E I Y 4261 CTGCGCTTTGTGGGTACCTGTTGTCTGAGGTTATTGCGTGTCTATACCTGTGAAATTTAC	
		1441 P V S A T G K A V V E E T S K L A E C I 4321 CCAGTGTCAGCTACAGGAAAAGCAGTTGTAGAAGAAACTAGCAAATTAGCAGAGTGTATT	
		1461 G K T R T L L R K I L S E P L D H C M V 4381 GGAAAAACCAGAACTTTGTTAAGAAAAATTTATCAGAACCACTTGATCACTGCATGGTG	
		1481 K L D N D P Q G Y L S Q P L S L L E A V 4441 AAATTGGATAATGATCCTCAAGGATATCTCAGTCAACCCTTGAGTCTTCTAGAAGCTGTC	
		1501 L Q E C H N T F T A C F H S F Y P T P A 4501 CTTCAGGAATGTCATAATACTTTCACTGCCTGCTTTCATTCTTTCTACCCAACTCCTGCC	
		1521 L Q W A C L C D L L N C L D Q D I Q E A 4561 TTACAGTGGGCTTGCCTTTGTGATCTGCTGAATTGTTTGGATCAGGATATCCAAGAAGCA	
		1541 N F K T S S S R L L A A V M S A L C H T 4621 AACTTCAAGACATCAAGTAGCCGACTCCTTGCAGCTGTTATGTCAGCTCTGTGTCACACG	
		1561 S V K L T S I F P I A Y D G E V L L R S 4681 TCTGTTAAGCTGACTTCCATCTTCCCGATTGCGTATGATGGAGAAGTATTACTACGATCA	
		1581 I V K Q V S T E N D S T L V H R F P L L 4741 ATTGTTAAACAAGTTAGTACAGAGAACGACTCAACACTAGTTCATCGTTTTCCCCTTTTG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1601 V A H M E K L S Q S E E N I S G M T S F 4801 GTGGCACATATGGAAAAACTCAGCCAGAGTGAAGAGAATATCTCAGGGATGACAAGCTTC 1621 R E V L E K M L V I V V L P V R N S L R 4861 CGTGAAGTTCTGGAGAAAATGCTGGTCATTGTTGTGCTACCAGTCAGGAACAGCCTGAGG 1641 R E N E L F S S H L V S N T C G L L A S 4921 AGAGAAAATGAACTCTTCTCCTCCCACCTCGTCTCTAACACCTGTGGATTACTGGCCAGC 1661 I V S E L T A S A L G S E V D G L N S L 4981 ATTGTCAGTGAACTGACAGCGTCAGCCCTGGGATCTGAGGTTGATGGACTTAATTCTCTT 1681 H S V K A S A N R F T K T S Q G R S W N 5041 CACTCTGTAAAAGCTAGTGCTAACCGATTTACAAAAACAAGTCAGGGCAGAAGTTGGAAC 1701 T G N G S P D A I C F S V D K P G I V V 5101 ACTGGGAACGGGTCCCCTGATGCAATCTGTTTTTCAGTAGACAAACCTGGAATAGTTGTG 1721 V G F S V Y G G G G I H E Y E L E V L V 5161 GTTGGTTTCTCTGTCTATGGAGGAGGTGGAATTCATGAATATGAATTAGAGGTGTTGGTT 1741 D D S E H A G D S T H S H R W T S L E L 5221 GATGATAGTGAACATGCAGGAGATTCAACTCATTCCCACAGATGGACATCTCTGGAATTA 1761 V K G T Y T T D D S P S D I A E I R L D 5281 GTGAAAGGAACGTACACAACGGATGACTCACCCAGTGATATAGCTGAGATCAGACTTGAC 1781 K V V P L K E N V K Y A V R L R N Y G S 5341 AAAGTGGTTCCTTTAAAGGAAAATGTTAAATATGCTGTGCGCTTGAGGAACTATGGAAGC 1801 R T A N G D G G M T T V Q C P D G V T F 5401 CGTACAGCCAATGGAGATGGAGGAATGACCACAGTTCAGTGCCCTGATGGTGTGACATTC 1821 T F S T C S L S S N G T N Q T R G Q I P 5461 ACATTCAGCACGTGCAGCTTGAGCAGTAACGGCACAAACCAAACCAGAGGACAGATCCCA 1841 Q I L Y Y R S E F D G D L Q S Q L L S K 5521 CAGATACTCTACTATAGGAGTGAATTTGATGGAGATTTACAATCCCAACTTCTGAGTAAA 1861 A N E E D K N C S R A L S V V S T V V R 5581 GCCAATGAAGAAGATAAAAACTGTAGCAGAGCATTGTCTGTTGTAAGCACTGTCGTTCGA 1881 A S K D L L H R A L A V D A D D I P E L	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		5641 GCCTCTAAGGACCTCCTGCACAGAGCTCTTGCTGTGGATGCTGATGACATTCCAGAACTG	
		1901 L S S S S L F S M L L P L I I A Y I G P	
		5701 CTGAGTTCTTCCAGTCTGTTTTCCATGCTGCTCCCCCTTATTATAGCCTACATAGGACCA	
		1921 V A A A I P K V A V E V F G L V Q Q L L	
		5761 GTAGCTGCTGCTATTCCCAAGGTGGCTGTAGAAGTCTTTGGCCTTGTCCAACAATTGCTT	
		1941 P S V A I L N Q K V A P P A F N P N Q S	
		5821 CCGTCAGTTGCCATTTTGAATCAGAAGTATGCACCGCCTGCCTTCAACCCTAATCAGTCG	
		1961 T D S T T G N Q P E Q G L S A C T T S S	
		5881 ACAGATAGCACCACAGGAAACCAGCCTGAACAGGGCCTCTCTGCTTGTACAACCTCCAGT	
		1981 H Y A V I E S E H P Y K P A C V M H Y K	
		5941 CACTATGCTGTCATAGAGAGTGAGCACCCGTATAAACCTGCCTGTGATGCATTACAAG	
		2001 V T F P E C V R W M T I E F D P Q C G T	
		6001 GTGACATTCCCAGAATGTGTGAGGTGGATGACAATCGAATTTGACCCTCAGTGTGGTACT	
		2021 A Q S E D V L R L L I P V R T V Q N S G	
		6061 GCACAGTCAGAAGATGTCCTTCGTTTGTTGATTCCTGTCAGAACTGTTCAGAATTCAGGA	
		2041 Y G P K L T S V H E N L N S W I E L K K	
		6121 TATGGACCAAAATTGACATCTGTTCATGAAAATCTTAATTCATGGATAGAATTAAAGAAA	
		2061 F S G S S G W P T M V L V L P G N E A L	
		6181 TTTTCAGGATCCTCTGGGTGGCCTACTATGGTTTTGGTGTTGCCAGGAAATGAGGCCCTT	
		2081 F S L E T A S D Y V K D D K A S F Y G F	
		6241 TTTTCATTGGAGACTGCATCAGATTATGTGAAAGATGACAAAGCTTCTTTCTATGGTTTT	
		2101 M C F A I G Y E F S P G P D E G V I Q L	
		6301 ATGTGTTTTGCAATTGGATATGAATTTAGCCCTGGACCTGATGAGGGAGTCATCCAATTG	
		2121 E K E L A N L G G V C A A A L M K K D L	
		6361 GAAAAAGAATTAGCCAATCTTGGTGGGGTTTGTGCAGCAGCTCTGATGAAGAAGGACCTA	
		2141 A L P I G N E L E E D L E I L E E A A L	
		6421 GCACTTCCTATTGGTAATGAATTAGAAGAAGACCTTGAAATTCTTGAGGAGGCTGCATTG	
		2161 Q V C K T H S G I L G K G L A L S H S P	
		6481 CAGGTGTGCAAAACCCATTCTGGAATTCTTGGAAAGGGTCTAGCTCTTTCTCATTCACCA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2181 T I L E A L E G N L P L Q I Q S N E Q S 6541	
WBC030E04.bFSP_20012410.abd	Equus caballus matrix metalloproteinase 1 precursor (MMP1)	1 AGGGAACTAGGGAGCTATCAGACTGCTTATCGGAGAAGGAAGACAGAGGCCAGCATGCT 61 CAGCCTTCCTCTGCTGCTGCTACTCTGGGGCATGGCTCTCACAGCTTCCCAACAGT 121 GCCTTCAGAAACACGAGAAGAAGATGTGAGATGGTCCAGAAATACCTGGAAAACTACTA 181 CAACCTGAAGAGTGATGGAGAGCAAATTGAAAAGCAGACACAGGAGCCCAGTCGTTGA 241 AAAGCTGAAGCAAATGCAGGAATTCTTTGGGCTGAAAGTGACTGGGAAGCCAGATGCTGA 301 AACCCTGAATGTGATGAAGCAGCCCAGATGCGGGGTGCCTGATGTGGCTGAGTTTGTCCT 361 CACCGAAGGGAACCCTCGGTGGGAGAACACACACCTGACCTACAGGATTGAAAATTACAC 421 ACCAGATTTACCAAGAGCAGATGTGGACCAGGCCATTGAGAAAGCCTTTCAACTCTGGAG 481 TAATGTCTCACCCCTGACCTTCACTAAAGTCTCTGAGGGTCAAGCGGACATAATGATATC 541 CTTTGTCAGGGGAGATCATCGTGACAATTCTCCCTTTGATGGACCTGGAGGGAAACCTCGC 601 CCATGCTTTTCAGCCAGGCCCACGTATTGGAGGGGATGCTCATTTTGATGAAGATGAAAC 661 ATGGACCAGCAATTTCAGAAATTACAACTTGTATCGAGTTGCAGCTCATGAATTTGGCCA 721 TTCCCTTGGACTCTCTCATTCTACTGATATTGGGGCTTTGATGTACCCCAACTACTTCTT 781 CACTGGTGATGTTCAGCTATCTCAGGATGACATCAATGGCATCCAGGCCATCTATGGACC 841 TTCCCAAAATCCCATCCAGCCAATTGGCCCACAAACCCCAGAAGTGTGTGATAGTAAGCT 901 AACCTTTGATGCTATAACTACGATTCGGGGAGAAGTGATGTTCTTTAAGACAGGTTCTA 961 CATGCGCATAAATCCTTACTACCCAGAAGCTGAGCTCAATTTCATTTCTATTTTCTGGCC 1021 ACAACTGCCAAATGGACTTCAAGCTGCTTATGAGGTTTCCCATAGAGATGAAGTCCGGTT 1081 TTTCAAAGGTAATAAGTACTGGGCTGTTAAGGGGCAGGATGTGCTCTACGGATACCCCAA 1141 GGACATCCACAGATCCTTCGGCTTTCCTAGCACTGTGAAGAATATCGATGCTGCTGTTTC 1201 TGAGGAAGATACTGGGAAAACGTACTTCTTTGTTGCTGACAAGTACTGGAGGTACGATGA 1261 ATATAAACGATCTATGGATGCAGGTTATCCCAAAATGATAGCAGATGACTTCTCCTGGAAT 1321 TGGCGACAAAGTTGATGCTGTTTTCAGAAAGATGGATTTTTCTATTTCTTTCACGGAAC 1381 AAGGCAATACAAATTTGATCCTAAAACTAAGAGAATTTTGACTCTCCAGAAAGCCAATAG 1441 CTGGTTCAACTGCAGAAAAAATTGACCATTACAAAGTTGAACAGAAAAATATATTTTGAG 1501 AACCCAAGGAAGATGTTTTCCTGAAGAGCCATACATTTAAATAAAATACAGAGCTGTTAC 1561 GTATAATCTTTATTTATATCTCATTCTGCAAATATTTTTTACAATTTAGAATGCAATGTTT 1621 CATGTACTGCTATATAATTTACTTCCACCAATGAGGTGAAGGAAGGTCAAGTTCTGATTTA 1681 CGGATTCATATGGGCCAATTTTGCAAAGAGAAGCTCTTTTCCAAAGTAGAAGACTCTG 1741 ACATTGATACTGGAGAGCAGCCTCAGAGATGGAGAGAAAGAAACAAGAGATACGAGTCTT 1801 CACCAGAGGAAAAGCAGCTCAAGAACATCTGAGCTGCTACTAGTATTATCCTAATATGCA 1861 AGGGATAATTTTTGTTACGGAAAATAAATCTTTTATGTTTGGAATAAAAAAAAAAAAA 1921 AAA 1 M L S L P L L L L L L W G M G S H S F P 1 ATGCTCAGCCTTCCTCTGCTGCTGCTACTCTGGGGCATGGGCTCTCACAGCTTCCCA	SEQ ID NO:139 SEQ ID NO:140

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		21 T V P S E T R E E D V E M V Q K Y L E N 61 ACAGTGCCTTCAGAAACACGAGAAGAAGATGTGGAGATGGTCCAGAAATACCTGGAAAAC 41 Y Y N L K S D G E Q I E K Q R H R S P V 121 TACTACAACCTGAAGAGTGATGGAGAGCAAATTGAAAAGCAGAGACACAGGAGCCCAGTC 61 V E K L K Q M Q E F F G L K V T G K P D 181 GTTGAAAAGCTGAAGCAAATGCAGGAATTCTTTGGCTGAAAGTGACTGGGAAGCCAGAT 81 A E T L N V M K Q P R C G V P D V A E F 241 GCTGAAACCCTGAATGTGATGAAGCAGCCCAGATGCGGGGTGCCTGATGTGGCTGAGTTT 101 V L T E G N P R W E N T H L T Y R I E N 301 GTCCTCACCGAAGGGAACCCTCGGTGGGAGAACACACACCTGACCTACAGGATTGAAAAT 121 Y T P D L P R A D V D Q A I E K A F Q L 361 TACACACCAGATTTACCAAGAGCAGATGTGGACCAGGCCATTGAGAAAGCCTTTCAACTC 141 W S N V S P L T F T K V S E G Q A D I M 421 TGGAGTAATGTCTCACCCTGACCTTCACTAAAGTCTCTGAGGGTCAAGCGGACATAATG 161 I S F V R G D H R D N S P F D G P G G N 481 ATATCCTTTGTCAGGGGAGATCATCGTGACAATTCTCCCTTTGATGGACCTGGAGGAAAC 181 L A H A F Q P G P R I G G D A H F D E D 541 CTCGCCCATGCTTTTCAGCCAGGCCCACGTATTGGAGGGATGCTCATTTTGATGAAGAT 201 E T W T S N F R N Y N L Y R V A A H E F 601 GAAACATGGACCAGCAATTTCAGAAATTACAACTTGTATCGAGTTGCAGCTCATGAATTT 221 G H S L G L S H S T D I G A L M Y P N Y 661 GGCCATTCCCTTGGACTCTCTCATTCTACTGATATTGGGGCTTTGATGTACCCCAACTAC 241 F F T G D V Q L S Q D D I N G I Q A I Y 721 TTCTTCACTGGTGATGTTCAGCTATCTCAGGATGACATCAATGGCATCCAGGCCATCTAT 261 G P S Q N P I Q P I G P Q T P E V C D S 781 GGACCTTCCCCAAAATCCCATCCAGCCAATTGGCCCACAAACCCCAGAAGTGTGTGATAGT 281 K L T F D A I T T I R G E V M F F K D R 841 AAGCTAACCTTTGATGCTATAACTACGATTCGGGGAGAAGTGATGTTCTTTAAAGACAGG 301 F Y M R I N P Y Y P E A E L N F I S I F	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		901 TTCTACATGCGCATAAATCCTTACTACCCAGAAGCTGAGCTCAATTTCATTTCTATTTTC 321 W P Q L P N G L Q A A Y E V S H R D E V 961 TGGCCACAACTGCCAAATGGACTTCAAGCTGCTTATGAGGTTTCCCATAGAGATGAAGTC 341 R F F K G N K Y W A V K G Q D V L Y G Y 1021 CGGTTTTTCAAAGGTAATAAGTACTGGGCTGTTAAGGGCAGGATGTGCTCTACGGATAC 361 P K D I H R S F G F P S T V K N I D A A 1081 CCCAAGGACATCCACAGATCCTTCGGCTTTCCTAGCACTGTGAAGAATATCGATGCTGCT 381 V S E E D T G K T Y F F V A D K Y W R Y 1141 GTTTCTGAGGAAGATACTGGGAAAACGTACTTCTTTGTTGCTGACAAGTACTGGAGGTAC 401 D E Y K R S M D A G Y P K M I A D D F P 1201 GATGAATATAAACGATCTATGGATGCAGGTTATCCCAAAATGATAGCAGATGACTTTCCT 421 G I G D K V D A V F Q K D G F F Y F F H 1261 GGAATTGGCGACAAAGTTGATGCTGTTTTTCAGAAAGATGGATTTTTCTATTTCTTTCAC 441 G T R Q Y K F D P K T K R I L T L Q K A 1321 GGAACAAGGCAATACAAATTTGATCCTAAAACTAAGAGAATTTTGACTCTCCAGAAAGCC 461 N S W F N C R K N - 1381 AATAGCTGGTTCAACTGCAGAAAAAATTGA	
WBC031B06.bFSP_20012510.abd	Homo sapiens progestin and adipoQ receptor family member XI (PAQR11)	1 atggcggagg agccggggag gcgggaggcg ggaggcggga ggtgttgggg ccgttgaagc 61 ggcctcctc cggccccag ccgccggttc tggccccagc cctgtcccga ccccggcct 121 ggcccactcc gaccctaccc ggccgaaggg ttccgctgga cacgcaggcg gcctccggag 181 cagcccaagc ccatgagggc cgcgcgcccg gccgccggtg ctgacgagac ggagctcctg 241 gccccggagg aggagcagag gatcaatgcg gttcaagaat cgattccagc ggttcatgaa 301 ccatcgagct ccagccaatg gccgctacaa gccaacttgc tatgaacatg ctgctaactg 361 ttacacacac gcattcctca ttgttccggc catcgtgggc agtgccctcc tccatcggct 421 gtctgatgac tgctgggaaa agataacagc atggatttat ggaatgggac tctgtgccct 481 cttcatcgtt tctacagtat ttcacattgt atcatggaaa aagagccact taaggacagt 541 ggagcattgt ttcacatgt gtgatagaat ggttatctat ttcttcattg ctgcttctta 601 tgctccatgg ttaaatcttc gtgaacttgg accctggca tctcatatgc gttggtttat 661 ctggctcatg gcagctggag gaaccattta tgtatttctc taccatgaaa aatataaggt 721 ggttgaactc ttttctatc tcacaatggg attctctcca gccttggtgg tgacatcaat 781 gaacaacacc gatggacttc aggaacttgc ctgtgggggc ttaatttatt gcttgggagt 841 tgtgttcttc aagagtgatg gcatcattcc atttgcccac gccatctggc acctgtttgt 901 ggccacggca gctgcagtgc attactacgc catttggaaa taccttacc gaagtcctac	SEQ ID NO:141

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		961 ggacttttatg cggcatttat gaccaatctg tactaattct ccaaaccagt attatttcaa 1021 ttatggcact tgggagtggg gtgagagcta aacattgcac agggaaagaa aaaaataac 1081 tgcactgact ttatatcttt tgaatataat tactgtgaaa gtataaaggc tgtgttctgg 1141 aatttctgc ctcacagcaa ataaataagg tagtgaatta attattcatt ccattccact 1201 atcatgaagg actctgaata gacttggcca actgatgttt acaaaccaga ctttatatt 1261 ttaattttac agatttact acatgatttt tctaaattac tatgtcaggt tgtaaaagtc 1321 agtgcaataa caaaccttcc tttttaagaa gaaaattgtt tctattactt tcccattcac 1381 taggtaaaga atcatggaca gaacttacac tacttttttac catgtttcat cttggcataa 1441 catggttctt ttttaaatag aaactttagt ttttttgtaaa ttttttaaaaa aatatttcat 1501 tgatatgcat ctctgcaggt cctcattcat gttgtaaatt tttgcagcaa gcagtcaaca 1561 ttccacaaac gaacaaacat tatacctctt ctgatagttt tattaagcat ggagaaattg 1621 ccaattttta aaaactgcag ttttccaaac ttttctgcca acctcttact ctgaattcag 1681 tgctgctttg ggacatatac ttgacctagc ttggtttacc agtgatggaa aagtatttg 1741 atatcattaa ctttttcaaa agatccaact ttttctctat gcctttgcca cattctcttc 1801 agggtctctt tccacagtgg ataaatgttt tttctgtatt atgacagtat tgttgtgatg 1861 gccatctgct ggaaactcct gaagagcatt atgtattaca gtgagcagtt gtattgcctg 1921 tttggtgccc aatggttaag tcattgtcac ttagctttat attgtcagtt tgatatttat 1981 tttaaattgt ggaactagat gcataaattc acatttctgc ctttcatttg catcttctca 2041 tatattgtgt ttttttttt tttcctagaa aaaatatatta aagcattgtt tgacaggtag 2101 aaactcatgt atctgtagtc catgagttat atcctggctc agtggagtga tatttatgta 2161 ttatttttac ttttctctca gtgtcttata ttaagattaa catgttgtta atagttgctt 2221 tgttgattaa tctctcttgt tggtgtttta ataaatgaaa taggcttgcc tttagatcgg 2281 gtgctgatat tgcctgtttc ctagtaatgg gctgatcaaa tgatcagtgg aattcttggt 2341 ttgatgataa ccttattaat tgaaatttttt tactgatgtg gctttaaaag aggtttattt 2401 tgtatatgtt tagaactctc tgattttgat gaattatatg ggagtgagaa acagaagaag 2461 tggtatttgc tggcgagtta aataggcaag gtacccagtg ataacaccaa ccaaaccact 2521 cctatctgca tgattctgaa catctggatg cctgttgttt tactgtgtat atttatttt 2581 taatatatta actttgtgga ttcatttaag gtctactcaa aagtaacact gtccaaacca 2641 ctaatatgta tgtaaaaatt gtgctgtata ctacaataaa gttgttactt ggatttgttc 2701 caaaaaaaaa aaaaaa 1 M R F K N R F Q R F M N H R A P A N G R 1 ATGCGGTTCAAGAATCGATTCCAGCGGTTCATGAACCATCGAGCTCCAGCCAATGGCCGC 21 Y K P T C Y E H A A N C Y T H A F L I V 61 TACAAGCCAACTTGCTATGAACATGCTGCTAACTGTTACACACACGCATTCCTCATTGTT 41 P A I V G S A L L H R L S D D C W E K I 121 CCGGCCATCGTGGGCAGTGCCCTCCTCCATCGGCTGTCTGATGACTGCTGGGAAAAGATA 61 T A W I Y G M G L C A L F I V S T V F H 181 ACAGCATGGATTTATGGAATGGGACTCTGTGCCCTCTTCATCGTTTCTACAGTATTTCAC	SEQ ID NO:142

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		81 I V S W K K S H L R T V E H C F H M C D 241 ATTGTATCATGGAAAAAGAGCCACTTAAGGACAGTGGAGCATTGTTTTCACATGTGTGAT 101 R M V I Y F F I A A S Y A P W L N L R E 301 AGAATGGTTATCTATTTCTTCATTGCTGCTTCTTATGCTCCATGGTTAAATCTTCGTGAA 121 L G P L A S H M R W F I W L M A A G G T 361 CTTGGACCCCTGGCATCTCATATGCGTTGGTTTATCTGGCTCATGGCAGCTGGAGGAACC 141 I Y V F L Y H E K Y K V V E L F F Y L T 421 ATTTATGTATTTCTCTACCATGAAAAATATAAGGTGGTTGAACTCTTTTTCTATCTCACA 161 M G F S P A L V V T S M N N T D G L Q E 481 ATGGGATTCTCTCCAGCCTTGGTGGTGACATCAATGAACACACCGATGGACTTCAGGAA 181 L A C G G L I Y C L G V V F F K S D G I 541 CTTGCCTGTGGGGGCTTAATTTATTGCTTGGGAGTTGTGTTCTTCAAGAGTGATGGCATC 201 I P F A H A I W H L F V A T A A A V H Y 601 ATTCCATTTGCCCACGCCATCTGGCACCTGTTTGTGGCCACGGCAGCTGCAGTGCATTAC 221 Y A I W K Y L Y R S P T D F M R H L - 661 TACGCCATTTGGAAATACCTTTACCGAAGTCCTACGGACTTTATGCGGCATTTATGA	
WBC031C11.bFSP_20012510.abd	Homo sapiens ribosomal protein L4, mRNA (cDNA clone MGC:87190 IMAGE:5259747).	1 CTTTTCCTGTGGCAGCAGCCGGGCTGAGAGGAGCGTGGCCTTCTCCTCCCTGCCATGG 61 CGTGTGCTCGTCCCACTGATATCAGTGTACTCCGAAAAGGGGGAGTCCTCTGGCAAAAATG 121 TCACTTTGCCTGCTGTGTTCAAGGCTCCCATTCGGCCAGATATTGTCAACTTTGTTCACA 181 CCAACTTGCGCAAAAACACAGACAGCCTTATGCCGTCAGCGAATTAGCAGGTCATCAAA 241 CCAGTGCTGAGTCTTGGGGTACTGGCAGAGCTGTGGCTCGGATTCCCAGAGTTCGAGGCG 301 GTGGTACTCACCGTTCTGGCCAGGGTGCTTTTGGAAACATGTGTCGTGGGGGCCGCATGT 361 TTGCACCAACCAAAACCTGGCGCCGTTGGCACCGCAGAGTGAACACAACACAGAAGCGAT 421 ATGCCATCTGCTCTGCCCTGGCTGCCTCAGCCTTACCAGCGTTGGTCATGTCTCAAAGGTC 481 ATCGTATTGAGGAAGTTCCTGAACTTCCTTTGGTAGTTGAAGATAAAGTTGAAGGCTACA 541 AGAAGACCAAGGAAGCTGTTTTGCTCCTTAAGAAACTTAAAGCCTGGAATGATATCAAAA 601 AGGTCTATGCCTCTCAGCGAATGAGAGCTGGCAAAGGCAAAATGAGAAACCGTCGCCGTA 661 TCCAGCGCAGGGGCCCGTGCATCATCTATAATGAGGATAATGGTATCATCAAGGCCTTCA 721 GAAACATCCCCTGGAATTACTCTGCTTAATGTAAGCAAGCTGAACATTTTGAAGCTTGCTC 781 CTGGTGGGCACGTGGGACGTTTTTGCATTTGGACTGAAAGCGCTTTCCGCAAGTTAGATG 841 ATCTTTATGGCACTTGGCGTAAAGCTGCTTCCCTCAAGAGTAACTACAACCTTCCCATGC 901 ACAAGATGCTCAATACAGACCTTAGCCGAATATTGAAGAGCCCAGATCCAAAGAGCCC 961 TCCGAGCACCACGCAAGAAGATTCATCGCAGGGTCCTGAAGAAGAATCCACTGAAAAACC 1021 TGAGAATCATGTTGAAGCTAAACCCGTATGCGAAGACCATGCGCAGGAACACCATTCTTC	SEQ ID NO:143

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1081 GCCAGGCCAAGAATCACAAACTCCGGTGGATAAGGCAGCAGCACTAGAAGCCAAAT 1141 CAGATGAGAAGGGGGTTCCAGGCAAGAAGCCTGTGGTAGGGAAGAAAGCAAAGAAGGCTG 1201 TTGACGTTAAGAAGCAGAAGAAGCCTTTGGTGGGAAAAAAGGCTGCAGCTACTAAGAAGC 1261 CAGCAGCTGAGAAGAAGCCTGCAGAAAAGAAACCCGCTGCAGAAGAAAAGAAGCCTGCTG 1321 CGTAAACTTGTTTGTTTATTTCATAAAGGTCACATCATTTTGGACAGCTCCTTTTGAATA 1381 AAGACCTGATTATACAGGCAGTGAGAAACAAAAAAAAAAAAAAAA 1 M A C A R P L I S V Y S E K G E S S G K 1 ATGGCGTGTGCTCGTCCACTGATATCAGTGTACTCCGAAAAGGGGGAGTCCTCTGGCAAA 21 N V T L P A V F K A P I R P D I V N F V 61 AATGTCACTTTGCCTGCTGTTCAAGGCTCCCATTCGGCCAGATATTGTCAACTTTGTT 41 H T N L R K N N R Q P Y A V S E L A G H 121 CACACCAACTTGCGCAAAAACAACAGACAGCCTTATGCCGTCAGCGAATTAGCAGGTCAT 61 Q T S A E S W G T G R A V A R I P R V R 181 CAAACCAGTGCTGAGTCTTGGGGTACTGGCAGAGCTGTGGCTCGGATTCCCAGAGTTCGA 81 G G G T H R S G Q G A F G N M C R G G R 241 GGCGGTGGTACTCACCGTTCTGGCCAGGGTGCTTTTGGAAACATGTGTCGTGGGGGCCGC 101 M F A P T K T W R R W H R R V N T T Q K 301 ATGTTTGCACCAACCAAAACCTGGCGCCGTTGGCACCGCAGAGTGAACACAACACAGAAG 121 R Y A I C S A L A A S A L P A L V M S K 361 CGATATGCCATCTGCTCTGCCCTGGCTGCCTCAGCCTTACCAGCGTTGGTCATGTCTAAA 141 G H R I E E V P E L P L V V E D K V E G 421 GGTCATCGTATTGAGGAAGTTCCTGAACTTCCTTTGGTAGTTGAAGATAAAGTTGAAGGC 161 Y K K T T K E A V L L L K K L K A W N D I 481 TACAAGAAGACCAAGGAAGCTGTTTTGCTCCTTAAGAAACTTAAGCCTGGAATGATATC 181 K K V Y Y A S Q R M R A G K G K M R N R R 541 AAAAAGGTCTATGCCTCTCAGCGAATGAGAGCTGGCAAAGGCAAAATGAGAAACCGTCGC 201 R I Q R R G P C I I Y N E D N G I I K A 601 CGTATCCAGCGCAGGGGCCCGTGCATCATCTATAATGAGGATAATGGTATCATCAAGGCC 221 F R N I P G I T L L N V S K L N I L K L 661 TTCAGAAACATCCCTGGAATTACTCTGCTTAATGTAAGCAAGCTGAACATTTTGAAGCTT	SEQ ID NO:144

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		241 A P G G H V G R F C I W T E S A F R K L 721 GCTCCTGGTGGGCACGTGGGACGTTTTTGCATTTGGACTGAAAGCGCTTTCCGCAAGTTA 261 D D L Y G T W R K A A S L K S N Y N L P 781 GATGATCTTTATGGCACTTGGCGTAAAGCTGCTTCCCTCAAGAGTAACTACAACCTTCCC 281 M H K M L N T D L S R I L K S P E I Q R 841 ATGCACAAGATGCTCAATACAGACCTTAGCCGAATATTGAAGAGCCCAGAGATCCAAAGA 301 A L R A P R K K I H R R V L K K N P L K 901 GCCCTCCGAGCACCACGCAAGAAGATTCATCGCAGGGTCCTGAAGAAGAATCCACTGAAA 321 N L R I M L K L N P Y A K T M R R N T I 961 AACCTGAGAATCATGTTGAAGCTAAACCCGTATGCGAAGACCATGCGCAGGAACACCATT 341 L R Q A K N H K L R V D K A A A A L E A 1021 CTTCGCCAGGCCAAGAATCACAAACTCCGGGTGGATAAGGCAGCAGCACTAGAAGCC 361 K S D E K G V P G K K P V V G K K A K K 1081 AAATCAGATGAGAAGGGGGTTCCAGGCAAGAAGCCTGTGGTAGGGAAGAAAGCAAAGAAG 381 A V D V K K Q K K P L V G K K A A A T K 1141 GCTGTTGACGTTAAGAAGCAGAAGAAGCCTTTGGTGGGAAAAAAGGCTGCAGCTACTAAG 401 K P A A E K K P A E K K P A A E E K K P 1201 AAGCCAGCAGCTGAGAAGAAGCCTGCAGAAAAGAAACCCGCTGCAGAAGAAAAGAAGCCT 421 A A - 1261 GCTGCGTAA	
WBC031D02.bFSP_20012510.abd	Homo sapiens syntenin (sycl) mRNA.	1 GGCACGAGGCGGGGGCGGTGCATGACGCGCCTCGGGGGCGGTCCTCGGGCGCGCACCGCT 61 CTCTTACACTCGGGTCTCGGAAGTCCGTGCCAGCGACCGAGGCGACGGCGAGCGGATCCC 121 AGCGGCCTAGAAAAATCCTGCAAAAATGTCTCTGTACCCATCTCTTGAAGACCTGAAGGT 181 AGACAAAGTAATTCAGGCTCAGACTGCCTATTCTGCAAACCCTGCCAACCCAGCAGTTTT 241 GTCTGAAGCTTCTGCTCCTCCCGTCTCTCAAGATGGAAATCTCTATCCTAAGTTGTATCC 301 GGAGCTCTCTCAGTACATGGGCCTGAGTTTAAACGATGAAGAAATACGTGCAAATATGGC 361 CATGATCCCTGGAGCACCAATTCAGGGGCAATTGGTAGCAAGACCTTCCAGTATGAACTA 421 TATGGTGGCTCCTGTAACCGGCAATGATGTTGGGATTCGTAGAGCCGAAATTAAGCAAGG 481 GATTCGTGAAGTCATTCTGTGTAAGGATCAAGATGGAAAAATTGGCTCCGGCTTAAATC 541 AATAGATAACGGAGTATTTGTGCAGCTTAGTCCAGGCAAATTCTCCAGCCTCGCTGGTTGG 601 CCTGAGGTTTGGGGACCAAGTACTCCAGATCAACGGGGAAAACTGTGCAGGCTGGAGCTC 661 TGATAAATCGCACAAGGTGCTCAAACAGGCTTTTGGAGAGAAGATTACTATGACTATTCG	SEQ ID NO:145

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		721 TGACAGGCCCTTCGAACGGACAATTACCATGCATAAGGATAGTACTGGACATGTTGGTTT	
		781 TATCTTTAAAAATGGAAAAATAACATCCATAGTGAAAGATAGTTCTGCAGCCAGAAATGG	
		841 TCTCCTCACAAAACATAACATCTGCCGAGATCAATGGATAGAATGTCATTGGGCTGAAGG	
		901 ACTCTCAAATTGCAGACATACTGTCAACATCTGGGACTGTAGTTACTATTACAATCTGCC	
		961 CTGCTTTTATCTTTGAACATATTATTAAGCGGATGGCACCAAGCATTATGAAAAGCCTAA	
		1021 TGGACCACACCATTCCTGAGGTTTAAAATTCACGGCACCATGGAAATGTAGCTGAACGTC	
		1081 TCCAGTTTCCTTCTTTGGCAACTTCTGTATTATGCACGTGAAGCCTTCCCGGAGCCAGCG	
		1141 AGCATATGCTGCATGAGGACCTTTCTATCTTACATTATGGCTGGGGATCTTACTCTTTCA	
		1201 TCTGATACCTTGTTCAGATTTCAAAATAGTTGTAGCCTTATCCTGGTTTTACAGATGTGA	
		1261 ACTTTCAAGAGATTTACTGACTTTCCTAGAATAGTTTCTCTACTGGAAACCTGATGCTTT	
		1321 TATAAGCCATTGTGATTAGGATGACTGTTACAGGCTTAGCTTTGTGTGAAAACCAGTCAC	
		1381 CTTTCTCCTAGGTAATGAGTAGTGCTGTCATATTACTTTAGTTCTATAGCATACTTGCAT	
		1441 CTTTAACATGCTATCATAGTACATTTAGAATGATTGCCTTTGATTTTTTTTTTAAATTC	
		1501 TGTGTGTGTGTGTTAAAATGCCAATTAAGAACACTGGTTTCATTCCATTGTAAGCATTA	
		1561 GACAGTGTATGTAGGTTGCAAGAGATTGTGTAGATTATCACTAAATTTTAACTACCTTCA	
		1621 CTTAATATGCTTAAACTGTCGCCTTAACTATGCTAAGCATCTAGAATAAAAGCCAAAATG	
		1681 TAACTACTGCTGCCTTTCTGAAACCCACCATGCAGTTCTGTATTAACTGAAATGTTCAGC	
		1741 AGCCCAGAGCAGTTTACTGGGAGATACTGAGCTATAGCATGCTGCTTAGTTGCATTTGA	
		1801 GATTTTCTAGTCATTGTGTAATGGAAACTTCTTTCTTCTAAAGTTACTGGTATCACTTT	
		1861 CTGAGAAATGAATCACTATATATTTAATGTAAAAATTCTTATAGGAAATAGGACAAACTT	
		1921 CTGACTCCCTTCTTTCATTTTTAGATTAAGTGGGATAAATACCTAATTTGGGCATTCTACT	
		1981 CTTAGCATTATGTAACCGTGCTACTTTGGCATGGTCATAGAATGTTTNCCTGGTAATTTG	
		2041 TTCCATGTCCCTGACTCCCTCCCTGCAAACAAAATGATAGTTGACACTTTATCCTGATTTTT	
		2101 TTCTTTTTTTTGGTTTATGTCTATTCTAATTAAATATGTATAAATAAGTTACATTTTAG	
		2161 TCTGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	
			SEQ ID NO:146
		1 M S L Y P S L E D L K V D K V I Q A Q T	
		1 ATGTCTCTGTACCCATCTCTTGAAGACCTGAAGGTAGACAAAGTAATTCAGGCTCAGACT	
		21 A Y S A N P A N P A V L S E A S A P P V	
		61 GCCTATTCTGCAAACCCTGCCAACCCAGCAGTTTTGTCTGAAGCTTCTGCTCCTCCCGTC	
		41 S Q D G N L Y P K L Y P E L S Q Y M G L	
		121 TCTCAAGATGGAAATCTCTATCCTAAGTTGTATCCGGAGCTCTCAGTACATGGGCCTG	
		61 S L N D E E I R A N M A M I P G A P I Q	
		181 AGTTTAAACGATGAAGAAATACGTGCAAATATGGCCATGATCCCTGGAGCACCAATTCAG	
		81 G Q L V A R P S S M N Y M V A P V T G N	
		241 GGGCAATTGGTAGCAAGACCTTCCAGTATGAACTATATGGTGGCTCCTGTAACCGGCAAT	
		101 D V G I R R A E I K Q G G I R E V I L C K	
		301 GATGTTGGGATTCGTAGAGCCGAAATTAAGCAAGGGATTCGTGAAGTCATTCTGTGTAAG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		121 D Q D G G K I G L R L K S I D N G V F V Q 361 GATCAGATGGAAAAATTGGGCTCCGGCTTAAATCAATAGATAACGGAGTATTTGTGCAG	
		141 L V Q A N S P A S L V G L R F G D Q V L 421 CTAGTCCAGGCAAATTCTCCAGCCTCGCTGGTTGGCCTGAGGTTTGGGGACCAAGTACTC	
		161 Q I N G E N C A G W S S D K S H K V L K 481 CAGATCAACGGGGAAAACTGTGCAGGCTGGAGCTCTGATAAATCGCACACAAGGTGCTCAAA	
		181 Q A F G E K I T M T I R D R P F E R T I 541 CAGGCTTTTGGAGAAGAAATTACTATTCGTGACAGGCCCTTCGAACGGACAATT	
		221 S I V K D S S A A R N G L L T K H N I C 661 TCCATAGTGAAAGATAGTTCTGCAGCCAGAAATGGTCTCCTCACAAACATAACATCTGC	
		241 R D Q W I E C H W A E G L S N C R H T V 721 CGAGATCAATGGATAGAATGTCATTGGGCTGAAGGACTCTCAAATTGCAGACATACTGTC	
		261 N I W D C S Y Y Y N L P C F Y L - 781 AACATCTGGGACTGTAGTTACTATTACAATCTGCCCTGCTTTTATCTTTGA	
WBC031F04.bFSP_20 012510.abd	Homo sapiens mRNA; cDNA DKFZp686K06110 (from clone DKFZp686K06110).	1 CTGATGAAACAGCAAAAGCTAGATATTGTTTCTTCTATACATAGAGGAAATAGCTTCTT 61 GCAACAGGAACAATTCAGGAGAAAACAGTTGTTTCTCCCCTTTAGATGATAGGTTGGGA 121 AGCAGGGTTGGCTCCGTCATAAATGATTTCTCCTAAACACTTCTCAGGTTTGGCCTATGCA 181 TGTGTGTTATAGATTGGGGATAGTTTGAAAACTCATTCTGTAGTATTATTCCTATGGGCA 241 GGGTGGTGAGTAGTGTGTAAATTCTTTGTCTTCTTTATGGGTCAGTATATCCACAGGCAC 301 ATTTCATGCTGCTTTGTCACTGAAAGTAAGGCAGCTGCAGTGGCAGGACCCTGTTCTAG 361 GACAGTTGATTGCCTCTATGATGAGACCTCAGAATTTCCTCTTTCCTAGTGCCCAAGACA 421 AGGAGCTTTGCTGATGTATTTCTGATAGCAGAAAAGGCCATTGAGCTTAGTGGTTGGTAC 481 CATATGGCAATTTACAATCTGGGAAATATTCTGATGATACATACTTTTCGAAGAATGCTA 541 GTTAGAATATTTAGATAGGACTCCTGAACTTTCTTTGAGAAGATGTTGATGACAACGAACT 601 AAAATCAGCCTAATCTGGGTCACATCCCAGGAAGATAAAGGTCTATAGGTGTGGAAGGC 661 TCTTTCTGGTCCTTTCAGTGAGCTATTTCCAATAGAGCCCGCCTATGCAGAGCTTCCCAC 721 TCTTGTGCATAGGATGTGGTTAAGCTCATGTCTCAGTGCCACAGTAGGTAGAGGATGCCA 781 TTGCAATGTAAAAGGCTATAAATAAAGCTCTCTTGTTTTTCCATAAAACAGTCTGCTCT 841 AGAACAGATTATAAAGGGCCAGAAGGAATCTCTTCTCATTTTCTTATTGAATAGAGAGT 901 GTATAAATTATTCCCTTACATAAAGGACAATTACTTTTTCTATATAGATCATATATAGAA 961 ATAGAGCTATAGAAAAAGTAATTAATTCTATATGATATGGCCTCAATTTTTAATTTTTAA	SEQ ID NO:147

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1021 ATTGTTTTTTATATGAAATAGTCTTAATTTTACTCTTTTTGCAGTTCACACAAAGATGAAT	
		1081 TCCTGCACTTCAAGATTACATTGTATATGTGATTCCTTGCTTCATTTTAAGGACTATGTT	
		1141 GTTTTCTTAAATGTGTTGATGAGTCTTTTATAACCTGTTTTAATAATGTTAAATTGAATTC	
		1201 ATTTTTCTTATTGTTAATACAAAACAGTAAATTTGAAGACTGAGAACCATATAAGAGGG	
		1261 TGATTGCACTTATTATGAAAAGATTTGAATCCTTCTTTGTGTGTGGGTGTGACCAGCC	
		1321 TTGCTATCAATTTCTTCTGTCATACACTGCCAAATTTTCTATTTAAGTATTGTGAAAACT	
		1381 CTGTTTTTTTTCAGGTCGAATGAGTGATTTGAGTGTAATTGGTCATCCAATAGATTCAGAA	
		1441 TCTAAAGAAGATGAACCTTGTAGTGAAGAAACAGATCCAGTGCATGATCTAATGGCTGAA	
		1501 ATTTTACCTGAATTCCCTGACATAATTGAAATAGACCTATACCACAGTGAAGAAAATGAA	
		1561 GAAGAAGAAGAAGAGTGTGCAAATGCTACTGATGTGACAACCACCCCATCTGTGCAGTAC	
		1621 ATAAAATGGGAAGCATCTCGTTACCACTGTGCCCAAGGACCCAGAAGCTGCAGAAGCTAGG	
		1681 CGTGGCCAGTTTGAAAGTGTTGCACCTTCTCAAAATTTCTCGGACAGCTCTGAAAGTGAT	
		1741 ACTCATCCATTTGTAATAGCCAAAACGGAATTGTCTACTGCTGTGCAACCTAATGAATCT	
		1801 ACAGAAACAACTCGAGTCTCTTGAAGTTACATGGAAGCCTGAGACTTACCCTGAAACATCA	
		1861 GAACATTTTTCAGGTGGTGAGCCTGATGTTTTCCCCACAGTCCCATTCCATGAGGAATTT	
		1921 GAAAGTGGACACAGCCAGAAAAGGGGCAGAATCAGTCACAGAGAGATACTGAAGTTGGT	
		1981 CATCAGGCACATGAACATACTACTGAACCTGTATCTCTGTTTCCTGAAGAGTCTTCAGGGAG	
		2041 ATTGCCATTGACCAAGAATCTCAGAAAATAGCCTTTGCAAGGGCTACAGAAGTAACATTT	
		2101 GGTGAAGAGGTAGAAAAAAGTACTTCTGTCACATACACTCCCACTATAGTTCCAAGTTCT	
		2161 GCATCAGCATATGTTTCAGAGGAAGAAGCAGTTACCCTAATAGGAAATCCTTGGCCAGAT	
		2221 GACCTGTTGTCTACCAAAGAAAGCTGGGTAGAAGCAACTCCTAGACAAGTTGTAGAGCTC	
		2281 TCAGGGAGTTCTTCGATTCCAATTACAGAAGGCTCTGGAGAAGCAGAAGAAGATGAAGAT	
		2341 ACAATGTTCACCATGGTAACTGATTTATCACAGAGAAATACTACTGATACACTCATTACT	
		2401 TTAGACACTAGCAGGATAATCACAGAAAGCTTTTTTGAGGTTCCTGCAACCACCATTTAT	
		2461 CCAGTTTCTGAACAACCTTCTGCAAAAGTGGTGCCTACCAAGTTTGTGAAGTGAAACAGAC	
		2521 ACTTCTGAGTGGATTTCCAGTACCACTGTTGAGGAAAAGAAAAGGAAGGAGGAGGAGGGA	
		2581 ACTACAGGTACGGCTTCTACATTTGAGGTATATTCATCTACACAGAGATCGGATCAATTA	
		2641 ATTTTACCCTTTGAATTAGAAAGTCCAAATGTAGCTACATCTAGTGATTCAGGTACCAGG	
		2701 AAAAGTTTTATGTCCTTGACAACACCAACACGGTCTGAAAGGGAAATGACAGATTCTACT	
		2761 CCTGTCTTTACAGAAACAAATACATTAGAAAATTTGGGGGCACAGACCACTGAGCACAGC	
		2821 AGTATCCATCAACCTGGGGTTCAGGAAGGCTGACCACTCTCCCACATAGTCCTGCCTCT	
		2881 GTCTTTATGGAGCAGGGCTCTGGAGAAGCTGCTGCCGACCCAGAAACCACCACTGTTTCT	
		2941 TCATTTTCATTAAACGTAGAGATATGCAATTCAAGCCGAAAAGGAAGTAGCTGGCACTTTG	
		3001 TCTCCGCATGTGGAAACTACATTCTCCACTGAGCCAACAGGACTGGTTTTGAGTACAGTA	
		3061 ATGGACAGAGTAGTTGCTGAAAATATAACCCAAACATCCAGGGAAATAGCGATTTCAGAG	
		3121 CGATTAGGAGAACCAAATTATGGGCAGAAATAAGGGCTTTCCACAGGTTTTCCTTTG	
		3181 GAGGAAGATTTCAGTGGCGACTTTAGAGAATACTCAACAGTGTCTCATCCCATAGCAAAA	
		3241 GAAGAAACGGTAATGATGGAAGGCTCTGGAGATGCAGCATTTAGGGACACCCAGACTTCA	
		3301 CCATCTACAGTACCTACTTCAGTTCACATCAGTCACATATCTGACTCAGAAGGACCCAGT	
		3361 AGCACCATGGTCAGCACTTCAGCCTTCCCCTGGGAAGAGTTTACATCCTCAGCTGAGGGC	
		3421 TCAGGTGAGCAACTGGTCACAGTCAGCAGCTCTGTTGTTCCAGTGCTTCCCAGTGCTGTG	
		3481 CAAAAGTTTTCTGGTACAGCTTCCTCCATTATCGACGAAGGATTGGGAGAAGTGGGTACT	
		3541 GTCAATGAAATTGATAGAAGATCCACCATTTTACCAACAGCAGAAGTGGAAGGTACGAAA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		3601 GCTCCAGTAGAGAAGGAGGAAGTAAAGGTCAGTGGCACAGTTTCAACAAACTTTCCCCAA	
		3661 ACTATAGAGCCAGCCAAATTATGGTCTAGGCAAGAAGTCAACCCTGTAAGACAAGAAATT	
		3721 GAAAGTGAAACAACATCAGAGGAACAAATTCAAGAAGAAAAGTCATTTGAATCCCCTCAA	
		3781 AACTCTCCTGCAACAGAACAAACAATCTTTGATTCACAGACATTTACTGAAACTGAACTC	
		3841 AAAACCACAGATTATTCTGTACTAACAACAAGAAAACTTACAGTGATGATAAAGAAATG	
		3901 AAGGAGGAAGACACTTCTTTAGTTAACATGTCTACTCCAGATCCAGATGCAAATGGCTTG	
		3961 GAATCTTACACAACTCTCCCTGAAGCTACTGAAAAGTCACATTTTCTTAGCTACTGCA	
		4021 TTAGTAACTGAATCTATACCAGCTGAACATGTAGTCACAGATTCACCAATCAAAAAGGAA	
		4081 GAAAGTACAAAACATTTTCCGAAAGGCATGAGGCCAACAATTCAAGAGTCAGATACTGAG	
		4141 CTCTTATTCTCTGGACTGGGATCAGGAGAAGAAGTTTTACCTACTCTACCAACAGAGTCA	
		4201 GTGAATTTTACTGAAGTGGAACAAATCAATAACACATTATATCCCCACACTTCTCAAGTG	
		4261 GAAAGTACCTCAAGTGACAAAATTGAAGACTATATAACAGAATGGAAAATGTGGCAAAAGAA	
		4321 GTTGGACCACTCTGGTATCTCAAACAGACATCTTTGAAGGTAGTGGGTCAGTAACCAGCACA	
		4381 ACATTAATAGAAATTTAAGTGACACTGGAGCAGAAGGACCCACGGTGGCACCTCTCCCT	
		4441 TTCTCCACGGACATCGGACATCCTCAAAATCAGACTGTCAGGTGGGCAGAAGAAATCCAG	
		4501 ACTAGTAGACCACAAACCATAACTGAACAAGACTCTAACAAGAATTCTTCAACAGCAGAA	
		4561 ATTAACGAAACAACAACCTCATCTACTGATTTTCTGGCTAGAGCTTATGGTTTTGAAATG	
		4621 GCCAAAGAATTTGTTACATCAGCACCAAAACCATCTGACTTGTATTATGAACCTTCTGGA	
		4681 GAAGGATCTGGAGAAGTGGATATTGTTGATTCATTTCACACTTCTGCAACTACTCAGGCA	
		4741 ACCAGACAAGAAAGCAGCACCACATTTGTTTCTGATGGGTCCCTGGAAAACATCCTGAG	
		4801 GTGCCAAGCGCTAAAGCTGTTACTGCTGATGGATTCCCCAACAGTTTCAGTGATGCTGCCT	
		4861 CTTCATTCAGAGCAGAACAAAAGCTCCCCTGATCCAACTAGCACACTGTCAAATACAGTG	
		4921 TCATATGAGAGGTCCACAGACGGTAGTTTCCAAGACCGTTTCAGGGAATTCGAGGATTCC	
		4981 ACCTTAAAACCTAACAGAAAAAAACCCACTGAAAATATTATCATAGACCTGGACAAAGAG	
		5041 GACAAGGATTTAATATTGACAATTACAGAGAGTACCATCCTTGAAATTCTACCTGAGCTG	
		5101 ACATCGGATAAAAATACTATCATAGATATTGATCATACTAACCTGTGTATGAAGACATT	
		5161 CTTGGAATGCAAACAGATATAGATACAGAGGTACCATCAGAACCACATGACAGTAATGAT	
		5221 GAAAGTAATGATGACAGCACTCAAGTTCAAGATCTATGAGGCAGCTGTCAACCTTTCT	
		5281 TTAACTGAGGAAACATTTGAGGGCTCTGCTGATGTTCTGGCTAGCTACACTCAGGCAACA	
		5341 CATGATGAATCAATGACTTATGAAGATAGAAGCCAACTAGATCACATGGGCTTTCACTTC	
		5401 ACAACTGGGATCCCTGCTCCTAGCACAGAAACAGAATTAGACGTTTTACTTCCCACGGCA	
		5461 ACATCCCTGCCAATTCCTCGTAAGTCTGCCACAGTTATTCCAGAGATTGAAGGAATAAAA	
		5521 GCTGAAGCAAAAGCCCTGGATGACATGTTTGAATCAAGCACTTTGTCTGATGGTCAAGCT	
		5581 ATTGCAGACCAAAGTGAAATAATAATACCAACATTGGGCCAATTTGAAAGGACTCAGGAGGAG	
		5641 TATGAAGACAAAAAACATGCTGGTCCTTCTTTTTCAGCCAGAATTCTCTTCAGGAGCTGAG	
		5701 GAGGCATTAGTAGACCATACTCCCTATCTAAGTATTGCTACTACCCACCTTATGGATCAG	
		5761 AGTGTAACAGAGGTGCCTGATGTGATGGAAGGATCCAATCCCCCATATTACACTGATACA	
		5821 ACATTAGCAGTTTCAACATTTGCGAAGTTGTCTTCTCAGACACCATCATCTCCCCTCACT	
		5881 ATCTACTCAGGCAGTGAAGCCTCTGGACACACAGAGATCCCCCAGCCCAGTGCTCTGCCA	
		5941 GGAATAGACGTCGGCTCATCTGTAATGTCCCCACAGGATTCTTTTAAGGAAATTCATGTA	
		6001 AATATTGAAGCGACTTTCAAACCATCAAGTGAGGAATACCTTCACATAACTGAGCCTCCC	
		6061 TCTTTATCTCCTGACACAAAATTAGAACCTTCAGAAGATGATGGTAAACCTGAGTTATTA	
		6121 GAAGAAATGGAAGCTTCTCCCACAGAACTTATTGCTGTGGAAGGAACTGAGATTCTCCAA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		6181 GATTTCCAAACAAAACCTATGGTCAAGTTTCTGGAGAAGCAATCAAGATGTTTCCCACC 6241 ATTAAAACACCTGAGGCTGGAACTGTTATTACAACTGCCGATGAAATTGAATTAGAAGGT 6301 GCTACACAGTGGCCACACTCTACTTCTGCTTCTGCCACCTATGGGGTCGAGGCAGGTGTG 6361 GTGCCTTGGCTAAGTCCACAGACTTCTGAGAGGCCCACGCTTTCTTCTTCTCCAGAAATA 6421 AACCCTGAAACTCAAGCAGCTTTAATCAGAGGCAGGATTCCACGATAGCAGCATCAGAA 6481 CAGCAAGTGGCAGCGAGAATTCTTGATTCCAATAATCAGGCAACTGTAAGCACTGCAGAG 6541 TTAAATACTGAGCTTGCAACACCATCATTTTCCCTTCTGGAAACTTCTAATGAAACCGAT 6601 TTCCTGATTGGCATTAATGAAGAGTCAGTGGAGGGCACAGCAGTCTATTTACCAGGACCA 6661 GATCGTTGCAAAACGAACCCGTGCCTTAACGGAGGCACCTGTTATCCTACTGAAACTTCC 6721 TACGTGTGCACCTGTGTGCCAGGATACAGCGGCGACCAGTGTGAGCTTGATTTTGATGAA 6781 TGTCACTCTAACCCCTGTCGCAATGGAGCCACGTGCATTGACGGTTTCAATACGTTCAGG 6841 TGCCTCTGCCTTCCGAGCTACATTGGTGCACTTTGTGAGCAAGACACCGAGACATGTGAC 6901 TACGGCTGGCACAAATTCCAAGGGCAGTGCTACAAGTACTTTGCCCACCGCCGCACGTGG 6961 GATGCAGCTGAGCGAGAATGCCGGCTGCAGGGCGCCCATCTCACAAGCATCCTGTCTCAT 7021 GAAGAACAAATGTTTGTGAATCGTGTGGGCCATGACTATCAGTGGATAGGCCTCAATGAC 7081 AAGATGTTTGAGCATGACTTCCGTTGGACTGATGGCAGCACCCTGCAATATGAGAACTGG 7141 AGGCCCAACCAGCCAGACAGCTTTTTTTCTGCTGGAGAAGATTGTGTCGTAATCATTTGG 7201 CACGAGAACGGCCAGTGGAATGATGTTCCCTGCAATTACCATCTCACCTATACTTGCAAG 7261 AAAGGAACAGTTGCTTGCGGCCAGCCCCCAGTTGTAGAAAATGCCAAGACCTTTGGAAAG 7321 ATGAAACCTCGTTATGAAATCAACTCCCTGATTAGATATCACTGTAAAGATGGTTTCATT 7381 CAACGCCACCCTTCCACTATCCGTTGCCTAGGAAATGGAAAATGGGCCATGCCTAAAATT 7441 ACCTGCATGAACCCATCTGCATACCAAAGGACTTATTCTATGAAATACTTTTAAAAATTCC 7501 TCATCAGCAAAGGACAATTCAATAAATACATCCAAACATGATCATCGTTGGAGCCGGAGG 7561 TGGCAGGAGTCGAGGCGCTGATCCCTAAAATGGCGAACATGTGTTTTCATCATTTCAGCC 7621 AAAGTCCTAACTTCCTGTGCCTTTCCTATCACCTCGAGAAGTAATTATCAGTTGGTTTGG 7681 ATTTTTGGACCACCGTTCAGTCATTTGGGTTGCCGTGCTCCCAAAACATTTTAAATGAA 7741 AGTATTGGCATTCAAAAAGACAGCAGACAAATGAAAGAAATGAGAGCAGAAAGTAAGC 7801 ATTTCTAGCCTATCTAATTTCTTTAGTTTTCTATTTGCCTCCAGTGCAGTCCATTTCCTA 7861 ATGTATACCAGCCTACTGTACTATTTAAAAAGCTCAATTTCAGCACCAATGGCAATGTAA 7921 ATAAGATGATTTAATGTTGATTTTAATCCTGTATATAAAATAAAAGTCATACTGAGTTTC 7981 GGGCGTATTTAATGATGATTATGGAGCCTTAGAGGTCTTTAATCATTGGTTCGGCTGCTT 8041 TTTGTACTTTGTTTAGGCTGGAAACGGTTTCACTTGCCCTTTGTCAGCAAGACTGAGGAC 8101 GGCTTTTCCTGGACAACTAACAAACAAAAGTCTTGTAGGTCACTGCGCCATCTCAGCCAT 8161 AGTAGTTGCAGTTTGCTTCCATGTGATTCTGAAGCCTGGCCAATGGGATCCGGACAAAAG 8221 TAGGGACTGCAATGTGAAACACCTCTTTGCTGCATTCTTTTTCTTCGCTTACAGAAAGG 8281 CCTGAATGGAGGACTTTTTTATGACCAGGAGCAGTTTTTAGGGGTCAAAGTGCTAATTAT 8341 TAACTCAACCAGGTCTACTTTTTAATGGCTTTCATAACACTAACTGGCAGATTACAGAT 8401 CAACACATTTCAAATGGATAGAGACCTAGGACTCTGGAGGGTGGGGATTGTTAAAACA 8461 C 1 M S D L S V I G H P I D S E S K E D E P 1 ATGAGTGATTTGAGTGTAATTGGTCATCCAATAGATTCAGAATCTAAAGAAGATGAACCT	SEQ ID NO:148

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		21 C S E E T D P V H D L M A E I L P E F P 61 TGTAGTGAAGAAACAGATCCAGTGCATGATCTAATGGCTGAAATTTTACCTGAATTCCCT 41 D I I E I D L Y H S E E N E E E E E E C 121 GACATAATTGAAATAGACCTATACCACAGTGAAGAAATGAAGAGAAGAAGAGTGT 61 A N A T D V T T T P S V Q Y I N G K H L 181 GCAAATGCTACTGATGTGACAACCACCCCATCTGTGCAGTACATAAATGGGAAGCATCTC 81 V T T V P K D P E A A E A R R G Q F E S 241 GTTACCACTGTGCCCAAGGACCCAGAAGCTGCAGAAGCTAGGCGTGGCCAGTTTGAAAGT 101 V A P S Q N F S D S S E S D T H P F V I 301 GTTGCACCTTCTCAAAATTTCTCGGACAGCTCTGAAAGTGATACTCATCCATTGTAATA 121 A K T E L S T A V Q P N E S T E T T E S 361 GCCAAAACGGAATTGTCTACTGCTGTGCAACCTAATGAATCTACAGAAACAACTGAGTCT 141 L E V T W K P E E T Y Y P E T S E H F S G G 421 CTTGAAGTTACATGGAAGCCTGAGACTTACCCTGAAACATCAGAACATTTTTCAGGTGGT 161 E P D V F P P T V P P F H E E E F E S G T A R 481 GAGCCTGATGTTTTCCCCACAGTCCCATTCCATGAGGAATTTGAAAGTGGAACAGCCAGA 181 K G A E S V T E E R D T E V G H Q A H E H 541 AAAGGGGCAGAATCAGTCACAGAGAGATACTGAAGTTGGTCATCAGGCACATGAACAT 201 T E E P V S L F P E E S S G E I A I D Q E 601 ACTGAACCTGTATCTCTGTTTCCTGAAGAGTCTTCAGGGGAGATTGCCATTGACCAAGAA 221 S Q K I A F A R A T E V T F G E E V E K 661 TCTCAGAAAATAGCCTTTGCAAGGGCTACAGAAGTAACATTTGGTGAAGAGGTAGAAAAA 241 S T S V T Y T P T I V P S S A S A Y V S 721 AGTACTTCTGTCACATACACTCCCACTATAGTTCCAAGTTCTGCATCAGCATATGTTTCA 261 E E E A V T L I G N P W P D D L L S T K 781 GAGGAAGAAGCAGTTACCCTAATAGGAAATCCTTGGCCAGATGACCTGTTGTCTACCAAA 281 E S W V E A T P R Q V V E L S G S S S I 841 GAAAGCTGGGTAGAAGCAACTCCTAGACAAGTTGTAGAGCTCTCAGGGAGTTCTTCGATT 301 P I T E G S G E A E E D E D T M F T M V	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		901 CCAATTACAGAAGGCTCTGGAGAAGCAGAAGAAGATGAAGATACAATGTTCACCATGGTA	
		321 T D L S Q R N T T D T L I T L D T S R I	
		961 ACTGATTTATCACAGAGAAATACTACTGATACACTCATTACTTTAGACACTAGCAGGATA	
		341 I T E S F F E V P A T T I Y P V S E Q P	
		1021 ATCACAGAAAGCTTTTTTGAGGTTCCTGCAACCACCATTTATCCAGTTTCTGAACAACCT	
		361 S A K V V P T K F V S E T D T S E W I S	
		1081 TCTGCAAAAGTGGTGCCTACCAAGTTTGTAAGTGAAACAGACACTTCTGAGTGGATTTCC	
		381 S T T V E E K K R K E E E G T T G T A S	
		1141 AGTACCACTGTTGAGGAAAAGAAAGGAAGGAGGAGGAGGGAACTACAGGTACGGCTTCT	
		401 T F E V Y S S T Q R S D Q L I L P F E L	
		1201 ACATTTGAGGTATATTCATCTACACAGAGATCGGATCAATTAATTTTACCCTTTGAATTA	
		421 E S P N V A T S S D S G T R K S F M S L	
		1261 GAAAGTCCAAATGTAGCTACATCTAGTGATTCAGGTACCAGGAAAAGTTTATGTCCTTG	
		441 T T P T R S E E R E M T D S T P V F T E T	
		1321 ACAACACCAACACGGTCTGAAAGGGAAATGACAGATTCTACTCCTGTCTTTACAGAAACA	
		461 N T L E N L G A Q T T E H S S I H Q P G	
		1381 AATACATTAGAAAATTGGGGGCACAGACCACTGAGCACAGCAGTATCCATCAACCTGGG	
		481 V Q E G L T T L P H S P A S V F M E Q G	
		1441 GTTCAGGAAGGGCTGACCACTCTCCCACATAGTCCTGCCTCTGTCTTTATGGAGCAGGGC	
		501 S G E A A A D P E T T T V S S F S L N V	
		1501 TCTGGAGAAGCTGCTGCCGACCCAGAAACCACCACTGTTTCTTCATTTTCATTAAACGTA	
		521 E Y A I Q A E K E V A G T L S P H V E T	
		1561 GAGTATGCAATTCAAGCCGAAAAGGAAGTAGCTGGCACTTTGTCTCCGCATGTGGAAACT	
		541 T F S T E P T G L V L S T V M D R V V A	
		1621 ACATTCTCCACTGAGCCAACAGGACTGGTTTTGAGTACAGTAATGGACAGAGTAGTTGCT	
		561 E N I T Q T S R E I A I S E R L G E P N	
		1681 GAAAATATAACCCAAACATCCAGGGAAATAGCGATTCAGAGCGATTAGGAGAACCAAAT	
		581 Y G A E I R G F S T G F P L E E D F S G	
		1741 TATGGGGCAGAAATAAGGGGCTTTCCACAGGTTTCCTTGGAGGAAGATTTCAGTGGC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		601 D F R E Y S T V S H P I A K E E T V M M 1801 GACTTTAGAGAATACTCAACAGTGTCTCATCCCATAGCAAAAGAAGAAACGGTAATGATG	
		621 E G S G D A A F R D T Q T S P S T V P T 1861 GAAGGCTCTGGAGATGCAGCATTTAGGGACACCCAGACTTCACCATCTACAGTACCTACT	
		641 S V H I S H I S D S E G P S S S T M V S T 1921 TCAGTTCACATCAGTCACATATCTGACTCAGAAGGACCCAGTAGCACCATGGTCAGCACT	
		661 S A F P W E E F T S S S A E G S G E Q L V 1981 TCAGCCTTCCCCTGGGAAGAGTTTACATCCTCAGCTGAGGGCTCAGGTGAGCAACTGGTC	
		681 T V S S S V V P V L P S A V Q K F S G T 2041 ACAGTCAGCAGCTCTGTTGTTCCAGTGCTTCCCAGTGCTGTGCAAAAGTTTTCTGGTACA	
		701 A S S I I D E G L G E V G T V N E I D R 2101 GCTTCCTCCATTATCGACGAAGGATTGGGAGAAGTGGGTACTGTCAATGAAATTGATAGA	
		721 R S T I L P T T A E V E G T K A P V E K E 2161 AGATCCACCATTTTACCAACAGCAGAAGTGGAAGGTACGAAAGCTCCAGTAGAGAAGGAG	
		741 E V K V S S G T V S T N F P Q T I E P A K 2221 GAAGTAAAGGTCAGTGGCACAGTTTCAACAAACTTTCCCCAAACTATAGAGCCAGCCAAA	
		761 L W S R Q E V N P V R Q E I E S E T T S 2281 TTATGGTCTAGGCAAGAAGTCAACCCTGTAAGACAAGAAATTGAAAGTGAAACAACATCA	
		781 E E Q I Q E E K S F E S P Q N S P A T E 2341 GAGGAACAAATTCAAGAAGAAAAGTCATTTGAATCCCCTCAAAACTCTCCTGCAACAGAA	
		801 Q T I F D S Q T F T E T E L K T T T D Y S 2401 CAAACAATCTTTGATTCACAGACATTTACTGAAACTGAACTCAAAACCACACAGATTATTCT	
		821 V L T T K K T Y S D D K E M K E E D T S 2461 GTACTAACAACAAAGAAAACTTACAGTGATGATAAAGAAATGAAGGAGGAAGACACTTCT	
		841 L V N M S T P D P D A N G L E S Y T T L 2521 TTAGTTAACATGTCTACTCCAGATCCAGATGCAAATGGCTTGGAATCTTACACAACTCTC	
		861 P E A T E K S H F F L A T A L V T E S I 2581 CCTGAAGCTACTGAAAAGTCACATTTTTCTTAGCTACTGCATTAGTAACTGAATCTATA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		881 P A E H V V T D S P I K K E E S T K H F 2641 CCAGCTGAACATGTAGTCACAGATTCACCAATCAAAAGGAAGAAAGTACAAACATTTT	
		901 P K G M R P T I Q E S D T E L L F S G L 2701 CCGAAAGGCATGAGGCCAACAATTCAAGAGTCAGATACTGAGCTCTTATTCTCTGGACTG	
		921 G S G E E V L P T L P T E S V N F T E V 2761 GGATCAGGAGAAGAAGTTTTACCTACTCTACCAACAGAGTCAGTGAATTTTACTGAAGTG	
		941 E Q I N N T L Y P H T S Q V E S T S S D 2821 GAACAAATCAATAACACATTATATCCCCACACTTCTCAAGTGGAAAGTACCTCAAGTGAC	
		961 K I E E D Y N R M E N V A K E V G P L V S 2881 AAAATTGAAGACTATAACAGAATGGAAAATGTGGCAAAGAAGTTGGACCACTCGTATCT	
		981 Q T D I F E G S G S V T S T T L I E I L 2941 CAAACAGACATCTTTGAAGGTAGTGGGTCAGTAACCAGCACACAACATTAATAGAAATTTTA	
		1001 S D T G A E G P T V A P L P F S T D I G 3001 AGTGACACTGGAGCAGAAGGACCCACGGTGGCACCTCTCCCTTTCTCCACGGACATCGGA	
		1021 H P Q N Q T V R W A E E I Q T S R P Q T 3061 CATCCTCAAAATCAGACTGTCAGGTGGGCAGAAGAAATCCAGACTAGTAGACCACAAACC	
		1041 I T E Q D S N K N S S T A E I N E T T T 3121 ATAACTGAACAAGACTCTAACACAGAATTCTTCAACAGCAGAAATTAACGAAACAACAACC	
		1061 S S T D F L A R A Y G F E M A K E F V T 3181 TCATCTACTGATTTTCTGGCTAGAGCTTATGGTTTTGAAATGGCCAAACGAATTTGTTACA	
		1081 S A P K P S D L Y Y E P S G E G S G E V 3241 TCAGCACCAAAACCATCTGACTTGTATTATGAACCTTCTGGAGAAGGATCTGGAGAAGTG	
		1101 D I V D S F H T S A T T Q A T R Q E S S 3301 GATATTGTTGATTCATTTCACACTTCTGCAACTACTCAGGCAACCAGACAAGAAAGCAGC	
		1121 T T F V S D G S L E K H P E V P S A K A 3361 ACCACATTTGTTTCTGATGGGTCCCTGGAAAAACATCCTGAGGTGCCAAGCGCTAAAGCT	
		1141 V T A D G F P T V S V M L P L H S E Q N 3421 GTTACTGCTGATGGATTCCCAACAGTTTCAGTGATGCTGCCTCTTCATTCAGAGCAGAAC	
		1161 K S S P D P T S T L S N T V S Y E R S T	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		3481 AAAAGCTCCCCTGATCCAACTAGCACACTGTCAAATACAGTGTCATATGAGAGGTCCACA	
		1181 D G S F Q D D R F R E E F E D S T L K P N R	
		3541 GACGGTAGTTTCCAAGACCGTTTCAGGGAATTCGAGGATTCCACCTTAAAACCTAACAGA	
		1201 K K P T E N N I I I D L D K E D K D L I L	
		3601 AAAAAACCCACTGAAAATATTATCATAGACCTGGACAAAGAGGACAAGGATTTAATATTG	
		1221 T I T E S T I L E I L P E L T S D K N T	
		3661 ACAATTACAGAGAGTACCATCCTTGAAATTCTACCTGAGCTGACATCGGATAAAAATACT	
		1241 I I D I D H T K P V Y E D I L G M Q T D	
		3721 ATCATAGATATTGATCATACTAAACCTGTGTATGAAGACATTCTTGGAATGCAAACAGAT	
		1261 I D T E V P S E P H D S N D E S N D D S	
		3781 ATAGATACAGAGGTACCATCAGAACCACATGACAGTAATGATGAAAGTAATGATGACAGC	
		1281 T Q V Q E I Y E A A V N L S L T E E T F	
		3841 ACTCAAGTTCAAGAGATCTATGAGGCAGCTGTCAACCTTTCTTTAACTGAGGAAACATTT	
		1301 E G S A D V L A S Y T Q A T H D E S M T	
		3901 GAGGGCTCTGCTGATGTTCTGGCTAGCTACACTCAGGCAACACATGATGAATCAATGACT	
		1321 Y E D R S Q L D H M G F H F T T G I P A	
		3961 TATGAAGATAGAAGCCAACTAGATCACATGGGCTTTCACTTCACAACTGGGATCCCTGCT	
		1341 P S T E T E L D V L L P T A T S L P I P	
		4021 CCTAGCACAGAAACAGAATTAGACGTTTTACTTCCCACGGCAACATCCCTGCCAATTCCT	
		1361 R K S A T V I P E I E G I K A E E A K A L	
		4081 CGTAAGTCTGCCACAGTTATTCCAGAGATTGAAGGAATAAAGCTGAAGCAAAAGCCCTG	
		1381 D D M F E S S S T L S D G Q A I A D Q S E	
		4141 GATGACATGTTTGAATCAAGCACTTTGTCTGATGGTCAAGCTATTGCAGACCAAAGTGAA	
		1401 I I P T L G Q F E R T Q E E Y E D K K H	
		4201 ATAATACCAACATTGGGCCAATTTGAAGGACTCAGGAGGAGTATGAAGACAAAAAACAT	
		1421 A G P S F Q P P E F S S G A E E A L V D H	
		4261 GCTGGTCCTTCTTTTCAGCCAGAATTCTCTTCAGGAGCTGAGGAGGCATTAGTAGACCAT	
		1441 T P Y L S I A T T H L M D Q S V T E V P	
		4321 ACTCCCTATCTAAGTATTGCTACTACCCACCTTATGGATCAGAGTGTAACAGAGGTGCCT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1461 D V M E G S N P P Y Y T D T T L A V S T 4381 GATGTGATGGAAGGATCCAATCCCCCATATTACACTGATACAACATTAGCAGTTTCAACA	
		1481 F A K L S S Q T P S S P L T I Y S G S E 4441 TTTGCGAAGTTGTCTTCTCAGACACCATCATCTCCCCTCACTATCTACTCAGGCAGTGAA	
		1501 A S G H T E I P Q P S A L P G I D V G S 4501 GCCTCTGGACACACAGAGATCCCCCAGCCCAGTGCTCTGCCAGGAATAGACGTCGGCTCA	
		1521 S V M S P Q D S F K E I H V N I E A T F 4561 TCTGTAATGTCCCCACAGGATTCTTTTAAGGAAATTCATGTAAATATTGAAGCGACTTTC	
		1541 K P S S E E Y L H I T E P P S L S P D T 4621 AAACCATCAAGTGAGGAATACCTTCACATAACTGAGCCTCCCTCTTTATCTCCTGACACA	
		1561 K L E P S E D D G K P E L L E E M E A S 4681 AAATTAGAACCTTCAGAAGATGATGGTAAACCTGAGTTATTAGAAGAAATGGAAGCTTCT	
		1581 P T E L I A V E G T E I L Q D F Q N K T 4741 CCCACAGAACTTATTGCTGTGGAAGGAACTGAGATTCTCCAAGATTTCCAAACAAAACC	
		1601 Y G Q V S G E A I K M F P T I K T P E A 4801 TATGGTCAAGTTTCTGGAGAAGCAATCAAGATGTTTCCCACCATTAAAACACCTGAGGCT	
		1621 G T V I T T A D E I E L E G A T Q W P H 4861 GGAACTGTTATTACAACTGCCGATGAAATTGAATTAGAAGGTGCTACACAGTGGCCACAC	
		1641 S T S A S A T Y G V E A G V V P W L S P 4921 TCTACTTCTGCTTCTGCCACCTATGGGTCGAGGCAGGTGTGGTGCCTTGGCTAAGTCCA	
		1661 Q T S E R P T L S S S P E I N P E T Q A 4981 CAGACTTCTGAGAGGCCCACGCTTTCTTCTTCCAGAAATAAACCCTGAAACTCAAGCA	
		1681 A L I R G Q D S T I A A S E Q Q V A A R 5041 GCTTTAATCAGAGGGCAGGATTCCACGATAGCAGCATCAGAACAGCAAGTGGCAGCGAGA	
		1701 I L D S N N Q A T V S T A E L N T E L A 5101 ATTCTTGATTCCAATAATCAGGCAACTGTAAGCACTGCAGAGTTAAATACTGAGCTTGCA	
		1721 T P S F S L L E T S N E T D F L I G I N 5161 ACACCATCATTTTCCCTTCTGGAAACTTCTAATGAAACCGATTTCCTGATTGGCATTAAT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1741 E E S V E G T A V Y L P G P D R C K T N 5221 GAAGAGTCAGTGGAGGGCACAGCAGTCTATTTACCAGGACCAGATCGTTGCAAAACGAAC	
		1761 P C L N G G T C Y P T E T S Y V C T C V 5281 CCGTGCCTTAACGGAGGCACCTGTTATCCTACTGAAACTTCCTACGTGTGCACCTGTGTG	
		1781 P G Y S G D Q C E L D F D E C H S N P C 5341 CCAGGATACAGCGGCGACCAGTGTGAGCTTGATTTTGATGAATGTCACTCTAACCCCTGT	
		1801 R N G A T C I D G F N T F R C L C L P S 5401 CGCAATGGAGCCACGTGCATTGACGGTTTCAATACGTTCAGGTGCCTCTGCCTTCCGAGC	
		1821 Y I G A L C E Q D T E T C D Y G W H K F 5461 TACATTGGTGCACTTTGTGAGCAAGACACCGAGACATGTGACTACGGCTGGCACAAATTC	
		1841 Q G Q C Y K Y F A H R R T W D A A E R E 5521 CAAGGGCAGTGCTACAAGTACTTTGCCCACCGCCGCACGTGGGATGCAGCTGAGCGAGAA	
		1861 C R L Q G A H L T S I L S H E E Q M F V 5581 TGCCGGCTGCAGGGCGCCCATCTCACAAGCATCCTGTCTCATGAAGAACAAATGTTTGTG	
		1881 N R V G H D Y Q W I G L N D K M F E H D 5641 AATCGTGTGGGCCATGACTATCAGTGGATAGGCCTCAATGACAAGATGTTTGAGCATGAC	
		1901 F R W T D G S T L Q Y E N W R P N Q P D 5701 TTCCGTTGGACTGATGGCAGCACCCTGCAATATGAGAACTGGAGGCCCAACCAGCCAGAC	
		1921 S F F S A G E D C V V I I W H E N G Q W 5761 AGCTTTTTTTCTGCTGGAGAAGATTGTGTCGTAATCATTTGGCACGAGAACGGCCAGTGG	
		1941 N D V P C N Y H L T Y T C K K G T V A C 5821 AATGATGTTCCCTGCAATTACCATCTCACCTATACTTGCAAGAAAGGAACAGTTGCTTGC	
		1961 G Q P P V V E N A K T F G K M K P R Y E 5881 GGCCAGCCCCCCAGTTGTAGAAAATGCCAAGACCTTTGGAAAGATGAAACCTCGTTATGAA	
		1981 I N S L I R Y H C K D G F I Q R H P S T 5941 ATCAACTCCCTGATTAGATATCACTGTAAAGATGGTTTCATTCAACGCCACCCTTCCACT	
		2001 I R C L G N G K W A M P K I T C M N P S 6001 ATCCGTTGCCTAGGAAATGGAAAATGGGCCATGCCTAAAATTACCTGCATGAACCCATCT	
		2021 A Y Q R T Y S M K Y F K N S S S A K D N	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		6061 GCATACCAAAGGACTTATTCTATGAAATACTTTAAAAATTCCTCATCAGCAAAGGACAAT	
		2041 S I N T S K H D H R W S R R W Q E S R R	
		6121 TCAATAAATACATCCAAACATGATCATCGTTGGAGCCGGAGGTGGCAGGAGTCGAGGCGC	
		2061 -	
		6181 TGA	
WBC031G11.bFSP_20012510.abd	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 14, mRNA	1 GCCGGCGGGGGGCGCAGCGGCCCGGAGGTGCGTGGTTGAGCGAAGCCGCGGGGCCCAACC	SEQ ID NO:149
		61 GCAGTCGCGGGGTCTGGGAGGAAGCAGTACCTTGAAGAGAAATTGGAGAGGGAGTCAATT	
		121 CCTAGGATAGCAGAGAGATGGACAACAGACAGAATGTCACCCCAGCTCTGATCTTTGCCA	
		181 TCACAGTTGCTACAATCGGCTCTTTCCAGTTTGGCTACAACACTGGGTCATCAATGCTC	
		241 CTGAGACGATCATAAAGGAATTTATCATAAAACTTTGACGGACAAGGCAAATGCCCCTC	
		301 CCTCTGAGGTGCTGCTCACGAATCTCTGGTCCTTGTCTGTGGCCATATTTTCCGTCGGGG	
		361 GTATGATCGGCCTCCTTTTCCGTCGACTCTTTGTTAACCGCTTTGGCAGGCGCAATTCAA	
		421 TGCTGATTGTCAACCTGTTGGCTGCCACTGGTGGCTGCCTTATGGGACTGTGTAAAATAG	
		481 CTGAGTCAGTTGAAATGCTGATCCTGGGCCGCTTGGTTATTGGCCTCTTCTGCGGACTCT	
		541 GCACAGGTTTTGTGCCCATGTACATTGGAGAGATCTCGCCTACTGCCCTGAGGGGTGCCT	
		601 TTGGCACTCTCAACCAGCTGGGCATAGTTATTGGAATTCTGGTGGCCCAGATCTTTGGTC	
		661 TGGAACTCATCCTTGGGTCTGAAGAGCTATGGCCGGTGCTATTAGGCTTTACCATCCTTC	
		721 CAGCTATCCTGCAAAGTGCAGCCCTTCCATGTTGCCCTGAAAGTCCCAGATTTTTGCTCA	
		781 TTAACAGAAAAAAAAGAGGAGAATGCTACGCGGATCCTCCAGCGGTTGTGGGGCACCCAGG	
		841 ATGTATCCCAAGACATCCAGGAGATGAAAGATGAGAGTGCAAGGATGTCACACAAGAAAAGC	
		901 AAGTCACCGTGCTGGAGCTCTTTAGAGTGTCCAGCTACCGACAGCCCATCATCATTTCCA	
		961 TTGTGCTCCAGCTCTCTCAGCAGCTCTCTGGGATCAATGCTGTGTTCTATTACTCAACAG	
		1021 GAATCTTCAAGGATGCAGGTGTTCAACAGCCCATCTATGCCACCATCAGCGCGGGTGTGG	
		1081 TTAATACTATCTTCACTTTACTTTCTCTATTTCTGGTGGAAAGGGCAGGAAGAAGGACTC	
		1141 TGCATATGATAGGCCTTGGAGGGATGGCTTTTTGTTCCACGCTCATGACTGTTTCTTTGT	
		1201 TATTAAAGAATCACTATAATGGGATGAGCTTTGTCTGTATTGGGGCTATCTTGGTCTTTG	
		1261 TGGCCTGTTTTTGAAATTGGACCAGGCCCCCATTCCCTGGTTTATTGTGGCCGAACTCTTCA	
		1321 GCCAGGGCCCCCGCCCAGCTGCGATGGCAGTGGCCGGCTGCTCCAACTGGACCTCCAACT	
		1381 TCCTAGTCGGATTGCTCTTCCCCTCTGCTGCTTACTATTTAGGAGCCTACGTTTTTATTA	
		1441 TCTTCACCGGCTTCCTCATTACCTTCTTGGCCTTTACCTTCTTCAAAGTCCCTGAGACCC	
		1501 GTGGCAGGACTTTTGAGGATATCACACGGGCCTTTGAAGGGCAGGCACACGGTGCAGATA	
		1561 GATCTGGGAAGGACGGCGTCATGGGATGAACAGCATCGAGCCTGCTAAGGAGACCACCA	
		1621 CCAATGTCTAAGTCATGCCTCCTTCCACCTCCCTCCCGGCATGGGAAAGCCACCTCTCCC	
		1681 TCAACAAGGGAGAGACTTTATCAGGATGAACCCAGGACTGCTTCTGAATGCTGCTACTTG	
		1741 ATTTCTTTCTCATCCCACGCACTCCATGAGCACCCCAAGGCTGCAGTTTGTTGGATCTTC	
		1801 AATGGCTTTTTAAATTTTATTTCCTGGACATCCTCTTCTGCTTAGGAGACCGAGTGAA	
		1861 CCTACCTTCATTTCAGGAGGGATTGGCCGCTTGGCACATGACAACTTTGCCAGCTTTTCC	
		1921 TCCCTTGGGTTCTGATATTGCCGCACTAGAGGATATAGGAGAGGAAAAGTAAGGTGCAGT	
		1981 TGCCCCAACCTCAGACTTACCAGGAAGCAGATACATATGAGTGTGGAAGCCGGAGGGTGT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2041 TTATGTAAGAGCACCTTCCTCACTTCCATACAGCTCTACGCGGCAAATTAACTTGAGTTT 2101 TATTTATCTTATCCTCTGGTTTAATTACATAAATATTTATTTTTTAAGTGTAATTTTGCC 2161 AAATAATAAAAACAGAAGGAAATTGAGATTAGAGGGAGGTGTTTAAAGAGAGGTTATAGA 2221 GTAAAAGATTTGATGCTGGAGAGGTTAAGGTGCAATAAGAATTCAGGGAGAAATGTTGTT 2281 CATTATTGGAGGGTAAATGATGTCGTGCCTGAGGTCTGTACATTACCTCTTAACAATTTC 2341 TGTCCTTCAGATGGAAACTCTTTGATTTCTCAGAAAAGTTGTATGCCTATTTAATAAAGC 2401 TACTCATTTCCTTTGGAACTTTATCTTTAAGATAATAGTTTACATGTAGTAGTACTTGAA 2461 ATCTAGGATTATTAACTAATATGGCATTGTAGTTAATGGCGGTTGATGGGTTCTAATTT 2521 TGGATGGAGTCCAGGGAAGAGAAAGTGATTTCTAGAAAGCCTGTTCCCCTCACTGACGA 2581 AATAACTCCTTGTAGTAGTCTCATTACTTTTGAAGTAATCCCGCCACCTATCTAGTGGGA 2641 GAGCCATCCAAATGAGAAACCTAAAATATAATTGGTTCTTGGTAGAGATTCATTATTTCTCC 2701 ACTTTGTTCTTTAGGAGATTTTAGGTGTTGATTTTCTGTTTTATTTTAACTCATACCTTT 2761 AAAGGAATTCCCCAAAGAATGTTTATAGCAAACTTGGAATTTGTAACCTCAGCTCTGGGA 2821 GAGGATTTTTTTTCTGAGCGATTATTATCTAAAGTGTGTTGTTTAGGCTCACGGCAC 2881 GCTTGCGTATGTCTGTTACCATGTCACTGTGGTCCTATGCCGAATGCCCTCAGGGACTT 2941 GAATCTTTCCAATAAACCAGGTTTAGACAGTATGAGTAAATGTGCGGTGTAGCCCATACT 3001 TGAGAGTATGAATGTATGTGCACTGTCACTTTGCTCTGGGTGGAAGTATGTTATTGTTGA 3061 CTTATTTTCTCTGTGTTTGTTCCTACAGCCCCTTTTTCATATGTTGCTTGGTCTCCCTTT 3121 CCCTCCTTGGTGCTTACACATTTCAGGCCCTTTAGCCAAACCCTTGCCTACGGCAGTATT 3181 TTAGTTCTCAGTTCTCACCATTCCCTCTGGTCATTGAGCCTTTGGATAAAAACTCATAGA 3241 GCTATGGACTGGGGCTTTGCTGGAAAGGTGGCCTTCCAACTTCACGTCAACTTCTGGCTC 3301 CTCAGTTTGGCAGTAAGGCAGGGAAGTTGTTTTCCCGTTTCTCAGTGACCAGATTGTGAA 3361 TATTTCCCAATGGATTTTCTATTATTAATGTTACTGTAGTTCTTTGTTTTGAAATAAAAA 3421 TTCTGAATGTAAAAAAAAAAAAAAA 1 M D N R Q N V T P A L I F A I T T V A T I 1 ATGGACAACAGACAGAATGTCACCCCAGCTCTGATCTTTGCCATCACAGTTGCTACAATC 21 G S F Q F G Y N T G V I N A P E T I I K 61 GGCTCTTTCCAGTTTGGCTACAACACTGGGGTCATCAATGCTCCTGAGACGATCATAAAG 41 E F I N K T L T D K A N A P P S E V L L 121 GAATTTATCAATAAAACTTTGACGGACAAGGCAAATGCCCCTCCCTCTGAGGTGCTGCTC 61 T N L W S L S V A I F S V G G M I G S F 181 ACGAATCTCTGGTCCTTGTCTGTGGCCATATTTTCCGTCGGGGTATGATCGGCTCCTTT 81 S V G L F V N R F G R R N S M L I V N L 241 TCCGTCGGACTCTTTGTTAACCGCTTTGGCAGGCGCAATTCAATGCTGATTGTCAACCTG 101 L A A T G G C L M G L C K I A E S V E M 301 TTGGCTGCCACTGGTGGCTGCCTTATGGGACTGTGTAAAATAGCTGAGTCAGTTGAAATG	SEQ ID NO:150

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		121 L I L G R L V I G L F C G L C T G F V P 361 CTGATCCTGGGCCGCTTGGTTATTGGCCTCTTCTGCGGACTCTGCACAGGTTTGTGCCC	
		141 M Y I G E I S P T A L R G A F G T L N Q 421 ATGTACATTGGAGAGATCTCGCCTACTGCCCTGAGGGGTGCCTTTGGCACTCTCAACCAG	
		161 L G I V I G I L V A Q I F G L E L I L G 481 CTGGGCATAGTTATTGGAATTCTGGTGGCCCAGATCTTTGGTCTGGAACTCATCCTTGGG	
		181 S E E L W P V L L G F T I L P A I L Q S 541 TCTGAAGAGCTATGGCCGGTGCTATTAGGCTTTACCATCCTTCCAGCTATCCTGCAAAGT	
		201 A A L P C C P E S P R F L L I N R K K E 601 GCAGCCCTTCCATGTTGCCCTGAAGTCCCAGATTTTTGCTCATTAACAGAAAAAAAGAG	
		221 E N A T R I L Q R L W G T Q D V S Q D I 661 GAGAATGCTACGCGGATCCTCCAGCGGTTGTGGGGCACCCAGGATGTATCCCAAGACATC	
		241 Q E M K D E S A R M S Q E K Q V T V L E 721 CAGGAGATGAAAGATGAGAGTGCAAGGATGTCACAGAAAAGCAAGTCACCGTGCTGGAG	
		261 L F R V S S Y R Q P I I I S I V L Q L S 781 CTCTTTAGAGTGTCCAGCTACCGACAGCCCATCATCATTTCCATTGTGCTCCAGCTCTCT	
		281 Q Q L S G I N A V F Y Y S T G I F K D A 841 CAGCAGCTCTCTGGGATCAATGCTGTGTTCTATTACTCAACAGGAATCTTCAAGGATGCA	
		301 G V Q Q P I Y A T I S A G V V N T I F T 901 GGTGTTCAACAGCCCATCTATGCCACCATCAGCGCGGGTGTGGTTAATACTATCTTCACT	
		321 L L S L F L V E R A G R R T L H M I G L 961 TTACTTTCTCTATTTCTGGTGGAAAGGGCAGGAAGAAGGACTCTGCATATGATAGGCCTT	
		341 G G M A F C S T L M T V S L L L K N H Y 1021 GGAGGGATGGCTTTTTGTTCCACGCTCATGACTGTTTCTTTGTTATTAAAGAATCACTAT	
		361 N G M S F V C I G A I L V F V A C F E I 1081 AATGGGATGAGCTTTGTCTGTATTGGGGCTATCTTGGTCTTTGTGGCCTGTTTTGAAATT	
		381 G P G P I P W F I V A E L F S Q G P R P 1141 GGACCAGGCCCCATTCCCTGGTTTATTGTGGCCGAACTCTTCAGCCAGGGCCCCCGCCCA	
		401 A A M A V A G C S N W T S N F L V G L L	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1201 GCTGCGATGGCAGTGGCCGGCTGCTCCAACTGGACCTCCAACTTCCTAGTCGGATTGCTC	
		421 F P S A A Y Y L G A Y V F I I F T G F L	
		1261 TTCCCCTCTGCTGCTTACTATTTAGGAGCCTACGTTTTTATTATCTTCACCGGCTTCCTC	
		441 I T F L A F T F F K V P E T R G R T F E	
		1321 ATTACCTTCTTGGCCTTTACCTTCTTCAAAGTCCCTGAGACCCGTGGCAGGACTTTTGAG	
		461 D I T R A F E G Q A H G A D R S G G K D G	
		1381 GATATCACACGGGCCTTTGAAGGGCAGGCACACGGTGCAGATAGATCTGGGAAGGACGGC	
		481 V M G M N S I E P A K E T T T N V -	
		1441 GTCATGGGGATGAACAGCATCGAGCCTGCTAAGGAGACCACCACCAATGTCTAA	
WBC032D03.bFSP_20012510.abd	Homo sapiens hypothetical protein MGC12966, mRNA	1 CGGCCAGGCTGGTACAGGCGGCTGCTCGCGGAGGCACTTCTCCGAGCGTGACGTGCGGAC	SEQ ID NO:151
		61 TCCGCTCCACTGCGGCCCGCCCGCCGGTCTAGCCGCCGCCTCCTTCGCTCCCTGAG	
		121 CACGCCAGGCGAGGGTCAGCTGCCGGGGCGACGCGGCGCGGAGAGGCGGGCGGGGGGC	
		181 TGTGGGAGCGCCGGTCTCTATATGGCGGCGGCTCTGTCGGGCCTGGCTGTCCGGCTCTCG	
		241 CGCTCGGCCGCCGCCCGCTCCTATGGGGTCTTCTGCAAGGGGCTGACTCGCACGCTGCTC	
		301 ATCTTCTTCGACCTGGCCTGGCGGCTGCGTATCAACTTCCCCTACCTCTACATCGTGGCT	
		361 TCCATGATGCTCAACGTCCGCCTGCAGGTTCATATTGAGATCCATTGAAGGCCCTCCCAG	
		421 ACTGACGAAGGCGTGACCTCAGGCCCACCGCATCCAAGAACACGAAGCATGAGGACAGA	
		481 AGAGGGCCCCCTCGGCACCTGCCTGGCACAAGTGCAGCAGGCCGGAGGAGGTGACTCGGAC	
		541 AAACTATCATGCAGCCTTAAGAAAAGAATGCCGGAGGGCCCTTGGCCTGCAGATGCACCC	
		601 TCCTGGATGAATAAGCCTGTGGTTGATGGAAATTCACAAAGTGAGGCATTATCACTGGAA	
		661 ATGAGAAAGGATCCGAGCGGGGCTGGCCTCTGGCTTCACAGTGGCGGCCCAGTGCTTCCA	
		721 TATGTGAGAGAATCAGTAAGAAGAAATCCAGCCTCAGCAGCCACTCCGAGCACAGCCGTG	
		781 GGTTTGTTCCCTGCTCCAACAGAGTGTTTGCTCGGGTGTCCTGCAGTGGTGTTGAAGCT	
		841 CTGGGGCGGCGAGACTGGCTGGGAGGAGGGCCCAGGGCCACTGACGGCCACAGAGGACAG	
		901 TGCCCCAAAGGAGAGCCTCGGGTGTCACGACTGCCACGCCATCAAAAAGTGCCGGAAATG	
		961 GGAAGTTTTCAGGATGACCCACCAAGTGCTTTTCCCAAGGGTCTGGGCTCTGAGTTGGAA	
		1021 CCCGCTTGCCTGCACTCCATCCTGTCTGCAACGCTGCACGTGTATCCCGAAGTGCTCCTG	
		1081 AGTGAGGAGACAAAACGCATTTTCCTTGACCGTTTAAAGCCCATGTTTTCAAAGCAAACA	
		1141 ATAGAATTCAAGAAAAATGCTTAAAAGCACCTCAGATGGTCTGCAGATGACACTGGGCTTG	
		1201 CTGGCTCTACAAGCTTTTGAATTAGCAAAGCCGTCACGCCATAGTTAAGGTACAAGCAGA	
		1261 ACAATAAAAATAGTGAGATTAATTTTAAAAATTGTCCTAGAATGATTTCTTTTGCATTAA	
		1321 ATCTGGCTGCAGACAGTGCAGCCCTTAGGTTCCTGCTGTAGTTTTGTACGACCTGGCAGA	
		1381 CTTAAGTAAATTGAGTTTAAATTCAAGCCAGTTGATGCGGAAGGAACTTTTTTGGCAT	
		1441 GTGTTAAATTGTGCTTTAAAAGACATATAAAGAATTGGGAAACATTTCAGGAGACGATCA	
		1501 TAGCCTGTATAAATACCAGATTAGAACATACGGATTTACCATGAAGTTCTGTCTTCAACA	
		1561 TCCATTCTAAAGGGCTACTGTCCCAAATCCTGTGTGTCCTTTTGACTTGTCTGATCACCC	
		1621 AATGGAAGTGGATACTTGTAAGTCTACACCACTGTACTTGGCGTTAAATCTTGCTGAGT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1681 TGCTGGTAGGCTGTTACCATTTCTGCGTTTTGTAAAATAATTTGGTCTGCAGCAATACT 1741 TGATTTCTTTTTCTCACATCCCTTTCCTTCCGCTTGAAATGTGATTTAAATGGAGGCCCTA 1801 CGGTGAAAGTTGCAATATTAACTTACTTTTAGAATAGTCCTTCCTCAAACTAGGAACCC 1861 TAGCAGTGTTACCTTAAACAAAAATGAGCTCGAGAAAAAAGTAGCTCAGTTACAGAGAAG 1921 CAAATCGAGTTATTTCCCACATAAAAAGTTTCCCAGATTCTAGAAATTGCAGTATCCTGT 1981 ACCCTAAAATTTTTCAAGGTGACTCCTGTTGTCGTCTGTTGATAACTTTAATAAAGGTCA 2041 TTTAAGGACATAAGTTTTTAAAGACTCCCAAAGTGAAACTTAAACATTTTCGGGATTATC 2101 GATTGCATATATATCAGTTTATGCTGTGTGCTGAATATTACTACACCGTGTGCTATTTTAGT 2161 GTTTTGGGAAAATGAAAAATAAAATCTGTTCTTTTAGCTTAAAAAAAAAAAAAAAAAAAA 2221 AAAAAAAA	
		1 M A A A L S G L A A V R L L S R S A A A A R S 1 ATGGCGGCGGCTCTGTCGGGCCTGGCTGTCCGGCTCTCGCGCTCGGCCGCCCGCCCGCTCC 21 Y G G V F C K G G L T T R T T L L I F F D L L A W 61 TATGGGGGTCTTCTGCAAGGGGCTGACTCGCACGCTGCTCATCTTCTTCGACCTGGCCTGG 41 R L R I N F P P Y L Y I V A S M M L N N V R 121 CGGCTGCGTATCAACTTCCCCTACCTCTACATCGTGGCTTCCATGATGCTCAACGTCCGC 61 L Q V H I E I H - 181 CTGCAGGTTCATATTGAGATCCATTGA	SEQ ID NO:152
WBC032H02.bFSP_20012510.abd	Homo sapiens mRNA; cDNA DKFZp686H1588	1 TCACTTCCGGCGTGCCTACGCCTCCTCTTGCGCTGTCCTGTTAATGGCGGGCAGTAGCCG 61 CTGAGGGGATTGCAGATAACCGCTTCCCGCACGGGGAAAGTCTACCCTGCCTGCCACTTT 121 CTGCTCGCCGTCAGCGCCGGAGCTCGCCAGCATGTCTGTGGTACCGCCCAATCGCTCGCA 181 GACCGGCTGGCCCCGGGGGGTCACTCAGTTCGGCAACACAAGTACATCCAGCAGACGAAGCC 241 CCTCACCCTGGAGCGCACCATCAACCTGTACCCCTCTTACCAATTATACTTTTGGTACAAA 301 AGAGCCCCCTCTACGAGAAGGACAGCTCTGTTGCAGCCAGATTTCAGCGCATGAGGGAAGA 361 ATTTGATAAAATTGGAATGAGGAGGACTGTAGAAGGGGTTCTGATTGTACATGAGCACCG 421 GCTACCCCATGTGTTACTGCTGCAGCTGGGAACACAACTTTCTTCAAATTACCTGGTGATGA 481 ACTTAACCCAAGAGAATATGAAGTTGAAGGACTAAAACGCTTAGTGACTGATATACTGGG 541 TCGTCAAGATGGAGACCTGCAAGACTGGGTCACTGATGACCGCATTGGTAACTGGTGGAG 601 ACCAAATTTTGAACCTCCTCACTATCCATATATTCCTGCACACAGTACAAAACATAAGGA 661 GCATAAGAATTTGTTTCTGGTTCAGCTTCAAGAAAAAGCCTTGTTTGCAGTCCCTAAAAA 721 TTACAAGCTGGTAGCTGCACCATTGTTTGAATTGTATGACAATGCACCAGGATATGGACC 781 CATCATTTCTAGTCTCCCTCAGCCGTTGAGCAGGTTCAATTTTATTTACAACTGAATTCC 841 TGCGCAGTGGAGAAGTAAAGAAGCCGCTTGTCTCTGTGAGCACAGCTATATACAGTGTA 901 GAATAAATGTGGTAGAAAAGTTTTTTGGTTTTATCTCTTTTGCGATCCCTAAATTGCCA 961 CCTTTCTATTGTTTGAATAGTAAAATTAATATGAAGAACTAGATAGTGGTGTAAACAAAT 1021 GTGATAATGTTTATTTACTTTCGGTTCTGCTCATACTTTTTTGTACAACATTAAAGAAAA 1081 TGGACTTTTTTTATTTTAATTTCTCATTAAACTTCTAAAATTCTTATAGGTGAGGATCAT	SEQ ID NO:153

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1141 TTTTCCCCCCCACCTTAGGATGGTGAATGTTGCAACACAATGACAGGTTTAAGTCAGTCAA	
		1201 GTTTATTGGACCCTTGCTTTGATACCATTCTTGGCACATACTCCAAGATTGTATTAGAT	
		1261 TTTTGTGATGAAGAGCTTCCATTACTTCTGAAAACTATATTTATCTGAGTGAGTCCAAGG	
		1321 TGCAACTCCTAAATGAATTGTGTTGCAGAGAACTCCCAGTATAATTCACTGACCAGTACA	
		1381 TTTTATAACCATCCAGGCCTTGGTTTGCAAGCAACAGACCTTAAACATACAGGAAACTAT	
		1441 TAAAATTGGCTCGATCAGTAGTCATAGGAATTGGTATAAGAAAGACTCATTTAGAGCTC	
		1501 AGAGTTTTCTTCACATAATGGGGGTATTAATTATTTGTGCTGTTGCGAAATTATGTGTCT	
		1561 TATTCTTAAGCCATGGTAAAAATAGGGATCTGTGAAGGAAATTTCTAAAATTGGATGTA	
		1621 TTAGGTTTTGAACTCTGAGATTGCACAAATATTCAATTAACTTGAAGTTGTGTACATAGA	
		1681 GAAGAAAATTTGGTTTTAGCAAATGACAGAGCCTTCAAAAATATTTTTGGAATAATGTGA	
		1741 ATCAACCGAAAACTGGGGGCAAGGCAGAGGACAGGTTTTCTCAGGTTAAGAGAAAAACGA	
		1801 AATTTTAAAAACTTTAAAAAATACTGATAAATTCGGATCAAATTTGGGGGAATAAAAAAT	
		1861 ATTAGAGCAAAGGAGTTTGCTGGTTGTGTCATTATTTAATGATCAAAGTATAGCATGTAT	
		1921 GCCTTATTACAGACTTGTTGACTATAGGCTTAATGTAAAAAGGAATCTTGCCAGATGTAG	
		1981 CTACTTAAGGAAAAAAGGGTTTTTAATAGAAATGAACTTTTGATTAGTATGGTGCCAGTC	
		2041 ACAGGGCTATTTTCCTGAATATTGGGTGATGTCAAAGGTATATGATACTTGAGGAAATCA	
		2101 GGCCAAGTGTAGCTGAGCAATTAATAAACACTCAAGTTTTTTTAGTTGGGGTCATGTCAA	
		2161 ACCCTCACATGGTGGTTAAGTAGTGACTAACTGTGCATGTCCTTCATGGTAGGTGAGCAC	
		2221 CAGTCTCCATGATCAAAAATGCCCCAGTTTCCTTTGAAAAAGCCACTAGTTCTGTGAATT	
		2281 GTCCTTTTCCCCTCCTGCCCCTAACAGTCCTACCCCTCTAGCCTACATTAGCATATTTCTC	
		2341 ATGTAATGTATTTTGCTGGTAAGCTCATCCATTAGCTGCGTCCTTCAGCTATTCCTTTAG	
		2401 ATTGGAGGAAGTGGATATGAAGATGGATTGATTCAGCTCACCTTCCATGATTGCTTTTGA	
		2461 GGGAAAAGCTACAGTGGCCACATTTCAGATGTTCACTTTTGCAATTTGTGGAGGGTGGAG	
		2521 AGAGGTAGACTTTTGTTGTGTTTTATAAAGTACTCTCAGTAAGGAGTGTTTGAGTTGA	
		2581 AGAGTCATCTGATTCGAGGCCACTCATGTTCTTTGTAACTTAAACTTTGACCAAGAAATT	
		2641 CTTCACTTCTCACTTCTTCACTTCCTTCCCAATATACAGTAAGTACGTGAGCCAGTCATCC	
		2701 ATACACTAAGGCCTAGTTGAGAAAAACCTTTGATTCAGGATGGCTGGGTTACTAACCTTG	
		2761 AAATGTAAGAGATCTGGTTTTTGGATGTAAAAGTTGCAACACACAAACGGAAGTCTTAAAA	
		2821 ACTTTTTGCTCTGGTCAGTTACAGGTGGATCCCCAATAATCTGTTTTTGGTTTCTGATG	
		2881 GAAATAATAGAATTAGGGGAAATCAAATCTGGTTGGTAGGTGTCTACAGTATTAGAAGAG	
		2941 GGTATAAGGGCACTGTTTAACACTAAGTTCTAATACTTCCAGAAACTGTGCATTCCAGAT	
		3001 CTACATACTAAATGCTCTTATCATTTTGAAATGGGCTCTTGATTAATAGACCCATATTTT	
		3061 TTAGTGGCTTCTATGTTGTATATTTGTCTAAAATGAAAGCTCTTTTGCGTTCTAAAACTA	
		3121 CAATATATGTCATCTTATTTTCCCTGAGTATCCAAGTATAGTGCAGATTCTATGTAAAAC	
		3181 TACTAAATGACACTGGAATATGTTTAGTAGATTAGGGGGAAAAACTATAAAGGTTTATAC	
		3241 AATTGTTTGTAGTTACATTTAGGATGGACTTATCCCTTTGGAGAAGAGTGAAGTTTGTTT	
		3301 TTTCGCCATGTGATGAAGACCACTGTGATTTTTTAAAAAAGTAGATAATACTTAAAATGG	
		3361 CGTAATAATTCTGCACTTGAATTTGTACTGTTAACAGCACATTTGGAAGATTTTAAAACT	
		3421 TTTTATTGTCTTATAAATAGCATTCACTTATTATTTTGGATATTTAAGGGTTCCATTAAG	
		3481 TTAACACTGTATTTGGACAAAGTGTGACCAAATTAGCCAGTCTGTTTTCTTCCATGTTTA	
		3541 ATTAGAAGTGAGAGGTAGAAGTACTTCAAATTCAACAGGCCAGCAAGCAATCGGCTTAAA	
		3601 ATTCCCTTTCTTTAAATGTTGTGCTCTTATGTTCTCCGCTTTTTAATGACTTTATTTTTAC	
		3661 AGTACTTGTTCAGTCACTTGAGATGAAATGCTTGGGGTAGCTTTTCCATCCTCAAACTTA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		3721 ATGTTTTTACTAGTTCATAGTGTTTGGAACAGTATATGCCAATCACTGAGACTGCATCAG 3781 AGTTTGCAATTTTGTATGTTTCATTGCCAAAGAAGGCTTAGTGGTTTGTCACTGTAATAC 3841 GAGTCAGCTTCTGTAGCATAAGGTTTGATTTCCTATAATTCTTCCACTTGTTTTTACATCA 3901 CTTATTATTTGGGTTAAAGTGGCCTCACTTCAAGCAGTTTGCCTTTGTTCTTTAAATATG 3961 TGATGAGAAACAATGCTGTAATTTGACTTGAGCCATAAAACACAATTTTAATATTAGCTT 4021 GTATTATATTTATCAAGGTTGTTTTGTGAAAAAACAGGCTAAAACCTAAGTAAGTCTAG 4081 ATTAAGCCAGGTTAGCTGTAATTTGTATTTTAGTGATGGATTGTATTGTAAGACTAGAGA 4141 TAAATTGGGAAAATGTATTATGCTTTTCTGTTGAGGAGAGATCAGTGCATTTAAAAACT 4201 TCAACTTTTGCTTACTGTGCTCACATCATAGTGTACAAGCGTCATTTATAGTTTGGCTTT 4261 GAGGATTTTTCTGGCATTAAGTTTATAGAAATGTATAAAGAAAGTGTTTGAAGTTTTGG 4321 TTATATTTTTATATTTGTAAAGTAAGTTTGGTTAAAGTGATCACTGTTCTTTTTTATTT 4381 TATTGTCATTTCAATAAAAAATATTTGAAAGAGAAAAAAAAAAAAAAAAA 1 M S V V P P N R S Q T G W P R G V T Q F 1 ATGTCTGTGGTACCGCCCAATCGCTCGCAGACCGGCTGGCCCCGGGGGTCACTCAGTTC 21 G N K Y I Q Q T K P L T L E R T T I N L Y 61 GGCAACAAGTACATCCAGCAGACGAAGCCCCTCACCCTGGAGCGCACCATCAACCTGTAC 41 P L T N Y T F G T K E P L Y E K D S S V 121 CCTCTTACCAATTATACTTTTGGTACAAAGAGCCCCTCTACGAGAAGGACAGCTCTGTT 61 A A R F Q R M R E E F D K L G M R R T V 181 GCAGCCAGATTTCAGCGCATGAGGGAAGAATTTGATAAAATTGGAATGAGGAGGACTGTA 81 E G V L I V H E H R L P H V L L L Q L G 241 GAAGGGGTTCTGATTGTACATGAGCACCGGCTACCCCATGTGTTACTGCTGCAGCTGGGA 101 T T F F K L P G D E L N P R E Y E V E G 301 ACAACTTTCTTCAAATTACCTGGTGATGAACTTAACCCAAGAGAATATGAAGTTGAAGGA 121 L K R L V T D I L G R Q D G D L Q D W V 361 CTAAAACGCTTAGTGACTGATATACTGGGTCGTCAAGATGGAGACCTGCAAGACTGGGTC 141 T D D R I G N W W R P N F E P P H Y P Y 421 ACTGATGACCGCATTGGTAACTGGTGGAGACCAAATTTTGAACCTCCTCACTATCCATAT 161 I P A H S T K H K E H K N L F L V Q L Q 481 ATTCCTGCACACAGTACAAAACATAAGGAGCATAAGAATTTGTTTCTGGTTCAGCTTCAA 181 E K A L F A V P K N Y K L V A A P L F E 541 GAAAAAGCCTTGTTTGCAGTCCCTAAAAATTACAAGCTGGTAGCTGCACCATTGTTTGAA	SEQ ID NO:154

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		201 L Y D N A P G Y G P I I S S L P Q P L S 601 TTGTATGACAATGCACCAGGATATGGACCCATCATTTCTAGTCTCCCTCAGCCGTTGAGC 221 R F N F I Y N - 661 AGGTTCAATTTTATTTACAACTGA	
WBC033A01.bFSP_20020801.esd	Homo sapiens mRNA; cDNA DKFZp686D0662 (from clone DKFZp686D0662).	1 AGTTGGAAAGAGACCACAGACTTTGAGGGAAGCTCACTCAGGATCTGCTCTCCGGCAAAG 61 TAGTAAGTGAGGTGCTGAGAGCAGAATGAGCTACTTTGTGGATTCTGCTGGGAGCAGCCC 121 CGTCCCTTACTCAGCGCCTCGTCCTGCAGTGGTGAGGCAAGGACCTAGCAACACTTATGA 181 AGATCCTCGAATGAACTGTGGTTTCCAGTCCAATTATCACCAGCAAAGACCTTGCTACCC 241 CTTTTGGGATGAGATGGCAACTCAGGAAGTTCCTACTGGTCTTGAACACTGTGTCTCAGA 301 TATGGAATGTGCAGATGTCCCACTATTAACTCCAAGCAGCAAAGAAATGATGTCTCAAGC 361 ATTAAAAGCTACTTTCAGTGGTTTCACTAAAGAACAGCAACGACTGGGGATCCCAAAAGA 421 CCCCCGGCAGTGGACAGAAACCCATGTTCGGGACTGGGTGATGTGGCTGTGAATGAATT 481 CAGCCTGAAAGGTGTAGACTTCCAGAAGTTCTGTATGAATGGAGCAGCCCTCTGCGCCCT 541 GGGTAAAGACTGCTTTCTCGAGCTGGCCCCAGACTTTGTTGGGGACATCTTATGGGAACA 601 TCTAGAGATCCTGCAGAAAGAGGATGTGAAACCATATCAAGTTAATGGAGTCAACCCAGC 661 CTATCCAGAATCCCGCTATACCTCGGATTACTTCATTAGCTATGGTATTGAGCATGCCCA 721 GTGTGTTCCACCATCGGAGTTCTCAGAGCCCAGCTTCATCACAGAGTCCTATCAGACGCT 781 CCATCCCATCAGCTCGGAAGAGCTCCTCTCCCTCAAGTATGAGAATGACTACCCCTCGGT 841 CATTCTCCGAGACCCTCTCCAGACAGACACCTTGCAGAATGACTACTTTGCTATCAAACA 901 AGAAGTCGTCACCCCAGACAACATGTGCATGGGAGGACCAGTCGTGGTAAACTCGGGGG 961 CCAGGACTCTTTTGAAAGCATAGAGAGCTACGATAGTTGTGATCGCCTCACCCAGTCCTG 1021 GAGCAGCCAGTCATCTTTCAACAGCCTGCAGCGTGTTCCCTCCTATGACAGCTTCGACTC 1081 AGAGGACTATCCGGCTGCCCTGCCCAACCACACAAGCCCAGGGCACCTTCAAGGACTATGT 1141 GCGGGACCGTGCTGACCTCAATAAGGACAAGCCTGTCATTCCTGCTGCTGCCCTAGCTGG 1201 CTACACAGGCAGTGGACCAATCCAGCTATGGCAGTTTCTTCTGGAATTACTCACTGATAA 1261 ATCCTGTCAGTCTTTTATCAGCTGGACAGGAGATGGCTGGGAATTCAAACTTTCTGACCC 1321 AGATGAGGTGGCCAGGAGATGGGGAAAGAGGAAAAACAAACCTAAGATGAATTATGAGAA 1381 ACTGAGCCGTGGCCTACGCTACTATTACGACAAAAACATCATCCACAAGACAGCGGGAA 1441 ACGCTACGTGTACCGCTTTGTGTGTGACCTGCAGAGCCTGCTGGGGTACACCCCTGAGGA 1501 GCTGCACGCCATGCTGGACGTCAAGCCAGATGCCGACGAGTGATGGCACTGAAGGGCTG 1561 GGGAAACCCTGCTGAGACCTTCCAAGGACAGCCGTGTTGGTTGGACTCTGAATTTTGAAT 1621 TGTTATTCTATTTTTTATTTTCCAGAACTCATTTTTTACCTTCAGGGTGGGAGCTAAGT 1681 CAGTTGCAGCTGTAATCAATTGTGCGCAGTTGGGAAAGGAAAGCCAGGACTTGTGGGGTG 1741 GGTGGGACCAGAAATTCTTGAGCAAATTTCAGGAGAGGGAAGGGCCTTCTCAGAAGC 1801 TTGAAGGCTCTGGCTTAACAGAGAAAGAGACTAATGTGTCCAATCATTTTTAAAATCAT 1861 CCATGAAAAAGTGTCTTGAGTTGTGGACCCATTAGCAAGTGACATTGTCACATCAGAACT 1921 CATGGAACTGATGTAAGGCAATTAATTTGCTTCTGTTTTTAGGTCTGGGAGGGCAAAAAA 1981 GAGGTGGGTGGGATGAAACATGTTTTGGGGGGGGATGCACTGAAAATCTGAGAACTATTT 2041 ACCTATCACTCTAGTTTTGAAGCAAAGATGGACTTCAGTGGGAGAGGGCCAAAACCGTTG 2101 TTGTGTTAAAATTTATTTTTATTAAATTTTGTGCCAGTATTTTTTTTCTTAAAAATCGTCT	SEQ ID NO:155

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2161 TAAGCTCTAAGGTGGTCTCAGTATTCGCGGTATCATGCAAGTTGGTTTTTATTTGCTGGC	
		2221 TGAGGATTCTGTCACAGTGAAAGAAAACTGTTTATATAGACCCCACTGGAAACGCAAAGG	
		2281 GCTGTCACTGAGATCGGGGATCCCAAATTCATGTGACTTATGTATGAAGGAAAAAATAAT	
		2341 GCTGATCTGAGTGCAAGGGAACTGTGCATGTGAATTTCATCTATAATTTAAAGAAGTTAT	
		2401 CACACCCTCTACTTATTTGCCATTAGTGAATTCTCGGGGTTTGGACTTAACGTTGAGCTA	
		2461 AGAAGCATTAAGTCTTTGAACTGAATGTATTTTGCAGCCCTGGTTTTGGACCACAGTAAA	
		2521 TGTAGGAGCTCTGTTGACACCATGGAAAGGAGGTCAAAGGAGGAACATTGACTTGGTTGT	
		2581 TTATTGGTTCTATGCCTATAACATGTATGACTTGGAATAAGGCTGTGTGCATGGGCATT	
		2641 ACCCCTCAGGTCTCAAGAAATAAGTCCTGAATGCATGTCATTCCGAACTAACACTCTACA	
		2701 CTTTCTCCTTTATGTTTTATTTTCCAAGAGTCCTCCATTTTTTGCACCCCCTCACCGCCA	
		2761 ACTCTGTTATTCAGTAGAGAGAAATGTACAGCTTTCTGATTGATGAGTGAAAAAGTAACT	
		2821 TGAGACACGACCTAAGTTGAAGAGTTTAGACTTGCTGAGTTTTAGAAGTGATGGAAATTA	
		2881 AGAGAGCATTTCAATAAAATGTGACTTGGCTGTCTTTGGAAGAAGTGCAAGGCTTTCC	
		2941 TTTGAAGAATTTAGGCTAGTTGAATTGGATGTCAGGTGAGAGTGTGTATGCAAAGTGAAT	
		3001 GGCACAGGTGATGCCAGGGCCTCTTGCTTGGGTCTGATGTCTTGGCACAGGGTAAGTGAA	
		3061 GGTTAATTCCAGAAGAGGAATGACTTGAAGGCAAAGGAAACTAAGGAAGGAGGTTCAG	
		3121 TGAGGAAAATAAGGTTGTCCATGAGATTTGAATAGATTTTTAGTTCCCCCAAGGTTTAAA	
		3181 TACAAACATAGTCAAGCAAGGTAGTCATCTTTCTGCTGGTTGTGAGGGGGAATCTGAAAA	
		3241 TGGAGTTTTAGAGGAAAAGTCAACATCTAACTATGTGAGGAAAAGTGCCTAATACAATTAG	
		3301 AATCTCCCTCACTCTATAGTTGCCCAGTTGAACGGATAAGGAGGAGGGGTGGCTTTTATG	
		3361 GACTTCCATGAGAGAAGGAAAGAAATATTTCAGGTAAGCTTCTCAGGGCTGGCCCTTTTT	
		3421 GGGATTTGGATGAGAAATTGGAAGTACTAACTACATTCTTCTAGCATATCTTTAAGAAAATTG	
		3481 ATTGTTATTTACTCCCAGATCCTCTTGCAGACCCAGAATTATCAGGAACATAGCTCTGTG	
		3541 ATTCATGAGTGTCCCCATACTGATGAATTGGAGCATCCATATGGAAAGCAAAGGCAGAAT	
		3601 TATCCCAGCTGTATTATTTTGATCTTTTGGATGCAGGTGCCTTAATGAAGCTCTCAAAAT	
		3661 ATTTTAGGAGCTGCTCAGGGAGTGTTGGGTGGAACTGTTTGGACTACATTGTTTTCTCTT	
		3721 AGATTATGTGATTTTTGTTGGGCACTGGCAAAAGGTGTGTGTGTGAATGTGTGCATGTGT	
		3781 GTGAATGTTGTGTGTGTGTGTGTGCGTGTTTGTGTGTGTGTGTGTGTTTG	
		3841 CAGACATGCAAAACTGCAGCTGAAATAATACCTTAGATTTCTAGGTAAGTCTTTCCACAT	
		3901 TTCAATAATGGGTAAGAGTAGAACCAGGGCCGGGTATCAATTATTGCTTGCTGTTTGCAA	
		3961 CCAGGCATAAAATCACTTTCTCAAATCATCCACCGTTCCTATTAAATTTATGCCGGAAAC	
		4021 ACTCCTTCTGTGAGTATAACTCCTGCAGTTCCTATAGCAGATAAGATATAAGAAAGTGCC	
		4081 TCCTAGTGCTCCTCCGCCCGCTTGTTTGCTAAAATTCCCTTTCTCTCTAAGTCCACCATT	
		4141 TTCAAGATTTGTAGATAGTGTATTAGTTAAGACAGCTTTGTCGATCTGGCCAGATGTTTT	
		4201 TTCTCCTTTGTCCAAAGGCCAGAGACCATCCCAGGAAGAGTGGTGGGTGGTTTATACACT	
		4261 GGAAAATGTTGCGTTTATGCTTTTTAAAAACACACGTTAACTTCAGAGGAAGGATGGCAA	
		4321 ATCTGGTCTAGCTGGGTGAAACCCTTATTTTCCCAGAGATGCCTTAACCTTTGTTGGTTT	
		4381 TGGCTTTAGGGTTCAGAGTCACTTTTGTTCCCTTCTCCATTCTGGAGAGGGACTTCCCCT	
		4441 ACATAGAGCCCTGATTTTTGTGGCTGTGGGGATTGGAGGTAGCATTCAAAGATCAGATGT	
		4501 GCTTTTCCTCACTTTGGAGATGAACACTCTGGGTTTTAGAGCATTAACCTGCCTAATCTT	
		4561 CATGGTGAAAATTACACCTTCTCTATTCTAGTCATGCTGTGCATGCTGCTGTCTCTGTTG	
		4621 GGGTCTATATAAATGTGTTGAAATGGTATCTACATTCCAAAGAAGTTTCAAGGAACCATA	
		4681 AATATATGTATACATATACATATATAAAATATATATTAAAATAAAATTATCAGGAATA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		4741 CTGCCTCAGTTATTGAACTTTTTTTTTTAAGAATACTTTTTTTTTTAAGCTGAGAAGTATA 4801 GGGGTGAAAAAGATGTTTATATTGTGTTTGACTATTTTCCAACTTGTATTTTTCATATAATT 4861 TATATTTTTTAAAAGCTGAAAATTTAAAAGCAAGATGAAAAAAGGAAAAGCAGGTGCTTT 4921 TTAAAAAATCAGAACTGAGGTAGCTTAGAGATGTAGCGATGTAAGTGTCTATGTGTTTTTA 4981 AAAAAAAAATGCAAAAAAAATTCTTATGGGGGAGTTTTTTGTTTGTTTATTTTAGTAGCTGA 5041 TGCTGGCACATCATTTTGCTGGAGATTTTTTTATATACTGTAGCCTGATTTCATATTGTA 5101 TTTTAAACTGTGTGAGATTAAAAACAAAGAATTTCATTCATAAAAAAAAAAAAAAAAAA 5161 AAAAAAAAAAAAAAAAAAAAAAA 1 M S Y F V D S A G S S P V P P Y S A P R R P 1 ATGAGCTACTTTGTGGATTCTGCTGGGAGCAGCCCCGTCCCTTACTCAGCGCCTCGTCCT 21 A V V R Q G P S N T Y E D P R M N C G F 61 GCAGTGGTGAGGCAAGGACCTAGCAACACTTATGAAGATCCTCGAATGAACTGTGGTTTC 41 Q S N Y H Q Q R P C Y P F W D E M A T Q 121 CAGTCCAATTATCACCAGCAAAGACCTTGCTACCCCTTTTGGGATGAGATGGCAACTCAG 61 E V P T G L E H C V S D M E C A D V P L 181 GAAGTTCCTACTGGTCTTGAACACTGTGTCTCAGATATGGAATGTGCAGATGTCCCACTA 81 L T P S S K E M M S Q A L K A T F S G F 241 TTAACTCCAAGCAGCAAAGAAATGATGTCTCAAGCATTAAAAGCTACTTTCAGTGGTTTC 101 T K E Q Q R L G I P P K D P R Q W T E T H 301 ACTAAAGAACAGCAACGACTGGGGATCCCAAAAGACCCCCGGCAGTGGACAGAAACCCAT 121 V R D W V M W A V N E F S L K G V D F Q 361 GTTCGGGACTGGGTGATGTGGGCTGTGAATGAATTCAGCCTGAAAGGTGTAGACTTCCAG 141 K F C M N G A A L C A L G K D C F L E L 421 AAGTTCTGTATGAATGGAGCAGCCCTCTGCGCCCTGGGTAAAGACTGCTTTCTCGAGCTG 161 A P D F V G D I L W E H L E I L Q K E D 481 GCCCCAGACTTTGTTGGGGACATCTTATGGGAACATCTAGAGATCCTGCAGAAAGAGGAT 181 V K P Y Q V N G V N P A Y P E S R Y T S 541 GTGAAACCATATCAAGTTAATGGAGTCAACCCAGCCTATCCAGAATCCCGCTATACCTCG 201 D Y F I S Y G I E H A Q C V P P S E F S 601 GATTACTTCATTAGCTATGGTATTGAGCATGCCCAGTGTGTTCCACCATCGGAGTTCTCA 221 E P S F I T E S Y Q T L H P I S S E E L	SEQ ID NO:156

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		661 GAGCCCAGCTTCATCACAGAGTCCTATCAGACGCTCCATCCCATCAGCTCGGAAGAGCTC	
		241 L S L K Y E N D Y P S V I L R D P L Q T 721 CTCTCCCTCAAGTATGAGAATGACTACCCCTCGGTCATTCTCCGAGACCCTCTCCAGACA	
		261 D T L Q N D Y F A I K Q E V V T P D N M 781 GACACCTTGCAGAATGACTACTTTGCTATCAAACAAGAAGTCGTCACCCCAGACAACATG	
		281 C M G R T S R G K L G G Q D S F E S I E 841 TGCATGGGGAGACCAGTCGTGGTAAACTCGGGGGCCAGGACTCTTTTGAAAGCATAGAG	
		301 S Y D S C D R L T Q S W S S Q S S F N S 901 AGCTACGATATGTTGTGATCGCCTCACCCAGTCCTGGAGCAGCCAGTCATCTTTCAACAGC	
		321 L Q R V P S Y D S F D S E D Y P A A L P 961 CTGCAGCGTGTTCCCTCCTATGACAGCTTCGACTCAGAGGACTATCCGGCTGCCCTGCCC	
		341 N H K P K G T F K D Y V R D R A D L N K 1021 AACCACAAGCCCAAGGGCACCTTCAAGGACTATGTGCGGGACCGTGCTGACCTCAATAAG	
		361 D K P V I P A A A L A G Y T G S G P I Q 1081 GACAAGCCTGTCATTCCTGCTGCCCTAGCTGGCTACACAGGCAGTGGACCAATCCAG	
		381 L W Q F L L E L L T D K S C Q S F I S W 1141 CTATGGCAGTTTCTTCTGGAATTACTCACTGATAAATCCTGTCAGTCTTTTATCAGCTGG	
		401 T G D G W E F K L S D P D E V A R R W G 1201 ACAGGAGATGGCTGGGAATTCAAACTTTCTGACCCAGATGAGGTGGCCAGGAGATGGGGA	
		421 K R K N K P K M N Y E K L S R G L R Y Y 1261 AAGAGGAAAAACAAACCTAAGATGAATTATGAGAAACTGAGCCGTGGCCTACGCTACTAT	
		441 Y D K N I I H K T A G K R Y V Y R F V C 1321 TACGACAAAAACATCATCCACAAGACAGCGGGAAACGCTACGTGTACCGCTTTGTGTGT	
		461 D L Q S L L G Y T P E E L H A M L D V K 1381 GACCTGCAGAGCCTGCTGGGGTACACCCCTGAGGAGCTGCACGCCATGCTGGACGTCAAG	
		481 P D A D E - 1441 CCAGATGCCGACGAGTGA	
WBC033D12.bFSP_20020801.esd	No Homology	1 AGGGCCTGGGAAGCCCTAACAATCCTGCTGCTGTCACGGCAGCCCCACAGGGACCCCACA	SEQ ID NO:157

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		61 CACTGCCCTGGGCAAGGACAGTGAGCTGTGCCCAAGGTCCAGATTGGCTGAGGCTCCTCC 121 CACCGCTCCTGTCCTCGCCAAACTCAGCTTCTCTGGACTGTGACGACAGCCCCAGGGCTG 181 GCTACCCTGACTGCCTCCCGCCTCCAGTGTGATGCATTTTGTACCCCCTTACTTTTTAT 241 TTATTTATTCTTGCTGAGGAAGATTGGCCCTGAGCTAACATCTGTGCCAGTCTTCCTCTA 301 TTTTTGTATGTGGGTCGCTGCCACGGCACCACTGATGAATGGTGTAGGTCCGCACCCAGG 361 ATCTGAATCTGAACCGTGTGTACCCCTTTATTTTTTCACAATACATGTCCCACATGGAAA 421 AACAGAACATTCTGGTAAGAAAAAAATAATTACAGTCAAACCTCCAAACCCAAAAAACCC 481 TACGCAGTGACTTAATATTTCTGTGTGAATCTTTCCAGGTTTTCACACTCTGAGTACACA 541 GACACACACACCTGTGCACGTGCACACACATGCCTTANAAAATTATAGTGGTTTGTTACC 601 TGTTAGGGTGTTTTAGCTTATTTAATCCTGGACGTGAAACAGGGTAAGCTGCCGTTTCTG 661 AGGGCTGCATGGCTTACACAGCGTGAACGTACCATAATTTTAAAATGCTCATGTCTTCAT 721 TTGCTTATCCAAGTGTAATTTAGAAGTGAAATTGCTGAGACAGAAGAAAAGAAGTATTTT 781 TAGAATTTTGATACTTACTGCCAAATTTTCTTTCAGGAGTTTGCCCCAGTTTGTTGTCC 841 CTTCGGTGGTGTATGAAACTGTTTGTTTCCCATAACTGAGCCTACGTGAGATATTTATA 901 TTGTCTTAATACCTTCCAATTTTATAAAGGAAAATAGTCTCTTGTTTCATTATGCATTC 961 CTTTGGTTACTTGTGATTTGAATGTGTTTTTACTTGTTTAATGGCTTTTTTTCTTTTGGC 1021 AGATTGCTTCAGAGACATGTGAAATCTTCACATATGAAAATGTGTCACTCGCTTTCTTCT 1081 GCAACTCTCTAGTGTCAGCGTGTAGAGCCCAATACTTCCCAGTATTTTCTAAGACTTTAA 1141 CGTTTTCTTCCTACCTTTGATTTTTAAGTAGTATTTATTTTCAACCTACTTGAACTATAT 1201 TTTGGAATAAAATGTGAACTATAGAGCTAGATTGATTTGTTTATTTAAGTTAATAAATTA 1261 GAATGGCCCTTCTTTTGTTTTGGTATCAGTAAAAAAAAAAAA	
WBC035E01.bFSP_20020901.abd	Homo sapiens splicing factor, arginine/serine-rich 2, mRNA (cDNA clone MGC:5480 IMAGE:3452024).	1 CTGCGGAGCCCGTCCGTGCTGTTCTACGGCAAGGCCTTTCCCAGTGTCCCCACGCGGAAG 61 GCAACTGCCTGAGAGGCGCGGCGTCGCACCGCCCAGAGCTGAGGAAGCCGGCGCCAGTTC 121 GCGGGGCTCCGGGCCGCCACTCAGAGCTATGAGCTACGGCCGCCCCCTCCCGATGTGGA 181 GGGTATGACCTCTCTCAAGGTGGACAACCTGACCTACCGCACCTCGCCCGGGACCGCTGAG 241 GCGCGTCTTCGAGAAGTACGGGCGCGTCGGCGACGTGTACATCCCGCGGGACCGCTACAC 301 CAAGGAGTCCCGCGGCTTCGCCTTCGTTCGCTTTCACGACAAGCGCGACGCTGAGGACGC 361 TATGGATGCCATGGACGGGGCCGTGCTGGACGGCCGCGAGCTGCGGGTGCAAATGGCGCG 421 CTACGGCCGCCCCCCGGACTCACACCACAGCCGCCGGGGACCGCCACCCCGCAGGTACGG 481 GGGCGGTGGCTACGGACGCCGGAGCCGCAGCCCTAGGCGGCGTCGCCGCAGCCGATCCCG 541 GAGTCGGAGCCGTTCCAGGTCTCGCAGCCGATCTCGCTACAGCCGCTCGAAGTCTCGGTC 601 CCGCACTCGTTCTCGATCTCGGTCGACCTCCAAGTCCAGATCCGCACGAAGGTCCAAGTC 661 CAAGTCCTCGTCGGTCTCCAGATCTCGTTCGCGGTCCAGGTCCGGTCTCGGTCCAGGAG 721 TCCTCCCCCAGTGTCCAAGAGGGAATCCAAATCCAGGTCGCGATCGAAGAGTCCCCCAA 781 GTCTCCTGAAGAGGAAGGAGCGGTGTCCTCTTAAGAAAATGATGTATCGGCAAGCAGTGT 841 AAACGGAGGACTTGGGGAAAAAGGACCACATAGTCCATCGAAGAAGTCCTTGGAGCGA 901 GCAGCTGGCTACCGAAAGGTTATTTTGTAACATTTGTCTAACTTCTTACTTGTTTTAAGC 961 TTTGCCTCAGGCGGCAAACTTCATTTTATGTGCCATTTTTGTTGCTGTTATTCAAATTTCT 1021 TGTAATTTAGTGAGGTGAACGACTTCAGATTTCATTATTGGCTTGGATATTTGAGGTAAA 1081 ACTTCCTTTTTGTTTATATAGTGCTGACTTTTTTTGTTTGAAATTGAACAGATTGGTAAC 1141 CTAAATTGTGGCCTCCTGACTTTTTAAGGAAACGTGCAGCCATTACACACAGCCTAAAGC	SEQ ID NO:158

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1201 TGTCAAGAGATTGACTCAACATTGCCTTCATTCCTTAAAATTAAAACCTACGAAAGTTGG 1261 TGTAAATTTGTTTGTATATGTTATTTACCTGCAGATCTAAATGGTAATCTGAACCCAAAT 1321 TTGTGTAAGACTTTTTCAGGTGAAAAGACTTGATTTTTTTGAGAGGATTGTTGACCAAACA 1381 CAATTCTAATCTCTTCTCTTATGTATTTTTGTGCACTAGGCGCAGTTGTGTAGCAGTTGA 1441 GTAATGCTGGTTAGCTGTTAAGGTGGCGTGTTGCAGTGCAGAGTGCTTGGCTGTTTCCTG 1501 TTTTCTCCTGATTGCTCCTGTGTAAAGATGCCTTGTCGTGCAGAAACAAATGGCTGTCCA 1561 GTTTATTAAAATGCCTGACAACTGCACTTCCAGTCACCCGGCCTTGCATATAAATAACG 1621 GAGCATACAGTGAGCACATCTAGCTGATGATAAATACACCTTTTTTTCCCTCTTCCCCCT 1681 AAAAATGGTAAATCTGATCATATCTACATGTATGAACTTAACATGGAAAATGTTAAGGAA 1741 GCAAATGGTTGTAACTTTGTAAGTACTTATAACATGGTGTATCTTTTTGCTTATGAATAT 1801 TCTGTATTATAACCATTGTTTCTGTAGTTTAATTAAAACATTTTCTTGGTGTTAGCTTTT 1861 CTCAGAAAAAAAAAAAAAAA	SEQ ID NO:159
		1 M S Y G R P P P D V E G M T S L K V D N 1 ATGAGCTACGGCCGCCCCCTCCCGATGTGGAGGGTATGACCTCTCTCAAGGTGGACAAC 21 L T Y R T S P D T L R R V F E K Y G R V 61 CTGACCTACCGCACCTCGCCCGACACGCTGAGGCGCGTCTTCGAGAAGTACGGGCGCGTC 41 G D V Y I P R D R Y T K E S R G F A F V 121 GGCGACGTGTACATCCCGCGGACCGCTACACCAAGGAGTCCCGCGGCTTCGCCTTCGTT 61 R F H D K R D A E D A M D A M D G A V L 181 CGCTTTCACGACAAGCGCGACGCTGAGGACGCTATGGATGCCATGGACGGGGCCGTGCTG 81 D G R E L R V Q M A R Y G R P P D S H H 241 GACGGCCGCGAGCTGCGGGTGCAAATGGCGCGCTACGGCCGCCCCCGGACTCACACCAC 101 S R R G P P P R R Y G G G G Y G R R S R 301 AGCCGCCGGGGACCGCCACCCCGCAGGTACGGGGGCGGTGGCTACGGACGCCGGAGCCGC 121 S P R R R R R S R S R S R S R S R S 361 AGCCCTAGGCGGCGTCGCCGCAGCCGATCCCGGAGTCGGAGCCGTTCCAGGTCTCGCAGC 141 R S R Y S R S K S R S S R T R S R S T 421 CGATCTCGCTACAGCCGCTCGAAGTCTCGGTCCCGCACTCGTTCTCGATCTCGGTCGACC 161 S K S R R S A R R R S K S S S S V S R S R 481 TCCAAGTCCAGATCCGCACGAAGGTCCAAGTCCTCGTCGGTCTCCAGATCTCGT 181 S R S R S S R S R S P P P V S K R E S 541 TCGCGGTCCAGGTCCCGGTCTCGGTCCAGGAGTCCTCCCCCCAGTGTCCAAGAGGGAATCC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		201 K S R S R S K S P P K S P E E E G A V S 601 AAATCCAGGTCGCGATCGAAGAGTCCCCCCAAGTCTCCTGAAGAGGAAGGAGCGGTGTCC 221 S - 661 TCTTAA	
WBC036E08.bFSP_20021001.abd	Homo sapiens annexin A2, mRNA	1 GCTCAGCATTTGGGGACGCTCGCAGCCCTCGGCGTCCGGCCCAGCTTCTATCAAAATGTC 61 TACTGTTCACGAAATTCTGTGCAAGCTCAGCTTGGAGGGTGATCACTCTACCCCGGCAAG 121 TGCTTACGGGTCAGTCAAGGCGTACACCAACTTCGATGCCGAGCGGGATGCGCTGAACAT 181 TGAAACAGCCATCAAGACCAAAGGTGTGGACGAGGTCACCATCGTCAACATTCTGACCAA 241 CCGCAGCAATGAACAGAGACAAGATATTGCCTTCGCCTACCAGAGAAGGACCAAAAAGGA 301 GCTTGCAGCAGCGCTGAAGTCAGCCTTGTCTGGCCACCTGGAGACGGTGATTCTGGCCT 361 GTTGAAAACACCTGCTCAGTATGATGCTTCTGAGCTGAAGGCTTCCATGAAGGGCTGGG 421 GACCGATGAGGACTCCCTCATTGAGATCATCTGCTCAAGGACCAACCAGGAGCTGCAGGA 481 AATTAACAGAGTCTACAAGGAAATGTACAAGACTGATCTGGAGAAGGACATCGTTTCTGA 541 CACATCTGGTGACTTCCGCAAGCTGATGGTTGCCCTCGCAAAGGGTAGAAGAGCAGAGGA 601 TGGCTCTGTCATTGATTATGAACTGATTGACCAAGATGCCCGGGATCTCTATGATGCTGG 661 AGTGAAGAGGAAAGGAACTGATGTTCCAAAGTGGATCAGCATCATGACCGAGCGCAGTGT 721 CTGTCACCTCCAGAAAGTATTTGAAAGGTACAAGAGCTACAGCCCTTATGACATCGTTGGA 781 GAGCATCAAGAAGGAGGTCAAAGGAGACCTGGAAAATGCTTTCCTGAACCTGGTCCAGTG 841 TATTCAGAACAAGCCCCTGTATTTTGCTGACCGACTGTACGACTCCATGAAGGGCAAGGG 901 CACGCGCGATAAGGTCCTGATCAGAATCATGGTCTCCCGCAGTGAAGTGGACATCGTTGAA 961 AATTAGGTCTGAATTCAAGAGAAAGTACGGCAAGTCCCTGTACTACTACATCCAGCAAGA 1021 CACCAAGGGCGACTACCAGAAGGCGCTGCTGTACCTGTTGTGGTGGGGATGACTGAAGCCC 1081 GACACGGCCTGAGCGTCAAGAAATGGTGCTCACCATGCTTCCTGCTAACAGTTCTAGAAA 1141 ACAGCTTGCGACTAACAGCCCCCTTGTGCCCATCCCTGTGAGGATGATGTTAGCCTTGTG 1201 CCCCCATCCTTATTTTAGATGCCTACGCGTTACCCGGCTTTCCCGTCTAGTCTCTCCTTT 1261 TAGCCAAAGAAATGAACATTCCAAGGAGTTGGCAGTGAAATCTATGATGTGAAACACTTT 1321 GCCTCTTTGTGTACTGTGTCGTAAACAGATGAATAAACTGAGTTTTTACTTTAAAAAAAA 1381 AAAAAAA	SEQ ID NO:160
		1 M S T V H E I L C K L S L E G D H S T P 1 ATGTCTACTGTTCACGAAATTCTGTGCAAGCTCAGCTTGGAGGGTGATCACTCTACCCCG 21 A S A Y G S V K A Y T N F D A E R D A L 61 GCAAGTGCTTACGGGTCAGTCAAGGCGTACACCAACTTCGATGCCGAGCGGGATGCGCTG 41 N I E T A I K T K G V D E V T I V N I L 121 AACATTGAAACAGCCATCAAGACCAAAGGTGTGGACGAGGTCACCATCGTCAACATTCTG 61 T N R S N E Q R Q D I A F A Y Q R R T K 181 ACCAACCGCAGCAATGAACAGAGACAAGATATTGCCTTCGCCTACCAGAGAAGGACCAAA	SEQ ID NO:161

Gene Name	GenBank HomoLogy	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		81 K E L L A A A L K S A L S G H L E T V I L 241 AAGGAGCTTGCAGCAGCGCTGAAGTCAGCCTTGTCTGGCCACCTGGAGACGGTGATTCTG 101 G L L K T P A Q Y D A S E L K A S M K G 301 GGCCTGTTGAAACACCTGCTCAGTATGATGCTTCTGAGCTGAAGGCTTCCATGAAGGGG 121 L G T D E D S L I E I I C S R T N Q E L 361 CTGGGGACCGATGAGGACTCCCTCATTGAGATCATCTGCTCAAGGACCAACCAGGAGCTG 141 Q E I N R V Y K E M Y K T D L E K D I V 421 CAGGAAATTAACAGAGTCTACAAGGAAATGTACAAGACTGATCTGGAGAAGGACATCGTT 161 S D T S G D F R K L M V A L A K G R R A 481 TCTGACACATCTGGTGACTTCCGCAAGCTGATGGTTGCCTCGCAAAGGGTAGAAGAGCA 181 E D G S V I D Y E L I D Q D A R D L Y D 541 GAGGATGGCTCTGTCATTGATTATGAACTGATTGACCAAGATGCCCGGGATCTCTATGAT 201 A G V K R K G T D V P K W I S I M T E R 601 GCTGGAGTGAAGAGGAAAGGAACTGATGTTCCAAAGTGGATCAGCATCATGACCGAGCGC 221 S V C H L Q K V F E R Y K S Y S P Y D M 661 AGTGTCTGTCACCTCCAGAAAGTATTTGAAAGGTACAAGAGCTACAGCCCTTATGACATG 241 L E S I K K K E V K G D L E N A F L N L V 721 TTGGAGAGCATCAAGAAGGAGGTCAAAGGAGACCTGGAAAATGCTTTCCTGAACCTGGTC 261 Q C I Q N K P L Y F A D R L Y D S M K G 781 CAGTGTATTCAGAACAAGCCCCTGTATTTTGCTGACCGACTGTACGACTCCATGAAGGGC 281 K G T R D K V L I R I M V S R S E V D M 841 AAGGGCACGCCGATAAGGTCCTGATCAGAATCATGGTCTCCCGCAGTGAAGTGGACATG 301 L K I R S E F K R K Y G K S L Y Y I Q 901 TTGAAAATTAGGTCTGAATTCAAGAGAAAGTACGGCAAGTCCCTGTACTACATCCAG 321 Q D T K G D Y Q K A L L Y L C G G D D - 961 CAAGACACCAAGGGCGACTACCAGAAGGCGCTGCTGTACCTGTGTGGTGGGGATGACTGA	
WBC037C09.bFSP_20021001.esd	Homo sapiens programmed cell death 4	1 AGTGACTCTCCGAGGCGGCGGCAGAGACAGAAGAGCGGGGTCGGGGCCGGCTGACCAGGA 61 ACCTGGGCGAGCAGCGGCGGGGGCCAGAGGGATTCTGAAGGAAGATTTCCATTAGGTAAT	SEQ ID NO:162

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
	(neoplastic transformation inhibitor), transcript variant 1, mRNA	121 TTGTTTTAATCAGTGCAAGCGAAATTAAGGGAAAATGGATGTAGAAAATGAGCAGATACTG 181 AATGTAAACCCTGCAGATCCTGATAACTTAAGTGACTCTCTCTTTCCGGTGATGAAGAA 241 AATGCTGGGACTGAGGAAGTAAAGAATGAAATAAATGGAAATTGGATTTCAGCATACTCC 301 ATTAACGAAGCTAGAATTAATGCCAAGGCAAAAAGGCGACTAAGGAAAAACTCATCCCGG 361 GACTCTGGCAGAGGCGATTCGGTCAGCGACAGTGGGAGTGACGCCCTTAGAAGTGGATTA 421 ACTGTGCCAACCAGTCCAAAGGCAAGGTTGCTGGATAGGCGATCCAGATCTGGGAAAGGA 481 AGGGGACTACCAAAGAAAGGTGGTGCAGGAGGCAAAGGTGTCTGGGGTACACCTGGACAG 541 GTGTATGATGTGGAGGAGGTGGATGTGAAGGATCCTAACTATGATGATGACCAGGAGAAC 601 TGTGTTTATGAAACTGTGGTTTTGCCTTTGGATGAAACGGCATTTGAGAAAACTTTAACA 661 CCAATCATACAGGAATATTTTGAGCATGGAGATACTAATGAAGTTGCGGAAATGCTAAGA 721 GATTTAAATCTTGGTGAAATGAAAAGTGGAGTACCAGTGTTGGCAGTGTCCTTGGCATTG 781 GAGGGAAAGGCTAGTCACAGAGAAATGACATCTAAGCTCCTTTCTGACCTTTGTGGGACG 841 GTAATGAGCACAAACGATGTAGAAAAGTCATTTGATAAATTGTTGAAAGATCTACCTGAA 901 TTAGCACTGGATACTCCTAGAGCACCACAGTTGGTGGGCCAGTTTATTGCTAGAGCTGTT 961 GGAGATGGAATTTTATGTAATACCTATATTGATAGTTACAAAGGAACTGTAGATTGTGTA 1021 CAGGCTAGAGCTGCCCTGGATAAGGCTACTGTGCTCCTGAGTATGTCTAAAGGTGGAAAG 1081 CGCAAAGACAGTGTGTGGGGCTCTGGAGGTGGGCAGCAGTCTGTTAACCACCTTGTTAAA 1141 GAGATTGATATGCTGCTGAAAGAATATTTACTCTCTGGAGACATATCTGAGGCTGAACAT 1201 TGCCTTAAGGAACTGGAAGTACCTCATTTTCACCATGAGCTTGTATATGAAGCCATTGTA 1261 ATGGTTTTAGAGTCAACTGGAGAAAGTACATTTAAGATGATTTTGGATTTATTAAAGTCC 1321 CTTTGGAAGTCTTCTACCATTACTGTAGACCAAATGAAAAGAGGTTATGAGAGAATTTAC 1381 AATGAAATTCCGGACATTAATCTGGATGTCCCACATTCATACTCTGTGCTGGAGCGGTTT 1441 GTAGAAGAATGTTTTCAGGCTGGAATAATTTCCAAACAACTCAGAGATCTTTGTCCTTCA 1501 AGGGGCAGAAAGCGTTTTGTAAGCGAAGGAGATGGAGGTCGTCTTAAACCAGAGAGCTAC 1561 TGAATATAAGAACTCTTGCAGTCTTAGATGTTATAAAAATATATATCTGAATTGTAAGAG 1621 TTGTTAGCACAAGTTTTTTTTTTTTTTTTAGCACTTGTTTTGGGTACAAGGCATTT 1681 CTGACATTTTATAAACCTACATTTAAGGGGAATTTTTTAAGGAAATGTTTTTTCTTTTTT 1741 TTTTGTTTTTCGAGGGGGCAAGGAGGGACAGAAAAGTAACCACTTCTTAAGTGGAATATT 1801 CTCATAAGCTACCTTTGTAAGTGCCATGTTTATGACCTAATCATTCCAAGTTTTGCATT 1861 GATGTCTGACTGCCACTCCTTTCTTTCAAGGACAGTGTTTTTGTAGTAAAATCACTGGTT 1921 TATACAAAGCTTTATTTAGGGGGTAAAGTTAAGCTGCTAAAACCCCATGTTGGCTGCTGC 1981 TGTTGAAATACTGTGCTTTGGGAGTAAAAAAAGAAAGTTATTTCTTTGTCTTAAAGAATT 2041 TTAAGAAAACGAGTTAGTCACAAGACTTATTCATCTTTCCAGGGAGCATACTGATTGGTC 2101 TTAAAGACTAGACAGTTAAGTAAATGGTGGCCGGAACATCTATTTTTCTACAACTGGAA 2161 AAATGAACCCAGTTCTAGAAGAATGTATGACAAAATAAACATGTGAAGCAGTAAAAAAA 2221 AAAAAAAAA 1 M D V E N E Q I L N V N P A D P D N L S 1 ATGGATGTAGAAAATGAGCAGATACTGAATGTAAACCCTGCAGATCCTGATAACTTAAGT 21 D S L F S G D E E N A G T E E V K N E I 61 GACTCTCTCTTTTCCGGTGATGAAGAAAATGCTGGGACTGAGGAAGTAAAGAATGAAATA	SEQ ID NO:163

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		41 N G N W I S A Y S I N E A R I N A K A K 121 AATGGAAATTGGATTTCAGCATACTCCATTAACGAAGCTAGAATTAATGCCAAGGCAAAA 61 R R L R K N S S R D S G R G D S V S D S 181 AGGCGACTAAGGAAAAACTCATCCCGGGACTCTGGCAGAGGCGATTCGGTCAGCGACAGT 81 G S D A L R S G L T V P T S P K G R L L 241 GGGAGTGACGCCCTTAGAAGTGGATTAACTGTGCCAACCAGTCCAAAGGGAAGGTTGCTG 101 D R R S R S G K G R G L P K K G G A G G 301 GATAGGCGATCCAGATCTGGGAAAGGAAGGGACTACCAAAGAAAGGTGGTGCAGGAGGC 121 K G V W G T P G Q V Y D V E E V D V K D 361 AAAGGTGTCTGGGGTACACCTGGACAGGTGTATGATGTGGAGGAGGTGGATGTGAAGGAT 141 P N Y D D D Q E N C V Y E T V V L P L D 421 CCTAACTATGATGATGACCAGGAGAACTGTGTTTATGAAACTGTGGTTTTGCCTTGGAT 161 E T A F E K T L T P I I Q E Y F E H G D 481 GAAACGGCATTTGAGAAAACTTTAACACCAATCATACAGGAATATTTTGAGCATGGAGAT 181 T N E V A E M L R D L N L G E M K S G V 541 ACTAATGAAGTTGCGGAAATGCTAAGAGATTTAAATCTTGGTGAAATGAAAGTGGAGTA 201 P V L A V S L A L E G K A S H R E M T S 601 CCAGTGTTGGCAGTGTCCTTGGCATTGGAGGGAAAGGCTAGTCACAGAGAAATGACATCT 221 K L L S D L C G T V M S T N D V E K S F 661 AAGCTCCTTTCTGACCTTTGTGGGACGGTAATGAGCACAAACGATGTAGAAAAGTCATTT 241 D K L L K D L P E L A L D T P R A P Q L 721 GATAAATTGTTGAAAGATCTACCTGAATTAGCACTGGATACTCCTAGAGCACCACAGTTG 261 V G Q F I A R A V G D G I L C N T Y I D 781 GTGGGCCAGTTTATTGCTAGAGCTGTTGGAGATGGAATTTTATGTAATACCTATATTGAT 281 S Y K G T V D C V Q A R A A L D K A T V 841 AGTTACAAAGGAACTGTAGATTGTGTACAGGCTAGAGCTGCCCTGGATAAGGCTACTGTG 301 L L S M S K G G K R K D S V W G S G G G 901 CTCCTGAGTATGTCTAAAGGTGGAAAGCGCAAAGACAGTGTGTGGGGCTCTGGAGGTGGG 321 Q Q S V N H L V K E I D M L L K E Y L L	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		961 CAGCAGTCTGTTAACCACCTTGTTAAAGAGATTGATATGCTGCTGAAAGAATATTTACTC 341 S G D I S E A E H C L K E L E V P H F H 1021 TCTGGAGACATATCTGAGGCTGAACATTGCCTTAAGGAACTGGAAGTACCTCATTTTCAC 361 H E L V Y E A I V M V L E S T G E S T F 1081 CATGAGCTTGTATATGAAGCCATTGTAATGGTTTTAGAGTCAACTGGAGAAAGTACATTT 381 K M I L D L L K S L W K S S T I T V D Q 1141 AAGATGATTTTGGATTTATTAAAGTCCCTTTGGAAGTCTTCTACCATTACTGTAGACCAA 401 M K R G Y E R I Y N E I P D I N L D V P 1201 ATGAAAAGAGGTTATGAGAGAATTTACAATGAAATTCCGGACATTAATCTGGATGTCCCA 421 H S Y S V L E R F V E E C F Q A G I I S 1261 CATTCATACTCTGTGCTGGAGCGGTTTGTAGAAGAATGTTTTCAGGCTGGAATAATTTCC 441 K Q L R D L C P S R G R K R F V S E G D 1321 AAACAACTCAGAGATCTTTGTCCTTCAAGGGCAGAAAGCGTTTGTAAGCGAAGGAGAT 461 G G R L K P E S Y - 1381 GGAGGTCGTCTTAAACCAGAGAGCTACTGA	
WBC038A02.bFSP_20021101.esd	Homo sapiens ribosomal protein L3, mRNA (cDNA clone MGC:70878 IMAGE:3852576).	1 GTTTGATGGCGTGATGTCTCACAGAAAGTTCTCCGCCCCCAGGCACGGGTCCCTGGGCTT 61 CTTGCCTCGGAAACGCAGCAGCCGGCACCCGGCAAGGTGAAGAGTTTCCCCAAGGATGA 121 CGCTTCGAAGCCCCGTGCACCTCACGGCCTTCCTTGGCTACCAGGGCGGCATGACCCACAT 181 CCTGCGTGAAGTCCATAGGCCCGGATTCCAAGTGAACCAGAAAGAAGTTGTGGAAGCTGT 241 GACCATTGTGGAGACGCCACCCATGGTGTTGTGGGCATTGTGTGGCTACGTGGAAACCCC 301 TCGGGGCCCTCGTACCTTCAAGACCATCTTTGCTGAGCACATAAGTGATGAGTGCAAAAG 361 GCGCTTCTACAAGAACTGGCATAAGTCTAAGAAGAAGGCCTTCACCAAATACTGCAAGAA 421 GTGGCAGGATGAGGACGGCAGGAAGCAGCTGGAGAAGGATTTCAGCAGCATGAAGAAGTA 481 CTGCCAGGTCATCCGTGTCATCGCCCACACCCAGATGCGCCTGCTCCCTCTGCGCCAGAA 541 GAAGGCGCATCTCATGGAGATCCAGGTGAACGGAGGCACAGTGGCCGAGAAACTGGACTG 601 GGCCCGCGAGAGGCTGGAGCAGCAGGTCCCTGTGAACCAGGTGTTTGGGCAGGACGAGAT 661 GATCGACGTCATCGGGGTGACCAAGGGCAAAGGCTACAAAGGGGTCACCAGCCGCTGGCA 721 CACCAAGAAGCTGCCCCGCAAGACCCACGAGGGCTGCGCAAGGTTGCCTGCATTGGGGC 781 CTGGCATCCCGCCCGAGTGGCCTTCTCCGTGGCGCGGGCCGGGCAGAAGGCTACCATCA 841 CCGCACGGAGATCAACAAGAAGATCTACAAGATTGGCCAGGGCTACCTCATCAAGGACGG 901 CAAGCTGATCAAGAACAATGCCTCCACTGATTACGACCTGTCTGACAAGAGCATCAACCC 961 TCTGGGTGGCTTTGTCCACTACGGTGAAGTGACCAACGACTTTGTCATGCTGAAAGGCTG 1021 TGTGGTGGGAACCAAGAAGCGAGTGCTGACCCTTCGCAAGTCCCTGCTGGTGCAGACGAA 1081 GCGGCGGCCCTGGAGAAGGTTGACCTCAAGTTCATCGACACCACCTCCAAGTTTGGCCA	SEQ ID NO:164

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1141 TGGCCGCTTCCAGACTGTGGAGGAGAAGAAAGCATTCATGGGACCACTTAAGAAAGACCG 1201 AATTGCAAAGGAGGAAGGAGCTTGATGCCAGCATCAGATCGTGCAGCTGGTGGGGTCCCA 1261 ATAAAAGTTATTTTCCACTGAAAAAAAAAAAAAAAAAAA 1 M S H R K F S A P R H G S L G F L P R K 1 ATGTCTCACAGAAAGTTCTCCGCCCCCAGGCACGGGTCCCTGGGCTTCTTGCCTCGGAAA 21 R S S R H R G K V K S F P K D D A S K P 61 CGCAGCAGCCGGCACCGCGGCAAGGTGAAGAGTTTCCCCAAGGATGACGCTTCGAAGCCC 41 V H L T A F L G Y Q G G M T H I L R E V 121 GTGCACCTCACGGCCTTCCTTGGCTACCAGGGCGGCATGACCCACATCCTGCGTGAAGTC 61 H R P G F Q V N Q K E V V E A V T I V E 181 CATAGGCCCGGATTCCAAGTGAACCAGAAAGAAGTTGTGGAAGCTGTGACCATTGTGGAG 81 T P P M V V V G I V G Y V E T P R G P R 241 ACGCCACCCATGGTGGTTGTGGGCATTGTGGGCTACGTGGAAACCCCTCGGGGCCCTCGT 101 T F K T I F A E H I S D E C K R R F Y K 301 ACCTTCAAGACCATCTTTGCTGAGCACATAAGTGATGAGTGCAAAAGGCGCTTCTACAAG 121 N W H K S K K K A F T K Y C K K W Q D E 361 AACTGGCATAAGTCTAAGAAGAAGGCCTTCACCAAATACTGCAAGAAGTGGCAGGATGAG 141 D G R K Q L E K D F S S M K K Y C Q V I 421 GACGGCAGGAAGCAGCTGGAGAAGGATTTCAGCAGCATGAAGAAGTACTGCCAGGTCATC 161 R V I A H T Q M R L L P L R Q K K A H L 481 CGTGTCATCGCCCACACCCAGATGCGCCTGCTCCCTCTGCGCCAGAAGAAGGCGCATCTC 181 M E I Q V N G G T V A E K L D W A R E R 541 ATGGAGATCCAGGTGAACGGAGGCACAGTGGCCGAGAAACTGGACTGGGCCCGCGAGAGG 201 L E Q Q V P V N Q V F G Q D E M I D V I 601 CTGGAGCAGCAGGTCCCTGTGAACCAGGTGTTTGGGCAGGACGAGATGATCGACGTCATC 221 G V T K G K G Y K G V T S R W H T K K L 661 GGGGTGACCAAGGGCAAAGGCTACAAAGGGGTCACCAGCCGCTGGCACACCAAGAAGCTG 241 P R K T H R G L R K V A C I G A W H P A 721 CCCCGCAAGACCCACCGAGGGCTGCGCAAGGTTGCCTGCATTGGGGCCTGGCATCCCGCC	SEQ ID NO:165

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		261 R V A F S V A R A G Q K G Y H H R T E I 781 CGAGTGGCCTTCTCCGTGGCGCGGGCCGGGCAGAAGGGCTACCATCACCGCACGGAGATC 281 N K K I Y K I G Q G Y L I K D G K L I K 841 AACAAGAAGATCTACAAGATTGGCCAGGGCTACCTCATCAAGGACGGCAAGCTGATCAAG 301 N N A S T D Y D L S D K S I N P L G G F 901 AACAATGCCTCCACTGATTACGACCTGTCTGACAAGAGCATCAACCCTCTGGGTGGCTTT 321 V H Y G E V T N D F V M L K G C V V G T 961 GTCCACTACGGTGAAGTGACCAACGACTTTGTCATGCTGAAAGGCTGTGTGGTGGGAACC 341 K K R V L T L R K S L L V Q T K R R A L 1021 AAGAAGCGAGTGCTGACCCTTCGCAAGTCCCTGCTGGTGCAGACGAAGCGGCGGCCCTG 361 E K V D L K F I D T T S K F G H G R F Q 1081 GAGAAGGTTGACCTCAAGTTCATCGACACCACCTCCAAGTTTGGCCATGGCCGCTTCCAG 381 T V E E K K A F M G P L K K D R I A K E 1141 ACTGTGGAGGAGAAGAAAGCATTTCATGGGACCACTTAAGAAAGACCGAATTGCAAAGGAG 401 E G A - 1201 GAAGGAGCTTGA	
WBC038B01.bFSP_20021101.esd	Homo sapiens ribosomal protein L15, mRNA.	1 CCTTTCCGTCTGGCGGCAGCCATCAGGTAAGCCAGATGGGCGCTTACAAGTACATCCAG 61 GAGCTATGGAGGAAGAAGCAGTCGGACGTGATGCGATTTCTTCTCAGGGTGCGCTGCTGG 121 CAGTACCGCCAGCTCTCGGCGCTCCACAGGGCGCCCCGCCCCGGCCCGATAAGGCG 181 CGCAGACTGGGCTACAAGGCCAAGGTTATGTCATATATCGCATTCGTGTGCGCCGT 241 GGTGGCCGCAAACGCCCCCGTTCCTAAGGGCGCGACCTACGGCAAGCCTGTGCATCATGGT 301 GTTAACCAGCTCAAGTTTGCTCGAAGCCTTCAGTCTGTTGCCGAGGAACGAGCTGGACGC 361 CACTGTGGGGCTCTGAGAGTTCTGAATTCTTACTGGGTTGGCGAAGATTCCACATACAAA 421 TTCTTTGAGGTGATCCTCATTGATCCATTCCATAAGGCTATTAGAAGAAATCCTGATACC 481 CAGTGGATCACCAAACCAGTCCACAAGCACAGGGAAATGAGAGGGCTGACATCTGCAGGC 541 CGCAAGAGCCGTGGCCTTGGAAAGGCCACAAGTTCCACCACACTATTGGTGGTTCTCGC 601 CGTGCAGCTTGGAGAAGGCGCAATACTCTGCAGCTTCACCGTTACCGCTAATATAAGTAA 661 TGTTTGTAAAATTCTTACCTAATAAACAATTTAGGACAGTCATGTCTGCTTACAGGTGTT 721 ATTTGTCTGTTAAAACTAGTCTGCAGATGTTTCTTGAATGCTTTGTCAAATTAAGAAAGT 781 TAAAGTGCAATAAATGTTTGAAGACAATAAGTGGTGGTGTATCTTGTTTCTAATAAGATAA 841 ACTTTTTTGTCTTTGCTTTATCTTATTAGGGAGTTGTATGTCAGTGTATAAAACATACTG 901 TCTGGTATACAGGCTTAATAAATTCTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1 M G A Y K Y I Q E L W R K K Q S D V M R	SEQ ID NO:166 SEQ ID NO:167

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1 ATGGGCGCTTACAAGTACATCCAGGAGCTATGGAGGAAGAAGCAGTCGGACGTGATGCGA 21 F L L R V R C W Q Y R Q L S A L H R A P 61 TTTCTTCTCAGGGTGCGCTGCTGGCAGTACCGCCAGCTCTCGGCGCTCCACAGGGCGCCC 41 R P T R P D K A R R L G Y K A K Q G Y V 121 CGCCCCACCCGGCCCGATAAGGCGCGCAGACTGGGCTACAAGGCCAAGCAAGGTTATGTC 61 I Y R I R V R R R G G R K R P V P K G A T 181 ATATATCGCATTCGTGTGCGCCGTGGTGGCCGCAAACGCCCCCGTTCCTAAGGGCGCGACC 81 Y G K P V H H G V N Q L K F A R S L Q S 241 TACGGCAAGCCTGTGCATCATGGTGTTAACCAGCTCAAGTTTGCTCGAAGCCTTCAGTCT 101 V A E E R A G R H C G A L R V L N S Y W 301 GTTGCCGAGGAACGAGCTGGACGCCACTGTGGGGCTCTGAGAGTTCTGAATTCTTACTGG 121 V G E D S T Y K F F E V I L I D P F H K 361 GTTGGCGAAGATTCCACATACAAATTCTTTGAGGTGATCCTCATTGATCCATTCCATAAG 141 A I R R N P D T Q W I T K P V H K H R E 421 GCTATTAGAAGAAATCCTGATACCCAGTGGATCACCAAACCAGTCCACAAGCACAGGGAA 161 M R G L T S A G R K S R G L G K G H K F 481 ATGAGAGGGCTGACATCTGCAGGCCGCAAGAGCCGTGGCCTTGGAAAGGGCCACAAGTTC 181 H H T I G G S R R R A A W R R R N T L Q L 541 CACCACACTATTGGTGGTTCTCGCCGTGCAGCTTGGAGAAGGCGCAATACTCTGCAGCTT 201 H R Y R - 601 CACCGTTACCGCTAA	
WBC038D08.bFSP_20021101.esd	No homology	1 GGACGTCAGTGAGAGCAGAGATGGCTGTGGGTGTGGAGTGAGGGTTCTACTGTGAGGTGA 61 GCTGCTCACTGCCGAGGAGAGTTACCGCAACCTGCACTCCGCGGCCACCTCACACTCTCG 121 ACTTGTCCAAACTGAATTCTTTCTTTCCTTTACCCGAACTTGTTATCCCTTTCAGCGTGG 181 GTTAAGGTGGGCACAGGAGGTTTATGAACCCCCTGAAATTGTATATGGAAGTTGGTGTAT 241 ATATGGCAAATGTATTTTTTTTTCCCCTAAGGAAAGGGTCCATATTATTCATCAGATTCT 301 GAATGGGATCTGTAATAGAAAAGTTTAAAAATTCCTATTTTGTAGGGATATAGAAAATTT 361 AAAAGGGATTTTAGAAGAAATATACAAAGATAAATCTGGGGGGAGTCAGTGAGGAAAAAA 421 TTAAGGAACTGTGATTTAATCTGGAGAATGGAATAAATTTAAGATATGTAGGGTATAAGG 481 AAGAACTTGAAAGATTCTAGAAAGGGTCAGAAAGTTAATATTTATATATGTGAAAAAGTC 541 TGAGGAGAGTAATTCTCATTTAATTCTCTACGTACCTTGCAACTTAAATTATCCCATTGC	SEQ ID NO:168

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		601 TCCTAGTATAGAACATCCTTATCCAGAACAAGTTTGCACAAAATTTATCTCAGTGTGCAT 661 TTGTTTCTTTTTATTTTTATCTAACTTATTTCTATATTATAAAATA	
		1 GTAGATGATCATTGGTGAGTGGGCATGGACAGGAAAAAAAGAGTCTGAAGTTAAGTGCAA 61 GAAGAAATGAGCAGGTAAAGCCAACGTTTTTGCTTCAAATGTTGCAATGAGATGGAAGAA 121 TAGGCTGCTTGATGTGTATTAAAAGAATGCTTGGTACAAGGGGAAAAAGTTGTATCTTGG 181 CTGCAAGATACCATTTAAGAATATCCTAGTGAAGTTATTTGACTATGGTTTGGCAGGAC 241 TTCTGAAAAAAGAAAAATAATAATAACCATGATATACATAGCCATGGTTAATCTGTTTGCT 301 TTTCACTTACTTTACAAGTATAATAATAAACTTGCCAAAACAAGTCGTTATCCATCTTTCTT 361 TTTCTTTTTTTTTTTGCAGGGACCTTGCTGCCTTTGATAAATCCCATGATCAAGCCATC 421 CGTACCTACCAGAGCACAGAGCAAGTATGCACCCTGTGACTGCCATGCTGGTGGGAAAA 481 GATTTAAAAGTGGATTAAGGACCTGCCTATTGCTGATTCCACACATTTCTCTTTTTTACA 541 TTGAATTCATAAAATAAATATGAAACTTCAGCTTGCA	SEQ ID NO:169
WBC038E02.bFSP_20021101.esd	Homo sapiens lysosomal-associated membrane protein 1, mRNA.	1 GGCCCAACCGCCGCCCGCGCCCCCGCTCTCCGCACCGTACCCGGCCGCCTCGCGCCATGG 61 CGGCCCCCGGCAGCGCCCGGCGACCCCTGCTGCTACTGCTGTTGCTGCTCGGCCC 121 TCATGCATTGTGCGTCAGCAGCAATGTTTATGGTGAAAAATGGCAACGGGACCGCGTGCA 181 TAATGGCCAACTTCTCTGCTGCCTTCTCAGTGAACTACGACACCAAGAGTGGCCCTAAGA 241 ACATGACCTTTGACCTGCCATCAGATGCCACACAGTGGTGCTCAACCGCAGCTCCTGTGGAA 301 AAGAGAACACTTCTGACCCCAGTCTCGTGATTGCTTTTGGAAGAGGACATACACTCACTC 361 TCAATTTCACGAGAAATGCAACACGTTACAGCGTCCAGCTCATGAGTTTTGTTTATAACT 421 TGTCAGACACACACCTTTTCCCCAATGCGAGCTCCAAAGAAATCAAGACTGTGGAATCTA 481 TAACTGACATCAGGGCAGATATAGATAAAAAATACAGATGTGTTAGTGGCACCCAGGTCC 541 ACATGAACAACGTGACCGTAACGCTCCATGATGCCACCATCCAGGCGTACCTTTCCAACA 601 GCAGCTTCAGCAGGGGAGAGACACGCTGTGAACAAGACAGGCCTTCCCCAACCACACGC 661 CCCCTGCGCCACCCAGCCCCTCGCCCTCACCCGTGCCCAAGAGCCCCTCTGTGGACAAGT 721 ACAACGTGAGCGGCACCAACGGGACCTGCCTGCTGGCCAGCATGGGCCTGCAGCTGAACC 781 TCACCTATGAGAGGAAGGACAACACGACGGTGACAAGGCTTCTCAACATCAACCCCAACA 841 AGACCTCGGCCAGCGGGAGCTGCGGCGCCCACCTGGTGACTCTGGAGCTGCACAGCGAGG 901 GCACCACCGTCCTGCTCTTCCACTTTGGAATGAATGCAACTTCTAGCCAGTTTTTCCTGC 961 AAGAAATCCAGTTGGATATGACTCTTCCTGACGCCAGAGACCCCACCTTCAAGGCTGCCA 1021 ACAGCTCGCTGAGGGCACTTCAGGCCACCATCGGGAACTCCTACAGGTGTAATGCCGAGG 1081 AGCGCCTGCGCGTCACAGAGGCCCTTTCTGTCAACGTCTTCAGAGTGTGGGTTCAGGCTT 1141 TCCAGGTGGAAGGTGACAAGTTTGGGTCCGTGGAGGAATGCCAGCTGGATGAGAACAACA 1201 TGATGATCCCCATTGCCGTGGGCGGTGCCCTGGCCGGGCTGGTCCTCATCGTCCTCATTG 1261 CCTACCTCATCGGCAGGAAGAGGAGCCACGCGGGCTACCAGACTATCTAGCCTGGTGCAC 1321 GCAGGCACAGCAGCTGCAGGGGCCTCTGTTCCTTTCTCTGGGCTTAGGGTCCTGTCGAAG 1381 GGGAGGCACACTTGCCTGCACACGATTTCCAAATCTGCTTTATCCAATTTGAAGTTCATC 1441 TTGCAACATTTACTATGCACAAAAGAGTAACTATTGAAATGACGGTGTTAATTTTGCTAA 1501 CTGGGTTAAATATTTTGCTAACTGGTTAAATGTTAATATTTACCAAAGTAGGATTTTGAG 1561 GGTGGGGGTGCTCTCTCTGAGGGGGTGGGGGTGCCGCTGTCTCTGAGGGGTGGGGGTGCC 1621 GCTGTCTCTGAGGGGTGGGGGTGCCGCTCTCTCTGAGGGGGTGGGGGTGCCGCTTTCTCT	SEQ ID NO:170

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1681 GAGGGGGTGGGGGGTGCCGCTCTCTCTGAGGGGGTGGGGGTGCTGCTCTCTCCGAGGGGTG 1741 GAATGCCGCTGTCTCTCTGAGGGGTGGGGGTGCCGCTCTTAAATTGGCTCCATATCATTTGAG 1801 TTTAGGGTTCTGGTGTTTGGTTTCTTCATTCTTTACTGCACTCAGATCTAAGCCTTACAA 1861 AGGGAGAGTCTCTGGCCGTCACACGTAGGACGCATGAAGGTCACTCGTGGTGAGGCTGAC 1921 ATGCTCACACATTACAACAGTAGAGAGGGAAAATCCTAAGACAGAGGAACTCCAGAGATG 1981 AGTGTCTGGAGCGCTTCAGTTCAGCTTTAAGGCCAGGACGGGCCACACGTGGCTGGCGG 2041 CCTCGTTCCAGTGGCGGCACGTCCTTGGCGTCTCTAATGTCTGCAGCTCAAGAGCTGGC 2101 ACTTTTTTAAATAGCAAACTGGGTGTTATTTTTATTTACTTCTTTGTAAAGTGGTTTTCG 2161 GTCTTCTGTTGACATTCGGGGTGATCCTGTTCTGCGCTGTGTACAATGTGAGATCGGTGC 2221 GTTCTCCTGATGTTTTGCCGTGGCTTGGGGATTGTACACGGGACCAGCTCACGTAATGCA 2281 TTGCCTGTAACAATGTAATAAAAAGCCTCTTTCTTTTAAAAAAAAAAAAAAAAAAAAAAA 2341 A	
		1 M A A P G S A R R P L L L L L L L L L 1 ATGGCGGCCCCCGGCAGCGCCCGGCGACCCCTGCTGCTACTGCTGTTGCTGCTGCTC 21 G L M H C A S A A M F M V K N G N G T A 61 GGCCTCATGCATTGTGCGTCAGCAGCAATGTTTATGGTGAAAAATGGCAACGGGACCGCG 41 C I M A N F S A A F S V N Y D T K S G P 121 TGCATAATGGCCAACTTCTCTGCTGCCTTCTCAGTGAACTACGACACCAAGAGTGGCCCT 61 K N M T F D L P S D A T V V L N R S S C 181 AAGAACATGACCTTTGACCTGCCATCAGATGCCACAGTGGTCGCTCAACCGCAGCTCCTGT 81 G K E N N T S D P S L V I A F G R G H T L 241 GGAAAAGAGAACACTTCTGACCCCAGTCTCGTGATTGCTTTTGGAAGAGGACATACACTC 101 T L N F T T R N A T R Y S V Q L M S F V Y 301 ACTCTCAATTTCACGAGAAATGCAACACGTTACAGCGTCCAGCTCATGAGTTTGTTTAT 121 N L S D T H L F P N A S S K E I K T V E 361 AACTTGTCAGACACACACCTTTTCCCCAATGCGAGCTCCAAGAAATCAAGACTGTGGAA 141 S I T D I R A D I D K K Y R C V S G T Q 421 TCTATAACTGACATCAGGGCAGATATAGATAAAAAATACAGATGTGTTAGTGGCACCCAG 161 V H M N N V T V T L H D A T I Q A Y L S 481 GTCCACATGAACAACGTGACCGTAACGCTCCATGATGCCACCATCCAGGCGTACCTTTCC 181 N S S F S R G E T R C E Q D R P S P T T 541 AACAGCAGCTTCAGCAGGGGAGACACGCTGTGAACAAGACAGGCCTTCCCCAACCACA	SEQ ID NO:171

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		201 A P P A P P S P S P S P V P K S P S V D 601 GCGCCCCCTGCGCCACCCAGCCCCTCGCCCTCACCCGTGCCCAAGAGCCCCTCTGTGGAC 221 K Y N V S G T N G T C L L A S M G L Q L 661 AAGTACAACGTGAGCGGCACCAACGGGACCTGCCTGCTGGCCAGCATGGGGCTGCAGCTG 241 N L T Y E R K D N T T V T R L L N I N P 721 AACCTCACCTATGAGAGGAAGGACAACACGACGGTGACAAGGCTTCTCAACATCAACCCC 261 N K T S A S G S C G A H L V T L E L H S 781 AACAAGACCTCGGCCAGCGGGAGCTGCGGCGCCCACCTGGTGACTCTGGAGCTGCACAGC 281 E G T T V L L F H F G M N A T S S Q F F 841 GAGGGCACCACCGTCCTGCTCTTCCACTTTGGAATGAATGCAACTTCTAGCCAGTTTTTC 301 L Q E I Q L D M T L P D A R D P T F K A 901 CTGCAAGAAATCCAGTTGGATATGACTCTTCCTGACGCCAGAGACCCCACCTTCAAGGCT 321 A N S S L R A L Q A T I G N S Y R C N A 961 GCCAACAGCTCGCTGAGGGCACTTCAGGCCACCATCGGGAACTCCTACAGGTGTAATGCC 341 E E R L R V T E A L S V N V F R V W V Q 1021 GAGGAGCGCCTGCGCGTCACAGAGGCCCTTTCTGTCAACGTCTTCAGAGTGTGGGTTCAG 361 A F Q V E G D K F G S V E E C Q L D E N 1081 GCTTTCCAGGTGGAAGGTGACAAGTTTGGGTCCGTGGAGGAATGCCAGCTGGATGAGAAC 381 N M M I P I A V G G A L A G L V L I V L 1141 AACATGATGATCCCCATTGCCGTGGGCGGTGCCCTGGCCGGGCTGGTCCTCATCGTCCTC 401 I A Y L I G R K R S H A G Y Q T I - 1201 ATTGCCTACCTCATCGGCAGGAAGAGGAGCCACGCGGGCTACCAGACTATCTAG	
WBC038G11.bFSP_20021101.esd	No Homology	1 GATGCCTGCAATACCTCTTATCATCGTTGTAACATTTCTTCCAAAATTAATGACCCAACC 61 CGTCCTCTCTGGGCCAGAGTTAAAGCGAGGCTTGGACAAGAAGAATCGGCCTATGCAGAC 121 TCAAAAGAGTTTATCCTGTGCCAGCACGGGAAAATTGGACCACCTAAACTGGATATCAGA 181 AAGAAAGACGACCAGATCATTATTGACATATCTCACCCTTTATTTGCTGTAAATGGATTT 241 GACCTGGAAGCCATGTATGATGATGAAAATGCTTGTTACGAATTCGTGTACAAGGTGTAT 301 GTGAAAATAAACGGAAGTGGAGAGAGCATGGAGAGAGTGTATGAATGCAGAGACGAGGAC 361 TGCAATGAGACCCACTGCCGCCTCGGCATCCCAGCGTCCTCCCTGAACTCTCAGTGCTGC 421 GCTGCAGCAGAGGGAGTCTCGGAACGATGGGAGTTCACAACTGACAAGTCCGAAGAACTC 481 TGCCTGACCGTTTTCGATGATGGCAGCCCAGAAGGTTCGGTTTGGATTCCAGTTGTTGCT	SEQ ID NO:172

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		541 GCTTTCCTACTCTTTCTAGTCATTCTGCTGGTTGCGTTGTTATTGTCGCATTAAGACG 601 AAGAATCTGTTTAAGAGAAGAAACAACCCTTTACCCAGTTCCTTGCTGTCTGTGGTAAGA 661 AGTGCCTCTTCAGAGCCAGACTCTGAATCAAAGCATATATCGCCTGTCACCTACCAGCCA 721 ATTGTCCCGGAGAACGATCACCTGTCTTCAGCAGCGGTGTCAGGGACGCAGGCTGAAGAC 781 AGTCC	
		1 GTGGACGAAGGTGGGAAGGAGTTCCCTGATCGGCTACAGACTGACAGCTGACTCCCAGGA 61 GTTCTCCTGAGCTCAGCCGAGGGGCCCGGCCCTGAAGGAAGGGCTCTGCCTGAGCAGTTC 121 TTCCTGAACGGCTTTGAGTTTGTGAAAAGATCTGATTTCTGAAATTGTGTCAATATTAAC 181 CACATGCAATGTCTGGTTCAGATCAAAATGTGAACTGCCTGTTGAACTTGGTCGCATTTG 241 GTCTGAAAACAGCAAACCAGTTTCAAAACCTGTCTTAGGAAAACAAGCGACATCAGCACC 301 TGGGAGCCTTTCTCCCGGCACGGCCAGCTGTGACAGTGGCACTCCCTGCCACCCTCTCC 361 TGCGACAGCGGTGGCATCTGTGGCGGATGTTTCTTCTCTGCGCCTCCGTGTGGGATTTGG 421 TTTGGAAGTTTGTGTAGATAGTACTTTTTAAATACCTGCTTTTGGAAGAAATCCTGGAAGC 481 TTTTCAAAACTGGCATTTAAAATCAGATTTGAGCCAGTGGAATTAATAGAGGGTGTAAAT 541 AGAGACGTGCATGTGTCTTCCAGGAGCATTGCACGTTGCCTGTAGAAAGTTTTAAATAAA 601 ACATTTTTAAAATTAAAAAAAAAAAAAAAAAA	SEQ ID NO:173
WBC039D09.bFSP_20021101.esd	Homo sapiens NPF/calponin-like protein, mRNA	1 AAGGGAACGGGGCCAGACTCAGCCCGACAGCGGGATTAGAGCCCTCCAGAATACCCATCA 61 TATAGCCCCTGAGGTGGCATGGTGATGTCTCCATGAGGGAACCCCTTCCCACTCATCCCTG 121 TCACGTATATCATAGTGTTCTTGACTGGGCCATTCATCTAAGATGGGATTTACCCTGTGA 181 AACAGGGAGAAGACTTATGGACCCCAAGCATCATTTCGAGTTGTAGTTTGAGTTTTTAAAA 241 GACATACATGCAAAGTTCCTTTGCTTTGGACCCTCTGCATTATTAAAGCTGCTGTATTGC 301 TAACCCAGAACTGCTCCAGTGTCTTGACTGATCATCATGGCTTCAGTTTGGAAGAGACTG 361 CAGCGTGTGGGAAAACATGCATCCAAGTTCCAGTTTGTGCCTCCTCCTACCAGGAGCTCATG 421 GTTGAGTGTACGAAGAAATGGCAACCAGATAAACTGGTGGTAGTTTGGACCAGAAGAAGC 481 CGAAGGAAGTCTTCTAAGGCACATAGCTGGCAACCTGGAATAAAAAATCCCTATCGTGGT 541 GTTGTTGTGGCCTGTTCCTGAAAACATTGAAATCACTGTAACACTTTTTAAGGATCCT 601 CATGCGGAAGAATTTGAAGACAAAGAGTGGACATTTGTCATAGAAAATGAATCCCCTTCT 661 GGTCGAAGGAAAGCTCTTGCTACTAGCAGCATCAATATGAAACAGTATGCAAGCCCTATG 721 CCAACTCAGACTGATGTCAAGTTAAAATTCAAGCCATTATCTATAAAAAGTTGTATCTGCC 781 GCTCTTCAGTTTTCATTATCTTGCATTTTTCTGAGGGAAGGAAAAGCCACAGATGAAGAC 841 ATGCAAAGTTTGGCTAGTTGATGAGTATGAAGCAGGCTGACATTGGCAATTTAGATGAC 901 TTCGAAGAAGATAATGAAGATGATGAGAACAAGAGTGAACCAAGAAGAAAAGGCAGCT 961 AAAATTACAGAGCTTATCAACAAACTTAACTTTTTGGATGAAGCAGAAAAGGACTTGGCC 1021 ACCGTGAATTCAAATCCATTTGATGATCCTGATGCTGCAGAATTAAATCCATTTGGAGAT 1081 CCTGACTCAGAAGAACCTATCACTGAAACAGCTTCACCTAGAAAAACAGAAGACTCTTTT 1141 TATAATAACAGCTATAATCCCTTTAAAGAGGTGCAGACTCCACAGTATTTGAACCCATTC 1201 GATGAGCCAGAAGCATTTGTGACCATAAAGGATTCTCCTCCCCAGTCTACAAAAAGAAAA 1261 AATATAAGACCTGTGGATATGAGCAAGTACCTCTATGCTGATAGTTCTAAAACTGAAGAA 1321 GAAGAATTGGATGAATCAAATCCTTTTATGAACCTAAATCAACTCCTCCTCCAAATAAT 1381 TTGGTAAATCCTGTTCAAGAACTAGAAACTGAAAGGCGAGTGAAAGAAAGGCCCCGGCT	SEQ ID NO:174

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1441 CCACCAGTCCTCTCACCAAAAACAGGAGTATTAAATGAAAACACAGTTTCTGCAGGAAAA	
		1501 GATCTCTCTACTTCTCCTAAGCCAAGCCCTATACCAAGTCCTGTTTTGGGGCGAAAGCCA	
		1561 AATGCTAGTCAGTCTTTGCTTGTATGGTGTAAAGAAGTTACAAAGAACTACCGAGGAGTA	
		1621 AAAATCACCAATTTTACTACATCGTGGAGAAATGGTTTATCTTTTTGTGCAATATTACAC	
		1681 CACTTTAGACCAGATTTAATTGACTACAAGTCTCTGAATCCTCAAGATATTAAAGAGAAC	
		1741 AACAAAAAGGCATACGATGGATTTGCCAGCATAGGAATTTCCCGATTATTGGAACCTTCT	
		1801 GATATGGTATTATTAGCAATTCCTGATAAACTGACTGTTATGACTTTATCTCTATCAAATA	
		1861 AGGGCACATTTCAGTGGCCAAGAACTAAATGTCGTTCAGATAGAGGAAAACAGCAGTAAA	
		1921 AGCACATATAAAGTTGGAAACTATGAAACAGATACAAACAGTTCTGTTGATCAAGAAAAA	
		1981 TTCTATGCAGAGCTTAGTGATCTGAAGCGGAGCCTGAACTACAACAGCCTATCAGCGGA	
		2041 GCAGTAGACTTCTTTATCACAGGATGACTCTGTATTTGTAAATGATAGCGGGGTTGGAGAG	
		2101 TCAGAAAGTGAGCATCAAACTCCTGATGATCACCTTAGTCCAAGCACAGCCTCCCCTTAC	
		2161 TGTCGCAGGACTAAAAGTGACACAGAACCCCAGAAGTCTCAGCAGAGCTCTGGAAGGACT	
		2221 TCAGGATCTGATGACCCTGGAATATGTTCCAATACAGATTCAACCCAAGCACAGGTTTTG	
		2281 TTAGGCAAAAAGAGACTATTGAAAGCTGAGACTTTAGAATTGAGTGACTTATATGTTAGT	
		2341 GATAAGAAGAAGGATATGTCTCCACCCTTTATTTGTGAGGAGACAGATGAACAAAAGCTT	
		2401 CAAACTCTAGACATCGGTAGTAACTTGGAGAAGAAAAATTAGAGAATTCCAGATCCTTA	
		2461 GAATGCAGATCAGATCCAGAATCTCCTATCAAAAAACACAGTTTATCTCCTACTTCTAAA	
		2521 CTTGGATACTCATATAGTAGAGATCTAGACCTTGCTAAGAAAAACATGCTTCCCTGAGG	
		2581 CAGACGGAGTCTGATCCAGATGCTGATAGAACCACTTTAAATCATGCAGATCATTCATCA	
		2641 AAAATAGTCCAGCATCGATTGTTATCTAGACAAGAAGAACTTAAGGAAAGAGCAAGAGTT	
		2701 CTGCTTGAGCAAGCAAGAAGATGCAGCCTTAAAGGCGGGGAATAAGCACAATACCCAAC	
		2761 ACAGCCACCCCATTCTGCAACAGGCAGCTAAGTGATCAGCAAGATGAAGAGCGACGTCGG	
		2821 CAGCTGAGAGAGAGAGCTCTGTCAGCTAATAGCAGAAGCTCGATCTGGAGTGAAGATGTCA	
		2881 GAACTTCCCAGCTATGGTGAAATGGCTGCAGAAAAGTTGAAAGAAAGGTCAAAGGCATCT	
		2941 GGAGAACAAAACAGTAAGTTGGTGGACTTGAAGCTGAAGAAGCTCCTAGAAGTTCAGCCA	
		3001 CAGGTGGCAAATTCACCCTCCAGTGCTGCCCAGAAAGCTGTAACTGAGAGCTCAGAGCAG	
		3061 GACATGAAAAGTGGCACAGAAGATCTCCGGACTGAACGATTACAAAAAACAACAGAACGT	
		3121 TTTAGAAATCCTGTTGTCTTCAGCAAAGATTCTACAGTCAGAAAAACTCAACTTCAGTCT	
		3181 TTCAGCCAATATATTGAGAATAGACCAGAGATGAAAAGGCAGAGATCAATACAGGAAGAT	
		3241 ACAAAGAAAGGAAATGAGGAGAAGGCAGCGATAACTGAAACTCAGAGGAAGCCATCAGAA	
		3301 GATGAAGTGCTTAATAAAGGTTCAAAGACACCAGTCAGTATGTTGTAGGAGAATTGGCA	
		3361 GCACTAGAGAATGAGCAAAAGCAAATTGACACCCGTGCCGCGCTGGTGGAGAAGCGCCTT	
		3421 CGCTATCTCATGGACACAGGAAGGAACACAGAAGAAGAAGCTATGATGCAGGAATGG	
		3481 TTTATGTTAGTTAATAAGAAAAATGCCTTAATAAGGAGAATGAACCAGCTGTCTTCTTCTG	
		3541 GAAAAAGAACATGATTTAGAACGCCGGTATGAACTGCTGAATCGGGAATTGCGGGCAATG	
		3601 CTGGCCATTGAAGACTGGCAGAAGACCGAGGCCCAGAAGCGACGCGAGCAACTCCTGCTG	
		3661 GATGAGCTGGTGGCCCTCGTGAAACAGCGCGACGCGCTAGTCAGGGACCTGGACGCGCAG	
		3721 GAGAAGCAGGCCGAAGAAGAAGATGAGCATTTGGAGCGAACTCTGGAGCAAAACAAAGGC	
		3781 AAGATGGCCAAGAAAGAGGAGAAATGTGTTCTTCAGTAGCCATCAGATCAGAAAGAATCT	
		3841 CTCCCAACATTTTAGAGTCTTGCTTCCCAAACCAGAAAAAGTCAGACTCATTGTTGATTT	
		3901 AAAACTTTAACATTTTGTTTGGCTGGATTTGTACTACTTTACCTCTACTTTACCACCACC	
		3961 ACCCTTTCCTCCCTCCTTTCCAAATAATATACAGAACTCCAAAATAGCTTCATTTAAGG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		4021 ATTTTTTTGTGAGTTAACAATTTCCTTGAAATCCTGTGAAATAGATTTGCACAGACACCT 4081 TGTGAGTGATTGGTATTGGAGGTGTTCAAGAAACTGTTCGAAAAAGAACAAAAACACTTC 4141 CCTCGTTATTTTCTCTCATTTTTTGATGAGAGGAAAATTTGAAACATTATTCTTGTTGTT 4201 GTTGGTAATAGCATAATGACAGTGGGAGGGGTACAAGGGGATAAGAAAAATGTCATGATT 4261 TTTTTCCGGTCCTGCCATATCTAACACTGACTCTGTTACCTAAATTTTATAGTTAGATCA 4321 TATTCAATCTGCTTATTAAACTGTGTTCTATTTACCAGTGGGATTTTCTGCAGTTGTTTT 4381 GCGTTTCACTGTAAGGATAATAGAGCTCCTCTCCTCGCTTTCTTCAGAGGATGGCTCTG 4441 TAACCTAGCCTGAGACAAGTCCTGTGATTTTAAAGGTGAGCTGTGAGGATGGGACTAATTG 4501 ACATGCATCAGTTTACAAAGACGGGCTTATCATCTGAGAATGCGCCATCTTTTTCTCTGG 4561 ATAATTATTTATTACTTCTAGCTTGGTTCCTACAATTTTGTTGGGTCTCAACATTGGCTC 4621 AAGAATGCTGTTAATATTTATTCTGTATTGATAAAAGTCTGTCTTGCCACTATGAGTAAA 4681 TCCCCCAATTAATATTTTCTTCTCTAGCATCGCACTGTCATTTTTTGTGAAAATGGTTAT 4741 CTGTTTATTTTATTACATATCTGAGTCATATATAAATTTTCAATAAAGCAGAAACTTTCT 4801 TACCTTAAAAAAAAAAAAAAA 1 M A S V W K R L Q R V G K H A S K F Q F 1 ATGGCTTCAGTTTGGAAGAGACTGCAGCGTGTGGGAAAACATGCATCCAAGTTCCAGTTT 21 V A S Y Q E L M V E C T K K W Q P D K L 61 GTGGCCTCCTACCAGGAGCTCATGGTTGAGTGTACGAAGAAATGGCAACCAGATAAACTG 41 V V V W T R R S R R R K S S K A H S W Q P 121 GTGGTAGTTTGGACCAGAAGAAGCCGAAGGAAGTCTTCTAAGGCACATAGCTGGCAACCT 61 G I K N P Y Y R G V V V V W P V P E N N I E I 181 GGAATAAAAAATCCCTATCGTGGTGTTGTTGTGGCCTGTTCCTGAAAACATTGAAATC 81 T V T L F K D P P H A E E F F E D K E W T F 241 ACTGTAACACTTTTTAAGGATCCTCATGCGGAAGAATTTGAAGACAAAGAGTGGACATTT 101 V I E N E S P S G R R R K A L A T S S I N 301 GTCATAGAAAATGAATCCCCTTCTGGTCGAAGGAAAGCTCTTGCTACTAGCAGCATCAAT 121 M K Q Y A S P M P T Q T D V K L K F K P 361 ATGAAACAGTATGCAAGCCCTATGCCAACTCAGACTGATGTCAAGTTAAAATTCAAGCCA 141 L S K K V V S A A L Q F S L S C I F L R 421 TTATCTAAAAAAGTTGTATCTGCCGCTCTTCAGTTTTCATTATCTTGCATTTTTCTGAGG 161 E G K A T D E D M Q S L A S L M S M K Q 481 GAAGGAAAAGCCACAGATGAAGACATGCAAAGTTTGGCTAGTTTGATGAGTATGAAGCAG 181 A D I G N L D D F E E D N E D D D E N R	SEQ ID NO:175

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		541 GCTGACATTGGCAATTTAGATGACTTCGAAGAAGATAATGAAGATGATGATGAGAACAGA	
		201 V N Q E E K A A K I T E L I N K L N F L 601 GTGAACCAAGAAGAAAAGGCAGCTAAAATTACAGAGCTTATCAACAAACTTAACTTTTTG	
		221 D E A E K D L A T V N S N P F D D P D A 661 GATGAAGCAGAAAAGGACTTGGCCACCGTGAATTCAAATCCATTTGATGATCCTGATGCT	
		241 A E L N P F G D D P D S E E P I T E T A S 721 GCAGAATTAAATCCATTTGGAGATCCTGACTCAGAAGAACCTATCACTGAAACAGCTTCA	
		261 P R K T E D S F Y N N S Y N P F K E V Q 781 CCTAGAAAAACAGAAGACTCTTTTTATAATAACAGCTATAATCCCTTTAAAGAGGTGCAG	
		281 T P Q Y L N P F D E P E A F V T I K D S 841 ACTCCACAGTATTTGAACCCATTCGATGAGCCAGAAGCATTTGTGACCATAAAGGATTCT	
		301 P P Q S T K R K N I R P V D M S K Y L Y 901 CCTCCCCAGTCTACAAAAAGAAAAAATATAAGACCTGTGATATGAGCAAGTACCTCTAT	
		321 A D S S K T E E E E L D E S N P F Y E P 961 GCTGATAGTTCTAAAACTGAAGAAGAATTGGATGAATCAAATCCTTTTTATGAACCT	
		341 K S T P P P N N L V N P V Q E L E T E R 1021 AAATCAACTCCTCCTCCAAATAATTTGGTAAATCCTGTTCAAGAACTAGAAACTGAAAGG	
		361 R V K R K A P P P V L S P K T G V L N 1081 CGAGTGAAAAGAAAGGCCCCGGCTCCACCAGTCCTCTCACCAAAAACAGGAGTATTAAAT	
		381 E N T V S A G K D L S T S P K P S P I P 1141 GAAAACACAGTTTCTGCAGGAAAAGATCTCTCTACTTCTCCTAAGCCAAGCCCTATACCA	
		401 S P V L G R K P N A S Q S L L V W C K E 1201 AGTCCTGTTTTGGGGCGAAAGCCAAATGCTAGTCAGTCTTTGCTTGTATGGTGTAAAGAA	
		421 V T K N Y R G V K I T N F T T S W R N G 1261 GTTACAAAGAACTACCGAGGAGTAAAAATCACCAATTTTACTACATCGTGGAGAAATGGT	
		441 L S F C A I L H H F R P D L I D Y K S L 1321 TTATCTTTTTGTGCAATATTACACCACTTTAGACCAGATTTAATTGACTACAAGTCTCTG	
		461 N P Q D I K E N N K K A Y D G F A S I G 1381 AATCCTCAAGATATTAAAGAGAACAACAAAAAGGCATACGATGGATTTGCCAGCATAGGA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		481 I S R L L E P S D M V L L A I P D K L T 1441 ATTTCCCGATTATTGGAACCTTCTGATATGGTATTATTAGCAATTCCTGATAAACTGACT	
		501 V M T Y L Y Q I R A H F S G Q E L N V V 1501 GTTATGACTTATCTCTATCAAATAAGGGCACATTTCAGTGGCCAAGAACTAAATGTCGTT	
		521 Q I E E N S S K S T Y K V G N Y E T D T 1561 CAGATAGAGGAAAACAGCAGTAAAAGCACATATAAAGTTGGAAACTATGAAACAGATACA	
		541 N S S V D Q E K F Y A E L S D L K R E P 1621 AACAGTTCTGTTGATCAAGAAAAATTCTATGCAGAGCTTAGTGATCTGAAGCGGGAGCCT	
		561 E L Q Q P I S G A V D F L S Q D D S V F 1681 GAACTACAACAGCCTATCAGCGGAGCAGTAGACTTCTTATCACAGGATGACTCTGTATTT	
		581 V N D S G V G E S E S E H Q T P D D H L 1741 GTAAATGATAGCGGGGTTGGAGAGTCAGAAAGTGAGCATCAAACTCCTGATGATCACCTT	
		601 S P S T A S P Y C R R T K S D T E P Q K 1801 AGTCCAAGCACAGCCTCCCCTTACTGTCGCAGGACTAAAAGTGACACAGAACCCCAGAAG	
		621 S Q Q S S G R T S G S D D P G I C S N T 1861 TCTCAGCAGAGCTCTGGAAGGACTTCAGGATCTGATGACCCTGGAATATGTTCCAATACA	
		641 D S T Q A Q V L L G K K R L L K A E T L 1921 GATTCAACCCAAGCACAGGTTTTGTTAGGCAAAAAGAGACTATTGAAGCTGAGACTTTA	
		661 E L S D L Y V S D K K K D M S P P F I C 1981 GAATTGAGTGACTTATATGTTAGTGATAGAAGGATATGTCTCCACCCTTTATTTGT	
		681 E E T D E Q K L Q T L D I G S N L E K E 2041 GAGGAGACAGATGAACAAAAGCTTCAAACTCTAGACATCGGTAGTAACTTGGAGAAAGAA	
		701 K L E N S R S L E C R S D P E S P I K K 2101 AAATTAGAGAATTCCAGATCCTTAGAATGCAGATCAGAATCCAGAATCTCCTATCAAAAAA	
		721 T S L S P T S K L G Y S Y S R D L D L A 2161 ACAAGTTTATCTCCTACTTCTAACTTGGATACTCATATAGTAGAGATCTAGACCTTGCT	
		741 K K K H A S L R Q T E S D P D A D R T T 2221 AAGAAAAAACATGCTTCCCTGAGGCAGACGGAGTCTGATCCAGATGCTGATAGAACCACT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		761 L N H A D H S S K I V Q H R L L S R Q E 2281 TTAAATCATGCAGATCATTCATCAAAAATAGTCCAGCATCGATTGTTATCTAGACAAGAA	
		781 E L K E R A R V L L E Q A R R D A A L K 2341 GAACTTAAGGAAAGAGCAAGAGTTCTGCTTGAGCAAGCAAGAAGATGCAGCCTTAAAG	
		801 A G N K H N T N T A T P F C N R Q L S D 2401 GCGGGGAATAAGCACAATACCAACACAGCCACCCCATTCTGCAACAGGCAGCTAAGTGAT	
		821 Q Q D E E R R R Q L R E E R A R Q L I A E 2461 CAGCAAGATGAAGAGCGACGTCGGCAGCTGAGAGAGAGCGCTCGTCAGCTAATAGCAGAA	
		841 A R S G V K M S E L P S Y G E M A A E K 2521 GCTCGATCTGGAGTGAAGATGTCAGAACTTCCCAGCTATGGTGAAATGGCTGCAGAAAAG	
		861 L K E R S K A S G E Q N S K L V D L K L 2581 TTGAAAGAAAGGTCAAAGGCATCTGGAGAACAAAACAGTAAGTTGGTGGACTTGAAGCTG	
		881 K K L L E V Q P Q V A N S P S S A A A Q K 2641 AAGAAGCTCCTAGAAGTTCAGCCACAGGTGGCAAATTCACCCTCCAGTGCTGCCCAGAAA	
		901 A V T E S S E Q D M K S G T E D L R T E 2701 GCTGTAACTGAGAGCTCAGAGCAGGACATGAAAAGTGGCACAGAAGATCTCCGGACTGAA	
		921 R L Q K T T E R F R N P V V F S K D S T 2761 CGATTACAAAAAACAACAGAACGTTTTAGAAATCCTGTTGTTCAGCAAAGATTCTACA	
		941 V R K T Q L Q S F S Q Y I E N R P E M K 2821 GTCAGAAAAACTCAACTTCAGTCTTTCAGCCAATATATTCAGAATAGACCAGAGATGAAA	
		961 R Q R S I Q E D T K K G N E E K A A I T 2881 AGGCAGAGATCAATACAGGAAGATACAAAGAAAGGAAATGAGGAGAAGGCAGCGATAACT	
		981 E T Q R K P S E D E V L N K G F K D T S 2941 GAAACTCAGAGGAAGCCATCAGAAGATGAAGTGCTTAATAAAGGGTTCAAAGACACCAGT	
		1001 Q Y V V G E L A A L E N E Q K Q I D T R 3001 CAGTATGTTGTAGGAGAATTGGCAGCACTAGAGAATGAGCAAAAGCAAATTGACACCCGT	
		1021 A A L V E K R L R Y L M D T G R N T E E 3061 GCCGCGCTGGTGGAGAAGCGCCTTCGCTATCTCATGGACACAGGAAGGAACACAGAAGAA	
		1041 E E A M M Q E W F M L V N K K N A L I R	

Gene Name	GenBank HomoLogy	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		3121 GAAGAAGCTATGATGCAGGAATGGTTTATGTTAGTTAATAAGAAAAATGCCTTATAAGG 1061 R M N Q L S L L E K E H D L E R R Y E L 3181 AGAATGAACCAGCTGTCTCTTCTGGAAAAAGAACATGATTTAGAACGCCGGTATGAACTG 1081 L N R E L R A M L A I E D W Q K T E A Q 3241 CTGAATCGGGAATTGCGGGCAATGCTGGCCATTGAAGACTGGCAGAAGACCGAGGCCCAG 1101 K R R E Q L L L D E L V A L V K Q R D A 3301 AAGCGACGCGAGCAACTCCTGCTGGATGAGCTGGTGGCCCTCGTGAAACAGCGCGACGCG 1121 L V R D L D A Q E K Q A E E E D E H L E 3361 CTAGTCAGGGACCTGGACGCGCAGGAGAAGCAGGCCGAAGAAGAGATGAGCATTTGGAG 1141 R T L E Q N K G K M A K K E E K C V L Q 3421 CGAACTCTGGAGCAAAACAAGGCAAGATGGCCAAGAAAGAGGAGAAATGTGTTCTTCAG 1161 - 3481 TAG	
WBC039F12.bFSP_20021101.esd	Leu-8 pan leukocyte antigen	1 ctcccttttgg gcaaggacct gagacccttg tgctaagtca agaggctcaa tgggctgcag 61 aagaactaga gaaggaccaa gcaaagccat gatatttcca tggaaatgtc agagcaccca 121 gagggactta tggaacatct tcaagtttgtg ggggtggaca atgctctgtt gtgatttcct 181 ggcacatcat ggaaccgact gctggactta ccattattct gaaaaccca 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 ggccccagtg 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 cccctggcca gcttcagctt tacctctgca tgtaccttca tctgctcaga 961 aggaactgag ttaattggga agaagaaaac catttgtgaa 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 gcccttggtg aaagaaattt cttggaatac taaaaatcat gagatccttt 1261 aaatccttcc atgaaacgtt ttgtgtggtg gcacctccta cgtcaaacat gaagtgtgtt	SEQ ID NO:176

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1321 tccttcagtg catctgggaa gatttctacc tgaccaacag ttccttcagc ttccatttcg 1381 cccctcattt atccctcaac ccccagccca caggtgttta tacagctcag ctttttgtct 1441 tttctgagga gaaacaaata agaccataaa gggaaaggat tcatgtggaa tataaagatg 1501 gctgactttg ctcttttctg actcttgttt tcagtttcaa ttcagtgctg tacttgatga 1561 cagacacttc 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 gtttctttta tcacgatatt attagtaaga aaacatcact gaaatgctag ctgcaagtga 2041 catctctttg atgtcatatg gaagagttaa aacaggtgga gaaattcctt gattcacaat 2101 gaaatgctct cctttcccct gccccagac cttttatccg acttacctag attctacata 2161 ttctttaaat ttcatctcag gcctccctca acccaccac ttcttttata actagtcctt 2221 tactaatcca acccatgatg agctcctctt cctggcttct tactgaaagg ttaccctgta 2281 acatgcaatt ttgcatttga ataaagcctg cttttaagt gtt 1 M G C R R T R E G P S K A M I F P W K C 1 ATGGGCTGCAGAAGAACTAGAGAAGGACCAAGCAAAGCCATGATATTTCCATGGAAATGT 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 TGTGATTTCCTGGCACATCATGGAACCGACTGCTGGACTTACCATTATTCTGAAAAACCC 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 TGGATAGGAATCCGGAAGATAGGAGGAATATGGACGTGGGTGGGAACCAACAAATCTCTC 121 T E E A E N W G D G E P N N K K N K E D 361 ACTGAAGAAGCAGAGAACTGGGGAGATGGTGAGCCCAACAACAAGAAGAACAAGGAGGAC 141 C V E I Y I K R N K D A G K W N D D A C 421 TGCGTGGAGATCTATATCAAGAGAAACAAAGATGCAGGCAAATGGAACGATGACGCCTGC	SEQ ID NO:177

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		161 H K L K A A L C Y T A S C Q P W S C S G 481 CACAAACTAAAGGCAGCCCTCTGTTACACAGCTTCTTGCCAGCCCTGGTCATGCAGTGGC 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 K T I C E S S G 901 ATCTGCTCAGAAGGAACTGAGTTAATTGGGAAGAAAACCATTTGTGAATCATCTGGA 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 TTGGCATTTATCATTTGGCTGGCAAGGAGATTAAAAAAGGCAAGAAATCCAAGAGAAGT 381 M N D P Y - 1141 ATGAATGACCCATATTAA	
WBC039G08.bFSP_20021101.esd	Human Lyn B protein mRNA.	1 GAAACTTTCACGCGAGCGGGAAATATGGGATGTATAAAATCAAAAGGGAAAGACAGCTTG 61 AGTGACGATGGAGTAGATTTGAAGACTCAACCAGTTCCAGAATCTCAGCTTTACCTGGA 121 CAGAGGTTTCAAACTAAAGATCCAGAGGAACAAGGAGACATTGTGGTAGCCTTGTACCCC 181 TATGATGGCATCCACCCGGACGACTTGTCTTTCAAGAAAGGAGAGAGATGAAAGTCCTG 241 GAGGAGCATGGAGAATGGTGGAAAGCAAAGTCCCTTTTAACAAAAAAGAAGGCTTCATC 301 CCCAGCAACTATGTGGCCAAACTCAACACCTTAGAAACAGAAGAGTGGTTTTTCAAGGAT	SEQ ID NO:178

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		361 ATAACCAGGAAGGACGCAGAAAGGCAGCTTTTGGCACCAGGAAATAGCGCTGGAGCTTTC 421 CTTATTAGAGAAAGTGAAACATTAAAGGAAGCTTCTCTCTCTGTCTGTCAGAGACTTTGAC 481 CCTGTGCATGGTGATGTTATTAAGCACTACAAAATTAGAAGTCTGGATAATGGGGCTAT 541 TACATCTCTCCACGAATCACTTTCCCTGTATCAGCGACATGATTAAACATTACCAAAAG 601 CAGGCAGATGGCTTGTGCAGAAGATTGGAGAAGGCTTGTATTAGTCCCAAGCCACAGAAG 661 CCATGGGATAAAGATGCCTGGGAGATCCCCCGGGAGTCCATCAAGTTGGTGAAAAGGCTT 721 GGCGCTGGGCAGTTTGGGGAAGTCTGGATGGGTTACTATACAACAGTACCAAGGTGGCT 781 GTGAAAACCCTGAAGCCAGGAACTATGTCTGTGCAAGCCTTCCTGGAAGAAGCCAACCTC 841 ATGAAGACCCTGCAGCATGACAAGCTCGTGAGGCTCTACGCTGTGGTCACCAGGGAGGAG 901 CCCATTTACATCATCACCGAGTACATGGCCAAGGGCAGTTTGCTGGATTTCCTGAAGAGC 961 GATGAAGGTGGCAAAGTGCTGCTTCCAAAGCTCATTGACTTTTCTGCTCAGATTGCAGAG 1021 GGAATGGCATACATTGAGAGGAAAAACTACATTCACCGGGACCTGCGAGCAGCAAACGTC 1081 CTGGTCTCCGAGTCGCTCATGTGCAAAATTGCGGATTTTGGGCTTGCTCGAGTGATTGAA 1141 GATAACGAGTACACAGCAGGAAGGTGCTAAATTCCCCATCAAGTGGACTGCTCCAGAA 1201 GCAATCAATTTTGGATGTTTCACTATTAAGTCTGACGTGTGGTCCTTCGGAATCCTCCTG 1261 TATGAAATCGTCACCTATGGGAAAATCCCCTACCCAGGGAGAACTAATGCCGACGTGATG 1321 ACTGCCCTGTCACAGGGCTACAGGATGCCCCCGCATGGAGAACTGCCCAGATGAGCTCTAT 1381 GACATCATGAAAATGTGCTGGAAAGAAAAGGCGGAAGAGAGGCCGACGTTTGATTACTTA 1441 CAGAGCGTCCTGGATGATTTCTACACTGCCACGGAAGGGCAGTATCAGCAGCAGCCTTAG 1501 AGCGCAGGAAGACCCGTC	SEQ ID NO:179
		1 M G C I K S K G K D S L S D D D G V D L K 1 ATGGGATGTATAAAATCAAAAGGGAAAGACAGCTTGAGTGACGATGGAGTAGATTTGAAG	
		21 T Q P V P E S Q L L P G Q R F Q T K D P 61 ACTCAACCAGTTCCAGAATCTCAGCTTTTACCTGGACAGAGGTTTCAAACTAAAGATCCA	
		41 E E Q G D I V V A L Y P Y D G I H P D D 121 GAGGACAAGGAGACATTGTGGTAGCCTTGTACCCCTATGATGGCATCCACCCGGACGAC	
		61 L S F K K G E K M K V L E E H G E W W K 181 TTGTCTTTCAAGAAAGGAGAGATGAAAGTCCTGGAGGAGCATGGAGAATGGTGGAAA	
		81 A K S L L T K K E G F I P S N Y V V A K L 241 GCAAAGTCCCTTTAACAAAAAAGAAGGCTTCATCCCCAGCAACTATGTGGCCCAAACTC	
		101 N T L E T E E W F F K D I T R K D A E E R 301 AACACCTTAGAAACAGAAGAGTGGTTTTTCAAGGATATAACCAGGAAGGACGCAGAAAGG	
		121 Q L L A P G N S A G A F L I R E S E T L 361 CAGCTTTTGGCACCAGGAAATAGCGCTGGAGCTTTCCTTATTAGAGAAAGTGAAACATTA	
		141 K G S F S L S V R D F D P V H G D V I K	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		421 AAAGGAAGCTTCTCTCTGTCTGTCAGAGACTTTGACCCTGTGCATGGTGATGTTATTAAG	
		161 H Y K I R S L D N G G Y Y I S P R I T F	
		481 CACTACAAAATTAGAAGTCTGGATAATGGGGGCTATTACATCTCTCCACGAATCACTTTT	
		181 P C I S D M I K H Y Q K Q A D G L C R R	
		541 CCCTGTATCAGCGACATGATTAAACATTACCAAAAGCAGGCAGATGGCTTGTGCAGAAGA	
		201 L E K A C I S P K P Q K P W D K D A W E	
		601 TTGGAGAAGGCTTGTATTAGTCCCAAGCCACAGAAGCCATGGATAAAGATGCCTGGGAG	
		221 I P R E S I K L V K R L G A G Q F G E V	
		661 ATCCCCCGGGAGTCCATCAAGTTGGTGAAAAGGCTTGGCGCTGGGCAGTTTGGGGAAGTC	
		241 W M G Y Y N N S T K V A V K T L K P G T	
		721 TGGATGGGTTACTATAACAACAGTACCAAGGTGGCTGTGAAAACCCTGAAGCCAGGAACT	
		261 M S V Q A F L E E A N L M K T L Q H D K	
		781 ATGTCTGTGCAAGCCTTCCTGGAAGAAGCCAACCTCATGAAGACCCTGCAGCATGACAAG	
		281 L V R L Y A V V T R E E P I Y I I T E Y	
		841 CTCGTGAGGCTCTACGCTGTGGTCACCAGGGAGGAGCCCATTTACATCATCACCGAGTAC	
		301 M A K G S L L D F L K S D E G G K V L L	
		901 ATGGCCAAGGGCAGTTTGCTGGATTTCCTGAAGAGCGATGAAGGTGGCAAAGTGCTGCTT	
		321 P K L I D F S A Q I A E G M A Y I E R K	
		961 CCAAAGCTCATTGACTTTTCTGCTCAGATTGCAGAGGGAATGGCATACATTGAGAGGAAA	
		341 N Y I H R D L R A A N V L V S E S L M C	
		1021 AACTACATTCACCGGGACCTGCGAGCAGCAAACGTCCTGGTCTCCGAGTCGCTCATGTGC	
		361 K I A D F G L A R V I E D N E Y T A R E	
		1081 AAAATTGCGGATTTTGGGCTTGCTCGAGTGATTGAAGATAACGAGTACACAGCAAGGGAA	
		381 G A K F P I K W T A P E A I N F G C F T	
		1141 GGTGCTAAATTCCCCATCAAGTGGACTGCTCCAGAAGCAATCAATTTTGGATGTTTCACT	
		401 I K S D V W S F G I L L Y E I V T Y G K	
		1201 ATTAAGTCTGACGTGTGGTCCTTCGGAATCCTCCTGTATGAAATCGTCACCTATGGGAAA	
		421 I P Y P G R T N A D V M T A L S Q G Y R	
		1261 ATCCCCTACCCAGGGAGAACTAATGCCGACGTGATGACTGCCCTGTCACAGGGCTACAGG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		441 M P R M E N C P D E L Y D I M K M C W K 1321 ATGCCCCGCATGGAGAACTGCCCAGATGAGCTCTATGACATCATGAAAATGTGCTGGAAA 461 E K A E E R P T F D Y L Q S V L D D F Y 1381 GAAAAGGCGGAAGAGAGGCCGACGTTTGATTACTTACAGAGCGTCCTGGATGATTTCTAC 481 T A T E G Q Y Q Q Q P - 1441 ACTGCCACGGAAGGGCAGTATCAGCAGCAGCCTTAG	
WBC040E12.bFSP_20021101.esd	Homo sapiens 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 121 AGCTTCCAGAGGACGGGAACACTTGCCTTTGAGCGGGTCTACACTGCCAACCAAAACTGT 61 V D A 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	SEQ ID NO:180 SEQ ID NO:181

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		301 TATCTGGGAGAGAGAAGGCAGAGCACACCCGGCTACATATTTGGGAAACGCATCATACTG 121 F L F L M S L A G I F N Y Y L I L F F G 361 TTCCTGTTCCTCATGTCCCTTGCTGGAATATTCAACTATTATCTCATCCTCTTTTTCGGA 141 S D F E N Y I K T I T T T I S P L L L I 421 AGTGACTTTGAAAACTACATAAAGACGATAACCACCACCATCTCCCCTCTACTTCTCATT 161 P - 481 CCCTAA	
WBC043B10.bFSP_20021401.esd	H.sapiens mRNA for P1 protein (P1.h).	1 CGGCACGAGGCGACTTTGGTGGAGGTAGTTCTTTGGCAGCGGGCATGGCGGGTACCGTGG 61 TGCTGGACGATGTGGAGCTGCGGGAGGCTCAGAGAGATTACCTGGACTTCCTGGACGACG 121 AGGAAGACCAGGGAATTTATCAGAGCAAAGTTCGGGAGCTGATCAGTGACAACCAATACC 181 GGCTGATTGTCAATGTGAATGACCTGCGCAGGAAAAACGAGAAGAGGGCTAACCGGCTTC 241 TGAACAATGCCTTTGAGGAGCTGGTTGCCTTCCAGCGGGCCTTAAAGGATTTTGTGGCCT 301 CCATTGATGCTACCTATGCCAAGCAGTATGAGGAGTTCTACGTAGGACTGGAAGGCAGCT 361 TTGGCTCCAAGCACGTCTCCCCGCGGACTCTTACCTCCTGCTTCCTCAGCTGTGTGGTCT 421 GTGTGGAGGGCATTGTCACTAAATGTTCTCTAGTTCGTCCCAAAGTCGTCCGCAGTGTCC 481 ACTACTGTCCTGCTACTAAGAAGACCATAGAGCGACGTTATTCTGATCTCACCACCCTGG 541 TGGCCTTTCCCTCCAGCTCTGTCTATCCTACCAAGGATGAGGAGAACAATCCCCTTGAGA 601 CAGAATATGGCCTTTCTGTCTACAAGGATCACCAGACCATCACCATCCAGGAGATGCCGG 661 AGAAGGCCCCAGCCGGCCAGCTCCCCCGCTCTGTGGACGTCATTCTGGATGATGACTTGG 721 TGGATAAAGCGAAGCCTGGTGACCGGGTTCAGGTGGTGGGAACCTACCGTTGCCTTCCTG 781 GAAAGAAGGGAGGCTACACCTCTGGGACCTTCAGGACTGTCCTGATTGCCTGTAATGTTA 841 AGCAGATGAGCAAGGATGCTCAGCCCTCTTTCTCTGCTGAGGATATAGCCAAGATCAAGA 901 AGTTCAGTAAAACCCGATCCAAGGATATCTTTGACCAGCTGGCCAAGTCATTGGCCCCAA 961 GTATCCATGGGCATGACTATGTCAAGAAAGCAATCCTCTGCTTGCTCTTGGGAGGGGTGG 1021 AACGAGACCTAGAAAATGGCAGCCACATCCGTGGGGACATCAATATTCTTCTAATAGGAG 1081 ACCCATCCGTTGCCAAGTCTCAGCTTCTGCGGTATGTGCTTTGCACTGCACCCCGAGCTA 1141 TCCCCACCACTGGCCGGGGCTCCTCTGGAGTGGGTCTGACGGCTGCTGTCACCACAGACC 1201 AGGAAACAGGAGAGCGCCGTCTGGAAGCAGGGGCCATGGTCCTGGCTGACCGAGGCGTGG 1261 TTTGCATCGATGAATTTGACAAGATGTCTGACATGGACCGCACGGCCATCCACGAAGTGA 1321 TGGAGCAGGGTCGAGTCACTATCGCCAAGGCTGGCATCCATGCTCGACTGAATGCCCGCT 1381 GCAGTGTTTTAGCAGCTGCCAACCCCGTCTATGGCAGGTATGATCAGTACAAGACCCCTA 1441 TGGAGAACATCGGGCTGCAGGACTCCCTGCTCTCCCGATTTGACTTGCTCTTCATCATGC 1501 TGGATCAGATGGACCCTGAGCAGGATCGGGAGATCTCGGACCATGTCCTTAGGATGCACC 1561 GTTACAGGGCACCTGGGGAGCAGGATGGCGATGCTATGCCTTTGGGTAGTGCTGTGGATA 1621 TCCTGGCTACAGACGATCCCAACTTTAGCCAGGAAGACCAGCAGGACACCCAGATTTATG 1681 AGAAGCATGACAACCTTCTGCATGGGACCAAGAAGAAAAAGGAGAAGATGGTGAATGCAG 1741 CTTTCATGAAGAAGTACATCCACGTGGCCAAAATCATCAAGCCCATCCTAACACAGGAGT 1801 CAGCTGCTTACATTGCAGAAGAGTACTCCCGCCTGCGCAGCCAAGACAGCATGAGCTCGG	SEQ ID NO:182

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1861 ACACCGCCAGGACATCTCCAGTTACAGCCCGGACGCTGGAAACTCTGATTCGCTTAGCCA 1921 CAGCCCATGCCAAGGCTCGCATGAGCAAGACGGTGGACCTGCAGGACGCCGAGGAAGCTG 1981 TGGAGTTGGTCCAGTATGCTTACTTTAAGAAGGTTCTGGAGAAGGAGAAGAAACGTAAGA 2041 AGCGAAGTGAGGATGAATCAGAGACAGAAGATGAAGAGGAGAAAAGCCAAGAGGACCAGG 2101 AGCAGAAGAGGAAGAGGAAGACTCGCCAGCCAGATGCCAAAGATGGGGATTCATACG 2161 ACCCCTATGACTTCAGTGACACAGAGGAGGAAATGCCTCAAGTACACACTCCAAAGACGG 2221 CAGACTCACAGGAGACCAAGGAATCCCAGAAAGTGGAGTTGAGTGAATCCAGGTTGAAGG 2281 CATTCAAGGTGCCCCTCTTGGATGTGTTCCGGGAAGCTCATGCGCAGTCAATCGGCATGA 2341 ATCGCCTCACAGAATCCATCAACCGGGACAGCGAAGAGCCCTTCTCTTCAGTTGAGATCC 2401 AGGCTGCTCTGAGCAAGATGCAGGATGACAATCAGGTCATGGTGTCTGAGGGCATCATCT 2461 TCCTCATCTGAGGAGGCCTCGTCTCTGAACTTGGGTTGTGCCGAGAGAGTTTGTTCTGTG 2521 TTTCCCACCCTCTCCCTGACCCAAGTCTTTGCCTCTTACTCCCTTAACAGTGTTGAATTCA 2581 ACTGAAGGCGAGGAATGTTGGTGATGAAGCTGAGTTCAGGAGTCGGTGGAAGCCTTGGGA 2641 ATGGGCAATGAAAGCTGCCGTGAGGTAAAGAGAAGAAAGTAGGAAGGACCAGACTATTG 2701 CTTCTTCATTGCAAAAGCACTGGCTCATCCGCCCTACTTCCCATCCCACACAAACCCAAT 2761 TGTAAATAACATATGACTTCTGATTAATTTCGGGGGCACAACTGTTTTCTGTTTGCTGTT 2821 TTTTTGTTTTGTTTTCTTCCTCCCGAGCACTTTGGTCCAGAATAGGCTTTGGATTGTTTT 2881 ATGCTGCTGGAGAGAAGCTCTGAGGCAAGTCATGGAGGCCAAAAAAAGCTTATGTGCAGTA 2941 GCATCAGTTAAGGTGAATATGTATTGTATCACAAACAAACCCAATATCCAGATGAATAT 3001 CCAAGACATTGAATAAACTTACCCATTTCGTACAAAAAAAGGGGGGCCCGGTAAAC	SEQ ID NO:183
		1 M A G T V V L D D V E L R E A Q R D Y L 1 ATGGCGGGTACCGTGGTGCTGGACGATGTGGAGCTGCGGGAGGCTCAGAGAGATTACCTG	
		21 D F L D D E E D Q G I Y Q S K V R E L I 61 GACTTCCTGGACGACGAGGAAGACCAGGGAATTTATCAGAGCAAAGTTCGGGAGCTGATC	
		41 S D N Q Y R L I V N V N D L R R K N E K 121 AGTGACAACCAATACCGGCTGATTGTCAATGTGAATGACCTGCGCAGGAAAAACGAGAAG	
		61 R A N R L L N N A F E E L V A F Q R A L 181 AGGGCTAACCGGCTTCTGAACAATGCCTTTGAGGAGCTGGTTGCCTTCCAGCGGGCCTTA	
		81 K D F V A S I D A T Y A K Q Y E E F Y V 241 AAGGATTTTGTGGCCTCCATTGATGCTACCTATGCCAAGCAGTATGAGGAGTTCTACGTA	
		101 G L E G S F G S K H V S P R T L T S C F 301 GGACTGGAAGGCAGCTTTGGCTCCAAGCACGTCTCCCCGCGGACTCTTACCTCCTGCTTC	
		121 L S C V V C V E G I V T K C S L V R P K 361 CTCAGCTGTGTGGTCTGTGTGGAGGGCATTGTCACTAAATGTTCTCTAGTTCGTCCCAAA	
		141 V V R S V H Y C P A T K K T I E R R Y S	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		421 GTCGTCCGCAGTGTCCACTACTGTCCTGCTACTAGAAGACCATAGAGCGACGTTATTCT	
		161 D L T T L V A F P S S S V Y P T K D E E 481 GATCTCACCACCCTGGTGGCCTTTCCCTCCAGCTCTGTCTATCCTACCAAGGATGAGGAG	
		181 N N P L E T E Y G L S V Y K D H Q T I T 541 AACAATCCCCTTGAGACAGAATATGGCCTTTCTGTCTACAAGGATCACCAGACCATCACC	
		201 I Q E M P E K A P A G Q L P R S V D V I 601 ATCCAGGAGATGCCGGAGAAGGCCCCAGCCGGCCAGCTCCCCCGCTCTGTGGACGTCATT	
		221 L D D D L V D K A K P G D R V Q V V G T 661 CTGGATGATGACTTGGTGGATAAAGCGAAGCCTGGTGACCGGTTCAGGTGGTGGGAACC	
		241 Y R C L P G K K G G Y T S G T F R T V L 721 TACCGTTGCCTTCCTGGAAAGAAGGGAGGCTACACCTCTGGGACCTTCAGGACTGTCCTG	
		261 I A C N V K K Q M S K D D A Q P S F S A E D 781 ATTGCCTGTAATGTTAAGCAGATGAGCAAGGATGCTCAGCCCTCTTTCTCTGCTGAGGAT	
		281 I A K I K K F S K T R S K D I F D Q L A 841 ATAGCCAAGATCAAGAAGTTCAGTAAAACCCGATCCAAGGATATCTTTGACCAGCTGGCC	
		301 K S L A P S I H G H D Y V K K A I L C L 901 AAGTCATTGGCCCCAAGTATCCATGGGCATGACTATGTCAAGAAAGCAATCCTCTGCTTG	
		321 L L G G V E R D L E N G S H I R G D I N 961 CTCTTGGGAGGGGTGGAACGAGACCTAGAAAATGGCAGCCACATCCGTGGGGACATCAAT	
		341 I L L I G D P S V A K S Q L L R Y V L C 1021 ATTCTTCTAATAGGAGACCCATCCGTTGCCAAGTCTCAGCTTCTGCGGTATGTGCTTTGC	
		361 T A P R A I P T T G R G S S G V G L T A 1081 ACTGCACCCCGAGCTATCCCCACCACTGGCCGGGGCTCCTCTGGAGTGGGTCTGACGGCT	
		381 A V T T D Q E T G E R R L E A G A M V L 1141 GCTGTCACCACAGACCAGGAAACAGGAGAGCGCCGTCTGGAAGCAGGGGCCATGGTCCTG	
		401 A D R G V V C I D E F D K M S D M D R T 1201 GCTGACCGAGGCGTGGTTTGCATCGATGAATTTGACAAGATGTCTGACATGGACCGCACG	
		421 A I H E V M E Q G R V T I A K A G I H A 1261 GCCATCCACGAAGTGATGGAGCAGGGTCGAGTCACTATCGCCAAGGCTGGCATCCATGCT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		441 R L N A R C S V L A A A N P V Y G R Y D 1321 CGACTGAATGCCCGCTGCAGTGTTTTAGCAGCTGCCAACCCCGTCTATGGCAGGTATGAT	
		461 Q Y K T P M E N I G L Q D S L L S R F D 1381 CAGTACAAGACCCCTATGGAGAACATCGGGCTGCAGGACTCCCTGCTCTCCCGATTTGAC	
		481 L L F I M L D Q M D P E Q D D R E I S D H 1441 TTGCTCTTCATCATGCTGGATCAGATGGACCCTGAGCCAGGATCGGGAGATCTCGGACCAT	
		501 V L R M H R Y R A P G E Q D G D A M P L 1501 GTCCTTAGGATGCACCGTTACAGGGCACCTGGGGAGCAGGATGGCGATGCTATGCCTTTG	
		521 G S A V D I L A T D D P N F S Q E D Q Q 1561 GGTAGTGCTGTGGATATCCTGGCTACAGACGATCCCAACTTTAGCCAGGAAGACCAGCAG	
		541 D T Q I Y E K H D N L L H G T K K K K E 1621 GACACCCAGATTTATGAGAAGCATGACAACCTTCTGCATGGGACCAAGAAGAAAAAGGAG	
		561 K M V N A A F M K K Y I H V A K I I K P 1681 AAGATGGTGAATGCAGCTTTCATGAAGAAGTACATCCACGTGGCCAAAATCATCAAGCCC	
		581 I L T Q E S A A Y I A E E Y S R L R S Q 1741 ATCCTAACACAGGAGTCAGCTGCTTACATTGCAGAAGAGTACTCCCGCCTGCGCAGCCAA	
		601 D S M S S D T A R T S P V T A R T L E T 1801 GACAGCATGAGCTCGGACACCGCCAGGACATCTCCAGTTACAGCCCGGACGCTGGAAACT	
		621 L I R L A T A H A K A R M S K T V D L Q 1861 CTGATTCGCTTAGCCACACCCATGCCAGGCTCGCATGAGCAAGACGGTGGACCTGCAG	
		641 D A E E A V E L V Q Y A Y F K K V L E K 1921 GACGCCGAGGAAGCTGTGGAGTTGGTCCAGTATGCTTACTTTAAGAAGGTTCTGGAGAAG	
		661 E K K R K K R S E D E S E T E D E E E K 1981 GAGAAGAAACGTAAGAAGCGAAGTGAGGATGAATCAGAGACAGAAGATGAAGAGGAGAAA	
		681 S Q E D Q E Q K R K K R R K K T R Q P D A K 2041 AGCCAAGAGGACCAGGAGCAGAAGAGGAAGAGAAGGAAGACTCGCCAGCCAGATGCCAAA	
		701 D G D S Y D P Y D F S D T E E E M P Q V 2101 GATGGGGATTCATACGACCCCTATGACTTCAGTGACACAGAGGAGGAAATGCCTCAAGTA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		721 H T P K T A D S Q E T K E S Q K V E L S 2161 CACACTCCAAAGACGGCAGACTCACAGGAGACCAAGGAATCCCAGAAAGTGGAGTTGAGT 741 E S R L K A F K V A L L D V F R E A H A 2221 GAATCCAGGTTGAAGGCATTCAAGGTGGCCCTCTTGGATGTGTTCCGGGAAGCTCATGCG 761 Q S I G M N R L T E S I N R D S E E P F 2281 CAGTCAATCGGCATGAATCGCCTCACAGAATCCATCAACCGGGACAGCGAAGAGCCCTTC 781 S S V E I Q A A L S K M Q D D N Q V M V 2341 TCTTCAGTTGAGATCCAGGCTGCTCTGAGCAAGATGCAGGATGACAATCAGGTCATGGTG 801 S E G I I F L I - 2401 TCTGAGGGCATCATCTTCCTCATCTGA	SEQ ID NO:184
WBC044E01.bFSP_20021501.esd	Human lymphocyte dihydropyrimidine dehydrogenase	1 ttcgactcg cgctccggct gctgtcactt ggctctctgg ctggagcttg aggacgcaag 61 gagggtttgt cactggcaga ctcgagactg taggcactgc catggcccct gtgctcagta 121 aggactcggc ggacatcgag agtatcctgg ctttaaatcc tcgaacacaa actcatgcaa 181 ctctgtgttc cacttcggcc aagaaattag acaagaaaca ttggaaaaga aatcctgata 241 agaactgctt taattgtgag aagctggaga ataatttga tgacatcaag cacacgactc 301 ttggtgagcg aggagctctc cgagaagcaa tgagatgcct gaaatgtgca gatgcccgt 361 gtcagaagag ctgtccaact aatcttgata ttaaatcatt catcacaagt attgcaaaca 421 agaactatta tggagctgct aagatgatat ttctgacaa cccacttggt ctgacttgtg 481 gaatggtatg tccaacctct gatcttgtg taggtggatg caatttatat gccactgaag 541 agggacccat taatattggt ggattgcagc aatttgctac tgaggtattc aaagcaatga 601 gtatcccaca gatcagaaat ccttcgctgc ctcccccaga aaaaatgtct gaagcctatt 661 ctgcaaagat tgctctttt ggtgctgggc ctgcaagtat aagttgtgct tccttttgg 721 ctcgattggg gtactctgac atcactatat ttgaaaaaca agaatatgtt ggtggtttaa 781 gtacttctga aattcctcag ttccggctgc cgtatgatgt agtgaatttt gagattgagc 841 taatgaagga ccttggtgta aagataattt gcggtaaaag cctttcagtg aatgaaatga 901 ctcttagcac tttgaaagaa aaaggctaca aagctgcttt cattggaata ggtttgccag 961 aacccaataa agatgccatc ttccaaggcc tgacgcagga ccagggattt tatacatcca 1021 aagacttttt gccacttgta gccaaaggca gtaaagcagg aatgtgcgcc tgtcactctc 1081 cattgccatc gatacgggga gtcgtgattg tacttggagc tggagacact gcctttgact 1141 gtgcaacatc tgctctacgt tgtggagctc gccgtgtgtt catcgtcttc agaaaaggct 1201 ttgttaatat aagagctgtc cctgaggaga tggaacttgc taaggaagaa aagtgtgaat 1261 ttctgccatt cctgtcccca cggaaggtta tagtaaaagg tgggagaatt gttgctatgc 1321 agtttgttcg gacagagcaa gatgaaactg gaaaatggaa tgaagatgaa gatcagatgg 1381 tccatctgaa agccgatgtg gtcatcagtg cctttggttc agttctgagt gatcctaaag 1441 taaaagaagc cttgagccct ataaaattta acagatgggg tctcccagaa gtagatccag 1501 aaactatgca aactagtgaa gcatgggtat ttgcaggtgg tgatgtcgtt ggtttggcta 1561 acactacagt ggaatcggtg aatgatggaa agcaagcttc ttggtacatt cacaaatacg	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1621 tacagtcaca atatggagct tccgtttctg ccaagcctga actacccctc ttttacactc	
		1681 ctattgatct ggtggacatt agtgtagaaa tggccggatt gaagtttata aatccttttg	
		1741 gtcttgctag cgcaactcca gccaccagca catcaatgat tcgaagagct tttgaagctg	
		1801 gatggggttt tgccctcacc aaaactttct ctcttgataa ggacattgtg acaaatgttt	
		1861 cccccagaat catccgggga accacctctg gccccatgta tggccctgga caaagctcct	
		1921 ttctgaatat tgagctcatc agtgagaaaa cggctgcata ttggtgtcaa agtgtcactg	
		1981 aactaaaggc tgactttcca gacaacattg tgattgctag cattatgtgc agttacaata	
		2041 aaaatgactg gacggaactt gccaagaagt ctgaggattc tggagcagat gccctggagt	
		2101 taaatttatc atgtccacat ggcatgggag aaagaggaat gggcctggcc tgtgggcagg	
		2161 atccagagct ggtgcggaac atctgccgct gggttaggca agctgttcag attcctttt	
		2221 ttgccaagct gacccaaat gtcactgata ttgtgagcat cgcaagagct gcaaaggaag	
		2281 gtggtgccaa tggcgttaca gccaccaaca ctgtcttcagg tctgatggga ttaaaatctg	
		2341 atggcacacc ttggccagca gtgggattg caaagcgaac tacatatgga ggagtgtctg	
		2401 ggacagcaat cagacctatt gctttgagag ctgtgacctc cattgctcgt gctctgcctg	
		2461 gatttcccat tttggctact ggtggaattg actctgctga aagtggtctt cagtttctcc	
		2521 atagtggtgc ttccgtcctc caggtatgca gtgccattca gaatcaggat ttcactgtga	
		2581 tcgaagacta ctgcactggc ctcaaagccc tgctttatct gaaaagcatt gaagaactac	
		2641 aagactggga tggacagagt ccagctactg tgagtcacca gaaagggaaa ccagttccac	
		2701 gtatagctga actcatggac aagaaactgc caagtttgg acctatctg gaacagcgca	
		2761 agaaaatcat agcagaaaac aagattagac tgaaagaaca aaatgtagct ttttcaccac	
		2821 ttaagagaaa ctgttttatc cccaaaaggc ctattcctac catcaaggat gtaataggaa	
		2881 aagcactgca gtaccttgga acatttggtg aattgagcaa cgtagagcaa gttgtggcta	
		2941 tgattgatga agaaatgtgt atcaactgtg gtaaatgcta catgacctgt aatgattctg	
		3001 gctaccaggc tatacagttt gatccagaaa cccacctgcc caccataacc gacacttgta	
		3061 caggctgtac tctgtgtctc agtgtttgcc ctattgtcga ctgcatcaaa atggtttcca	
		3121 ggacaacacc ttatgaacca aagagaggcg taccctatc tgtgaatccg gtgtgttaag	
		3181 gtgatttgtg aaacagttgc tgtgaacttt catgtcacct acatatgctg atcttttaaa	
		3241 atcatgatcc ttgtgttcag ctctttccaa attaaaacaa atatacattt tctaaataaa	
		3301 aatatgtaat ttcaaaatac atttgtaagt gtaaaaaatg tctcatgtca atgaccattc	
		3361 aattagtggt cataaaatag aataatttct ttctgaggat agtagttaaa taactgtgtg	
		3421 gcagttaatt ggatgttcac tgccagttgt cttatgtgaa aaattaactt ttttgtggca	
		3481 attagtgtga cagtttccaa attgccctat gctgtgctcc atatttgatt tctaattgta	
		3541 agtgaaatta agcatttga aacaaagtac tctttaacat acaagaaaat gtatccaagg	
		3601 aaacatttta tcattaaaaa ttacctttaa ttttaatgct gtttctaaga aaatgtagtt	
		3661 agctccataa agtacaaatg aagaaagtca aaaaattatt tgctatggca ggataagaaa	
		3721 gcctaaaatt gagtttgtag aacttatta agtaaaatcc ccttcgctga aattgcttat	
		3781 tttggtgttt ggatagagga tagggagaat atttactaac taaataccat tcactactca	
		3841 tgcgtgagat gggtgtacaa actcatcctc ttttaatggc atttctcttt aaactatgtt	
		3901 cctaacaaaa tgagatgata ggatagatcc tggttaccac tcttttgctg tgcacatacg	
		3961 ggctctgact ggtttaata gtcaccttca tgattatagc aactaatgtt tgaacaaagc	
		4021 tcaaagtatg caatgcttca ttattcaaga atgaaaaata taatgttgat aatatatatt	
		4081 aagtgtgcca aatcagtttg actactctct gttttagtgt ttatgtttaa aagaaatata	
		4141 ttttttgtta ttattagata atattttgt atttcttat tttcataatc agtaaatagt	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		4201 gtcatataaa ctcatttatc tcctcttcat ggcatcttca atatgaatct ataagtagta 4261 aatcagaaag taacaatcta tggcttattt ctatgacaaa ttcaagagct agaaaaataa 4321 aatgtttcat tatgcacttt tagaaatgca tatttgccac aaaacctgta ttactgaata 4381 atatcaaata aaatatcata aagcatttt 1 M A P V L S K D S A D I E S I L A L N P 1 ATGGCCCCCTGTGCTCAGTAAGGACTCGGCGGACATCGAGAGTATCCTGGCTTTAAATCCT 21 R T Q T H A T L C S T S A K K L D K K H 61 CGAACACAAACTCATGCAACTCTGTGTTCCACTTCGGCCAAGAAATTAGACACAAGAAACAT 41 W K R N P D K N C F N C E K L E N N F D 121 TGGAAAAGAAATCCTGATAAGAACTGCTTTAATTGTGAGAAGCTGGAGAATAATTTTGAT 61 D I K H T T L G E R G A L R E A M R C L 181 GACATCAAGCACACACGACTCTTGGTGAGCGAGGAGGCTCTCCGAGAAGCAATGAGATGCCTG 81 K C A D A P P C Q K S C P T N L D I K S F 241 AAATGTGCAGATGCCCCGTGTCAGAAGAGCTGTCCAACTAATCTTGATATTTAAATCATTC 101 I T S I A N K N Y Y G A A K M I F S D N 301 ATCACAAGTATTGCAAACAAGAACTATTATGGAGCTGCTAAGATGATATTTTCTGACAAC 121 P L G L T C G M V C P T S D L C V G G C 361 CCACTTGGTCTGACTTGTGGAATGGTATGTCCAACCTCTGATCTTTGTGTAGGTGGATGC 141 N L Y A T E E G P I N I G G L Q Q F A T 421 AATTTATATGCCACTGAAGAGGGACCCATTAATATTGGTGGATTGCAGCAATTTGCTACT 161 E V F K A M S I P Q I R N P S L P P P E 481 GAGGTATTCAAAGCAATGAGTATCCCACAGATCAGAAATCCTTCGCTGCCTCCCCCAGAA 181 K M S E A Y S A K I A L F G A G P A S I 541 AAAATGTCTGAAGCCTATTCTGCAAAGATTGCTCTTTTTGGTGCTGGGCCTGCAAGTATA 201 S C A S F L A R L G Y S D I T T I F E K Q 601 AGTTGTGCTTCCTTTTTGGCTCGATTGGGGTACTCTGACATCACTATATTTGAAAAACAA 221 E Y V G G L S T S E I P Q F R L P Y D V 661 GAATATGTTGGTGGTTTAAGTACTTCTGAAATTCCTCAGTTCCGGCTGCCGTATGATGTA 241 V N F E I E L M K D L G V K I I C G K S 721 GTGAATTTTGAGATTGAGCTAATGAAGGACCTTGGTGTAAAGATAATTTGCGGTAAAAGC	SEQ ID NO:185

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		261 L S V N E M T L S T L K E K G Y K A A F 781 CTTTCAGTGAATGAAATGACTCTTAGCACTTTGAAAGAAAAAGGCTACAAAGCTGCTTTC	
		281 I G I G L P E P N K D A I F Q G L T Q D 841 ATTGGAATAGGTTTGCCAGAACCCAATAAAGATGCCATCTTCCAAGGCCTGACGCAGGAC	
		301 Q G F Y T S K D F L P L V A K G S K A G 901 CAGGGGTTTTATACATCCAAAGACTTTTTGCCACTTGTAGCCAAAGGCAGTAAAGCAGGA	
		321 M C A C H S P L P S I R G V V I V L G A 961 ATGTGCGCCTGTCACTCTCCATTGCCATCGATACGGGGAGTCGTGATTGTACTTGGAGCT	
		341 G D T A F D C A T S A L R C G A R R V F 1021 GGAGACACTGCCTTTGACTGTGCAACATCTGCTCTACGTTGTGGAGCTCGCCGTGTGTTC	
		361 I V F R K G F V N I R A V P E E M E L A 1081 ATCGTCTTCAGAAAAGGCTTTGTTAATATAAGAGCTGTCCCTGAGGAGATGGAACTTGCT	
		381 K E E K C E F L P F L S P R K V I V K G 1141 AAGGAAGAAAAGTGTGAATTTCTGCCATTCCTGTCCCCACGGAAGGTTATAGTAAAAGGT	
		401 G R I V A M Q F V R T E Q D E T G K W N 1201 GGGAGAATTGTTGCTATGCAGTTTGTTCGGACAGAGCAAGATGAAACTGGAAAATGGAAT	
		421 E D E D Q M V H L K A D V V I S A F G S 1261 GAAGATGAAGATCAGATGGTCCATCTGAAAGCCGATGTGGTCATCAGTGCCTTTGGTTCA	
		441 V L S D P K V K E A L S P I K F N R W G 1321 GTTCTGAGTGATCCTAAAGTAAAAGAAGCCTTGAGCCCTATAAAATTTAACAGATGGGGT	
		461 L P E V D P E T M Q T S E A W V F A G G 1381 CTCCCAGAAGTAGATCCAGAAACTATGCAAACTAGTGAAGCATGGGTATTTGCAGGTGGT	
		481 D V V G L A N T T V E S V N D G K Q A S 1441 GATGTCGTTGGTTTGGCTAACACTACAGTGGAATCGGTGAATGATGGAAAGCAAGCTTCT	
		501 W Y I H K Y V Q S Q Y G A S V S A K P E 1501 TGGTACATTCACAAATACGTACAGTCACACAATATGGAGCTTCCGTTTCTGCCAAGCCTGAA	
		521 L P L F Y T P I D L V D I S V E M A G L 1561 CTACCCCTCTTTTACACTCCTATTGATCTGGTGGACATTAGTGTAGAAATGGCCGGATTG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		541 K F I N P F G L A S A T P A T S T S M I 1621 AAGTTTATAAATCCTTTGGTCTTGCTAGCGGCAACTCCAGCCACCAGCACATCAATGATT	
		561 R R A F E A G W G F A L T K T F S L D K 1681 CGAAGAGCTTTTGAAGCTGGATGGGGTTTTGCCCTCACCAAAACTTTCTCTCTTGATAAG	
		581 D I V T N V S P R I I R G T T S G P M Y 1741 GACATTGTGACAAATGTTTCCCCCAGAATCATCCGGGGAACCACCTCTGGCCCCATGTAT	
		601 G P G Q S S F L N I E L I S E K T A A Y 1801 GGCCCTGGACAAAGCTCCTTTCTGAATATTGAGCTCATCAGTGAGAAAACGGCTGCATAT	
		621 W C Q S V T E L K A D F P D N I V I A S 1861 TGGTGTCAAAGTGTCACTGAACTAAAGGCTGACTTTCCAGACAACATTGTGATTGCTAGC	
		641 I M C S Y N K N D W T E L A K K S E D S 1921 ATTATGTGCAGTTACAATAAAAATGACTGGACGGAACTTGCCAAGAAGTCTGAGGATTCT	
		661 G A D A L E L N L S C P H G M G E R G M 1981 GGAGCAGATGCCCTGGAGTTAAATTTATCATGTCCACATGGCATGGGAGAAAGAGGAATG	
		681 G L A C G Q D P E L V R N I C R W V R Q 2041 GGCCTGGCCTGTGGCAGGATCCAGAGCTGGTGCGGAACATCTGCCGCTGGGTTAGGCAA	
		701 A V Q I P F F A K L T P N V T D I V S I 2101 GCTGTTCAGATTCCTTTTTTTGCCAAGCTGACCCCAAATGTCACTGATATTGTGAGCATC	
		721 A R A A K E G G A N G V T A T N T V S G 2161 GCAAGAGCTGCAAAGGAAGGTGGTGCCAATGGCGTTACAGCCACCAACACTGTCTCAGGT	
		741 L M G L K S D G T P W P A V G I A K R T 2221 CTGATGGGATTAAAATCTGATGGCACACCTTGGCCAGCAGTGGGGATTGCAAAGCGAACT	
		761 T Y G G V S G T A I R P I A L R A V T S 2281 ACATATGGAGGAGTGTCTGGGACAGCAATCAGACCTATTGCTTTGAGAGCTGTGACCTCC	
		781 I A R A L P G F P I L A T G G I D S A E 2341 ATTGCTCGTGCTCTGCCTGGATTTCCCATTTTGGCTACTGGTGGAATTGACTCTGCTGAA	
		801 S G L Q F L H S G A S V L Q V C S A I Q 2401 AGTGGTCTTCAGTTTCTCCATAGTGGTGCTTCCGTCCTCCAGGTATGCAGTGCCATTCAG	
		821 N Q D F T V I E D Y C T G L K A L L Y L	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2461 AATCAGGATTTCACTGTGATCGAAGACTACTGCACTGGCCTCAAAGCCCTGCTTTATCTG 841 K S I E E L Q D W D G Q S P A T V S H Q 2521 AAAAGCATTGAAGAACTACAAGACTGGGATGGACAGAGTCCAGCTACTGTGAGTCACCAG 861 K G K P V P R I A E L M D K K L P S F G 2581 AAAGGGAAACCAGTTCCACGTATAGCTGAACTCATGGACAAGAAACTGCCAAGTTTTGGA 881 P Y L E Q R K K I I A E N K I R L K E Q 2641 CCTTATCTGGAACAGCGCAAGAAAATCATAGCAGAAAACAAGATTAGACTGAAAGAACAA 901 N V A F S P L K R N C F I P K R P I P T 2701 AATGTAGCTTTTTCACCACTTAAGAGAAACTGTTTTATCCCCAAAAGGCCTATTCCTACC 921 I K D V I G K A L Q Y L G T F G E L S N 2761 ATCAAGGATGTAATAGGAAAAGCACTGCAGTACCTTGGAACATTTGGTGAATTGAGCAAC 941 V E Q V V A M I D E E M C I N C G K C Y 2821 GTAGAGCAAGTTGTGGCTATGATTGATGAAGAAATGTGTATCAACTGTGGTAAATGCTAC 961 M T C N D S G Y Q A I Q F D P E T H L P 2881 ATGACCTGTAATGATTCTGGCTACCAGGCTATACAGTTTGATCCAGAAACCCACCTGCCC 981 T I T D T C T G C T L C L S V C P I V D 2941 ACCATAACCGACACTTGTACAGGCTGTACTCTGTGTCTCAGTGTTTGCCCTATTGTCGAC 1001 C I K M V S R T T P Y E P K R G V P L S 3001 TGCATCAAAATGGTTTCCAGGACAACACCTTATGAACCAAAGAGAGGCGTACCCTTATCT 1021 V N P V C - 3061 GTGAATCCGGTGTGTTAA	
WBC047A01.bFSP_20021401.esd	H.sapiens mRNA for BS69 protein.	1 GGAGCATAATGCTAAAGAAGTAAACAGGTCATGGCACGTTTAACAAAAAGACGACAGGCG 61 ATACAAAAGCTATCCAGCATCTTTGGGCAGCCATTGAGATTATACGGAACCAGAAGCAGA 121 TTGCCAACATTGACCGTATTACAAAATGTGAAACAACTACATTATTCTTGAACCTATGGT 181 GATTTTTACATCATTACACAGATATGTCATTTTCATTAGTTGTATCATTGTTATAAACTG 241 GTATATGTCTCGAGTCCACGGTATGCACCCTAAAGAGACCACCCGTCAGCTGAGCTTAGC 301 TGTGAAAGATGGTCTTATTGTCGAAACTCTAACAGTGGGCTGCAAAGGTTCAAAAGCTGG 361 TATTGAACAAGAAGGATATTGGTTGCCAGGAGATGAGATTGACTGGGAAACAGAAAATCA 421 TGACTGGTATTGTTTTGAATGCCATTTGCCTGGAGAGGTGTTGATATGTGACCTGTGTTT 481 TCGTGTGTATCATTCCAAGTGTTTGTCTGATGAGTTCAGGCTTAGAGACAGCAGTAGTCC 541 CTGGCAGTGCCCAGTTTGCAGGAGCATTAAGAAGAAGAATACAAACAAACAGGAGATGGG	SEQ ID NO:186

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		601 CACATACCTCAGATTCATTGTCTCCCGCATGAAGGAGAGGGCTATAGATCTTAATAAAAA 661 GGGGAAGGACAATAAACACCCGATGTACAGGAGGCTGGTGCACTCAGCTGTGGACGTTCC 721 CACCATTCAAGAGAAAGTGAATGAAGGGAAATACCGAAGTTATGAAGAGTTCAAAGCTGA 781 TGCCCAATTGCTTCTCCACAATACCGTGATTTTCTATGGAGCAGACAGTGAGCAAGCTGA 841 CATTGCGAGGATGCTATATAAAGACACATGTCATGAGCTGGATGAACTGCAGCTTTGCAA 901 GAATTGCTTTTACTTGTCAAATGCTCGTCCTGACAACTGGTTCTGTTATCCTTGTATACC 961 TAATCATGAGCTGGTTTGGGCTAAAATGAAAGGTTTTGGGTTTTGGCCAGCCAAAGTCAT 1021 GCAGAAAGAAGACAATCAAGTCGACGTTCGCTTCTTTGGCCACCACCACCAGAGGGCCTG 1081 GATTCCTTCTGAAAACATTCAAGATATCACAGTCAACATTCATCGGCTGCACGTGAAGCG 1141 CAGTATGGGTTGGAAAAAGGCCTGTGATGAGCTGGAGCTGCATCAGCGTTTCCTACGAGA 1201 AGGGAGATTTTGGAAATCTAAGAATGAGGACCGAGGTGAGGAAGAGGCAGAATCCAGTAT 1261 CTCCTCCACCAGTAATGAGCAGCTAAAGGTCACTCAAGAACCAAGAGCAAAGAAAGGACG 1321 ACGTAATCAAAGTGTGGAGCCCAAAAAGGAAGAACCAGAGCCTGAAACAGAAGCAGTAAG 1381 TTCTAGCCAGGAAATACCCACGATGCCTCAGCCCATCGAAAAAGTCTCCGTGTCAACTCA 1441 GACAAAGAAGTTAAGTGCCTCTTCACCAAGAATGCTGCATCGGAGCACCCAGACCACAAA 1501 CGACGGCGTGTGTCAGAGCATGTGCCATGACAAATACACCAAGATCTTCAATGACTTCAA 1561 AGACCGGATGAAGTCGGACCACAAGCGGGAGACAGAGCGTGTTGTCCGAGAAGCTCTGGA 1621 GAAGCTGCGTTCTGAAATGGAAGAAGAAAAGAGACAAGCTGTAAATAAAGCTGTAGCCAA 1681 CATGCAGGGTGAGATGGACAGAAAATGTAAGCAAGTAAAGGAAAAGTGTAAGGAGGAATT 1741 TGTAGAAGAAATCAAGAAGCTGGCAACACAGCACAAGCAACTGATTTCTCAGACCAAGAA 1801 GAAGCAGTGGTGCTACAACTGTGAGGAGGAGGCCATGTACCACTGCTGCTGGAACACATC 1861 CTACTGCTCCATCAAGTGCCAGCAGGAGCACTGGCACGCCGAGCACAAGCGCACCTGCCG 1921 CCGGAAGAGATGAAGGCGGCTCTTCCTGGGAGCGCCGACGACGACTCTTCTCAGACACAG 1981 CGGTTTTTGTTTCCAAGAAGCCAAAATTGTTTAGAATTTGCTTCCCATTTTGCACCAGCC 2041 TTTAAACACTTTTCGTGAAGAAATTTTGCACAGTAGTTTAAATCTTTTGTTAATGCTCCT 2101 CCAGAGTTTTTCAGGGGGTAAAAGTAACATCAGTGGAGGGTATTATTTTAAATAAACTTT 2161 AGTGAGAATTTGTTGCATTTTCAGCAAATTTTAAAACATTTTTAGGTTTTACAGAGATTT 2221 TAACCTTTAAACAAAAGATCTTTAAAAAACAACAGGTGAATACAAGTGAGTTTAACAAAG 2281 AAGCATTTAAAGTAGATCTGAATGTGAGAACTGTTTCAGAAATAAAACATACTACCTTGA 2341 TGTGAAATTTATTTCTTAACCTTGTTGAGCTGGTTTTGTTCAGCTTAATTTACTGTTTAA 2401 AGGCATTATCTATTGGTTATGCCAGTGGGTATATGATTGAATTTAGGGAACAGGGTTGAC 2461 ACAGCAGGTGCTAGTCCTGCATATTTTTTCGTAAATATTTCCCAATTGTGTTTTTCATTA 2521 TTTCTTTTCAATATATAACTTTTATAACAAATTATTAGCTTTGATCTTGTAGTTTAAAAT 2581 TGCAGGGAACTGGGGTAATCTTTTACTGAGCTGGATCTTAGAGAAAATGAATATTTAAAT 2641 TTTAAAGTTTGCACATTTCATCTTTGTCCTAACATGAGTGCTTGTAACAAAATAAAACAA 2701 CAAAAACAAAGCCT 1 M S R V H G M H P K E T T R Q L S L A V 1 ATGTCTCGAGTCCACGGTATGCACCCTAAAGAGACCACCCGTCAGCTGAGCTTAGCTGTG 21 K D G L I V E T L T V G C K G S K A G I 61 AAAGATGGTCTTATTGTCGAAACTCTAACAGTGGGCTGCAAAGGTTCAAAAGCTGGTATT	SEQ ID NO:187

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		41 E Q E G Y W L P G D E I D W E T E N H D 121 GAACAAGAAGGATATTGGTTGCCAGGAGATGAGATTGACTGGGAAACAGAAAATCATGAC	
		61 W Y C F E C H L P G E V L I C D L C F R 181 TGGTATTGTTTTGAATGCCATTTGCCTGGAGAGGTGTTGATATGTGACCTGTGTTTTCGT	
		81 V Y H S K C L S D E F R L R D S S S P W 241 GTGTATCATTCCAAGTGTTTGTCTGATGAGTTCAGGCTTAGAGACAGCAGTAGTCCCTGG	
		101 Q C P V C R S I K K K N T N K Q E M G T 301 CAGTGCCCAGTTTGCAGGAGCATTAAGAAGAAGAATACAAACAAACAGGAGATGGGCACA	
		121 Y L R F I V S R M K E R A I D L N K K G 361 TACCTCAGATTCATTGTCTCCCGCATGAAGGAGAGGGCTATAGATCTTAATAAAAAGGGG	
		141 K D N K H P M Y R R L V H S A V D V P T 421 AAGGACAATAAACACCCGATGTACAGGAGGCTGGTGCACTCAGCTGTGGACGTTCCCACC	
		161 I Q E K V N E G K Y R S Y E E F K A D A 481 ATTCAAGAGAAAGTGAATGAAGGGAAATACCGAAGTTATGAAGAGTTCAAAGCTGATGCC	
		181 Q L L L H N T V I F Y G A D S E Q A D I 541 CAATTGCTTCTCCACAATACCGTGATTTTCTATGGAGCAGACAGTGAGCAAGCTGACATT	
		201 A R M L Y K D T C H E L D E L Q L C K N 601 GCGAGGATGCTATATAAAGACACATGTCATGAGCTGGATGAACTGCAGCTTTGCAAGAAT	
		221 C F Y L S N A R P D N W F C Y P C I P N 661 TGCTTTTACTTGTCAAATGCTCGTCCTGACAACTGGTTCTGTTATCCTTGTATACCTAAT	
		241 H E L V W A K M K G F G F W P A K V M Q 721 CATGAGCTGGTTTGGGCTAAAATGAAAGGTTTTGGGTTTTGGCCAGCCAAAGTCATGCAG	
		261 K E D N Q V D D V R F F G H H H Q R A W I 781 AAAGAAGACAATCAAGTCGACGTTCGCTTCTTTGGCCACCACCACCAGAGGCCTGGATT	
		281 P S E N I Q D I T V N I H R L H V K R S 841 CCTTCTGAAAACATTCAAGATATCACAGTCAACATTCATCGGCTGCACGTGAAGCGCAGT	
		301 M G W K K A C D E L E L H Q R F L R E G 901 ATGGGTTGGAAAAAGGCCTGTGATGAGCTGGAGCTGCATCAGCGTTTCCTACGAGAAGGG	
		321 R F W K S K N E D R G E E E A E S S S I S	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		961 AGATTTTGGAAATCTAAGAATGAGGACCGAGGTGAGGAAGAGGCAGAATCCAGTATCTCC	
		341 S T S N E Q L K V T Q E P P R A K K G R R 1021 TCCACCAGTAATGAGCAGCTAAAGGTCACTCAAGAACCAAGAGCAAAGAAAGGACGACGT	
		361 N Q S V E P K K E E P E P E T E A V S S 1081 AATCAAAGTGTGGAGCCCAAAAAGGAGAACCAGAGCCTGAAACAGAAGCAGTAAGTTCT	
		381 S Q E I P T M P Q P I E K V S V S T Q T 1141 AGCCAGGAAATACCCACGATGCCTCAGCCCATCGAAAAAGTCTCCGTGTCAACTCAGACA	
		401 K K L S A S S P R M L H R S T Q T T N D 1201 AAGAAGTTAAGTGCCTCTTCACCAAGAATGCTGCATCGGAGCACCCAGACCACAAACGAC	
		421 G V C Q S M C H D K Y T K I F N D F K D 1261 GGCGTGTGTCAGAGCATGTGCCATGACAAATACACCAAGATCTTCAATGACTTCAAAGAC	
		441 R M K S D H K R E T E R V V R E A L E E K 1321 CGGATGAAGTCGGACCACAAGCGGGAGACAGAGCGTGTTGTCCGAGAAGCTCTGGAGAAG	
		461 L R S E M E E E K R Q A V N K A V A N M 1381 CTGCGTTCTGAAATGGAAGAAAAGAGACAAGCTGTAAATAAAGCTGTAGCCAACATG	
		481 Q G E M D R K C K Q V K E K C K E E F V 1441 CAGGGTGAGATGGACAGAAAATGTAAGCAAGTAAAGGAAAAGTGTAAGGAGGAAATTGTA	
		501 E E I K K L A T Q H K Q L I S Q T K K K 1501 GAAGAAATCAAGAAGCTGGCAACACAGCACAAGCAACTGATTTCTCAGACCAAGAAGAAG	
		521 Q W C Y N C E E E E A M Y H C C W N T S Y 1561 CAGTGGTGCTACAACTGTGAGGAGGAGGCCATGTACCACTGCTGCTGGAACACATCCTAC	
		541 C S I K C Q Q E H W H A E E H K R T C R R 1621 TGCTCCATCAAGTGCCAGCAGGAGCACTGGCACGCCGAGCACAAGCGCACCTGCCGCCGG	
		561 K R - 1681 AAGAGATGA	
WBC048H02.bFSP_20021501.esd	Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 2-like	1 CTGCAAGGCGGCGGCAGGAGAGGTTGTGGTGCTAGTTTCTCTAAGCCATCCAGTGCCATC 61 CTCGTCGCTGCAGCGACACCGCTCTCGCCGCCGCCATGACTGAGCAGATGACCCTTCGTG 121 GCACCCTCAAGGGCCACAACGGCTGGGTAACCCAGATCGCTACCACCCCGCAGTTCCCAG 181 ACATGATACTGTCGGCCTCGCGAGACAAGACCATCATCATGTGGAAGCTGACCAGGGATG	SEQ ID NO:188

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
	1 (GNB2L1), mRNA.	241 AGACCAACTACGGCATCCCACAGCGTGCTCTTCGAGGTCACTCCCACTTTGTTAGTGACG 301 TGGTGATCTCTTCAGATGGCCAGTTTGCCCTCTCAGGCTCCTGGGATGGAACGCTTCGCC 361 TCTGGGATCTCACAACGGGCACCACCACACGCCGATTTGTGGGCCATACCAAGGATGTGC 421 TGAGTGTGGCATTCTCCTCTGACAACCGGCAGATTGTCTCTGGCTCCCGAGATAAAACCA 481 TCAAGCTATGGAATACTCTGGGTGTATGCAAATACACTGTCCAGGATGAGAGCCACTCGG 541 AGTGGGTGTCTTGTGTCCGCTTCTCACCCAACAGTAGCAATCCCATCATTGTCTCCTGTG 601 GCTGGGACAAGCTAGTCAAGGTGTGGAATTTGGCAAACTGCAAGCTGAAGACCAATCACA 661 TCGGCCACACAGGCTACCTGAACACTGTCACTGTCTCTCCGGATGGATCCCTCTGTGCTT 721 CTGGAGGCAAGGATGGCCAGGCCATGCTTTGGGATTTAAATGAAGGCAAGCACCTTTACA 781 CACTAGATGGTGTGGGGACATCATCAACGCCTTGTGCTTCAGTCCCAATCGCTACTGGCTCT 841 GTGCTGCCACAGGCCCCAGCATCAAGATCTGGGACTTGGAGGGCAAGATCATTGTAGATG 901 AACTGAAGCAAGAAGTTATCAGTACCAGCAGGCAAGGCAGAGCCACCCCAGTGCACTTCTC 961 TTGCCTGGTCTGCTGATGGCCAGACTCTGTTTGCTGGCTACACGGACAACCTGGTGAGAG 1021 TGTGGCAGGTGACCATCGGCACCCGCTAGAAATACATGGCAAGCTTTAGAAATAAAAAAA 1081 AAATGGCTTTTC	SEQ ID NO:189
		1 M T E Q M T T L R G T L K G H N G W V T Q 1 ATGACTGAGCAGATGACCCTTCGTGGCACCCTCAAGGGCCACAACGGCTGGGTAACCCAG 21 I A T T P Q F P D M I L L S A S R D K T I 61 ATCGCTACCACCCCGCAGTTCCCAGACATGATACTGTCGGCCTCGCGAGACAAGACCATC 41 I M W K L T R D E T N Y G I P Q R A L R 121 ATCATGTGGAAGCTGACCAGGGATGAGACCAACTACGGCATCCCACAGCGTGCTCTTCGA 61 G H S H F V S D V V I S S D G Q F A L S 181 GGTCACTCCCACTTTGTTAGTGACGTGGTGATCTCTTCAGATGGCCAGTTTGCCCTCTCA 81 G S W D G T L R L W D L T T G T T T R R 241 GGCTCCTGGGATGGAACGCTTCGCCTCTGGGATCTCACACAACGGGCACCACCACGCCGA 101 F V G H T K D V L S V A F S S D N R Q I 301 TTTGTGGGCCATACCAAGGATGTGCTGAGTGTGGCATTCTCCTCTGACAACCGGCAGATT 121 V S G S R D K T I K L W N T L G V C K Y 361 GTCTCTGGCTCCCGAGATAAAACCATCAAGCTATGGAATACTCTGGGTGTATGCAAATAC 141 T V Q D E S H S E W V S C V R F S P N S 421 ACTGTCCAGGATGAGAGCCACTCGGAGTGGGTGTCTTGTGTCCGCTTCTCACCCAACAGT 161 S N P I I V S C G W D K L V K V W N L A 481 AGCAATCCCATCATTGTCTCCTGTGGCTGGGACAAGCTAGTCAAGGTGTGGAATTTGGCA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		181 N C K L K T N H I G H T G Y L N T V T V 541 AACTGCAAGCTGAAGACCAATCACATCGGCCACACAGGCTACCTGAACACTGTCACTGTC 201 S P D G S L C A S G G K D G Q A M L W D 601 TCTCCGGATGGATCCCTCTGTGCTTCTGGAGGCAAGGATGGCCAGGCCATGCTTTGGGAT 221 L N E G K H L Y T L D G G D I I N A L C 661 TTAAATGAAGGCAAGCACCTTTACACACTAGATGGTGGGGACATCATCAACGCCTTGTGC 241 F S P N R Y W L C A A T G P S I K I W D 721 TTCAGTCCCAATCGCTACTGGCTCTGTGCTGCCACAGGCCCCAGCATCAAGATCTGGGAC 261 L E G K I I V D E L K Q E V I S T S S K 781 TTGGAGGGCAAGATCATTGTAGATGAACTGAAGCAAGAAGTTATCAGTACCAGCAGCAAG 281 A E P P Q C T S L A W S A D G Q T L F A 841 GCAGAGCCACCCCAGTGCACTTCTCTTGCCTGGTCTGCTGATGGCCAGACTCTGTTTGCT 301 G Y T D N L V R V W Q V T I G T R - 901 GGCTACACGGACAACCTGGTGAGAGTGTGGCAGGTGACCATCGGCACCCGCTAG	
WBC107.bFSP	Homo sapiens nuclear receptor subfamily 1, group D, member 2, mRNA (cDNA clone IMAGE:3912370) - Partial.	1 gggggctgca ggaagccgcc gcgccgccgc ttttgttgtc agggacccag cgaggagcgc 61 cgctcgccgg ccgccgccac cctctctcgc tgcagcctgc tgtgcgctgc acggcctggg 121 gcccgggagc ccgccgcgct ctgcccatga ggggcccccg cgaccaccgc tgcttccagc 181 ccggggcggc gcggcgctga ggcggcggcg gcggcgctgc ccctctgcg ggaagcgggc 241 ggccccgggc gcctccgcga gggcaccatg gagtgaatg caggaggtgt gattgcctat 301 atcagttctt ccagctcagc ctcaagccat gcctcttgtc acagtgaggg ttctgagaat 361 agtttccagt cctcctcctc ttctgttcca tcttctccaa atagcttctaa ttctgatacc 421 aatggtaatc ccaagaatgg tgatctcgcc aatattgaag gcatcttgaa gaatgatcga 481 atagattgtt ctatgaaaac aagcaaatcg agtgcacctg ggatgacaaa aagtcatagt 541 ggtgtgacaa aatttagtgg catggttcta ctgtgtaaag tctgtgggga tgtggcgtca 601 ggattccact atggagttca tgcttgcgaa ggctgtaagg gtttctttcg gagaagtatt 661 caacaaaaca tccagtacaa gaagtgcctg aagaatgaaa actgttctat aatgagaatg 721 aataggaaca gatgtcagca atgtcgcttc aaaaagtgtc tgtctgttgg aatgtcaaga 781 gatgctgttc ggtttggtcg tattcctaag cgtgaaaaac agaggatgct aattgaaatg 841 caaagtgcaa tgaagaccat gatgaacagc cagttcagtg gtcacttgca aaatgacaca 901 ttagtagaac atcatgaaca gacagccttg ccagcccagg aacagctgcg acccaagccc 961 caactggagc aagaaaacat caaaagctct tctcctccat cttctgattt tgcaaaggaa 1021 gaagtgattg gcatggtgac cagagctcac aaggatacct ttatgtataa tcaagagcag 1081 caagaaaact cagctgagag catgcagccc aagagaggag aacggattcg caagaacatg 1141 gagcaatata atttaaatca tgatcattgc ggcaatgggc ttagcagcca tttccctgt 1201 agtgagagcc agcagcatct caatggacag ttcaaaggga ggaatataat gcattaccca	SEQ ID NO:190

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1261 aatggtcatg ccatttgtat tgcaaatgga catgtatga acttctccaa tgcttatact	
		1321 caaagagtat gtgatagagt tccgatagat ggatatttctc agaatgagaa caagaatagt	
		1381 tacctgtgca acactggagg aagaatgcat ctggtttgtc caatgagtaa gtctccatat	
		1441 gtggatcctc ataaatcagg acatgaaatc tgggaagaat tttcgatgag cttcactcca	
		1501 gcagtgaaag aagtggtgga attgcaaag cgtatttcctg ggttcagaga tctcctctcag	
		1561 catgaccagg tcaaccttt aaaggctggg actttgagg tttaatggt acggttcgca	
		1621 tcattatttg atgcaaagga acgtactgtc acctttttaa gtggaaagaa atatagtgtg	
		1681 gatgatttac actcaatggg agcagggat ctgctaaact ctatgtttga atttagtgag	
		1741 aagctaaatg ccctccaact tagtgatgaa gagatgagtt tgtttacagc tgttgtcctg	
		1801 gtatctgcag atcgatctgg aatagaaaac gtcaactctg tggaggcttt gcaggaaact	
		1861 ctcattcgtg cactaaggac cttaataatg aaaaaccatc caaatgaggc ctctatttttt	
		1921 acaaaactgc ttctaaagtt gccagatctt cgatctttaa acaacatgca ctctgaggag	
		1981 ctcttggcct ttaaagttca ccctaaggc ctttgtttat ttaaacatga actgatggta	
		2041 actgtacatt ttgtgctaaa atgcatattt atatgtgtat accatatgtg gagatagaaa	
		2101 agacctttaa gacaataaaa gattgtaggc tatcctgta atcatgcaat agctgttcgg	
		2161 atgagaact cttcagccat gattagacgt tgactgcatc tccctgatag accaatcagc	
		2221 tgtgtcgcac ttaaactgga gaagttacac tgaagtataa tcacactgaa tgttatactt	
		2281 ttcatctgc caaaaccaaa aaccatttg atctccctgt ggttatcaat ataacgcaca	
		2341 atcacaagtg tatgaggact tagaaattaa tcctttgtgg taggagttct gttgaatgat	
		2401 ggaaatctta ttactaccac aagactattt gttctggtaa ttggagactt cgggatttag	
		2461 gagatctcca tgtctgtatt tactctacca ctgctaaagt gtgtggtcct gggtagttta	
		2521 cttgcttgcg gaaaatgaga attgatggtg tccccaatgc cccacctcac agagttacta	
		2581 aaaaatgtct gtaaagcata ttacctcctt gggagatagg cactatgtaa ataaggtaaa	
		2641 atttctgtta ttacaattat tcataataat attctttttct tatttctaag cctttctggg	
		2701 aaatcatttc agtccacacc aaccatatta ttcagggttc ctgccatatg tgtggggtat	
		2761 cctactgata cacacgtatt caaagtttat gggtacaaca aagacatagt acatgtacat	
		2821 aatatgtatg tgaatatagt taaatatatt tcttcacaat atttaaact gtgaagaact	
		2881 ttatcataca ggaaacttaa aacaagaggt gtcaaaagac ccaaattagg tgcatttac	
		2941 ttgtttatga tggcataacc attgctttaa aatgtttaga cagtagaata ttgaatttat	
		3001 gctctatttt tgtttattta agcaacactt aatgtaaaag tgcaacaggc aattgaatcc	
		3061 aaatttcaac gacaaaaaaa aaaaacatgt attttagagt tcatctttgg caaaatcttt	
		3121 ggttcagggt actagttgtt taaaagttga ttcatattct taccttgtgc tgagaaaggt	
		3181 tgcattgctg ccccttatac acatgctgca gcttgatgtt aaagaatttt tattctttct	
		3241 gaagaactaa ttaatgtttta aagcaactgt ttaatatgat ggcatgtgtg tgtgtgcgtg	
		3301 cgtgtgtatg ttctgagtcc acttctttttt tcctaaataa cactacaggg atttgtcat	
		3361 attagattta atttataatt tgaaaaatca tctagtgtgt gacctacagg cttagaaatg	
		3421 gtatagtcaa agacatttta tccacatttc taatagtgga cttgattaag tagataagat	
		3481 cagcatctgt ttatggtatt aggagaaata gccaaagttg aggatttat gtatgttttc	
		3541 ctgtttacct ggaaaataagc aattaattgg atttttggt aaagattgcc ttctgtataa	
		3601 tgtttggatt atataaaatt gcaaaaatga taacagcccg ctttactgta ctaagcctgt	
		3661 tactcttcatg acgtgtgagc agaatgcctt atttgtaat cttgtttaac ttgttgctac	
		3721 tgggacttga tttactgtgg cactagttaa gtaagttaaa aaaaagttaa accctctcat	
		3781 tattaaagag gaaaggcgat ggtgatgtct gtagtacaat ataaaccata attgtgattt	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		3841 accttaagta ggtataactc ttatgggata tacagtatag tttttgtgaa tctttacatg 3901 atagcattat cttttataa ttttttttcc taagataaac aaatgcatag tttctttcta 3961 tgggtgatag aaacagcttt ttgaagtaat gaaaacctca aaagatcatg ttgattctta 4021 attttgcct tttgcataag cttctttata acatgtatct ttaaaacaat taagtcttta 4081 ggaatgtgta accagaacta tgttagtatt gcttataaaa ctttagttag gttccaatata 4141 tacatatata catctctata taggtatata gatttgcatt ttgtcttgta aaattttatt 4201 tgataaaatt cttcctgtag gtaatgggaa acaaaattaa tagttcatat gtcactcata 4261 gatttctat atttgaaagt agcccaatat aaaacttttg attctaaaat taaaccagca 4321 gcctattaca agcaaaaaaa aaaaaaaaa 1 M E V N A G G V I A Y I S S S S S A S S 1 ATGGAGGTGAATGCAGGAGGTGTGATTGCCTATATCAGTTCTTCCAGCTCAGCCTCAAGC 21 H A S C H S E G S E N S F Q S S S S S V 61 CATGCCTCTTTGTCACAGTGAGGGTTCTGAGAATAGTTTCCAGTCCTCCTCCTCTTCTGTT 41 P S S P N S S N S D T N G N P K N G D L 121 CCATCTTCTCCAAATAGCTCTAATTCTGATACCAATGGTAATCCCAAGAATGGTGATCTC 61 A N I E G I L K N D R I D C S M K T S K 181 GCCAATATTGAAGGCATCTTGAAGAATGATCGAATAGATTGTTCTATGAAAACAAGCAAA 81 S S A P G M T K S H S G V T K F S G M V 241 TCGAGTGCACCTGGGATGACAAAAAGTCATAGTGGTGTGACAAAATTTAGTGGCATGGTT 101 L L C K V C G D V A S G F H Y G V H A C 301 CTACTGTGTAAAGTCTGTGGGGATGTGGCGTCAGGATTCCACTATGGAGTTCATGCTTGC 121 E G C K G F F R R S I Q Q N I Q Y K K C 361 GAAGGCTGTAAGGGTTTCTTTCGGAGAAGTATTCAACAAAACATCCAGTACAAGAAGTGC 141 L K N E N C S I M R M N R N R C Q Q C R 421 CTGAAGAATGAAAACTGTTCTATAATGAGAATGAATAGGAACAGATGTCAGCAATGTCGC 161 F K K C L S V G M S R D A V R F G R I P 481 TTCAAAAAGTGTCTGTTGGAATGTCAAGAGATGCTGTTCGGTTTGGTCGTATTCCT 181 K R E K Q R M L I E M Q S A M K T M M N 541 AAGCGTGAAAAACAGAGGATGCTAATTGAAATGCAAAGTGCAATGAAGACCATGATGAAC 201 S Q F S G H L Q N D T L V E H H E Q T A 601 AGCCAGTTCAGTGGTCACTTGCAAAATGACACATTAGTAGAACATCATGAACAGACAGCC	SEQ ID NO:191

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		221 L P A Q E Q L R P K P Q L E Q E N I K S 661 TTGCCAGCCCAGGAACAGCTGCGACCCAAGCCCCAACTGGAGCAAGAAACATCAAAAGC	
		241 S S P P S S D F A K E E V I G M V T R A 721 TCTTCTCCTCCATCTTCTGATTTTGCAAAGGAAGAAGTGATTGGCATGGTGACCAGAGCT	
		261 H K D T F M Y N Q E Q Q E N S A E S M Q 781 CACAAGGATACCTTTATGTATAATCAAGAGCAGCAAGAAACTCAGCTGAGAGCATGCAG	
		281 P K R G E R I R K N M E Q Y N L N H D H 841 CCCAAGAGAGGAGAACGGATTCGCAAGAACATGGAGCAATATAATTTAAATCATGATCAT	
		301 C G N G L S S H F P C S E S Q Q H L N G 901 TGCGGCAATGGGCTTAGCAGCCATTTTCCCTGTAGTGAGAGCCAGCAGCATCTCAATGGA	
		321 Q F K G R N I M H Y P N G H A I C I A N 961 CAGTTCAAAGGGAGGAATATAATGCATTACCCAAATGGTCATGCCATTTGTATTGCAAAT	
		341 G H C M N F S N A Y Y T Q R V C D R V P I 1021 GGACATTGTATGAACTTCTCCAATGCTTATACTCAAAGAGTATGTGATAGAGTTCCGATA	
		361 D G F S Q N E N K N S Y Y L C N T G G R M 1081 GATGGATTTTCTCAGAATGAGAACAAGAATAGTTACCTGTGCAACACTGGAGGAAGAATG	
		381 H L V C P M S K S P Y Y V D P H K S G H E 1141 CATCTGGTTTGTCCAATGAGTAAGTCTCCATATGTGGATCCTCATAAATCAGGACATGAA	
		401 I W E E F S M S F T P A V K E V V E F A 1201 ATCTGGGAAGAATTTTCGATGAGCTTCACTCCAGCAGTGAAAGAAGTGGTGGAATTTGCA	
		421 K R I P G F R D L S Q H D Q V N L L K A 1261 AAGCGTATTCCTGGGTTCAGAGATCTCTCTCAGCATGACCAGGTCAACCTTTTAAAGGCT	
		441 G T F E V L M V R F A S L F D A K E R T 1321 GGGACTTTTGAGGTTTTAATGGTACGGTTCGCATCATTATTTGATGCAAAGGAACGTACT	
		461 V T F L S G K K Y S V D D L H S M G A G 1381 GTCACCTTTTTAAGTGGAAAGAAATATAGTGTGGATGATTTACACTCAATGGGAGCAGGG	
		481 D L L N S M F E F S E K L N A L Q L S D 1441 GATCTGCTAAACTCTATGTTTGAATTTAGTGAGAAGCTAAATGCCCTCCAACTTAGTGAT	
		501 E E M S L F T A V V L V S A D R S G I E	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1501 GAAGAGATGAGTTTGTTTACAGCTGTTGTCCTGGTATCTGCAGATCGATCTGGAATAGAA 521 N V N S V E A L Q E T L I R A L R T L I 1561 AACGTCAACTCTGTGGAGGCTTTGCAGGAAACTCTCATTCGTGCACTAAGGACCTTAATA 541 M K N H P N E A S I F T K L L L K L P D 1621 ATGAAAAACCATCCAAATGAGGCCTCTATTTTTACAAAACTGCTTCTAAAGTTGCCAGAT 561 L R S L N N M H S E E L L A F K V H P - 1681 CTTCGATCTTTAAACAACATGCACTCTGAGGAGCTCTTGGCCTTTAAAGTTCACCCTTAA	
WBC117.gRSP	No homology	1 GACTTTATTTGAGGTAAGAAGGCAGAGCAGGATCAGAGAGTTCGAGAACAGGCATGGCAT 61 TATCTGGCTTGTATTTTTAAAGGGTGCCTCTGGTAGAATTATCTATTTTGTTTTCATGAA 121 GAGTCCTGTAATTATTGCCACGTTGCAGGTGAAGAATCTGAGGCTCAGAGAGGTTGAGTC 181 ATTGCTCAGGTTGGCACAGCTGGTGAGCGGCAGAGCTGGGTTTCCTAGTTACCTCCGTCT 241 GACTGCAGAATCCAAATCTTCGTCCACCATACTGGGCTTGCCCTGGTCCCTTCCTAATTC 301 CTTTAGCTTTGTAAAACATGTCTAAATTTGGAGTATCCAGAGAGTTGTGACTGTGTCGCC 361 TTCTATCACTGTTGACTTCAACCCCATCTCTTCCTGATGCATCCCCTAGGATGTGAGAGC 421 TCACTCTTATGGCTCCACCTGGGTTTCTCATGTTTGGTGCTACCATCCTTAACCTTTCAC 481 CAAGGGGCTCAAGATGTTTCCCATGATGATCCAGCCTTTCCGTTCTTCCCTTTGCTGGCA 541 ATTATACGTGCTTACCTTTCTCGGACAGGACCCACTTTCCGGGTGACTGCATGCAAACTC 601 TCCCTTTCTCTTTTTAGATGTTAATAGCAGAGTTATCAAGAACGAATGCTCTGAAGAGAA 661 CATGGCCTTTAGCTTGAAAGCCAAAGGGGATAAGATGACGATTTCATGCTCCACAATTAA 721 AGAATCTGGATCCACAGGTACAGACCCACTCCGGAGAATCAGGGTGGGTAGTTATGGTAC 781 ACTCAGTCAACAAACACTTATCGATCACCTCTTAGGTGCCAAGACCTATGCCAGGTGGTG 841 GGGAAATCAATGATGGGAGAGGCAAAAATGG	SEQ ID NO:192
		1 GTTATGGTACACTCAGCCACCAACACTTATCGGATCCCCTTTTTAGGGGCCAAGACCTAT 61 GCCAGGTGGGGGGAAATCAATGATGGAAGAGGCAGAAATGGCCTCAGGAAAGTTTCCCAC 121 CTGCTAGGAAAGGCAGACATTGAAAAAATAATCTTGCAGTACCGGAGTATTGAAAGCTTA 181 CCTATCTAATACAGCAGCCACTGGCCACTTTTGTCATTCAGCACTTGAAATGTGGCCAGG 241 TTGTGAATTTAAAATACCTACCAGATTTCAAAGACTTGGTCCAAAAAAAAAAATGGAGGA 301 TGTAAAATAGCTCACTCATAATTTTTTCTATTGATCAAGTGTTGAAACGATACTATTTTG 361 CATGTATTGAATTAATATATTATTAAAATGAATTTTACCTGTTTTCTACTCTAAAATGTG 421 GCTATTAGAAAATTTAAAATTGCGTATGTGGCTCATAGTATATTTCTAGCAGATAGTGCT 481 GATCTGTATCAGGGGCTGGGAAACTTTTCCTGTAGAGGGCCGCTTTGTAAATATTTTAGG 541 CTTTGAGGGCAACACAATTTCTGTCGCAACCATTCGACCCTGCCGTCATCATGCAAAAGC 601 ATTCATCAGCAGCGTGTAAATGAATGGGTGTGTCTGTGTTGCAATAGAGCTTTTATTTAA 661 AAAAAAAAAAAA	SEQ ID NO:193
WBC21.bFSP	No Homology	1 TTCGCATACCACTTGTGGACATTATAAATTGCTGATTTCCAGTCTCCATTCCCAGAGATT	SEQ ID NO:194

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		61 CTGATTCTGTAGGGGTGACCTGGGGCCCAGGATCAAATCTTTCTAACCAGTTCCACAGGT 121 GATTCTGATGTACGTATACAGAGTTTGAGAACTATCACTTTAGAGCACGGGTTGGAAAAT 181 TACAACCCACAGATCAAATCCGGCCTGCTGCTTTTTTGGTGTGATAAAGTTTTATTGGAA 241 TGCAGCTACACTTATTTGTTTGCATATTGTCTATGTCTGTTTCAGCACTGCAACAGCAGA 301 GTTGAGTAGTTACAGCAGACACCATACGGCCATAAAGCTGAAGATATTTACTATCTGGAC 361 CTTTACAGAAAAAGTTTGCAAACTCTTGCTCTAAAGCTAAATGAACATTTCTCCTTAAAT 421 AATTTAAACTCTGTTGCAATCCTGATCATTCCTGCCAAACACAATTGTAGATAGAATAAC 481 TGTTTTTTCAGAATTTAGTCTGAGAATGTTAGTTCTTGTATAGTCCACACTTCTCTAGG 541 ACCTTTGGCAAATCAAGAATGCTGTGACTCCTGAGTGGTCAATAGAAGATATACATTTC 601 CTTGGCCTTACCACAAGTGATTGAAAGTGAAGCATATGGTTCTATAGTCTGCGTATCTCA 661 TAATAGTCCTTAGTAATCTCATGCATTAGGAGGCAATCATCAAGTAGAGACTCTTTCATC 721 CATAAGCCCCCAAACCAAACTACTTACCTGATTGTCAAGAAGAAAAGCATTGCTGTATCT 781 ATTTTTGAAGAGAGGCATTAGTGGCTTTGGCTAAAGTTTAACAAAGCTAACCACATCCCC 841 TCCCTTCAGCCAGCCAGCCATCTGATTCCCCTAAATGCGTAGAAATAAAGATGTAGTGCT 901 GCAAATGTATTTTGACTTTTTCAAGTTATGCTGTTTCCTCTATTCTTGGATAAATCATAG 961 TAGGTTAATAATACAGAAATGAGATTGCATATTTCTCTTTAGTAGAAATTAGCAAAATTA 1021 GCTTTTTTTTGCTACAACTTAAGACACTTGATGTATTCCTCTGTGTTTTATGTTACTGTAA 1081 ACTCAACATACGGTGAGTTTTGTGGTATTTGACCTGTTAGGCAAAATCACTATTTTCACT 1141 TTGACTGACATTTATAATGTTCTGTTCATGAAATAAAATTCTTCTGTCTAAAAAAAAAAA 1201 AAAAAAA	
WBC215.gRSP	Homo sapiens CDC14 cell division cycle 14 homolog A (S. cerevisiae) (CDC14A), transcript variant 1, mRNA	1 cgaagaggat ccggagcagc tgctgccagc ccgcgggcac tgaagtcctc ccggctgccg 61 ctcgagtagc cacgggcgcg atcgggacca gaagtctcct cctccatgat cactttggaa 121 gccgggggag aagactttgc cctgccctga gagctggtct gcgttcccca ggcgcggcgg 181 cggcggagca gcagctgcag cagccgagtc caaataggag cggccacagc caggggcgtg 241 tgcgcccccgc gcggagcgag ctcgggttcc cctcggaatg tccccggggc gcccggcgcg 301 ctgaccccga agccgcctcc gccttcggcg cctgctgcct ccctcggcca ggcttgttgt 361 tcgggactgt gagcttcctg gctcctgggc agtgggggaag ccccgggggg cgagtgacct 421 cagctggcca cgacccagcc ctccccgctg cgtatctcgc ttaagatggc agcggagtca 481 ggggaactaa tcggggcttg tgagttcatg aaagatcggt tatattttgc tactttaagg 541 aatagaccaa aaagcacagt aaatacccac tatttctcca tcgatgagga gctggtctat 601 gaaaatttct atgcagattt tggaccgctg aacttggcaa tggtgtacag atattgctgc 661 aaactaaaca agaaactaaa atcatacagt ttgtcaagaa agaaaatagt gcactacacc 721 tgttttgacc aacggaaaag agcaaatgca gcatttttga taggtgccta tgcagtaatc 781 tatttaaaga agacaccaga agaagcctac agagcactcc tgtctggctc aaacccccgc 841 tatcttccat tcagggatgc ttccctttgga aattgcactt acaatctcac cattctcgac 901 tgtttgcagg gaatcagaaa gggattacaa catggatttt ttgactttga gacatttgat 961 gtggatgaat atgaacatta tgagcgagtt gaaaatggtg acttcaactg gattgttcca 1021 ggaaaatttt tagcatttag tggacacact cctaaaagca aaattgagaa tggttatcct 1081 cttcacgccc ctgaagccta ctttccttat ttcaaaaagc ataatgtgac tgcagttgtg 1141 aggctaaaca aaaagattta tgaggcaaag cgcttcacag acgctggctt cgagcactat 1201 gacctcttct tcatagatgg cagcacaccc agtgacaaca tcgtgcgaag gttcctgaac	SEQ ID NO:195

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1261 atctgtgaga acaccgaagg ggccatcgcc gttcactgca aagctggtct tggaagaaca 1321 gggacattga tagcctgtta tgtaatgaaa cactacaggt ttacacatgc tgaaataatt 1381 gcttggatta gaatatgccg gccaggctct attataggac cccagcagca cttcctggaa 1441 gaaaaacaag catcgttgtg ggtccaagga gacattttcc gatccaaact gaaaaatcga 1501 ccatccagtg aaggaagtat taataaaatt ctttctggcc tagatgatat gtcttattggt 1561 ggaaatcttt caaaaacaca aaacatggaa cgatttggag aggataactt agaagatgat 1621 gatgtggaaa tgaaaaatgg tataacccag ggagacaaac tacgtgcctt aaaaagtcag 1681 agacagccac gtacctcacc atcctgtgca tttaggtcag atgatacaaa aggacatcca 1741 agagcagtgt cccagccttt cagattaagt tcatccctgc aaggatctgc agttactttg 1801 aagacatcaa aaatggcact gtcccttca gcaacggcca agaggatcaa cagaacttct 1861 ttgtcttcgg gtgccactgt aagaagcttt tccataaact ccggctagc cagttctcta 1921 gggaacttga atgctgcaac agatgatcca gagaacaaaa agacctcctc atcctctaag 1981 gcaggcttca cagccagccc gtttaccaac ctcttgaatg gcagctccca gccaactacc 2041 agaaattacc ctgagctcaa caataatcag tacaacagaa gcagcaacag caacgggggc 2101 aacctgaaca gccccccagg ccccacagc gccaagacag aggagcacac caccatcctc 2161 cgaccctcct acaccgggct ttcttcttct tcagcgagat tcctgagccg ttctatccct 2221 tcccttcagt ctgaatatgt tcattactaa ggccttgcca ctccagtgaa agctgttctt 2281 ctcttagaca caatttcttc atctggacga gcagtggaga gggaaagcaa cttcttgctg 2341 gaagaatatc tctgccttct taccttaaat taaaaagagc actaagataa caccttcaag 2401 agacttgaaa acagaaaact ggttaatgac tactataaat gcactgaaac tatgttatgg 2461 agatttccat acttttaaag acagttttaa tgttgaattt ggtatttgga agggttattt 2521 ttaatgtatt ttggtaatac atttattatt atatttacat gtacagtgtt acattatata 2581 tgtattgtga actttaaaag actattttga taaatttata aatatataaa attatgtaaa 2641 aactacacta tattttgatt tagattttcc tgctgtttgc taccaaaaat ttgtatttta 2701 aatctgttta gttttagtat ggttttgtct ctaatgaata aataattcct tcttattaag 2761 aagaagtaag ggagaaagtt tttagaaagt gattttatg ctcgcactat aaatatggca 2821 ggtcagttca ttcttttggg aagtcagttt agttacactg agtttatcca agtttatctc 2881 taccaagagt ataatggcat gggatggctt atttaggaca attcccttc ctattgtttt 2941 tgttgctgag ccaatttgag ttagttttgc atcctgtggg gctttaaaat acagcatgca 3001 gtgaaagatc agaattcact gaatatttct tctgagagca tggtttcatg gttttctct 3061 atgaaatgac tcaatattcc aaatgttttt ttttccttcc tcctttcaaa agagttctta 3121 acccaattag gatatcctgc tttgggtatg aggttgttgt tgcctgtaat cacacatggt 3181 ttgacatcag tttaaatca atggagagaa aaaactgaaa aagatgctgc taagtagttc 3241 tctgtattaa aggagatatt tttaaaacag ggtacaaccc cctgctgcac acgctagcat 3301 atctggaacc tactatgaaa atgaaaggac ccttataggt actcacagcc ctttcatgta 3361 agtatgatct gatatttagg tcttcagaag cctgtaggtt tcatttctat gaggaatcga 3421 ggagcgttac atcctgatat ccttccaggc tgcttaagaa tggactgctt cgacactgaa 3481 agtgctagtt aaatggattc atatgaagtg ctttactccc aaccattgag ttatttataa 3541 tgtatttatt aggggagggt accttgagtc tattatatat gcttcatcaa aacatcttgt 3601 tcatgttttа tgtttttaaa aaaggcattt gaatgaatgt ttgactcagg tttgttaaat 3661 taacttcagt aactgcagta ccaaaaatta cactcaactg atgaaaaaaa cgaattgtat 3721 gatttaggaa tcaaaaacta aaataagtgg aattatgtat cttttctaaa gttaaaaaag 3781 taaaatattt tattatgagt tattataaaa attggttaat tgtataggaa gatgacagta	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		3841 ttttttcaa gttatcataa aaagtaattc agatgacatt tgagaagtag gggaaaggga 3901 atcatgttga cagttttagt tctgtgaaca ctaatttgtg tgaagctatt aaaatgattg 3961 taaagttgac tactgtaaat ttcccataat tatgtgtgta tatgtgtcat atgtatgtac 4021 atgtatatgt ctaaaaatta ctttacacat gtgcctacat agacacacca agaagtggat 4081 gtatataata tagaaagtat atagcaaagt aattttactc tgataataaa aattgtttga 4141 catgtatttt gttatgaata gtttatcttc caaaagatat tttgctctat tttaaagtgt 4201 agaagaatac actgctaata aataataaaa gttttattca atttaaaaaa aaaaaaaaaa 4261 aa	SEQ ID NO:196
		1 M A A E S G E L I G A C E F M K D R L Y 1 ATGGCAGCGGAGTCAGGGGAACTAATCGGGGCTTGTGAGTTCATGAAAGATCGGTTATAT	
		21 F A T L R N R P K S T V N T H Y F S I D 61 TTTGCTACTTTAAGGAATAGACCAAAAAGCACAGTAAATACCCACTATTTCTCCATCGAT	
		41 E E L V Y E N F Y A D F G P L N L A M V 121 GAGGAGCTGGTCTATGAAAATTTCTATGCAGATTTTGGACCGCTGAACTTGGCAATGGTG	
		61 Y R Y C C K L N K K L K S Y S L S R K K 181 TACAGATATTGCTGCAAACTAAACAAGAAACTAAAATCATACAGTTTGTCAAGAAAGAAA	
		81 I V H Y T C F D Q R K R A N A A F L I G 241 ATAGTGCACTACACCTGTTTTGACCAACGGAAAAGAGCAAATGCAGCATTTTGATAGGT	
		101 A Y A V I Y L K K T P E E A Y R A L L S 301 GCCTATGCAGTAATCTATTTAAAGAAGACACCAGAAGAAGCCTACAGAGCACTCCTGTCT	
		121 G S N P P Y L P F R D A S F G N C T Y N 361 GGCTCAAACCCCCCCTATCTTCCATTCAGGGATGCTTCCTTTGGAAATTGCACTTACAAT	
		141 L T I L D C L Q G I R K G L Q H G F F D 421 CTCACCATTCTCGACTGTTTGCAGGGAATCAGAAAGGGATTACAACATGGATTTTTTGAC	
		161 F E T F D V D E Y E H Y E R V E N G D F 481 TTTGAGACATTTGATGTGGATGAATATGAACATTATGAGCGAGTTGAAAATGGTGACTTC	
		181 N W I V P G K F L A F S G P H P K S K I 541 AACTGGATTGTTCCAGGAAAATTTTTAGCATTTAGTGGACCACATCCTAAAAGCAAAATT	
		201 E N G Y P L H A P E A Y F P Y F K K H N 601 GAGAATGGTTATCCTCTTCACGCCCCTGAAGCCTACTTTCCTATTTCAAAAAGCATAAT	
		221 V T A V V R L N K K I Y E A K R F T D A	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		661 GTGACTGCAGTTGTGAGGCTAAACAAAAAGATTTATGAGGCAAAGCGCTTCACAGACGCT	
		241 G F E H Y D L F F I D G S T P S D N I V 721 GGCTTCGAGCACTATGACCTCTTCTTCATAGATGGCAGCACACCCAGTGACAACATCGTG	
		261 R R F L N I C E N T E G A I A V H C K A 781 CGAAGGTTCCTGAACATCTGTGAGAACACCGAAGGGCCATCGCCGTTCACTGCAAAGCT	
		281 G L G R T G T L I A C Y V M K H Y R F T 841 GGTCTTGGAAGAACAGGGACATTGATAGCCTGTTATGTAATGAAACACTACAGGTTTACA	
		301 H A E I I A W I R I C R P G S I I G P Q 901 CATGCTGAAATAATTGCTTGGATTAGAATATGCCGGCCAGGCTCTATTATAGGACCCCAG	
		321 Q H F L E E K Q A S L W V Q G D I F R S 961 CAGCACTTCCTGGAAGAAAAACAAGCATCGTTGTGGGTCCAAGGAGACATTTTCCGATCC	
		341 K L K N R P S S E G S I N K I L S G L D 1021 AAACTGAAAAATCGACCATCCAGTGAAGGAAGTATTAATAAAATCTTTCTGGCCTAGAT	
		361 D M S I G G N L S K T Q N M E R F G E D 1081 GATATGTCTATTGGTGGAAATCTTTCAAAAACACAAAACATGGAACGATTTGGAGAGGAT	
		381 N L E D D D V E M K N G I T Q G D K L R 1141 AACTTAGAAGATGATGTGGAAATGAAAAATGGTATAACCCAGGGAGACAAACTACGT	
		401 A L K S Q R Q P R T S P S C A F R S D D 1201 GCCTTAAAAAGTCAGAGACAGCCACGTACCTCACCATCCTGTGCATTTAGGTCAGATGAT	
		421 T K G H P R A V S Q P F R L S S S L Q G 1261 ACAAAAGGACATCCAAGAGCAGTGTCCCAGCCTTTCAGATTAAGTTCATCCCTGCAAGGA	
		441 S A V T L K T S K M A L S P S A T A K R 1321 TCTGCAGTTACTTTGAAGACATCAAAAATGGCACTGTCCCCTTCAGCAACGGCCAAGAGG	
		461 I N R T S L S S G A T V R S F S I N S R 1381 ATCAACAGAACTTCTTTGTCTTCGGGTGCCACTGTAAGAAGCTTTTCCATAAACTCCCGG	
		481 L A S S L G N L N A A T D D P E N K K T 1441 CTAGCCAGTTCTCTAGGGAACTTGAATGCTGCAACAGATGATCCAGAGAACAAAAAGACC	
		501 S S S S K A G F T A S P F T N L L N G S 1501 TCCTCATCCTCTAAGGCAGGCTTCACAGCCAGCCCGTTTACCAACCTCTTGAATGGCAGC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		521 S Q P T T R N Y P E L N N N Q Y N R S S 1561 TCCCAGCCAACTACCAGAAATTACCCTGAGCTCAACAATAATCAGTACAACAGAAGCAGC 541 N S N G G N L N S P P G P H S A K T E E 1621 AACAGCAACGGGGGCAACCTGAACAGCCCCCCAGGCCCCCACAGCGCCAAGACAGAGGAG 561 H T T I L R P S Y T G L S S S S A R F L 1681 CACACCACCATCCTCCGACCCTCCTACACCGGGCTTTCTTCTTCTTCAGCGAGATTCCTG 581 S R S I P S L Q S E Y V H Y - 1741 AGCCGTTCTATCCCTTCCCTTCAGTCTGAATATGTTCATTACTAA	
WBC309.bFSP	Homo sapiens hypothetical protein MGC5576, mRNA	1 GACATGACACAAGTGGCACATCCCGGACATGGGGTCCCAGCATTCCGCCTCTGCTCGCCC 61 CTCTTCCTGCAGGCGAAAGAAAGATGACAGGGAGGATTTTCTGGCTGAACGGGAGCAGGA 121 AGAAGCCATCGCTCAGTTTCCGTATGTGGAGTTCACCGGTCGAGATAGCATCACCTGTCT 181 CACGTGCCAAGGGACCGGCTACATTCCAACAGAGCAAGTAAATGAATTGGTGGCTTTGAT 241 CCCACACAGTGATCAGAGGTTGCGCCCTCAGAGAACTAAGCAATATGTACTCCTGTCTGT 301 CTTGCTGTGTCTCCTGGCATCTGGGTTGGTGGTTTTCTTCCTCTTTCCACATTCAGTCCT 361 TGTGGATGACGATGGCATCAAAGTGGTGAAAGTCACGTTTAATAAGCAGGACTCCCTGGT 421 GATCCTCGCCATCACGGCCACCCTGAAAATCAGGAACTCCAACTTCTACTCTGTGGCCGT 481 GACCAGCCTGTCCACCCAGGTTCAGTACATGAACACCGTGGTTGGGTCATATGTGACAGC 541 AAATGTCTCCCTTATTCCACCTCGGAGCGAGCACCTGGTGAATTTTACTGTGAAGGCTGA 601 GATGGGAGGACCGTATTCCTATGTGTACTTCTTCTGCACATTGCCGGATATCCTGATTCA 661 CAACATAGTGATCTTCATGCGAACTTCAGTGAAGATTTCATACATTGGCCTCATGACCCA 721 GAGCTCCTTGGAGACACATCACTATGTGGATTGTGGAGGAAATTCCACAGCTATTTAACA 781 ACTGCTATTGGTTCTTCCACACAGCGCCTGTAGAAGAGAGCACAGCATATGTTCCCAAGG 841 CCTGAGTTCTGGACCTACCCCCACGTGGTGTAAGCAGAGGAGGAATTGGTTCACTTAACT 901 CCCAGCAAACATCCTCCTACCACTTGGGAGGAAAACTCCTCTCTGTAGCACCATTTCTGT 961 TTCTGAGAACCAGCAGAATCACTGCCCAGTGCCTGGCCATATGCCCAGCAAATTAATAGG 1021 CACTCCAAGAAGGTTTGAAGAATGTAATTCAGATCTTTTCAGCTGTTCTTGGGCCGTTAT 1081 AAATTGAAATCATACTGTGGTTCTAGGTTATCAGACCATGGAGTGATGTGGAGCTAGGAT 1141 TGTGAGTGACCTGCAGGCCATTATCAGTGCCTCATCTGTGCAGAAGTGGCAGCAGAGAGG 1201 GACCATCCAAATACCTAAGAGAAAACAGACCTAGTCAGGATATGAATTTGTTTCAGCTGT 1261 TCCCAAAGGCCTGGGAGCTTTTTGAAAAGAAAGAAAAAAGTGTGTTGGCTTTTTTTTTTT 1321 TTTAGAGAGTTACACTTGTTTTTACCAAGAACCTTTATGGGCTTTGATTTACCCTTCATC 1381 CATTGGCTGGAACATGGATTGGGGATTTGGTAGAAAAATAAACCCTGCTTTTGATTCAAA 1441 AAAAAAAAAAAAAAAA 1 M G S Q H S A S A R P S S C R R K K D D 1 ATGGGGTCCCAGCATTCCGCCTCTGCTCGCCCCTCTTCCTGCAGGCGAAAGAAAGATGAC	SEQ ID NO:197 SEQ ID NO:198

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		21 R E E D F L L A E E R R E E Q E E E A I A Q F P Y V 61 AGGGAGGATTTTCTGGCTGAACGGAGCAGGAAGAAGCCATCGCTCAGTTTCCGTATGTG 41 E F T G R D S I T C L T C Q G T G Y I P 121 GAGTTCACCGGTCGAGATAGCATCACCTGTCTCACGTGCCAAGGGACCGGCTACATTCCA 61 T E Q V N E L V A L I P H S D Q R L R P 181 ACAGAGCAAGTAAATGAATTGGTGGCTTTGATCCCACACAGTGATCAGAGGTTGCGCCCT 81 Q R T K Q Y V L L S V L L C L L A S G L 241 CAGAGAACTAAGCAATATGTACTCCTGTCTGTCTTGCTGTGTCTCCTGGCATCTGGGTTG 101 V V F F L F P H S V L V D D D D G I K V V 301 GTGGTTTTCTTCCTCTTTCCACATTCAGTCCTTGTGGATGACGATGGCATCAAAGTGGTG 121 K V T F N K Q D S L V I L A I T A T L K 361 AAAGTCACGTTTAATAAGCAGGACTCCCTGGTGATCCTCGCCATCACGGCCACCCTGAAA 141 I R N S N F Y S V A V T S L S T Q V Q Y 421 ATCAGGAACTCCAACTTCTACTCTGTGGCCGTGACCAGCCTGTCCACCCAGGTTCAGTAC 161 M N T V V G S Y V T A N V S L I P P R S 481 ATGAACACCGTGGTTGGGTCATATGTGACAGCAAATGTCTCCCTTATTCCACCTCGGAGC 181 E H L V N F T V K A E M G G P Y S Y V V Y 541 GAGCACCTGGTGAATTTTACTGTGAAGGCTGAGATGGGAGGACCGTATTCCTATGTGTAC 201 F F C T L P D I L I H N I V I F M R T S 601 TTCTTCTGCACATTGCCGGATATCCTGATTCACAACATAGTGATCTTCATGCGAACTTCA 221 V K I S Y I G L M T Q S S L E T H H Y V 661 GTGAAGATTTCATACATTGGCCTCATGACCCAGAGCTCCTTGGAGACACATCACTATGTG 241 D C G G N S T A I - 721 GATTGTGGAGGAAATTCCACAGCTATTTAA	
WBC310.bFSP	Homo sapiens lymphoid enhancer-binding factor 1, mRNA (cDNA clone MGC:60112 IMAGE:6054813).	1 CCCACGCGTCCGCCCACGCGTCCGCCCCTCTGTCTTTCCTGCTGTTGCGCGGGTGCTCCC 61 ACAGCGGAGCCGAGATTACAGAGCCGCCGGGATGCCCCCAACTCTCCGGAGGAGGTGGCGG 121 CGGCGGGGGGGACCCGGAACTCTGCGCCACGGACGAGATGATCCCCTTCAAGGACGAGGG 181 CGATCCTCAGAAGGAAAAGATCTTCGCCGAGATCAGTCATCATCCGAAGAGGAAGGCGATTT 241 AGCTGACATCAAGTCTTCCTTGGTGAACGAGTCTGAAATCATCCCGGCCAGCAACGGACA	SEQ ID NO:199

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		301 CGAGGTGGCCAGACAAGCACAAACCTCTCAGGAGCCCTACCACGACAAGGCCAGAGAACA 361 CCCCGATGACGGAAAGCATCCAGATGGAGGCCTCTACACACAAGGGACCCTCCTACTCGAG 421 TTATTCCGGTACATAATGATGCCAAATATGAATAACGACCCATACATGTCAAATGGATC 481 TCTTTCTCCACCCATCCCGAGAACATCAAATAAAGTGCCCGTGGTGCAGCCATCCCATGC 541 GGTCCATCCTCTCACCCCCCTCATCACTTACAGTGACGAGCACTTTTCTCCAGGATCACA 601 CCCGTCACACATCCCCATCAGATGTCAACTCCCAAACAAGGCATGTCCAGACATCCTCCAGC 661 TCCTGATATCCCTACTTTTTATCCCTTGTCTCCGGGTGGTGTTGGACAGATCACCCCACC 721 TCTTGGCTGGCAAGGTCAGCCTGTATATCCCATCACGGGTGGATTCAGGCAACCCTACCC 781 ATCCTCACTGTCAGTCGACACTTCCATGTCCAGGTTTTCCCATCATATGATTCCCGGTCC 841 TCCTGGTCCCCCACACAACTGCCATCCCCTCATCCAGCTATTGTAACACCTCAGGTCAAACA 901 GGAACATCCCCACACTGACAGTGACCTAATGCACGTGAAGCCTCAGCATGAACAGAGAAA 961 GGAGCAGGAGCCCAAAAAGACCTCACATTAAGAAGCCTCTGAATGCTTTATGTTATACAT 1021 GAAAGAAATGAGAGCGAATGTCGTTGCTGAGTGTACTCTAAAAGAAAGTGCAGCTATCAA 1081 CCAGATTCTTGGCAGAAGGTGCCATGCCCTCTCCCGTGAAGAGCAGGCTAAATATTATGA 1141 ATTAGCACGGAAAGAAAGACAGCTACATATGCAGCTTTATCCAGGCTGGTCTGCAAGAGA 1201 CAATTATGGTAAGAAAAAAGAAGAGAGAGAAGAAACTACAGGAATCTGCATCAGGTAC 1261 AGGTCCAAGAATGACAGCTGCCTACATCTGAAACATGGTGGAAAACGAAGCTCATTCCCG 1321 ACGTGCAAAGCCAAGGCAGCGACCCCGGGGCCTCTACTGGAGATGGAAGCTTGTTGAAAA 1381 CCCAGACTGTGTCCAGGGCTTGCCCAGTCGACCCCAAAGGAGAATTGACACCAACTTCAC 1441 CCTGAGGTCACTGCTAGAGACGCTGATCCACAAAGACAATCACTGCCACCCCCCTTCAT 1501 CTACTGCAAGAGCCAAGTTCCAAAATAAAGCGTAAAGGATTTTTTAGAAGAAAAGTAAAA 1561 AGCACATGAGAATGCTGGCAGGCCCTGGGTCAGCTGAGCAGCTTTCCCCCTCAGCTCCGC 1621 CGTGCACTTCCCAGAGCATCTCGCGTCCATACCTGAACCCTTGGGCGAGGACAGTAACTT 1681 GGCTGCATTTGCCTGTCATGCGCAACTGGAGCCAGCAACCAGCACATCCATCAGCACCCC 1741 AGTGGAGGAGTTCATGGAAGAGTTCCCTCTTTGTTTCTGCTTCATTTTTCTTCTTTTCT 1801 TTTCTCCTAAAGCTTTTCTTTAACAGTGCAAAAGGATCGTTTTTTTTTGCTTTTTAAAC 1861 TTGAATTTTTTTAATTTACACTTTTTAGTTTTAACTTTCTCTGTTGTATATTTTGCTAGC 1921 TATGAGCTTTGAAGTAAAATTGAAAGTTCTGGAAAAGTTTGAAATAATGACATAAAAAGA 1981 AGCCTTCTTTTTCTGAGACAGCTTGTCTGGTAAGTGGCTTCTCTGTGAATTGCCTGTAAC 2041 ACATAGTGGCTTCTCCGCCCTTGTAAGGTGTTCAGTAGAGCTAAATAAATGTAATAGCCA 2101 AACCCACTCTGTTGGTAGCAATTGGCAGCCCTATTTCAGTTTATTTTTTCTCTGTTTTC 2161 TTCTTTTCTTTTTTTTAAACAGTAAACCTTAACAGATGCGTTCAGCAGACTGGTTTGCAGT 2221 GAATTTTCATTTCCTTCCTTCTTGTTGTAAAAAGCCCAGCACTTGAATTGTTC 2281 TTACTTTAAATGTTCTGTATTTGTATCTGTTTTTTATTAACCGATTAGTGGGATTTTATGC 2341 CAGTTGTTAAAATGAGCAATGATGTACCCATTTTTTTTTAAATAGCAAGGCACAGCCTTCG 2401 CCCCAAACTGTCATCTAACGTTTGTCATTCCAGTTTGAGTTAATGTGCTGAGCATTTTTT 2461 AAAAGAAGCTTTGTAATAAAACATTTTTAAAAATTGTCAAAAAAAAAAAAAAAAAA 1 M P Q L S G G G G G G G G D P P E L C A T 1 ATGCCCCAACTCTCCGGAGGAGGTGGCGGCGGCGGGGGGACCCGGAACTCTGCGCCACG 21 D E M I P F F K D E G D P Q K E K I F A E 61 GACGAGATGATCCCCTTCAAGGACGAGGGCGATCCTCAGAAGGAAAAGATCTTCGCCGAG SEQ ID NO:200	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		41 I S H P E E E G D L A D I K S S L V N E 121 ATCAGTCATCCCGAAGAGGAAGGCGATTTACTGACATCAAGTCTTCCTTGGTGAACGAG	
		61 S E I I P A S N G H E V A R Q A Q T S Q 181 TCTGAAATCATCCCGGCCAGCAACGGACACGAGGTGGCCAGACAAGCACAAACCTCTCAG	
		81 E P Y H D K A R E H P D D G G K H P D G G 241 GAGCCCTACCACGACAAGGCCAGAGAACACCCCGATGACGGAAAGCATCCAGATGGAGGC	
		101 L Y N K G P S Y S S Y S G Y I M M P N M 301 CTCTACAACAAGGGACCCTCCTACTCGAGTTATTCCGGGTACATAATGATGCCAAATATG	
		121 N N D P Y M S N G S L S P P I P R T S N 361 AATAACGACCCATACATGTCAAATGGATCTCTTTCTCCACCCATCCCGAGAACATCAAAT	
		141 K V P P V V Q P S H A V H P L T P L I T Y 421 AAAGTGCCCGTGGTGCAGCCATCCCATGCGGTCCATCCTCTCACCCCCCTCATCACTTAC	
		161 S D E H F S P G S H P S H I P S D V N S 481 AGTGACGAGCACTTTTCTCCAGGATCACACCGTCACACATCCCATCAGATGTCAACTCC	
		181 K Q G M S R H P P A P P D I P T F Y P L S 541 AAACAAGGCATGTCCAGACATCCTCCAGCTCCTGATATCCCTACTTTTATCCCTTGTCT	
		201 P G G V G Q I T P P L G W Q G Q P V Y P 601 CCGGGTGGTGTTGGACAGATCACCCCACCTCTTGGCTGGCAAGGTCAGCCTGTATATCCC	
		221 I T G G F R Q P Y P S S L S V D T S M S 661 ATCACGGGTGGATTCAGGCAACCCTACCCATCCTCACTGTCAGTCGACACTTCCATGTCC	
		241 R F S H H M I P G P P G P H T T G I P H 721 AGGTTTTCCCATCATATGATTCCCGGTCCTCCTGGTCCCCACACAACTGGCATCCCTCAT	
		261 P A I V T P Q V K Q E H P H T D S D L M 781 CCAGCTATTGTAACACCTCAGGTCAAACAGGAACATCCCCACACTGACAGTGACCTAATG	
		281 H V K P Q H E Q R K E Q E P K R P H I K 841 CACGTGAAGCCTCAGCATGAACAGAGAAAGGAGCAGGAGCCAAAAAGACCTCACATTAAG	
		301 K P L N A F M L Y M K E M R A N V V A E 901 AAGCCTCTGAATGCTTTTATGTTATACATGAAAGAAATGAGAGCGAATGTCGTTGCTGAG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		321 C T L K E S A A I N Q I L G R R W H A L 961 TGTACTCTAAAAGAAAGTGCAGCTATCAACCAGATTCTTGGCAGAAGGTGGCATGCCCTC 341 S R E E Q A K Y Y E L A R K E R Q L H M 1021 TCCCGTGAAGAGCAGGCTAAATATTATGAATTAGCACGGAAAGAAAGACAGCTACATATG 361 Q L Y P G W S A R D N Y G K K K K R R K 1081 CAGCTTTATCCAGGCTGGTCTGCAAGACAATTATGGTAAGAAAAAGAAGAGGAAGAGA 381 E K L Q E S A S G T G P R M T A A Y I - 1141 GAGAAACTACAGGAATCTGCATCAGGTACAGGTCCAAGAATGACAGCTGCCTACATCTGA	
WBC311.bFSP	Homo sapiens THAP domain containing 5, mRNA (cDNA clone MGC:61780 IMAGE:5165075), complete cds	1 gtgaggcctt ggacctgtgg cctttgggct tgggtgtctc ctgtccgctc tgccagtgag 61 tcctcagctc tccgtacgtg gcccgtcgcc cgcggcaaga cggagggaag gcgctagttc 121 agtttagcta gcaatgccct tcttgcgcga ggactgctgg ctggtggcga ggcccaggag 181 cctgtttggg tgttaacagt taaaacagta aagtttgcgc gggcttctgt ggttttcagt 241 cttttcccca cttcacgtga tctcatttca ttgagcaaca ttaaccacca tttaagatac 301 gtgaaacctg cgaagtggaa aggtgcacgc aaagttaatt tacacccccc gcgagatttc 361 ctctacatga caaagaaaga ctggaaaagt ggttaaagaa tatgaagcga gattcatggg 421 ttcccagtaa ataccagttt ctatgtagtg accatttttac tcctgactct cttgacatca 481 gatggggtat tcgatattta aaacaaactg cagttccaac aatatttttct ttgcctgaag 541 acaatcaggg aaaagaccct tctaaaaaaa aatcccagaa gaaaaacttg gaagatgaga 601 aagaagtatg cccaaaagcc aagtcagaag aatcatttgt attaaatgag acaaagaaaa 661 atatagttaa cacagatgtg ccccatcaac atccagaatt acttcattca tcttccttgg 721 taaagccacc agctcccaaa acaggaagta tacaaaataa catgttaact cttaatctag 781 ttaaacaaca tactgggaaa ccagaatcta ccttggaaac atcagttaac caagatacag 841 gtagaggtgg tttcacaca tgtttgaga atctaaattc tacaactatt actttgacaa 901 cttcaaattc agaaagtatt catcaatctt tggaaactca agaagttctt gaagtaacta 961 ccagtcatct tgctaatcca aactttacaa gtaattccat ggaaataaag tcagcacagg 1021 aaaatccatt cttattcagc acaattaatc aaacagttga agaattaaac acaaataaag 1081 aatctgttat tgccatttt gtacctgctg aaaattctaa accctcagtt aattctttta 1141 tatctgcaca aaaagaaacc acggaaatgg aagacacaga cattgaagac tccttgtata 1201 aggatgtaga ctatgggaca gaagtttac aaatcgaaca ttcttactgc agacaagata 1261 taaataagga acatctttgg cagaaagtct ctaagctaca ttcaaagata actcttctag 1321 agttaaaaga gcaacaaact ctaggtagat tgaagtcttt ggaagctctt ataaggcagc 1381 taaagcagga aaactggcta tctgaagaaa acgtcaagat tatagaaaac cattttacaa 1441 catatgaagt cactatgata tagaataact aggttttaaa actatggctg ttaaataagc 1501 ttttttccagc caaaccaaac tacatgtaaa gtgaactgtt tcctgtataa agttctcatc 1561 ttaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1621 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1 M L T L N L V K Q H T G K P E S T L E T	SEQ ID NO:201 SEQ ID NO:202

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1 ATGTTAACTCTTAATCTAGTTAAACAACATACTGGGAAACCAGAATCTACCTTGGAAACA 21 S V N Q D T G R G G F H T C F E N L N S 61 TCAGTTAACCAAGATACAGGTAGAGGTGGTTTTCACACATGTTTTGAGAATCTAAATTCT 41 T T I T L T T S N S E S I H Q S L E T Q 121 ACAACTATTACTTTGACAACTTCAAATTCAGAAAGTATTCATCAATCTTTGGAAACTCAA 61 E V L E V T T S H L A N P N F T S N S M 181 GAAGTTCTTGAAGTAACTACCAGTCATCTTGCTAATCCAAACTTTACAAGTAATTCCATG 81 E I K S A Q E N P F L F S T I N Q T V E 241 GAAATAAAGTCAGCACAGGAAAATCCATTCTTATTCAGCACAATTAATCAAACAGTTGAA 101 E L N T N K E S V I A I F V P A E N S K 301 GAATTAAACACAAATAAAGAATCTGTTATTGCCATTTTTGTACCTGCTGAAAATTCTAAA 121 P S V N S F I S A Q K E T T E M E D T D 361 CCCTCAGTTAATTCTTTTATATCTGCACAAAAAGAAACCACGGAAATGGAAGACACAGAC 141 I E D S L Y K D V D Y G T E V L Q I E H 421 ATTGAAGACTCCTTGTATAAGGATGTAGACTATGGGACAGAAGTTTTACAAATCGAACAT 161 S Y C R Q D I N K E H L W Q K V S K L H 481 TCTTACTGCAGACAAGATATAAATAAGGAACATCTTTGGCAGAAAGTCTCTAAGCTACAT 181 S K I T L L E L K E Q Q T L G R L K S L 541 TCAAAGATAACTCTTCTAGAGTTAAAAGAGCAACAAACTCTAGGTAGATTGAAGTCTTTG 201 E A L I R Q L K Q E N W L S E E N V K I 601 GAAGCTCTTATAAGGCAGCTAAAGCAGGAAAACTGGCTATCTGAAGAAAACGTCAAGATT 221 I E N H F T T Y E V T M I - 661 ATAGAAAACCATTTTACAACATATGAAGTCACTATGATATAG	
WBC327.bFSP	Homo sapiens maltase-glucoamylase mRNA.	1 ATTGCTAAGCCATCCTTCAGACAGAGAGGGAGCGGCTGCAAGAGGTAATGAGAGATGGCA 61 AGAAAGAAGCTGAAAAAATTTACTACTTTGGAGATTGTGCTCAGTGTTCTTCTGCTTGTG 121 TTGTTTATCATCAGTATTGTTCTAATTGTGCTTTTAGCCAAAGAGTCACTGAAATCAACA 181 GCCCCAGATCCTGGGACAACTGGTACCCCAGATCCTGGGACAACTGGTACCCCAGATCCT 241 GGAACAACTGGTACCACACATGCTAGGACAACGGGTCCCCCAGATCCTGGAACAACTGGT 301 ACCACTCCTGTTTCTGCTGAATGTCCAGTGGTAAATGAATTGGAACGAATTAATTGCATC 361 CCTGACCAGCCGCCAACAAAGGCCACATGTGACCAACGTGGCTGTTGCTGGAATCCCCAG	SEQ ID NO:203

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		421 GGAGCTGTAAGTGTTCCCTGGTGCTACTATTCCAAGAATCATAGCTACCATGTAGAGGGC	
		481 AACCTTGTCAACACAAATGCAGGATTCACAGCCCGGTTGAAAAATCTGCCTTCTTCACCA	
		541 GTGTTTGGAAGCAATGTTGACAATGTTCTTCTCACAGCAGAATATCAGACATCTAATCGT	
		601 TTCCACTTTAAGTTGACTGACCAAACCAATAACAGGTTTGAAGTGCCCCACGAACACGTG	
		661 CAGTCCTTCAGTGGAAATGCTGCTGCTTCTTTGACCTACCAAGTTGAAATCTCCAGACAG	
		721 CCATTTAGCATCAAAGTGACCAGAAGAAGCAACAATCGTGTTTTGTTTGACTCGAGCATT	
		781 GGGCCCCTACTGTTTGCTGACCAGTTCTTGCAGCTCTCCACTCGACTGCCTAGCACTAAC	
		841 GTGTATGGCCTGGGAGAGCATGTGCACCAGCAGTATCGGCATGATATGAATTGGAAGACC	
		901 TGGCCCATATTTAACAGAGACACAACTCCCAATGGAAACGGAACTAATTTGTATGGTGCG	
		961 CAGACATTCTTCTTGTGCCTTGAAGATGCTAGTGGATTGTCCTTTGGGGTGTTTCTGATG	
		1021 AACAGCAATGCCATGGAGGTTGTCCTTCAGCCTGCGCCAGCCATCACTTACCGCACCATT	
		1081 GGGGGCATTCTCGACTTCTATGTGTTCTTGGGAAACACTCCAGAGCAAGTTGTTCAAGAA	
		1141 TATCTAGAGCTCATTGGGCGGCCAGCCCTTCCTCCTACTGGCGCTTGGATTTCACCTC	
		1201 AGTCGTTACGAATATGGAACCTTAGACAACATGAGGGAAGTCGTGGAGAGAAATCGCGCA	
		1261 GCACAGCTCCCTTATGATGTTCAGCATGCTGATATTGATGGATGAGACGAAGGGAC	
		1321 TTCACTTATGATTCAGTGGATTTTAAAGGCTTCCCTGAATTTGTCAACGAGTTACACAAT	
		1381 AATGGACAGAAGCTTGTCATCATTGTGGATCCAGCCATCTCCAACAACTCTTCCTCAAGT	
		1441 AAACCCTATGGCCCATATGACAGGGGTTCAGATATGAAGATATGGTGAATAGTTCAGAT	
		1501 GGAGTGACTCCCACTCATTGGGGAGGTCTGGCCTGGACAAACTGTGTTTCCTGATTATACC	
		1561 AATCCCAACTGTGCTGTTTGGTGGACAAAGGAATTTGAGCTTTTCACAATCAAGTAGAG	
		1621 TTTGATGGAATCTGGATTGATATGAATGAAGTCTCCAACTTTGTTGATGGTTCGGTCTCA	
		1681 GGATGTTCCACAAACACCTAAATAATCCCCCATTCACTCCCAGAATCCTGGATGGGTAC	
		1741 CTGTTCTGCAAGACTCTCTGTATGGATGCAGTGCAGCACTGGGGCAAGCAGTATGACATT	
		1801 CACAATCTGTATGGCTACTCCATGGCGGTCGCCACAGCAGAAGCTGCCAAGACTGTGTTC	
		1861 CCTAATAAGAGAAGCTTCATTCTGACCCGTTCTACCTTTGCGGCTCTGGCAAGTTTGCA	
		1921 GCACATTGGTTAGGAGACAACACTGCCACCTGGGATGACCTGAGATGGTCCATCCCTGGC	
		1981 GTGCTTGAGTTCAACCTTTTTGCCATCCCAATGGTGGGTCCTGACATATGTGGCTTTGCT	
		2041 TTGGACACCCCTGAGGAGCTCTGTAGGCGGTGGATGCAGTTGGGTGCATTTTATCCGTTT	
		2101 TCTAGAAATCACAATGGCCAAGGCTACAAGGACCAGGATCCTGCCTCCTTTGGAGCTGAC	
		2161 TCCCTGCTGTTGAATTCCTCCAGGCACTACCTTAACATCCGCTATACTCTATTGCCCTAC	
		2221 CTATACACCCTTTCTTCTTCCGTGCTCACAGCCGAGGGGACACGGTGGCCCAGGCCCCTTTTG	
		2281 CATGAGTTCTACGAGGACAACAGCACTTGGGATGTGCACCAACAGTTCTTATGGGGCCC	
		2341 GGCCTCCTCATCACTCCAGTTCTGGATGAAGGTGCAGAGAAGTGATGGCATATGTGCCT	
		2401 GATGCTGTCTGGTATGACTACGAGACTGGGAGCCAAGTGAGATGAGGAAGCAAAAGTC	
		2461 GAGATGGAACTTCCTGGAGACAAAATTGGACTTCACCTTCGAGGAGGCTACATCTTCCCC	
		2521 ACACAGCAGCCAAATACAACACTCTGGCCAGTCGAAAGAACCCTCTTGGTCTTATCATT	
		2581 GCCCTAGATGAGAACAAAGAAGCAAAAGGAGAACTTTTCTGGGATGATGGGGAAACGAAG	
		2641 GATACTGTGGCCAATAAAGTGTATCTTTATGTGAGTTTTCTGTCACTCAAAACCGCTTG	
		2701 GAGGTGAATATTTCACAATCAACCTACAAGGACCCCAATAATTTAGCATTTAATGAGATT	
		2761 AAAATTCTTGGGACGGAGGAACCTAGCAATGTTACAGTGAAACACAATGGTGTCCCAAGT	
		2821 CAGACTTCTCCTACAGTCACTTATGATTCTAACCTGAAGGTTGCCATTATCACAGATATT	
		2881 GATCTTCTCCTGGGAGAAGCATACACAGTGGAATGGAGCATAAAGATAAGGGATGAAGAA	
		2941 AAAATAGACTGTTACCCTGATGAGAATGGTGCTTCTGCCGAAAACTGCACTGCCCGTGGC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		3001 TGTATCTGGGAGGCATCCAATTCTTCTGGAGTCCCTTTTTGCTATTTTGTCAACGACCTA	
		3061 TACTCTGTCAGTGATGTTCAGTATAATTCCCATGGGGCCACAGCTGACATCTCCTTAAAG	
		3121 TCTTCCGTTTATGCCAATGCCTTCCCTCCACACCCGTGAACCCCCTTCGCCTGGATGTC	
		3181 ACTTACCATAAGAATGAAATGCTGCAGTTCAAGATTTATGATCCCAACAAGAATCGGTAT	
		3241 GAAGTTCCAGTCCCTCTGAACATACCCAGCATGCCATCCAGCACCCCTGAGGGTCAACTC	
		3301 TATGATGTGCTCATTAAGAAGAATCCATTTGGGATTGAAATTCGCCGGAAGAGTACAGGC	
		3361 ACTATATAATTTGGGACTCTCAGCTCCTTGGCTTTACCTTCAGTGACATGTTTATCCGCATC	
		3421 TCCACCCGCCTTCCCTCCAAGTACCTCTATGGCTTTGGGGAAACTGAGCACACAGGTCCTAT	
		3481 AGGAGAGACTTGGAGTGGCACACTTGGGGGATGTTCTCCCGAGACCAGCCCCCCAGGGTAC	
		3541 AAGAAGAATTCCTATGGTGTCTCCACCCTACTACATGGGGCTGGAGGAGGACGGCAGTGCC	
		3601 CATGGAGTGCTCCTGCTGAACAGCAATGCCATGGATGTGACGTTCCAGCCCCTGCCTGCC	
		3661 TTGACATACCGCACCACAGGGGGAGTTCTGGACTTTTATGTGTTCTTGGGGCCGACTCCA	
		3721 GAGCTTGTCACCCAGCAGTACACTGAGTTGATTGGCCGGCCTGTGATGGTACCTTACTGG	
		3781 TCTTTGGGGTTCCAGCTGTGTCGCTATGGCTACCAGAATGACTCTGAGATCGCCAGCTTG	
		3841 TATGATGAGATGGTGGCTGCCCAGATCCCTTATGATGTGCAGTACTCAGACATCGACTAC	
		3901 ATGGAGCGGCAGCTGGACTTCACCCTCAGCCCCAAGTTTGCTGGGTTTCCAGCTCTGATC	
		3961 AATCGCATGAAGGCTGATGGGATGCGGGTCATCCTCATTCTGGATCCAGCCATTTCTGGC	
		4021 AATGAGACACAGCCTTATCCTGCCTTCACTCGGGGCGTGGAGGATGACGTCTTCATCAAA	
		4081 TACCCAAATGATGGAGACATTGTCTGGGGAAAGGTCTGGCCTGATTTCCTGATGTTGTT	
		4141 GTGAATGGGTCTCTAGACTGGGACAGCCCAAGTGGAGCTATATCGAGCTTATGTGGCCTTC	
		4201 CCAGACTTTTTCCGTAATTCAACTGCCAAGTGGTGGAAGAGGGAAATAGAAGAACTATAC	
		4261 AACAATCCACAGAATCCAGAGAGGAGCTTGAAGTTTGATGGCATGTGGATTGATATGAAT	
		4321 GAACCATCAAGCTTCGTGAATGGGGCAGTTTCTCCAGGCTGCAGGGACGCCTCTCTGAAC	
		4381 CACCCTCCCTACATGCCACATTTGGAGTCCAGGGACAGGGGCCTGAGCAGCAAGACCCTT	
		4441 TGTATGGAGAGTCAGCAGATCCTCCCAGACCAGGCTCCCTGGTGCAGCACTACAACGTGCAC	
		4501 AACCTGTATGGGTCGTCCCAGACCAGACCCACATACGAAGCCGTGCAGGAGGTGACGGGA	
		4561 CAGCGAGGGGTCGTCATCACCCGCTCCACATTTCCCTCTTCTGGCCGCTGGGCAGGACAT	
		4621 TGGCTGGGAGACAACACGGCCGCATGGGATCAGCTGAAGAAGTCTATCATTGGCATGATG	
		4681 GAGTTCAGCCTCTTCGGCATATCCTATACGGGAGCAGATATCTGTGGGTTCTTTCAAGAT	
		4741 GCTGAATATGAGATGTGTGTTCGCTGGATGCAGCTGGGGGCCTTTTACCCCTTCTCAAGA	
		4801 AACCACAACACCATTGGGACCAGGAGACAAGACCCTGTGTCCTGGGATGTTGCTTTTGTG	
		4861 AATATTTCCAGAACTGTCCTGCAGACCAGATACACCCTGTTGCCATATCTGTATACCTTG	
		4921 ATGCATAAGGCCCACACGGAGGGCGTCACTGTTGTGCGGCCTCTGCTCCATGAATTTGTG	
		4981 TCAGACCAGGTGACATGGGACATAGACAGTCAGTTCCTGCTGGGCCCAGCCTTCCTGGTC	
		5041 AGCCCTGTCCTGGAGCGTAATGCCAGAAATGTCACTGCATATTTCCCTAGAGCCCGCTGG	
		5101 TATGATTACTACACGGGTGTGGATATTAATGCAAGAGGAGAGTGGAAGACCTTGCCAGCC	
		5161 CCTCTTGACCACATTAATCTTCATGTCCGTGGGGGCTACATCCTGCCCTGGCAAGAGCCT	
		5221 GCACAGAACACCCACTTAAGCCGTCAGAAATTCATAGGTTTCAAGGTTGCATTGGATGAC	
		5281 GATGGGACTGCTGAAGGTTGTCTCTTCTGGGATGATGGGCAAAGCATTGATACCTATGAA	
		5341 AAAGGACTCTATTATCTGGCCAACTTTTCTGCCAGCCAGAATACGATGCAGAGTCATGTA	
		5401 ATTTTCAACCAATACATCGTTGACACAAACCCTTTGAAACTGGGCTACATTGAGATCTGG	
		5461 GGAGTGGGCAGTGCTCCTGTTTCCAATGTCAGTGTCTCTCTGAGCAGCACAGTTATAACA	
		5521 CCCGCCTTCACCTACAACCCTACAACACAGGTGTTAAACATCGATGTGACCAGCAGAGAC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		5581 ATCAGCCTACATAATTTCATCTCATTGACATGGAGCAGCACTCTGTGAATTTTTAGAGCA 5641 AGATCCTAATTATGAAAGGCTTTGAAACTCCTTGTACATCATACCCATAAAATTACTGTG 5701 TGTTGCTAATTGGTTCAAGCCCCAATATGGTTAAAATATTTCATTAATTTTGTTGTATGTT 5761 TTTTGTGTGAACCCTAAAGGTTAAACCTTAGCCCTGTAATATAGGCAGTAGGGAAGTGTG 5821 AAAAATCTATGGGGTACCTTAATGTCTCTGTGTGATCAGTATGGTACTGATCACTCATCA 5881 TACAACATTTGTTGAAGATGCTCTGGGCCCATGATGAAGTGTGTGTATGTCCACGTTTGT 5941 AATCATAGAATGGACCCCATTCTTTTGTTAAATACACAAGAGAAAGCTTTCTGTGACAGT 6001 TCCAGGTCTTGAAGCTAATCAGCATCTCCAAGAAAGTATCCAGAAAGAACATCTGCTAGTT 6061 GGTTATAGGCGGTGGGAGGAATAATATACCTAATTGGTTATAGGTGGGGGAGCATGATA 6121 AGCAAAGAAAAGGCAAACACAAGGAAAGATCAGATGAAACAGAAGATGATAGTAAAAGTG 6181 ATCCTAAGTAAGAACATAATGTAAAATTGTCAGCAGCCTCATGGGGAGGTGAAAGGAAGA 6241 GCCAACTCACCTGAAGAAGAAGGGTCTTGAGAAATCCTTAGCATAAAGGGCTACTGGTGAG 6301 ATTGAGATCTGAGCAGGCAAAGCTCAAAAGAGAGTTTGGAGGTTAAAAATAATTTATTTT 6361 TGCAGTGGTGTGCTTTGAAATTTGTCAGTCTTATTTCTAATGTATATAACCACAGTTCCC 6421 ATAAATGCATGAAATTTATATGCCAGAGAAAAATAAACAAGTGAATTTGCAAGTGAAAA 6481 AAAAAAAAAAAAAAAAAAAAAAAAA	SEQ ID NO:204
		1 M A R K K L K K F T T L E I V L S V L L 1 ATGGCAAGAAAGAAGCTGAAAAAATTTACTACTTTGGAGATTGTGCTCAGTGTTCTTCTG	
		21 L V L F I I S I V L L I V L L A K E S L K 61 CTTGTGTTGTTTATCATCAGTATTGTTCTAATTGTGCTTTTAGCCAAAGAGTCACTGAAA	
		41 S T A P D P G T T G T P D P G T T G T P 121 TCAACAGCCCCAGATCCTGGGACAACTGGTACCCCAGATCCTGGACAACTGGTACCCCA	
		61 D P G T T G T T H A R T T T G P P P D P G T 181 GATCCTGGAACAACTGGTACCACACATGCTAGGACAACGGGTCCCCCAGATCCTGGAACA	
		81 T G T T P V S A E C P V V N E L E R I N 241 ACTGGTACCACTCCTGTTTCTGCTGAATGTCCAGTGGTAAATGAATTGGAACGAATTAAT	
		101 C I P D Q P P T K A T C D Q R G C C W N 301 TGCATCCCTGACCAGCCGCCAACAAAGGCCACATGTGACCAACGTGGCTGTTGCTGGAAT	
		121 P Q G A V S V P W C Y Y S K N H S Y H V 361 CCCCAGGGAGCTGTAAGTGTTCCCTGGTGCTACTATTCCAAGAATCATAGCTACCATGTA	
		141 E G N L V N T N A G F T A R L K N L P S 421 GAGGGCAACCTTGTCAACACAAATGCAGGATTCACAGCCCCGGTTGAAAAATCTGCCTTCT	
		161 S P V F G S N V D N V L L T A E Y Q T S 481 TCACCAGTGTTTGGAAGCAATGTTGACAATGTTCTTCTCACAGCAGAATATCAGACATCT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		181 N R F H F F K L T T D Q T N N N R F E E V P H E 541 AATCGTTTCCACTTTAAGTTGACTGACCAAACCAATAACAGGTTTGAAGTGCCCCACGAA	
		201 H V Q S F S G N A A A S L T Y Q V E I S 601 CACGTGCAGTCCTTCAGTGGAAATGCTGCTTCTTTGACCTACCAAGTTGAAATCTCC	
		221 R Q P F S I K V T R R S N N R V L F D S 661 AGACAGCCATTTAGCATCAAAGTGACCAGAAGAAGCAACAATCGTGTTTTGTTTGACTCG	
		241 S I G P L L F A D Q F L Q L S T R L P S 721 AGCATTGGGCCCCTACTGTTTGCTGACCAGTTCTTGCAGCTCTCCACTCGACTGCCTAGC	
		261 T N V Y G L G E H V H Q Q Y R H D M N N W 781 ACTAACGTGTATGGCCTGGGAGAGCATGTGCACCAGCAGTATCGGCATGATATGAATTGG	
		281 K T W P I F N R D T T P N G N G T N L Y 841 AAGACCTGGCCCATATTTAACAGAGACACAACTCCCAATGGAAACGGAACTAATTTGTAT	
		301 G A Q T F F L C L E D A S G L S F G V F 901 GGTGCGCAGACATTCTTCTTGTGCCTTGAAGATGCTAGTGGATTGTCCTTTGGGGTGTTT	
		321 L M N S N A M E V V L Q P A P A I T Y R 961 CTGATGAACAGCAATGCCATGGAGGTTGTCCTTCAGCCTGCGCCAGCCATCACTTACCGC	
		341 T I G G I L D F Y V F L G N T P E Q V V 1021 ACCATTGGGGGCATTCTCGACTTCTATGTGTTCTTGGGAAACACTCCAGAGCAAGTTGTT	
		361 Q E Y L E L I G R P A L P S Y W A L G F 1081 CAAGAATATCTAGAGCTCATTGGCGCGGCCAGCCCTTCCCTCCTACTGGGCGCTTGGATTT	
		381 H L S R Y E Y G T L D N M R E V V E R N 1141 CACCTCAGTCGTTACGAATATGGAACCTTAGACAACATGAGGGAAGTCGTGGAGAGAAAT	
		401 R A A Q L P Y D V Q H A D I D Y M D E R 1201 CGCGCAGCACAGCTCCCTTATGATGTTCAGCATGCTGATATTGATTATATGGATGAGAGA	
		421 R D F T Y D S V D F K G F P E F V N E L 1261 AGGGACTTCACTTATGATTCAGTGGATTTTAAGGCTTCCCTGAATTTGTCAACGAGTTA	
		441 H N N G Q K L V I I V D P A I S N N S S 1321 CACAATAATGGACAGAAGCTTGTCATCATTGTGGATCCAGCCATCTCCAACAACTCTTCC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		461 S S K P Y G P Y D R G S D M K I W V N S 1381 TCAAGTAAACCCTATGGCCCATATGACAGGGTTCAGATATGAAGATATGGTGAATAGT	
		481 S D G V T P L I G E V W P G Q T V F P D 1441 TCAGATGGAGTGACTCCACTCATTGGGGAGGTCTGGCCTGGACAAACTGTGTTTCCTGAT	
		501 Y T N P N C A V W W T K E F E L F H N Q 1501 TATACCAATCCCAACTGTGCTGTTTGGTGGACAAAGGAATTTGAGCTTTTTCACAATCAA	
		521 V E F D G I W I D M N E V S N F V D G S 1561 GTAGAGTTTGATGGAATCTGGATTGATATGAATGAAGTCTCCAACTTTGTTGATGGTTCG	
		541 V S G C S T N N L N N P P F T P R I L D 1621 GTCTCAGGATGTTCCACAAACAACCTAAATAATCCCCCATTCACTCCCAGAATCCTGGAT	
		561 G Y L F C K T L C M D A V Q H W G K Q Y 1681 GGGTACCTGTTCTGCAAGACTCTCTGTATGGATGCAGTGCAGCACTGGGGCAAGCAGTAT	
		581 D I H N L Y G Y S M A V A T A E A A K T 1741 GACATTCACAATCTGTATGGCTACTCCATGGCGGTCGCCACAGCAGAAGCTGCCAAGACT	
		601 V F P N K R S F I L T R S T F A G S G K 1801 GTGTTCCCTAATAAGAGAAGCTTCATTCTGACCCGTTCTACCTTTGCGGGCTCTGGCAAG	
		621 F A A H W L G D N T A T W D D L R W S I 1861 TTTGCAGCACATTGGTTAGGAGACAACACTGCCACCTGGGATGACCTGAGATGGTCCATC	
		641 P G V L E F N L F G I P M V G P D I C G 1921 CCTGGCGTGCTTGAGTTCAACCTTTTTGGCATCCCAATGGTGGGTCCTGACATATGTGGC	
		661 F A L D T P E E L C R R W M Q L G A F Y 1981 TTTGCTTTGGACACCCCTGAGGAGCTCTGTAGGCGGTGATGCAGTTGGGTGCATTTTAT	
		681 P F S R N H N G Q G Y K D Q D P A S F G 2041 CCGTTTTCTAGAAATCACAATGGCCAAGGCTACAAGGACCAGGATCCTGCCTCCTTTGGA	
		701 A D S L L L N S S R H Y L N I R Y T L L 2101 GCTGACTCCCTGCTGTTGAATTCCTCCAGGCACTACCTTAACATCCGCTATACTCTATTG	
		721 P Y L Y T L F F R A H S R G D T V A R P 2161 CCCTACCTATACACCCTTTTCTTCCGTGCTCACAGCCGAGGGACACGGTGGCCAGGCCC	
		741 L L H E F Y E D N S T W D V H Q Q F L W	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2221 CTTTTGCATGAGTTCTACGAGGACAACAGCACTTGGGATGTGCACCAACAGTTCTTATGG	
		761 G P G L L I T P V L D E G A E K V M A Y	
		2281 GGGCCCGGCCTCCTCATCACTCCAGTTCTGGATGAAGGTGCAGAGAAAGTGATGGCATAT	
		781 V P D A V W Y D Y E T G S Q V R W R K Q	
		2341 GTGCCTGATGCTGTCTGGTATGACTACGAGACTGGGAGCCAAGTGAGATGGAGGAAGCAA	
		801 K V E M E L P G D K I G L H L R G G Y I	
		2401 AAAGTCGAGATGGAACTTCCTGGAGACAAAATTGGACTTCACCTTCGAGGAGGCTACATC	
		821 F P T Q Q P N T T T L A S R K N P L G L	
		2461 TTCCCCACACAGCAGCCAAATACAACCACTCTGGCCAGTCGAAAGAACCCTCTTGGTCTT	
		841 I I A L D E N K E A K G E L F W D D G E	
		2521 ATCATTGCCCTAGATGAGAACAAAGAAGCAAAAGGAGAACTTTTCTGGGATGATGGGGAA	
		861 T K D T V A N K V Y L L C E F S V T Q N	
		2581 ACGAAGGATACTGTGGCCAATAAAGTGTATCTTTTATGTGAGTTTTCTGTCACTCAAAAC	
		881 R L E V N I S Q S T Y K D P N N L A F N	
		2641 CGCTTGGAGGTGAATATTTCACAATCAACCTACAAGGACCCCAATAATTTAGCATTTAAT	
		901 E I K I L G T E E P S N V T V K H N G V	
		2701 GAGATTAAAATTCTTGGGACGGAGGAACCTAGCAATGTTACAGTGAAACACAATGGTGTC	
		921 P S Q T S P T V T Y D S N L K V A I I T	
		2761 CCAAGTCAGACTTCTCCTACAGTCACTTATGATTCTAACCTGAAGGTTGCCATTATCACA	
		941 D I D L L L G E A Y T V E W S I K I R D	
		2821 GATATTGATCTTCTCCTGGGAGAAGCATACACAGTGGAATGGAGCATAAAGATAAGGGAT	
		961 E E K I D C Y P D E N G A S A E N C T A	
		2881 GAAGAAAAAATAGACTGTTACCCTGATGAGAATGGTGCTTCTGCCGAAAACTGCACTGCC	
		981 R G C I W E A S N S S G V P F C Y F V N	
		2941 CGTGGCTGTATCTGGGAGGCATCCAATTCTTCTGGAGTCCCTTTTGCTATTTTGTCAAC	
		1001 D L Y S V S D V Q Y N S H G A T A D I S	
		3001 GACCTATACTCTGTCAGTGATGTTCAGTATAATTCCCATGGGGCCACAGCTGACATCTCC	
		1021 L K S S V Y A N A F P S T P V N P L R L	
		3061 TTAAAGTCTTCCGTTTATGCCAATGCCTTCCCCTCCACACCCGTGAACCCCCTTCGCCTG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1041 D V T Y H K N E M L Q F K I Y D P N K N 3121 GATGTCACTTACCATAAGAATGAAATGCTGCAGTTCAAGATTTATGATCCCAACAAGAAT	
		1061 R Y E V P V P L N I P S M P S S T P E G 3181 CGGTATGAAGTTCCAGTCCCTCTGAACATACCCAGCATGCCATCCAGCACCCCTGAGGGT	
		1081 Q L Y D V L I K K N P F G I E I R R K S 3241 CAACTCTATGATGTGCTCATTAAGAAGAATCCATTTGGGATTGAAATTCGCCGGAAGAGT	
		1101 T G T I I W D S Q L L G F T F S D M F I 3301 ACAGGCACTATAATTTGGGACTCTCAGCTCCTTGGCTTTACCTTCAGTGACATGTTTATC	
		1121 R I S T R L P S K Y L Y G F G E T E H R 3361 CGCATCTCCACCCGCCTTCCCTCCAAGTACCTCTATGGCTTTGGGGAAACTGAGCACAGG	
		1141 S Y R R D L E W H T W G M F S R D Q P P 3421 TCCTATAGGAGACGACTTGGAGTGGCACACTTGGGGGATGTTCTCCCGAGACCAGCCCCCA	
		1161 G Y K K N S Y G V H P Y Y M G L E E D G 3481 GGGTACAAGAAGAATTCCTATGGTGTCCACCCCTACTACATGGGGCTGGAGGAGGACGGC	
		1181 S A H G V L L L N S N A M D V T F Q P L 3541 AGTGCCCATGGAGTGCTCCTGCTGAACAGCAATGCCATGGATGTGACGTTCCAGCCCCTG	
		1201 P A L T Y R T T G G V L D F Y V F L G P 3601 CCTGCCTTGACATACCGCACCACAGGGGGAGTTCTGGACTTTTATGTGTTCTTGGGCCG	
		1221 T P E L V T Q Q Y T E L I G R P V M V P 3661 ACTCCAGAGCTTGTCACCCAGCAGTACACTGAGTTGATTGGCCGGCCTGTGATGGTACCT	
		1241 Y W S L G F Q L C R Y G Y Q N D S E I A 3721 TACTGGTCTTTGGGTTCCAGCTGTGTCGCTATGGCTACCAGAATGACTCTGAGATCGCC	
		1261 S L Y D E M V A A Q I P Y D V Q Y S D I 3781 AGCTTGTATGATGAGATGGTGGCTGCCCAGATCCCTTATGATGTGCAGTACTCAGACATC	
		1281 D Y M E R Q L D F T L S P K F A G F P A 3841 GACTACATGGAGCGGCAGCTGGACTTCACCCTCAGCCCCAAGTTTGCTGGGTTTCCAGCT	
		1301 L I N R M K A D G M R V I L L D P A I 3901 CTGATCAATCGCATGAAGGCTGATGGGATGCGGGTCATCCTCATTCTGGATCCAGCCATT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1321 S G N E T Q P Y P A F T R G V E D D V F 3961 TCTGGCAATGAGACACAGCCTTATCCTGCCTTCACTCGGGGCGTGGAGGATGACGTCTTC	
		1341 I K Y P N D G D I V W G K V W P D F P D 4021 ATCAAATACCCAAATGATGGAGACATTGTCTGGGGAAAGGTCTGGCCTGATTTTCCTGAT	
		1361 V V V N G S L D W D S Q V E L Y R A Y V 4081 GTTGTTGTGAATGGGTCTCTAGACTGGGACAGCCAAGTGGAGCTATATCGAGCTTATGTG	
		1381 A F P D F F R N S T A K W W K R E I E E 4141 GCCTTCCCAGACTTTTTCCGTAATTCAACTGCCAAGTGGTGGAAGAGGGAAATAGAAGAA	
		1401 L Y N N P Q N P E R S L K F D G M W I D 4201 CTATACAACAATCCACAGAATCCAGAGAGGAGCTTGAAGTTTGATGGCATGTGGATTGAT	
		1421 M N E P S S F V N G G A V S P G C R D A S 4261 ATGAATGAACCATCAAGCTTCGTGAATGGGGCAGTTTCTCCAGGCTGCAGGGACGCCTCT	
		1441 L N H P P Y M P H L E S R D R G L S S K 4321 CTGAACCACCCTCCCTACATGCCACATTTGGAGTCCAGGGACAGGGGCCTGAGCAGCAAG	
		1461 T L C M E S Q Q I L P D G S L V Q H Y N 4381 ACCCTTTGTATGGAGAGTCAGCAGATCCTCCCAGACGGCTCCCTGGTGCAGCACTACAAC	
		1481 V H N L Y G W S Q T R P T Y E A V Q E V 4441 GTGCACAACCTGTATGGGTGGTCCCAGACCAGACCCACATACGAAGCCGTGCAGGAGGTG	
		1501 T G Q R G V V I T R S T F P S S G R W A 4501 ACGGGACAGCGAGGGGTCGTCATCACCCGCTCCACATTTCCCTCTTCTGGCCGCTGGGCA	
		1521 G H W L G D N T A A W D Q L K K S I I G 4561 GGACATTGGCTGGGAGACAACACGGCCGCATGGATCAGCTGAAGAAGTCTATCATTGGC	
		1541 M M E F S L F G I S Y T G A D I C G F F 4621 ATGATGGAGTTCAGCCTCTTCGGCATATCCTATACGGGAGCAGATATCTGTGGGTTCTTT	
		1561 Q D A E Y E M C V R W M Q L G A F Y P F 4681 CAAGATGCTGAATATGAGATGTGTTCGCTGGATGCAGCTGGGGGCCTTTTACCCCTTC	
		1581 S R N H N T I G T R R Q D P V S W D V A 4741 TCAAGAAACCACAACACCATTGGGACCAGGAGACAAGACCCTGTGTCCTGGGATGTTGCT	
		1601 F V N I S R T V L Q T R Y T L L P Y L Y	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		4801 TTTGTGAATATTTCCAGAACTGTCCTGCAGACCAGATACACCCTGTTGCCATATCTGTAT	
		1621 T L M H H K A H T T E G V T V V R P L L H E	
		4861 ACCTTGATGCATAAGGCCCACACGGAGGGCGTCACTGTTGTGCGGCCTCTGCTCCATGAA	
		1641 F V S D Q V T W D I D S Q F L L G P A F	
		4921 TTTGTGTCAGACCAGGTGACATGGGACATAGACAGTCAGTTCCTGCTGGGCCCAGCCTTC	
		1661 L V S P V L E R N A R N V T A Y F P R A	
		4981 CTGGTCAGCCCTGTCCTGGAGCGTAATGCCAGAAATGTCACTGCATATTTCCCTAGAGCC	
		1681 R W Y D Y Y T G V D I N A R G E W K T L	
		5041 CGCTGGTATGATTACTACACGGGTGTGGATATTAATGCAAGAGGAGAGTGGAAGACCTTG	
		1701 P A P L D H I N L H V R G G Y I L P W Q	
		5101 CCAGCCCCTCTTGACCACATTAATCTTCATGTCCGTGGGGGCTACATCCTGCCCTGGCAA	
		1721 E P A Q N T H L S R Q K F I G F K V A L	
		5161 GAGCCTGCACAGAACACCCACTTAAGCCGTCAGAAATTCATAGGTTTCAAGGTTGCATTG	
		1741 D D D G T A E G C L F W D D G Q S I D T	
		5221 GATGACGATGGGACTGCTGAAGGTTGTCTCTTCTGGGATGATGGGCAAAGCATTGATACC	
		1761 Y E K G L Y Y L A N F S A S Q N T M Q S	
		5281 TATGAAAAAGGACTCTATTATCTGGCCAACTTTTCTGCCAGCCAGAATACGATGCAGAGT	
		1781 H V I F N Q Y Y I V D T N P L K L G Y Y I E	
		5341 CATGTAATTTTCAACCAATACATCGTTGACACAAACCCTTTGAAACTGGGCTACATTGAG	
		1801 I W G V G S A P V S N V S V S L S S T V	
		5401 ATCTGGGGAGTGGGCAGTGCTCCTGTTTCCAATGTCAGTGTCTCTCTGAGCAGCACAGTT	
		1821 I T P A F T Y N P T T Q V L N I D V T S	
		5461 ATAACACCCGCCTTCACCTACAACCCTACAACACAGGTGTTAAACATCGATGTGACCAGC	
		1841 R D I S L H N F I S L T W S S T L -	
		5521 AGAGACATCAGCCTACATAATTTCATCTCATTGACATGGAGCAGCACTCTGTGA	
WBC33.gRSP	No Homology	1 GGGACGAAGTTTCCATGACATCATAAGCAGAGATGGCAGAAACATCAAGGATTCTGGGGA	SEQ ID NO:205
		61 TTACTTCTTATCAAGACTCAGAGAGTGTGGTGACCACACAAAGTCCCCCTTCTGCTAAGGGA	
		121 CTGGCCCTGGATTTATGACCCCTGTGGAGTGGTAGCCACTAGCTGTGAAGAGGTCTCAGC	
		181 CCAGGCCCCTTCAGTACTCTTTTCTCCCTGTATAGAAGGCATCATTTGTCTTTCTTTCCCC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		241 AGAACCTTCCAAGACCTGGCCCTGACTTCTGCATGATAAACTGCTATCAGGAACCCTATA 301 TCAGTTAAAACACATTATCCCTCTCTCCACTCTCTTGGGAAGCCGGAATTTGAGACTGGGTG 361 GGGGCTTGGGATATTTTTAATAGAGCTTATCTTCAGCTAGTGGTTAGTTATGATTCTAA 421 AACTTTGGGAGCCTGAGAGATTTGTTAAAAATATAGACACTTGGGCCCCACTCTAGGCAT 481 GCAGTCCCCAGGTGATTCTGAAGCAGCCCCTATTCAGAGTCTCTGGTTTAGAGGAAGAAC 541 TGAGGCCACTTAGACTATTGAGTCCTTCATGCCTGTTCCTGTCTACCATAGGTGGGATAA 601 GAGTTTGTTCTTAGAGTAAGAGTAATTTAATGAACCTCAAGACAGTTTAATGAGAGTGGG 661 AGTTTCCTAGACCAGGCTTCCCAAAGGAGAAAAGGATT 1 TTTTTTTTTTTTTTTGAAAAGTTAAACTGTCTTTATTCACAACCAACATTATCATCTACGT 61 AGGATGTCTAACAGGATGTACCAAAAAAAGCTACCAGCATTAATAAGTGAGTTTAGGAAG 121 TTTTCAGGGTACAAGATCAATGTACTAAAGTAACTGTATTCTATATATTATCAATGAAC 181 AATTGGAAATTGAAATTTTAAAAATACCATATACAATAGCATCAAAAAATATGAAATATT 241 TAGGGCTAAATCTGACAGAAGATGTGTTCATGGATTGGAACACTCAATATCAGTAAGTTG 301 TCTGTTCTCCCCAAGTTGATCTATAAATTTGATGCAATCCTGATCATGATTCCAGGAGAC 361 CTTTTGTAGTAATGAGAAGTCAATTCGTTTGGGAGGGCAAGGACTGAGAATAGCCAAAC 421 TGCTTTCTTTAAAAGTTGTAACCCAGCCTTTCCAATCCTGAGTATTTATCCAATAGAAAT 481 GAAAGCATACGCTCACATGATGACTTATATACACCGAATGTTCGTAGCACTTTATTTGTAAT 541 AACCAAAACAGGAGACAACCCAAAGACTGTCAACAGGTGAATGGATAAAGCAGCTTGTG 601 GTATATCCATACAATGAAATACTAATGAACAATAAAAGGAATGAACTATTGAT	SEQ ID NO:206
WBC335.bFSP	Homo sapiens radixin, mRNA (cDNA clone MGC:48283 IMAGE:5284438)	1 ATTGCGGAGCTGTCTGCGGTGGCGGCGGCGCCTCTCGTCTCCCGCGGCCCAGCGCTCGCA 61 CCACCGCTTCTCCCTCCCTGTCGCAGCCGCCGCCGCGCAGCGCCCCAGCCACACGCCG 121 GCGGGCAGAAGCCGCCCGCTCTCCGGAAAGTGATAACAGAATTCATTGAAGTGGAGAATT 181 TTTAAAGAAGGTAACAAAAAGAGAAAGAAATGCCGAAACCAATCAACGTAAGAGTAACT 241 ACAATGGATGCTGAGCTGGAATTTGCCATTCAGCCCAATACAACTGGCAAACAACTTTTT 301 GACCAGGTGGTGAAAACAGTTGGTTTGCGTGAGGTCTGGTTTTTTGGGCTGCAGTATGTA 361 GACAGCAAAGGTTATTCTACATGGCTTAAACTAAATAAAAAGGTAACACAGCAGGATGTT 421 AAAAAAGAGAATCCTTTACAGTTCAAGTTTAGAGCTAAATTCTTTCCTGAAGATGTTTCT 481 GAGGAATTAATTCAAGAAATAACCCAGAGACTCTTCTTCTTGCAAGTTAAAGAAGCCATC 541 TTAAATGATGAGATATATTGCCCGCCAGAAACTGCAGTTCTTTTGGCTTCCTATGCTGTC 601 CAAGCCAGTATGGAGATTACAATAAAGAGATTCATAAGCCAGGCTACCTGGCTAATGAT 661 AGACTCCTACCCCAGCGTGTATTGGAACAACACAACTAACAAAAGAACAGTGGGAAGAA 721 AGAATACAGAACTGGCATGAAGAACATAGAGGAATGTTAAGGGAGGATTCTATGATGGAA 781 TACCTGAAGATTGCACAGATCTAGAAATGTATGGAGTCAACATTTTTGAAATAAAAAAT 841 AAAAAAGGAACTGAATTGTGGCTAGGTGTTGATGCTTTGGGTCTGAATATTTATGAGCAT 901 GACGACAAGTTAACACCTAAAATTGGTTTTCCCTGGAGTGAAATCAGAAATATTTCATTT 961 AATGACAAAAAATTTGTTATAAAGCCAATCGACAAAAAGGCACCTGATTTTGTGTTTTAT 1021 GCACCTCGTCTGAGAATCAATAAGAGGATTTTGGCCTTATGTATGGGAAACCATGAACTA 1081 TACATGCGAAGAAGGAAGCCTGATACTATTGAAGTACAACAGATGAAGGCTCAGGCTAGG 1141 GAGGAGAAACATCAGAAGCAGTTGGAAAGGGCACAATTAGAGAATGAAAAGGAGAAAAGA 1201 GAAATAGCAGAAAAGGAAAAGGAAAGAATAGAACGTGAAAAGGAAGAGCTAATGGAACGT	SEQ ID NO:207

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1261 CTAAAACAAATTGAAGAGCAGACAATTAAAGCTCAGAAAGAACTAGAAGAACAGACTCGA	
		1321 AAAGCTCTAGAACTGGATCAAGAACGAAAACGAGCAAAAGAAGAAGCAGAACGACTTGAA	
		1381 AAGGAGCGTCGAGCTGCTGAAGAGGCAAAGTCTGCCATAGCAAAACAAGCTGCCGACCAG	
		1441 ATGAAGAATCAGGAGCAGCTAGCAGCAGAACTTGCTGAATTCACTGCCAAGATTGCACTT	
		1501 CTAGAGGAAGCCAAGAAGAAAAAGGAAGAGGAAGCTTACTGAGTGGCAACACAAAGCTTTT	
		1561 GCAGCCCAGGAAGACTTGGAAAAGACCAAAGAAGAGTTAAAAACTGTGATGTCTGCCCCC	
		1621 CCTCCACCTCCACCACCACGTCATTCCTCCAACAGAAAACGAACATGATGAACACGAT	
		1681 GAGAATAATGCTGAAGCTAGTGCTGAATTATCAAATGAAGGGGTAATGAACCATAGAAGC	
		1741 GAGGAAGAACGTGTAACCGAAACACAGAAAAATGAGCGTGTTAAGAAGCAACTTCAGGCA	
		1801 TTAAGTTCAGAATTAGCCCAAGCCAGATGAAACCAAGAAAACACAAAATGATGTTCTT	
		1861 CATGCTGAGAATGTTAAAGCAGGCCGTGATAAGTACAAGACTCTGCGACAGATTCGACAA	
		1921 GGCAATACAAAGCAGCGTATCGATGAGTTTGAAGCAATGTGAGAGCTGTTATTTTGCATA	
		1981 TATGTTCTTCATAAGCTGAACCACCACAGAGAAAAGCAGGCCTTTGCAGATATGATGGA	
		2041 ATGCATCCCACCTTGCCAAAGCACTTACACCAGTTTGACTGTGCTAGCTAAAAGACAAAT	
		2101 TTAAGGGGAGCTCTTCAACATTAAGGCAGTATGATATCATGCTTGGTTTTCTTTTTTCTT	
		2161 TTGGTCCAGGGAATGGAGAATGGTGTTCCATTGCCTCTTTTCACATTTTTTTTCTTTTTC	
		2221 TTTTTTTTTTCTGTTGAAGATTAACACTAATTATCACGTCTGACAAATGTGTATGTGTGG	
		2281 TTTCAGTTCTGTGTACATTTTAAAGGATAATGGTGAACATTTTAATGGGTTTCCCTTGCC	
		2341 CTTTCCATATTTAACCTATTTCCACATTCTCTCTCACTCACATTTCTCAGTGTGCCCTT	
		2401 CTCTTATCTGCCGTGTCCATAGCCATAATTCCACCATACAGATCATTGGCAGTGTTTAAA	
		2461 ATGAGGGTAGGTGACAGGGTGGACAGTGTTTGATCATCATGTAGAATATGGCTATGAATC	
		2521 AGGAAAGAGATTAGAACATTTAATAATGTATGTACAGCTGGTGCTTAGTTTTTTTTAAT	
		2581 CTAAATTTAATTACATTATTTGGATATTTGATGTTTGCTTACTAAATTACAGTCATCTTTG	
		2641 ACAGCTGAATTGATTGGTGTTTCATCTCCTGTCACCCTTTGGCTTTCTTTACTTACCAAT	
		2701 TCACAAAGGTGTAGACAGCAGGTAGTAGGTCCCTAGGAAAATTTATTATTGATGAAACAGCCT	
		2761 CTGCAAGATTTTAAAAGTTTTGTTCTTTCATAGATTGATTTAGAAAAACAAATGATTAGT	
		2821 TAAAAAAAGAAAATATACATTTGTTGGTAACTAAATGTTATTTTTTTAAAACCTGGACCTTT	
		2881 CTGGAAGGGCAGCCTATGAAAACATTAGTCCCAGAGAAGGGACAATAAATACTACCTCAC	
		2941 TACTACACCTGCGATGACTGGTTGTTCAAACACAACAGAGTGTGTCAGCTGTATGTTTTA	
		3001 TAATACATAACCATAGCCTCGATCATCAAGAAATACTTTCGAAATTTCATTTTCCTTCAG	
		3061 AATATCTTAAGAGTGCTAAATTTTTAACTGCCTTTTTGTCGAGTCAAACTGTGGGATTCT	
		3121 GATTTGTATTAAAATTGTAAGCTCCTCACTGGTATATCTATCATCCTGGAGGGGGTGTTGTA	
		3181 TGGCTGAGCAAGAGAGAGAGAATGAGAGAGAGACTGTGTGTGTGTGTGTGTG	
		3241 TACTCTGTGTGTATGAGAGAGAGAGAGAAATGCTAACCTTGTAGCATGTGAAGAATGT	
		3301 CTGTACCTTGATACGATAGTTACATAATCAGTATATATTTGGTTTCTAGATCACTGTGCTTA	
		3361 TTTTGTTTCAATCTCTGACTAAAAATACTTAAATTTGGTTTGTTAATTCTTATTTTAGAA	
		3421 ATTATAATTTTAGTTTATATTAATTTCGGTTATAGCTTACTGAAGAAATCTTTCCAGTTA	
		3481 GAAGGAGGTTCTAATATTCACATGTTCTAATACTTTGTTTATTGTAAAACAGCTAAATTT	
		3541 GGAGATACGTAAAGCCTTGTTTTCTCTGTGTGGTTCAGCTACTTTCCATTTGGTATTACA	
		3601 CAGTCAAATTTACATTTATCTATTAAAATTGCCATTTTATTAAACATTTTCATGCACAGT	
		3661 AGATTCAAGTTGTGTCTGAAAATATCTCTTGTGCTTTTTTGATTTTGCTGACTTTAAAAG	
		3721 GATTAATCTGGGCAGACATTATGTAAAAGAAGGTTGCGTTTAATATATTTTTTGAACTT	
		3781 TGTAGGACAAAACATAGCTGGTTAACCTTGAAGTGACTGTTGTACCATGGTTGTGCACAT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		3841 GCTTCAGAATCCTATGGAAGAGAATATTCCTACTTGCAGTACATCAAAGGAATGGATGGT 3901 GGACCCTACTATTCATGTTTTGAGACATAAATGTTCACTTTAAAGCAATTGCATAATAGA 3961 TAAAAACCTGAACTTTCATTGGATTTTTATTAATTTTCTTCATTTTGAATTGTGTGCACT 4021 ACCATTGTCACATCAGTTTGATATCAGTGTTGAAAAATTACCAGTTATATTTGCTGTTTA 4081 TAATCTATTTGTAGATTAGGATTAAAATGGATTTAATCCATTTTTAAAGCTGTGTGAATT 4141 TTTCTAAACAGGAACAACTATTTGCAATATAGGTTTTCATAGTGATTAAACCAATTATAA 4201 CTTTTATTATTAGCAATTGAGAGCACATGTTCATATAGCAATGTAAAAATATATTAATGA 4261 GTATTTGGTAAATTCCAACAGGCTTTTACCATTAGCATAATTTTGTGTTGTACAATTAAG 4321 TTACAATTACATCTATAATTTTGGATAACATTCATTGGTTAACAATAAAGTGACAAAAGC 4381 TCAAAAAAAAAAAAAAAAAAAGAAAAAAAAAAAAAAAA	
		1 M P K P I N V R V T T M D A E L E F A I 1 ATGCCGAAACCAATCAACGTAAGAGTAACTACAATGGATGCTGAGCTGGAATTTGCCATT	SEQ ID NO:208
		21 Q P N T T G K Q L F D Q V V K T V G L R 61 CAGCCCAATACAACTGGCAAACAACTTTTTGACCAGGTGGTGAAAACAGTTGGTTTGCGT	
		41 E V W F F G L Q Y V D S K G Y S T W L K 121 GAGGTCTGGTTTTTTGGGCTGCAGTATGTAGACAGCAAAGGTTATTCTACATGGCTTAAA	
		61 L N K K V T Q Q D V K K E N P L Q F K F 181 CTAAATAAAAAGGTAACACAGCAGGATGTTAAAAAAGAGAATCCTTTACAGTTCAAGTTT	
		81 R A K F F P E D V S E E L I Q E I T Q R 241 AGAGCTAAATTCTTTCCTGAAGATGTTTCTGAGGAATTAATTCAAGAAATAACCCAGAGA	
		101 L F F L Q V K E A I L N D E I Y C P P E 301 CTCTTCTTCTTGCAAGTTAAAGAAGCCATCTTAAATGATGAGATATATTGCCCGCCAGAA	
		121 T A V L L A S Y A V Q A K Y G D Y N K E 361 ACTGCAGTTCTTTTGGCTTCCTATGCTGTCCAAGCCAAGTATGGAGATTACAATAAAGAG	
		141 I H K P G Y L A N D R L L P Q R V L E Q 421 ATTCATAAGCCAGGCTACCTGGCTAATGATAGACTCCTACCCCAGCGTGTATTGGAACAA	
		161 H K L T K E Q W E E R I Q N W H E E H R 481 CACAAACTAACAAAAGAACAGTGGGAAGAAAGAATACAGAACTGGCATGAAGAACATAGA	
		181 G M L R E D S M M E Y L K I A Q D L E M 541 GGAATGTTAAGGGAGGATTCTATGATGGAATACCTGAAGATTGCACAAGATCTAGAAATG	
		201 Y G V N Y F E I K N K K G T E L W L G V 601 TATGGAGTCAACTATTTTGAAATAAAAAATAAAAAAGGAACTGAATTGTGGCTAGGTGTT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		221 D A L G L N I Y E H D D K L T P K I G F 661 GATGCTTTGGGTCTGAATATTTATGAGCATGACGACAAGTTAACACCTAAAATTGGTTTT	
		241 P W S E I R N I S F N D K K F V I K P I 721 CCCTGGAGTGAAATCAGAAATATTTCATTTAATGACAAAAAATTTGTTATAAAGCCAATC	
		261 D K K A P D F V F Y A P P R L R I N K R I 781 GACAAAAAGGCACCTGATTTTGTGTTTATGCACCTCGTCTGAGAATCAATAAGAGGATT	
		281 L A L C M G N H E L Y M R R R K P D T I 841 TTGGCCTTATGTATGGGAAACCATGAACTATACATGCGAAGAAGGAAGCCTGATACTATT	
		301 E V Q Q M K A Q A R E E K H Q K Q L E R 901 GAAGTACAACAGATGAAGGCTCAGGCTAGGGAGGAGAAACATCAGAAGCAGTTGGAAAGG	
		321 A Q L E N E K E K R E I A E K E K E R I 961 GCACAATTAGAGAATGAAAAGGAGAAAAGAGAAATAGCAGAAAAGGAAAAGGAAAGAATA	
		341 E R E K E E E L M E R L K Q I E E Q T I K 1021 GAACGTGAAAAGGAAGAGCTAATGGAACGTCTAAAACAAATTGAAGAGCAGACAATTAAA	
		361 A Q K E L E E E Q T R K K A L E L D Q E R K 1081 GCTCAGAAAGAACTAGAAGAACAGACTCGAAAAGCTCTAGAACTGGATCAAGAACGAAAA	
		381 R A K E E A E R L E K E R R A A E E A K 1141 CGAGCAAAAGAAGAAGCAGAACGACTTGAAAAGGAGCGTCGAGCTGCTGAAGAGGCAAAG	
		401 S A I A K Q A A D Q M K N Q E Q L A A E 1201 TCTGCCATAGCAAAACAAGCTGCCGACCAGATGAAGAATCAGGAGCAGCTAGCAGCAGAA	
		421 L A E F T A K I A L L E E A K K K K E E 1261 CTTGCTGAATTCACTGCCAAGATTGCACTTCTAGAGGAAGCCAAGAAGAAAAAGGAAGAG	
		441 E A T E W Q H K A F A A Q E D L E K T K 1321 GAAGCTACTGAGTGGCAACACAAAGCTTTTGCAGCCCAGGAAGACTTGGAAAAGACCAAA	
		461 E E L K T V M S A P P P P P P P V I P 1381 GAAGAGTTAAAAACTGTGATGTCTGCCCCCCCTCCACCTCCACCACCAGTCATTCCT	
		481 P T E N E H D E E H D E N N A E E A S A E L 1441 CCAACAGAAACGAACATGATGAACACGATGAGAATATAATGCTGAAGCTAGTGCTGAATTA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		501 S N E G V M N H R S E E E R V T E T Q K 1501 TCAAATGAAGGGGTAATGAACCATAGAAGCGAGGAAGAACGTGTAACCGAAACACAGAAA 521 N E R V K K K Q L Q A L S S E L A Q A R D 1561 AATGAGCGTGTTAAGAAGCAACTTCAGGCATTAAGTTCAGAATTAGCCCAAGCCAGAGAT 541 E T K K T Q N D V L H A E N V K A G R D 1621 GAAACCAAGAAAACACAAATGATGTTCTTCATGCTGAGAATGTTAAAGCAGGCCGTGAT 561 K Y K T L R Q I R Q G N T K Q R I D E F 1681 AAGTACAAGACTCTGCGACAGATTCGACAAGGCAATACAAAGCAGCGTATCGATGAGTTT 581 E A M - 1741 GAAGCAATGTGA	
WBC374.bFSP	No Homology	1 AGTTTCTGCTTTTTGTTTTAGAATAAATCGTCAGGGAAATGAAGAGGATGCTTTTGT 61 TTTGGGTTATGGTCAAGAACTGATTAAATAATTTAGTGTCTCTGGCACACACTAAAACCA 121 TATACTTCAGTTGTGATCTTGGTGACATATCTGTTGGCTTAGGTTTTATTACATTTATTA 181 TCGCAGATGTTCGGTTGACCAAGTAGTTCATTACTTTCTCTTAATTTTTTTAAATTTTAA 241 TTTGGGCTTCTAACTGCAGCGTTTGAGAACTCAGCATCCTTGTTTTCTGCAAATACTGAT 301 TAAAATAAAATGCTGTAAAACGTGTTGTAAACATTGTAATTACCTTCCCATGTCTTTGT 361 TGTACTTGTGCAGAAATGTTTTCACATTCCTTTGTCCGGAGAAAAAATCTTTGCTTTCAT 421 TTTGATTATGTTGCTTACCTTGAAATCAATAGGTTTTGATATTTTCTCTTGGAAGATTTT 481 ATATCTTTTTGGGAATATGTAATATATGATCTCTAATAAAAGATAAATCTCAAAAAAAAA 541 AAAAAAAAAACTCG	SEQ ID NO:209
WBC964.gRSP	No Homology	1 GGGACCAAGGCAGAGGCTGAGCTGGGGATGTTCCCCAGTACATTCAGGAAACTCCTGCAC 61 ACAGTCAACGTACCCTCCTTCAGCAAGGCGCCCTCCAGCAGGCCCCAGCAGACCAGCTAC 121 GAACCCCCGTCTTGTTCCGGACCAAAGACCACTTTCCCTTGTTGCAGTGAAAGACCTTGG 181 GTGTGAGTCTGCTAGCCAACACTGCAGAGGACGCTGAGATTATCTCGAGTATTAAATCC 241 ATTGAAAATCCTACTATAGACATCCCATGATGTTGGAGAGTATGGAATTTTACAGTTTAT 301 TTTTTGCACACCCTATTTCTCACTGTCTTCATTATTTCACGTAGGATGTATGATTTTCTA 361 TGTCTTCCACTTCTAACCTGAAAGCTGCTTGGTGGGGGGACTGGAGAAGCAAAATGGATC 421 TGTGCGCTGTGGCAGAACTGTTATTTTTATGGATTTTACAGCTCAACTACACAGTGTTACC 481 TTTTCAAAATTTATATATACTCCCTAAAGCCTTGTTATTATTTGATCCTAATAGTGATTCA 541 GTTTTCTATAGCTTACTTTTAGGGTAGATGGTAAATTATTTAACATTATATTATTAACTTTC 601 CATATCATGGATAGTAAACCGAAGGAAATTATACAATTTCTGAGAAAATGTATTATTTAA 661 ACTAATTCTGAAGTTGTATTTGAAATATGACCTCACAATCTTAATTTGTCCATAGCAAA 721 CATGTCTATATATGGTTGCAGCATTTGGTTTATAATTTAAATATTAAATAAGGTTTTAAA 781 TTTTGTTGGAAAAAAAAAAAAAAAAAAA	SEQ ID NO:210

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1 TTTTTTTTTTTTTTTTTTTTCCAACAAAATTTAAAACCTTTATTAATATTTAAATTTATAAA 61 CCAAATGCTGCAACCATATATAGACATGTTTGCTATGGACAAATTAAGATTGTGAGGTCA 121 TATTTTCAAATACAACTTCAGAATTAGTTTAAATAATACATTTTCTCAGAAATTGTATAA 181 TTTCCTTCGGTTTACTATCCATGATATGGAAAGTTTAATATAATGTTAAATAATTTACCA 241 TCTACCCTAAAAGTAAGCTATAGAAAACTGAATCACTATTAGGATCAAATAATAACAAGG 301 CTTTAGGAGTATATATAAATTTTGAAAAGGTAACACTGTTAGTTGAGCTGTAAAATCCAT 361 AAAAATAACAGTTCTGCCACAGCGCACAGATCCATTTTGCTTCTCCAGTCCCCCCACCAA 421 GCAGCTTTCAGGTTAGAAGTGGAAGACATAGAAAATCATACATCCTACGTGAAATAATGA 481 AGACAGTGAGAAATAGGGTGTGCAAAAAATAAACTGTAAAATTCCATACTCTCCAACATC 541 ATGGATGTCTATTAAGTAGGGATTTTCAATGGATTTAATACTCGAGATAATCTCAGCGTC 601 CTCTTGCAGTGGTGGC	SEQ ID NO:211
B1961827	Homo sapiens actin related protein 2/3 complex subunit 1B (41 kD) (ARPC1B) mRNA.	1 gcgcgtcgac tgcccagagt ccgcggccgg ggcgcgggag gagccaagcc gccatggcct 61 accacagctt cctggtggag cccatcagct gccacgcctg gaacaaggac cgcacccaga 121 ttgccatctg ccccaacaac catgaggtgc atatctatga aaagagcggt gccaaatgga 181 ccaaggtgca cgagctcaag gagcacaacg ggcaggtgac aggcatcgac tgggcccccg 241 agagtaaccg tatgtgacc tgcggcacag accgcaacgc ctacgtgtgg acgctgaagg 301 gccgcacatg gaagcccacg ctggtcatcc tgcggatcaa ccgggctgcc cgctgcgtgc 361 gctgggcccc caacgagaac aagtttgctg tgggcagcgg 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 cccttgggg aactgatgtt cgaatccagc agtagctgcg 661 gctgggtaca tggcgtctgt ttctcagcca gcgggagccg ctggcctgg gtaagccacg 721 acagcaccgt ctgcctggct gatgccgaca agaagatggc cgtcgcgact ctggcctctg 781 aaacactacc actgctggcg ctgaccttca tcacagacaa cagcctggtg gcagcgggcc 841 acgactgctt cccggtgctg 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 ctgctccctc aaaaagggag gggacagatg 1321 gggagctttt cttacctatt caaggaatac gtgccttttt cttaaatgct ttcatttatt 1381 gaaaaaaaa 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 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	SEQ ID NO:212 SEQ ID NO:213

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		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	
		61 A P E S N R I V T C G T D R N A Y 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 TCCATCTGTTATTTCGAGCAGGAGAATGACTGGTGGGTTTGCAAGCACATCAAGAAGCCC	
		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 AGCTGCGGCTGGTACATGGCGTCTGTTTCTCAGCCAGCGGGAGCCGCGTGGCCTGGGTA	
		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 GCGGGCCACGACTGCTTCCCGGTGCTGTTCACCTATGACGCCGCCGCGGGGATGCTGAGC	
		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 A G 901 CGCTTCCAGAACCTGGACAAGAAGCGAGCTCCGAGGGTGGCACGGCTGCGGGCGCGGGC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		321 L D S L H K N S V S Q I S V L S G G K A 961 CTAGACTCGCTGCACACAGAACAGCGTCAGCCAGATCTCGGTGCTCAGCGGCGGCAAGGCC 341 K C S Q F C T T G M D D G G M S I W D V K 1021 AAGTGCTCGCAGTTCTGCACCACTGGCATGGATGGCGGCATGAGTATCTGGGATGTGAAG 361 S L E S A L K D L K I K - 1081 AGCTTGGAGTCAGCCTTGAAGGACCTCAAGATCAAATGA	
B1961438	No homology	1 GCACGAGGCAGCCAGCAGCTTTGGAGCCCCCACAACCTGGACACTCACATCGAAGTCTCT 61 GCCTAGCCACCCTCTCCCTGAGCCCATCTCAGATGGCCCCTCCCCCCCAGGCTGCCAGGTG 121 GCTGGGGTGAGGTCAGGTGGCAGGCCCAGAATAGGCCCAGTCATCCACTCCCCCCTCT 181 CAGGATTGCAGGAGTCTGAGCTATTCCCGGCCACCTCTATCTCCCACCCCACCTTCTCCA 241 CCATAGCCAGGGGCTGGGCCCCGTAGGTGAAACAAGCGGGTGAAACCCCTCTGGGGCCCA 301 GACATGCAAACCTCTGGCACCACTGGGTCCTGGCTGAACCCCTGGGTGGTGTGCAGCTTC 361 CCCTCTGGTCTCAGTTTCCTTTCCTGAAAAGCGAGGAGTTGGAGGCAACGTTCTCCTCCT 421 GGCCTGTGGCCCTCAGAGGAGAAGGACTGGAAGGAACTTCAGAGAATCCTCACTCCCCTC 481 ATTTTACAGATGAGGAAACT 1 CCTTTCCTGAAAAGCGAGGAGTTGGAGGCAACGTTCTCCTCCTGGCCTGTGGCCCTCAGA 61 GGAGAAGGACTGGAAGGAACTTCAGAGAATCCTCACTCCCCTCATTTTACAGATGAGGAA 121 ACTGAGGCCCAGAGTGGGCAGAGACTTGGCATCATTGTCATCCAGCAAATAACAGAAGGG 181 AAGTTCCTTGGGGAAGAACCAGGAGCAGAGGTCTGGGGAGAGGTGGGCAAGGAGGGGGTC 241 AGTCTCCCCTAGTCCAGAAAAGGGCCTCACCTGCCAGGGGCCTCCAGTCTCTGGCCCTCT 301 GTCCTGCGCATTGCTTTCCAAGGAGCCTTCTTGAGGTCACTGCATTTGATCTTCATGGCG 361 GCACCTGGAAGAGACATGAGCGTTTGTGTTTGCTTTAAAAAAAGCATTTTTCATTTTA 421 AAAAATCAGGTGTGCTTTGTAGACACTTTGGAAAGTTCAGGAGAGTAATCCAGGGTGGA 481 GTCTATGCAGAAATGACCCATAATCCAGCAACGCCAGGCCCCTGAGTGGTGGCTTCTATG 541 TAGCTGTAATCGTACTATACAT	SEQ ID NO:214 SEQ ID NO:215
B1961499	Homo sapiens SUI1 isolog	1 cggcacgagc gccgccgagg attcagcagc ctccccctg agccccctcg cttcccgacg 61 ttccgttccc cctgccgcgc cttctcccgc caccgccgcc gccgccttcc gcaggccgtt 121 tccaccgagg aaaaggaatc gtatcgtatg tccgctatcc agaacctcca ctctttcgac 181 cctttgctg atgcaagtaa gggtgatgac ctgcttcctg ctggcactga ggattatatc 241 catataagaa ttcaacagag aaacggcagg aagacccttа ctactgtcca agggatcgct 301 gatgattacg ataaaaagaa actagtgaag gcgtttaaga aaaagtttgc ctgcaatggt 361 actgtaattg agcatccgga atatggagaa gtaattcagc tacagggtga ccaacgcaag 421 aacatatgcc agttcctcgt agagattgga ctggctaagg acgatcagct gaaggttcat	SEQ ID NO:216

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFTER:
		481 gggttttaag tgcttgtggc tcactgaagc ttaagtgagg atttccttgc aatgagtaga 541 atttcccttc tctcccttgt cacaggttta aaaacctcac agcttgtata atgtaaccat 601 ttggggtccg cttttaactt ggactagtgt aactccttca tgcaataaac tgaaaagagc 661 catgctgtct agtcttgaag tccctcattt aaacagaggt caagcaatag gcgcctggca 721 gtgtcaagcc tgaaaccaag caataccgtc atgtttcagc caagcccaga gccctaagat 781 tacaaacaac tatggccgga acctcctcag ctctccctct gcagagttcc ctaccctaag 841 agaatgttac cacctgaaca gtcctcggtg aatctgagag gagaggatgg ggtaaggcag 901 aagcaccagc tgtactacta gaagggagct tttggtggta gatcccctgg tgtctccaac 961 ctgactaggt ggacagagct caaagaggcc ctcttaccgc tagcgaggtg ataggacatc 1021 tggcttgcca caaaggtctg ttcgaccaga catatcctag ctaagggatg tccaaacatc 1081 agaatgtgag gccaaccttc tatcagagtt aaactttgga caagggaaca aatctcaaac 1141 tgatccatca gtcatgtagc tagctgtaga gcttgcaact taatagcagc agctgcccaa 1201 tgccatgtga agtaacaaac tggttttttg ttttttttc cccttcagtt ttaatgttat 1261 gtgtaatgta tttaaaccct tatttaaata aaacttgttt tcagaaaaaa aaaaaaaaaa 1321 aaaa 1 M S A I Q N L H S F D P F A D D A S K G D 1 ATGTCCGCTATCCAGAACCTCCACTCTTTCGACCCCTTTGCTGATGCAAGTAAGGGTGAT 21 D L L P A G T E D Y I H I R I Q Q R N G 61 GACCTGCTTCCTGCTGGCACTGAGGATTATATCCATATAAGAATTCAACAGAGAAACGGC 41 R K T L T T V Q G I A D D Y D K K K L V 121 AGGAAGACCCTTACTACTGTCCAAGGGATCGCTGATGATTACGATAAAAGAAACTAGTG 61 K A F K K K F A C N G T V I E H P E Y G 181 AAGGCGTTTAAGAAAAAGTTTGCCTGCAATGGTACTGTAATTGAGCATCCGGAATATGGA 81 E V I Q L Q G D Q R K N I C Q F L V E I 241 GAAGTAATTCAGCTACAGGGTGACCAACGCAAGAACATATGCCAGTTCCTCGTAGAGATT 101 G L A K D D Q L K V H G F - 301 GGACTGGCTAAGGACGATCAGCTGAAGGTTCATGGGTTTTAA	SEQ ID NO:217
B1961539	Human mRNA for 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	SEQ ID NO:218

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		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 GTTCAAAAAGAGCTGGCGAACTTCCTCAAGAGTAAGAAGGATGAGAAAGCCATAAAT 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:219
B1961620	IL1T11A mRNA for immunoglobulin-like transcript 11 protein	1 cacggctgga gaccatggga agcagtgccg ggacaccttc cctcattgcc ttcagtgac 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 acccctccga gctggtggtg acaggattct acaccaaacc caccctcca gccctgccga 421 gcccactggt gatctcagga gggaatgtga ccctccagtg tggctcaaag cttggatttg 481 ccaggtttgt tctcactaag gaaggagaaa acaagacctc ctggaccctg gattcacagc 541 gacaacccaa tgggcagttc caggccctgt tccctgtggg ccctgtgatc ccttccaca 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 841 tgcacagttc agagtagtag agccttgaaa gtaaatcttg tgcacccagg aggttcctga 901 agagcatctg tggtgtatga tcagtgaact gtctgcaggt cattgtgagg tgtagtagtt 961 atcgttcatg tgcagggaca atgtccgctc ctttctgcca ttaactgag ggacattcct 1021 tcacaagcac tttgagtta 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	SEQ ID NO:220 SEQ ID NO:221

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		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	
B1961856	No Homology	1 GCACGAGGGAAGAGGGTCTCCTTCCACCCCAAGGAATTTTTTTTAATCAGAAGACCTTGA 61 AAAGGGGGATATAACTTTGAACAATTTAATTTCTTGGCCGTGTTTAGTAACAGTTCCTAT 121 GCATGGTTTTTAACGTATAAATTTGCTTTCTTCCCTCTCCCACCTGATTCTGCCTCTTTA 181 ATGAATATTTTTACTGGGGTTGAAACTCAATGCCTTATGTGCTCACTCAGTTTCCCTTCT 241 GCAGCTTGTTTTTTCTCACTATCTGTATGTGTTCAGATTGTGTCAAATGCTGGCAAAACC 301 TCTAAGACTGTCAAGAAAGGCTTGAAAGTTGATTTGTCCTAGTGCAAATTCAAGATAAAT 361 GTCTTAATGTTTTTTGGCTATGTAGTACATAGGAACAGAAAATAACTTAAATAAAGTCAT 421 TTTTGTAATTTAAAAAAAAAAAAAAAAAA 1 GCACGAGGGAAGAGGGTCTCCTTCCACCCCAAGGAATTTTTTTTAATCAGAAGACCTTGA 61 AAAGGGGGATATAACTTTGAACAATTTAATTTCTTGGCCGTGTTTAGTAACAGTTCCTAT 121 GCATGGTTTTTAACGTATAAATTTGCTTTCTTCCCTCTCCCACCTGATTCTGCCTCTTTA 181 ATGAATATTTTTACTGGGGTTGAAACTCAATGCCTTATGTGCTCACTCAGTTTCCCTTCT 241 GCAGCTTGTTTTTTCTCACTATCTGTATGTGTTCAGATTGTGTCAAATGCTGGCAAAACC 301 TCTAAGACTGTCAAGAAAGGCTTGAAAGTTGATTTGTCCTAGTGCAAATTCAAGATAAAT 361 GTCTTAATGTTTTTTGGCTATGTAGTACATAGGAACAGAAAATAACTT	SEQ ID NO:222 SEQ ID NO:223
B1961872	No homology	1 GCACGAGCCGAGCCCTGAGCAAAACCCTCCCCATCCGCTGTATTTATCTCTATTTAATAT	SEQ ID NO:224

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		61 TTATGCTCTGTGTATAAGGATGAATTAGAGTTGTCATTTTCTCTTCACTGGATGTTTATT 121 TATAAAGATTTGACCTGTTCATGCGTCTGTGGAGCAGCCCTCCGTCTCCCGGCTATATAG 181 TAATCTTAGGTAGAGTGTTGCCTTGTGGGTTACCGTTTGCTCTGAGACTTCTCGGATGGA 241 CCCACCCTCCTCCAGCCCTGGCTGCCAGCGCCGCGGGGCCGCGTGCTGGGCCTGCCGGGG 301 CCTGGCGCCGAGCCGTGTCCAATAAAGTTCTCGGATGTGACTGGAAAAAAAAAAAAAAAA 361 AA	
B1961880	Equus caballus tissue inhibitor of metalloproteinase-1 (TIMP-1) mRNA, complete cds	1 aggcagagca cccaccatgg ccccctttgc accctggtc tccggcattc tgttgttgct 61 gtggctcaca gcccccagca gggcctgtac gtgtgtccca ccccacccgc agacggcctt 121 ctgcagctct gagttcgtca tcagggccaa gttcgtgggg acctcagaag tcaaccagac 181 caccttacag cggcgttatg agatcaagat gaccaagatg ttcaaagggt tcagcgcctt 241 gggggatgcc cctgacacct ggtttgtcta cacccccgct atggagagcc tctgcggata 301 cttccacagg tcggagaacc gcagcgagga gtttctcatc gccggacaac tattggacga 361 gaagctgtac atcaccacct gcagtttcgt ggctccctgg aacagtctga gctccgctca 421 gcgccagggc ttcaccaaga cctacgccgc cggctgtggg gaatgctcag tgtttccctg 481 ttcatccatc ccctgcaaac tgcagagtga cactgattgc ttgtggacgg accagctcct 541 cacaggctct gacaagggct tccagagccg ctacctcgcc tgcctgcccc gggagccagg 601 gctgtgcacc tggcagtccc ttcggccccg gacggcctga atcctgtctc cagcagaagc 661 tgaagcttgc acagtgttca ccctctttcc cattcctatc tttctttctc caagacagtg 721 aaataaagaa ctaccaccca aa 1 M A P F A P L V S G I L L L L W L T A P 1 ATGGCCCCCTTTGCACCCCTGGTCTCCGGCATTCTGTTGTTGCTGTGGCTCACAGCCCCC 21 S R A C T C V P P H P Q T A F C S S E F 61 AGCAGGGCCTGTACGTGTGTCCCACCCCACCCGCAGACGGCCTTCTGCAGCTCTGAGTTC 41 V I R A K F V G T S E V N Q T T L Q R R 121 GTCATCAGGGCCAAGTTCGTGGGGACCTCAGAAGTCAACCAGACCACCTTACAGCGGCGT 61 Y E I K M T K M F K G F S A L G D A P D 181 TATGAGATCAAGATGACCAAGATGTTCAAAGGGTTCAGCGCCTTGGGGGATGCCCCTGAC 81 T W F V Y T P A M E S L C G Y F H R S E 241 ACCTGGTTTGTCTACACCCCCGCTATGGAGAGCCTCTGCGGATACTTCCACAGGTCGGAG 101 N R S E E F L I A G Q L L D E K L Y I T 301 AACCGCAGCGAGGAGTTTCTCATCGCCGGACAACTATTGGACGAGAAGCTGTACATCACC 121 T C S F V A P W N S L S S A Q R Q G F T 361 ACCTGCAGTTTCGTGGCTCCCTGGAACAGTCTGAGCTCCGCTCAGCGCCAGGGCTTCACC	SEQ ID NO:225 SEQ ID NO:226

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		141 K T Y A A G C G E C S V F P C S S I P C 421 AAGACCTACGCCGGCCGGCTGTGGGGAATGCTCAGTGTTTCCCTGTTCATCCATCCCCTGC 161 K L Q S D T D C L W T D Q L L T G S D K 481 AAACTGCAGAGTGACACTGATTGCTTGTGGACGGACCAGCTCCTCACAGGCTCTGACAAG 181 G F Q S R Y L A C L P R E P G L C T W Q 541 GGCTTCCAGAGCCGCTACCTCGCCTGCCCCGGGAGCCAGGGCTGTGCACCTGGCAG 201 S L R P R T A - 601 TCCCTTCGGCCCCGGACGGCCTGA	
B1961900	PREDICTED: Homo sapiens zinc finger, SWIM domain containing 6 (ZSWIM6), mRNA	1 atggcatcgt ggcgtcgcga cggcgtgtgc gtgtcgcgct tcctagtgcc gtttataggg 61 tcccggcact tccgctgtcg gacgcggctg cctttccgcc ggggcatcgc gctgttggaa 121 agcggctgcg tagacaacgt cctgcaagtc gttccgcgcg cgcccgcacc cctgcgggtg 181 tcctcactgg cccggacggt cctcctgagc ggagcgccca tttcctccct ccctccctg 241 ccccccgtcg cccggacgg gccagcgcga gtgggaaatg aatcagcagg acgcgccct 301 ccgtgggctc cgcgcccccg gcccgcgctc ccctacccgc cctcctccgg ggagcacatc 361 ctggagggct gttcgccggt ttcgggggtg gatgtggaca aaggcgcggg cggacggccg 421 gcctccggcg agggtgtgtg tggcgggggct ggctccgacg ggcgagcggc cgcggcgctc 481 ccgggtcgct gtggcgtctg gcccgggcga gctccactgg ccgcccgggg tttaaatgtc 541 gttttctttg cgcctcctca gtctccaagc ggcgcagagg agaggtggcg gcggaccgga 601 ctccgtctcc ggagggacat ctcgcccgta ggacgcttac taattaaagg gcgcgagcct 661 gaggaggagc tgctagcgct tccctttttct ctgaagctgc ctccagacac ccctgtgcgg 721 gccgcggcgc agccctgtg cccgcgccgc cgagttttgt ttgcgctgtg tggtcaggtc 781 gtggtgcccc gggcgagccg cggtcggcag ttgcggattt gccgctcgca gccaaagggg 841 cgagcgggct gcaggagcgc gaggcagagg gctcggcggc cgctcccgcg tcccgcggcc 901 gcggcagccc ggcacgaccc agcactttgt tctcatttcc aggaactct tctgtttgct 961 gatgaggaaa ggttatcttt ccaggcagca tccaggaatg gtcttttgaa tgtcttcatg 1021 cctcttgtg acctcattcc tgctgccatc gtacttatcc ctgctcagat taactgcctg 1081 cgtgttcaac tttattccat agttggatct acctgtctgc tggagatctt cattggttct 1141 gtcgctttgg agccaccaca gatgatgatg gagcctacag ttatctgttg ctgctgttgg 1201 agggtaagtc tctccggccc ggtttccctc ggtgtgctac tgtgcgcgcg atccagcacc 1261 atgggaagc gggacaatcg ggtggcctat atgaacccaa tagcaatggc gagatcaagg 1321 ggtccaatcc agtcttcagg gccaacaata caggattatc tgaatcgacc aaggcctacc 1381 tgggaagaag taaaagagca actagaaaag gaaaagaaag gctccaaggc tttggctgaa 1441 ttgaagaaa aaatgaatga gaactggaag aaagaactgg aaaaacacag agagaaattg 1501 ttaagtggaa gtgagagctc atccaaaaaa agacagagaa agaaaaaaga aaagaagaaa 1561 tctggtaggt attcatcttc ttcttcatca agctctgatt cttccagcag ttcttctgat 1621 tctgaagatg aggataagaa acaaggaaaa cagagaaaga aaaagaagaa ccgttcacat 1681 aaatcttctg aaagctccat gtcagaaact gaatcagaca gtaaggatag tttaaaaaag	SEQ ID NO:227

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1741 aaaaagaagt caaaagatgg aactgagaaa gaaaaggata ttaaaggact cagcaaaaag 1801 agaaagatgt attctgaaga taaaccttta tcatctgagt ccttgtcaga atcagagtat 1861 attgaggagc tgcttatcat gggcacagct gacaaaacca gaagagcctt tctatggtgc 1921 catgaatgct gtcttctcct ccatggtctg gaagcagcca tggccaaact tggaggtggt 1981 gtcaatgaac ttaaggtcaa tcttctccag aggccgccgt ttggttggca ctggcaagga 2041 cttgtgaagg ccattgccct tggtcaacct gatgacgtcg atcatcttgt cctgctcaaa 2101 catctggttc acaggtacct gctgctcaag cctctcgtgg gcccagtcca gcttcttggc 2161 catggtgcct cccttacct ggatctccat caggtgggcc ttcctctggt gcagaggaag 2221 caggcacatc tgggtgtagg caatgatgca gatgacttgg cggtacttct tcatgctgct 2281 gaagtccttc tccagctgct tcttgccatc ctcatcctga catttcttgc agtacttggt 2341 aaaggccttc ttcttagatt tatgccggtt tttatagaaa tgtctcttgc atgcatcgct 2401 gatgtgctca gcgaagacag tattgaaggt ctggaggcct cgaggggttt ccacgaagcc 2461 cacaatggcc acaaccacca tgggtggtat ctccacaatg gtcacagcct ctatcacttc 2521 cttctttgtc acctggatc ctggcctgtc gacttcccgc atgatgttgg tcatgccagc 2581 cttgtatccc aggaaggctg tgaggtggac cagcttggaa gggtcatcct taggaaagct 2641 cttcaccttc ccatgatgct tcctgctgcg ctgctgaggc aggaagccga gggaccatg 2701 tctgggagcg gagaaccttc tctgagggct ttcgaagctt cccaccagtg ggtttgtctg 2761 aactgtttag gaatgcggcc gcggtcgcca gctgacgtca gcgccgccgg ttcagccgca 2821 ggccagagtc agagactgac agcgcgaggg gcgggggttgg gagtcaggat ggggcgaggc 2881 ctgcgtgtga ctgatggcgc ggggcgcggg cggcgtttcc acttgagcgg cacagtgaca 2941 gaacctgcaa tacaatcgga gccagaaact gtttgcaacg tggccatcag ctttgatcgt 3001 tgcaagatta cctcagtgac ctgcagctgt ggaaacaagg acatatttta ttgtgcccat 3061 gttgtggcac tgtctttata ccgcatccgc aagccagatc aggtcaaact gcatcttcct 3121 atttcagaga ctctctttca aatgaataga gaccaactgc aaaagtttgt acagtatttg 3181 atcacagtgc accacacaga agttttgcca actgctcaaa aattagcaga tgaaattctt 3241 tcccaaaatt cagaaatcaa ccaagttcat ggtgctcctg atccaacagc aggtgctagt 3301 atagatgatg aaaactgctg gcacttagat gaagagcagg ttcaagaaca ggttaaactg 3361 ttcctttccc agggcgggta ccacggatca gggaagcagc ttaatttgct ctttgcaaag 3421 gtgcgggaga tgttaaagat gagggactcc aatgggggccc gcatgttgac cttgataaca 3481 gagcaattca tggctgaccc tcgcctgtca ctttggcggc aacaaggcac tgcaatgact 3541 gacaaataca ggcagctctg ggatgagctg ggtgctctgt ggatgtgtat agttttaaac 3601 cccactgca agttggagca aaaggccagt tggctaaaac agctgaagaa atggaatagt 3661 gttgatgtct gtccatggga agatggaaat catggcagtg aattacccaa cttaaccaat 3721 gttctgcctc agggtgcaaa tgccaaccaa gattcatcga acaggccaca tcggacagtg 3781 ttcacccgag ccatcgaggc atgcgatctc cactggcagg atagccactt gcagcacatt 3841 atcagcagtg acctatacac caactactgt taccatgacg acactgaaaa ctccctcttc 3901 gactcccgcg ggtggccctc ctggcatgaa catgttccta cagcctgtgc aagagtggac 3961 gcattacgtt ctcatgggta ccccagagaa gcactgagac tagcaatagc tattgttaat 4021 acattaagac gacagcagca gaaacagttg gaaatgttcc gaacccaaaa aaaagagcta 4081 cccataaaa acataacctc gataaccaat ctggagggct gggttggaca tcccctggac 4141 cctgtgggca ctctcttcag tagccttatg gaagcctgcc gcattgatga tgagaacctc 4201 tctgggttct cagattttac agagaatatg ggacagtgca agtctctgga ataccagcat 4261 ctacctgcac acaaattctt agaagaaggg gaatcctatt taacgctggc tgtggaagta	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		4321 gccctgatag ggctaggaca gcagcgtatc atgcctgatg ggctgtacac acaagagaaa 4381 gtttgccgga atgaggagca gctcatttct aagcttcagg aaattgaatt ggatgacaca 4441 ctggtgaaaa tttttcgcaa gcaagcagtc ttcctattag aagccggacc atatagtggt 4501 ttaggtgaaa taatccatcg ggagagcgtt ccaatgcaca catttgccaa gtatcttctc 4561 acctcttcc tacctcacga tgctgaattg gcatacaaaa ttgcactgag agcaatgcgg 4621 ttactagtat tggaatctac tgctccatca ggagacctca cccgcccaca ccacattgca 4681 tcagttgttc ccaaccgcta ccctcgctgg ttcactctaa gccacattga gtcccagcag 4741 tgtgagctgg catccaccat gctaactgca gccaaaggcg atgttcggag gctggaaaca 4801 gtattagaat ccatccagaa aaacattcac tcctcatcac acatcttcaa gcttgcccaa 4861 gatgcattta aaatagcaac tctcatggac agtttgccag acatcactct tttgaaagtg 4921 tctctggagc tgggcctgca ggttatgcga atgacactgt caaccttaaa ttggcgacgg 4981 cgggagatgg tgaggtggct ggtaacgtgt gctactgaag tcgggtttta tgccctggac 5041 agcatccatgc agacctggtt tacactcttt actcccaccg aggccacaag tatagttgca 5101 actaccgtga tgtccaacag caccatcgtc cgcctccacc tggactgcca ccagcaggaa 5161 aagctggcca gcagcgcccg gacacttgca ctgcagtgtg ccatgaagga tccacagaac 5221 tgtgccctct ctgcgctaac cctttgtgaa aaggatcaca tagcttttga gacggcgtac 5281 caaattgttc tcgacgctgc tacgactggc atgagctata cacagctctt tacaatagca 5341 cggtacatgg agcaccgcgg gtacccccatg agggcctaca agctggccac cctggccatg 5401 acccatctca acctgagcta caatcaggac acacaccctg ccattaatga tgttttgtgg 5461 gcctgtgcgc ttagccactc cattggtaaa aatgagcttg cagctataat acctctggtg 5521 gtcaagagtg tcaagtgtgc aacggtactg tcagacattt tgcgcagatg cactctgacc 5581 actcctggca tggtgggact tcatgggagg aggaactctg gtaagctcat gtcactggac 5641 aaagcccccc tgaggcaact cttggatgcc acgatcgggg cctacatcaa cacaacgcac 5701 tcacggctca cacacatcag tcctcggcac tatagtgagt ttatagagtt cctcagcaaa 5761 gcccgagaga cctcttaat ggcgcatgat ggacacattc agtttacaca gtttattgac 5821 aacctgaaac aaatctacaa aggcaaaaag aaactgatga tgttggttcg ggagaggttt 5881 ggttgataga tcttgtatga atgggtggg gggtgggggat gggagggatg gtttgttttt 5941 acttgagcct gcctttgtac cctttttaac ttaaagaaca gagccacacc ggtattatat 6001 gtgtatagtt atattgcgtt tgcagactaa attgtcatgt tgtgaaagtt tgtgtgtttt 6061 ttatttttc cctatttctt tctttccttt atttttattat ttttttttaat ttttttttc 6121 tggttttgta tgagagagag gttaaaaagg tttggtttac actgagtata tgttgtcaag 6181 tggcaaaagt ccacatagct ctcctgtttt ctgtatacgt tcacagcctc aaaaaaaata 6241 attgaaatgg ctttaaaaac caaacaaaac acttccatcc tgtgataagt acctcgaatg 6301 gattcagctt tactcctttg taactcatct ttacatttcc agcatattta aacaaaccaa 6361 caaaatgaaa tactaatagt aaaaaggctg acccatgtgg ctttgcagtg ctgttcgtcc 6421 agaagcatgg cacacgatgc ttgtgcatgt ggaaacttag cgactgtcaa catacattct 6481 cagggattta tccaaaaaaa ttaaaaaaag aatgagagca tttattgtac tgtatatata 6541 ttatagtata tgtctgaata ttgaaaatat aacattaact aatttataaa aaatattcta 6601 tgtaatgcaa aatacttgaa gctgcagtag cttgtttta aacaaaaaca aaaaaaaaac 6661 tgagagaaaa cctatcagaa ggactaaaag tacgccttgc ttcagggttg gctcaggtgg 6721 tgaacttcat gctgggcatc tatgcagagc caccttttgg attgcatggt tggactgaga 6781 tctattggga gaaattatat atgtatatat atttatacaa cttatgtata catatatata 6841 tgtatacaca cagacacaca cacacaccac caacaaccac cactacacca cacatgctta	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		6901 taacaggcac tagaataaag agggacaaca aaatacacag ccagagcagc aagccttagc 6961 attaagaata tacaatatgc cggaattggg gttcgtgcct cctagcctag gaaacttaaa 7021 agaaatatcc ttttgacaca aaacacaaaa tgttttccaa aacaattgac ataatgatac 7081 attacgcctt tgcagtgagc taataataag ctaacctttg tgcacaaata acattatata 7141 tattatatat ctattctgca taggtatttt gactttgtgc aggacagaaa gttgtgtagg 7201 tatgactgtt ctacttttca gttttctttt ttttaatat atttttatttt ctctagaaat 7261 tactcaaaca aaagcagcct tctatctttgc cttgtcttaa tgctttaaaa taaccaaact 7321 ggagatctaa ctaccaaact gttcattata ttattaaata ccaactttgg ttacagtata 7381 gtgtctttac tttagctgat ggttctgtaa cctttgtgctt tttaaagcaa tttttatgtt 7441 ttggtgcaaa agttgtccag tgtctcttgt tcccttcact agagaacatg cttagaggta 7501 tgtttgtagg tatttttgtt tagaagaact attcatgcg ctccatttta tttattataa 7561 taggtaaaaa gaaaaaaaaa ggttgtaatt catcacccat gtaaacatgc tcatgaagtt 7621 gaaagtaatt aagatttgat acactgatat caatttattt atgtaactaa atcactgttt 7681 tataaacttg ttaatgatca acaatttttg ttttgattaa aattagtttt ttgaaagtt 1 M A S W R R D G V C V S R F L V P F I G 1 ATGGCATCGTGGCGTCGCGACGGCGTGTGCGTGTCGCGCTTCCTAGTGCCGTTTATAGGG 21 S R H F R C R T R L P F R R G I A L L E 61 TCCCGGCACTTCCGCTGTCGGACGCGGCTGCCTTTCCGCCGGGCATCGCGCTGTTGGAA 41 S G C V D N V L Q V V P R A P A P L R V 121 AGCGGCTGCGTAGACAACGTCCTGCAAGTCGTTCCGCGCGCCCGCACCCCTGCGGGTG 61 S S L A R T V L L S G A P I S S L P S L 181 TCCTCACTGGCCCGGACGGTCCTCCTGAGCGGAGCGCCCATTTCCTCCCTCCCTTCCCTG 81 P P V A P D G P P A R V G N E S A G R A P 241 CCCCCCGTCGCCCCGGACGGGCCAGCGCGAGTGGGAAATGAATCAGCAGGACGCGCCCCT 101 P W A P P R P P A L P Y P P S S G E H I 301 CCGTGGGCTCCGCGCCCCCGGCCCGCGCTCCCCTACCCGCCCTCCTCCGGGGAGCACATC 121 L E G C S P V S G V D V D K G A G G R P 361 CTGGAGGGCTGTTCGCCGGTTTCGGGGGTGGATGTGGACAAAGGCGCGGGCGGACGGCCG 141 A S G E G V C G G A G S D G R A A A L 421 GCCTCCGGCGAGGGTGTGTGTGGCGGGCTGGCTCCGACGGGCGAGCGGCCGCGGCGCTC 161 P G R C G V W P G R A P L A A R G L N V 481 CCGGGTCGCTGTGGCGTCTGGCCCGGGCGAGCTCCACTGGCCGCCCGGGGTTTAAATGTC 181 V F F A P P Q S P S G A E E R W R R T G	SEQ ID NO:228

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		541 GTTTTCTTTGCGCCTCCTCAGTCTCCAAGCGGCGCAGAGGAGGTGGCGCGGACCGGA	
		201 L R L R R D I S P V G R L L I K G R E P	
		601 CTCCGTCTCCGGAGGGACATCTCGCCCGTAGGACGCTTACTAATTAAAGGCGCGAGCCT	
		221 E E E L L A L P F S L K L P P D T P V R	
		661 GAGGAGGAGCTGCTAGCGCTTCCCTTTTCTCTGAAGCTGCCTCCAGACACCCCTGTGCGG	
		241 A A A Q P L C P A A R V L F A L C G Q V	
		721 GCCGCGGCGCAGCCCTTGTGCCCCGCCCGAGTTTGTTGCGCTGTGTGGTCAGGTC	
		261 V V P R A S R G R Q L R I C R S Q P K G	
		781 GTGGTGCCCCGGGCGAGCCGCGGTCGGCAGTTGCGGATTTGCCGCTCGCTCAGCCAAAGGGG	
		281 R A G C R S A R Q R A R R P L P R R P R G	
		841 CGAGCGGGCTGCAGGAGCGCGAGGCAGAGGGCTCGGCGGCCGCTCCCGCGTCCCCGCGGC	
		301 A A A R H D P A L C S H F Q E T L L F A	
		901 GCGGCAGCCCGGCACGACCCAGCACTTTGTTCTCATTTTCAGGAAACTCTTCTGTTTGCT	
		321 D E E R L S F Q A A S R N G L L N V F M	
		961 GATGAGGAAAGGTTATCTTTCCAGGCAGCATCCAGGAATGGTCTTTTGAATGTCTTCATG	
		341 P S C D L I P A A I V L I P A Q I N C L	
		1021 CCTTCTTGTGACCTCATTCCTGCTGCCATCGTACTTATCCCTGCTCAGATTAACTGCCTG	
		361 R V Q L Y S I V G S T C L L E I F I G S	
		1081 CGTGTTCAACTTTATTCCATAGTTGGATCTACCTGTCTGCTGGAGATCTTCATTGGTTCT	
		381 A A L E P P Q M M M E P T V I C C C C W	
		1141 GCTGCTTTGGAGCCACCACAGATGATGAGGCCTACAGTTATCTGTTGCTGCTGTTGG	
		401 R V S L S G P V S L G V L L C A R S S T	
		1201 AGGGTAAGTCTCTCCGGCCCGTTTCCCTCGGTGTGCTACTGTGCGCGCGATCCAGCACC	
		421 M G K R D N R V A Y M N P I A M A R S R	
		1261 ATGGGGAAGCGGACAATCGGGTGGCCTATATGAACCCAATAGCAATGGCGAGATCAAGG	
		441 G P I Q S S G P T I Q D Y L N R P R P T	
		1321 GGTCCAATCCAGTCTTCAGGGCCAACAATACAGGATTATCTGAATCGACCAGGCCTACC	
		461 W E E V K E Q L E E K E K K G S K A L A E	
		1381 TGGGAAGAAGTAAAAGAGGCAACTAGAAAAGGAAAGAAAGGCTCCAAGGCTTTGGCTGAA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		481 F E E K M N E N W K K E L E K H R E K L 1441 TTTGAAGAAAAAATGAATGAGAACTGGAAGAAAGAACTGGAAAAACACAGAGAAATTG	
		501 L S G S E S S S K K R Q R K K K E K K K K 1501 TTAAGTGGAAGTGAGAGCTCATCCAAAAAAAGACAGAGAAAGAAAAAAGAAAAGAAA	
		521 S G R Y S S S S S S S S S D S S S S S S D 1561 TCTGGTAGGTATTCATCTTCTTCTTCATCAAGCTCTGATTCTTCCAGCAGTTCTTCTGAT	
		541 S E D E D K K Q G K Q R K K K K N R S H 1621 TCTGAAGATGAGGATAAGAAACAAGGAAAACAGAGAAAGAAAAGAAGAACCGTTCACAT	
		561 K S S E S S M S E T E S S D S K D S L K K K 1681 AAATCTTCTGAAAGCTCCATGTCAGAAACTGAATCAGACAGTAAGGATAGTTTAAAAAG	
		581 K K K S K D G T E K E K D I K G L S K K K 1741 AAAAAGAAGTCAAAAGATGGAACTGAGAAAGAAAAGGATATTAAAGGACTCAGCAAAAAG	
		601 R K M Y S E D K P L S S E E S L S S E E S E Y 1801 AGAAAGATGTATTCTGAAGATAAACCTTTATCATCTGAGTCCTTGTCAGAATCAGAGTAT	
		621 I E E L L I M G T A D K T R R A F L W C 1861 ATTGAGGAGCTGCTTATCATGGGCACAGCTGACAAAACCAGAAGAGCCTTTCTATGGTGC	
		641 H E C C L L L H G L E A A M A K L G G G G 1921 CATGAATGCTGTCTTCTCCTCCATGGTCTGGAAGCAGCCATGGCCAAACTTGGAGGTGGT	
		661 V N E L K V N L L Q R P P P F G W H W Q G 1981 GTCAATGAACTTAAGGTCAATCTTCTCCAGAGGCCGCCGTTTGGTTGGCACTGGCAAGGA	
		681 L V K A I A L G Q P D D D V D H L V L L K 2041 CTTGTGAAGGCCATTGCCCTTGGTCAACCTGATGACGTCGATCATCTTGTCCTGCTCAAA	
		701 H L V H R Y L L L K P L V G P V Q L L G 2101 CACTTGGTTCACAGGTACCTGCTGCTCAAGCCTCTCGTGGGCCCAGTCCAGCTTCTTGGC	
		721 H G A S L Y L D L H Q V G L P L V Q R K 2161 CATGGTGCCTCCCTTTACCTGGATCTCCATCAGGTGGGCCTTCCTCTGGTGCAGAGGAAG	
		741 Q A H L G V G N D A D D L A V L L H A A 2221 CAGGCACATCTGGGTGTAGGCAATGATGCAGATGACTTGGCGGTACTTCTTCATGCTGCT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		761 E V L L Q L L L A I L I L T F L A V L G 2281 GAAGTCCTTCTCCAGCTGCTTCTTGCCATCCTCATCCTGACATTTCTTGCAGTACTTGGT	
		781 K G L L L R F M P V F I E M S L A C I A 2341 AAAGGCCTTCTTCTTAGATTTATGCCGGTTTTTATAGAAATGTCTCTTGCATGCATCGCT	
		801 D V L S E D S I E G L E A S R G F H E A 2401 GATGTGCTCAGCGAAGACAGTATTGAAGGTCTGGAGGCCTCGAGGGTTTCCACGAAGCC	
		821 H N G H N H H G W Y L H N G H S L Y H F 2461 CACAATGGCCACAACCACCATGGGTGGTATCTCCACAATGGTCACAGCCTCTATCACTTC	
		841 L L V H L G S W P V D F P H D V G H A S 2521 CTTCTTGTTCACCTTGGATCCTGGCCTGTCGACTTCCCGCATGATGTTGGTCATGCCAGC	
		861 L V S Q E G C E V D Q L G R V I L R K A 2581 CTTGTATCCCAGGAAGGCTGTGAGGTGGACCAGCTTGGAAGGGTCATCCTTAGGAAAGCT	
		881 L H L P M M L P A A L L R Q E A E G P M 2641 CTTCACCTTCCCATGATGCTTCCTGCTGCGCTGCTGAGGCAGGAAGCCGAGGGACCCATG	
		901 S G S G E P S L R A F E A S H Q W V C L 2701 TCTGGGAGCGGAGAACCTTCTCTGAGGGCTTTCGAAGCTTCCCACCAGTGGGTTTGTCTG	
		921 N C L G M R P R S P A D V S A A G S A A 2761 AACTGTTTAGGAATGCGGCCGGTCGCCAGCTGACGTCAGCGCCGGCCGGTTCAGCCGCA	
		941 G Q S Q R L T A R G A G L G V R M G R G 2821 GGCCAGAGTCAGAGACTGACAGCGCGAGGGGCGGGGTTGGGAGTCAGGATGGGGCGAGGC	
		961 L R V T D G A G A G R R F H L S G T V T 2881 CTGCGTGTGACTGATGGCGCGGGGGCGGGGCGCGTTTCCACTTGAGCGGCACAGTGACA	
		981 E P A I Q S E P E T V C N V A I S F D R 2941 GAACCTGCAATACAATCGGAGCCAGAAACTGTTTGCAACGTGGCCATCAGCTTTGATCGT	
		1001 C K I T S V T C S C G N K D I F Y C A H 3001 TGCAAGATTACCTCAGTGACCTGCAGCTGTGGAAACAAGGACATATTTTATTGTGCCCAT	
		1021 V V A L S L Y R I R K P D Q V K L H L P 3061 GTTGTGGCACTGTCTTTATACCGCATCCGCAAGCCAGATCAGGTCAAACTGCATCTTCCT	
		1041 I S E T L F Q M N R D Q L Q K F V Q Y L	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		3121 ATTTCAGAGACTCTCTTTCAAATGAATAGAGACCAACTGCAAAAGTTTGTACAGTATTTG	
		1061 I T T V H H T E V L P T A Q K L A D E I L 3181 ATCACAGTGCACCACACAGAAGTTTTGCCAACTGCTCAAAAATTAGCAGATGAAATTCTT	
		1081 S Q N S E I N Q V H G A P D P T A G A S 3241 TCCCAAAATTCAGAAATCAACCAAGTTCATGGTGCTCCTGATCCAACAGCAGGTGCTAGT	
		1101 I D D E N C W H L D E E Q V Q E Q V K L 3301 ATAGATGATGAAAACTGCTGGCACTTAGATGAAGAGCAGGTTCAAGAACAGGTTAAACTG	
		1121 F L S Q G G Y H G S G K Q L N L L L F A K 3361 TTCCTTTCCCAGGGCGGGTACCACGGATCAGGGAAGCAGCTTAATTTGCTCTTTGCAAAG	
		1141 V R E M L K M R D S N G A R M L T L I T 3421 GTGCGGGAGATGTTAAAGATGAGGGACTCCAATGGGGCCCGCATGTTGACCTTGATAACA	
		1161 E Q F M A D P R L S L W R Q Q G T A M T 3481 GAGCAATTCATGGCTGACCCTCGCCTGTCACTTTGGCGGCAACAAGGCACTGCAATGACT	
		1181 D K Y R Q L W D E L G A L W M C I V L N 3541 GACAAATACAGGCAGCTCTGGGATGAGCTGGGTGCTCTGTGGATGTGTATAGTTTTAAAC	
		1201 P H C K L E Q K A S W L K Q L K K W N S 3601 CCCCACTGCAAGTTGGAGCAAAAGGCCAGTTGGCTAAAACAGCTGAAGAAATGGAATAGT	
		1221 V D V C P W E D G N H G S E L P N L T N 3661 GTTGATGTCTGTCCATGGGAAGATGGAAATCATGGCAGTGAATTACCCAACTTAACCAAT	
		1241 A L P Q G A N A N Q D S S N R P H R T V 3721 GCTCTGCCTCAGGGTGCAAATGCCAACCAAGATTCATCGAACAGGCCACATCGGACAGTG	
		1261 F T R A I E A C D L H W Q D S H L Q H I 3781 TTCACCCGAGCCATCGAGGCATCGATCTCCACTGGCAGGATAGCCACTTGCAGCACATT	
		1281 I S S D L Y T N Y C Y H D D T E N S L F 3841 ATCAGCAGTGACCTATACACCAACTACTGTTACCATGACGACACTGAAAACTCCCTCTTC	
		1301 D S R G W P L W H E H V P T A C A R V D 3901 GACTCCCGCGGGTGGCCCCTCTGGCATGAACATGTTCCTACAGCCTGTGCAAGAGTGGAC	
		1321 A L R S H G Y P R E A L R L A I A I V N 3961 GCATTACGTTCTCATGGGTACCCCAGAAGCACTGAGACTAGCAATAGCTATTGTTAAT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1341 T L R R R Q Q Q K Q L E M F R T Q K K E L 4021 ACATTAAGACGACAGCAGCAGAAACAGTTGGAAATGTTCCGAACCCAAAAAAAAGAGCTA	
		1361 P H K N I T S I T N L E G W V G H P L D 4081 CCCCATAAAAACATAACCTCGATAACCAATCTGGAGGGCTGGGTTGGACATCCCCTGGAC	
		1381 P V G T L F S S L M E A C R I D D E N L 4141 CCTGTGGGCACTCTCTTCAGTAGCCTTATGGAAGCCTGCCGCATTGATGATGAGAACCTC	
		1401 S G F S D F T E N M G Q C K S L E Y Q H 4201 TCTGGGTTCTCAGATTTACAGAGAATATGGGACAGTGCAAGTCTCTGGAATACCAGCAT	
		1421 L P A H K F L E E G E S Y L T L A V E V 4261 CTACCTGCACACAAATTCTTAGAAGAGGGGAATCCTATTTAACGCTGGCTGTGTGGAAGTA	
		1441 A L I G L G Q Q R I M P D G L Y T Q E K 4321 GCCCTGATAGGGCTAGGACAGCAGCGTATCATGCCTGATGGGCTGTACACACAAGAGAAA	
		1461 V C R N E E Q L L I S K L Q E I E L D D T 4381 GTTTGCCGGAATGAGGAGCAGCTCATTTCTAAGCTTCAGGAAATTGAATTGGATGACACA	
		1481 L V K I F R K Q A V F L L E A G P Y S G 4441 CTGGTGAAAATTTTTCGCAAGCAAGCAGTCTTCCTATTAGAAGCCGGACCATATAGTGGT	
		1501 L G E I I H R E S V P M H T F A K Y L F 4501 TTAGGTGAAATAATCCATCGGGAGAGCGTTCCAATGCACACATTTGCCAAGTATCTCTTC	
		1521 T S L L P H D A E L A Y K I A L R A M R 4561 ACCTCTCTCCTACCTCACGATGCTGAATTGGCATACAAAATTGCACTGAGAGCAATGCGG	
		1541 L L V L E S T A P S G D L T R P H H I A 4621 TTACTAGTATTGGAATCTACTGCTCCATCAGGAGACCTCACCCGCCCACACCACATTGCA	
		1561 S V V P N R Y P R W F T L S H I E S Q Q 4681 TCAGTTGTTCCCAACCGCTACCCTCGCTGGTTCACTCTAAGCCACATTGAGTCCCAGCAG	
		1581 C E L A S T M L T A A K G D V R R L E T 4741 TGTGAGCTGGCATCCACCATGCTAACTGCAGCCAAAGGCGATGTTCGGAGGCTGGAAACA	
		1601 V L E S I Q K N I H S S S H I F K L A Q 4801 GTATTAGAATCCATCCAGAAAAACATTCACTCCTCATCACACATCTTCAAGCTTGCCCAA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1621 D A F K I A T L M D S L P D I T L L K V 4861 GATGCATTTAAAATAGCAACTCTCATGGACAGTTTGCCAGACATCACTCTTTTGAAAGTG	
		1641 S L E L G L Q V M R M T L S T L N W R R 4921 TCTCTGGAGCTGGGCCTGCAGGTTATGCGAATGACACTGTCAACCTTAAATTGGCGACGG	
		1661 R E M V R W L V T C A T E V G V Y A L D 4981 CGGGAGATGGTGAGGTGGCTGGTAACGTGTGCTACTGAAGTCGGGGTTTATGCCCTGGAC	
		1681 S I M Q T W F T L F T P T E A T S I V A 5041 AGCATCATGCAGACCTGGTTTACACTCTTTACTCCCACCGAGGCCACAAGTATAGTTGCA	
		1701 T T V M S N S T I V R L H L D C H Q Q E 5101 ACTACCGTGATGTCCAACAGCACCATCGTCCGCCTCCACCTGGACTGCCACCAGCAGGAA	
		1721 K L A S S A R T L A L Q C A M K D P Q N 5161 AAGCTGGCCAGCAGCGCCCGGACACTTGCACTGCAGTGTGCCATGAAGGATCCACAGAAC	
		1741 C A L S A L T L C E K D H I A F E T A Y 5221 TGTGCCCTCTCTGCGCTAACCCTTTGTGAAAAGGATCACATAGCTTTTGAGACGGCGTAC	
		1761 Q I V L D A A T T G M S Y T Q L F T I A 5281 CAAATTGTTCTCGACGCTGCTACGACTGGCATGAGCTATACACAGCTCTTTACAATAGCA	
		1781 R Y M E H R G Y P M R A Y K L A T L A M 5341 CGGTACATGGAGCACCGCGGGTACCCCATGAGGGCCTACAAGCTGGCCACCCTGGCCATG	
		1801 T H L N L S Y N Q D T H P A I N D V L W 5401 ACCCATCTCAACCTGAGCTACAATCAGGACACACACCCTGCCATTAATGATGTTTTGTGG	
		1821 A C A L S H S L G K N E L A A I I P L V 5461 GCCTGTGCGCTTAGCCACTCCCTTGGTAAAAATGAGCTTGCAGCTATAATACCTCTGGTG	
		1841 V K S V K C A T V L S D I L R R C T L T 5521 GTCAAGAGTGTCAAGTGTGCAACGGTACTGTCAGACATTTTGCGCAGATGCACTCTGACC	
		1861 T P G M V G L H G R R N S G K L M S L D 5581 ACTCCTGGCATGGTGGGACTTCATGGGAGGAGGAACTCTGGTAAGCTCATGTCACTGGAC	
		1881 K A P L R Q L L D A T I G A Y I N T T H 5641 AAAGCCCCCTTGAGGCAACTCTTGGATGCCACGATCGGGGCCTACATCAACACACGCAC	
		1901 S R L T H I S P R H Y S E F I E F L S K	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		5701 TCACGGCTCACACACATCAGTCCTCGGCACTATAGTGAGTTTATAGAGTTCCTCAGCAAA	
		1921 A R E T F L M A H D G H I Q F T Q F I D	
		5761 GCCCGAGAGACCTTCTTAATGGCGCATGATGGACACATTCAGTTTACACAGTTTATTGAC	
		1941 N L K Q I Y K G K K K L M M L V R E R F	
		5821 AACCTGAAACAAATCTACAAAGGCAAAAAGAAACTGATGATGTTGGTTCGGGAGAGGTTT	
		1961 G -	
		5881 GGTTGA	
B1961932	Equus caballus interleukin-4 receptor alpha-chain mRNA.	1 GGGCGCTGCCGAGCCTGGCTGCCCTGGATCCCGCACTTCCCGCTCGGGCGCTGGACGGCG	SEQ ID NO:229
		61 AATGGGCCAGGGGCGCGCAGGTGCAGTAGGGTCTCCCAATGGGGTGCCTTTGCCCCGGGC	
		121 TCACGCTCCCTGTGAGCTGCCTGATCCTGGTGTGGGCGGCAGGCTCTGGGAGCGTTAAGG	
		181 TCCTGCGTCTCACCGCCTGCTTCTCCGACTACATCAGCGCCTCCACCTGTGAGTGGAAGA	
		241 TGGACCGTCCCACCAACTGCAGTGCCCAGCTCCGTCTGTCCTACCAGCTGAACGACGAGT	
		301 TCTCTGACAACCTCACGTGTATCCCCGAGAACAGAGAAGATGAAGTGTGCGTGTGCCGTA	
		361 TGCTGATGGACAACATCGTCAGCGAGGACGTCTATGAGCTGGACCTGTGGCTGGGAACC	
		421 AACTGCTGTGGAACAGCTCCTTCAAGCCCAGCCGGCACGTGAAACCCAGGGCCCCTCAAA	
		481 ACCTCACGGTTCACGCCATCTCCCACACGTGGCTGCTGACGTGGAGCAACCCGTACCCTT	
		541 TGAAGAATCACCTGTGGTCTGAGCTTACCTACCTGGTCAACATCTCCAAGGAGGACGACC	
		601 CCACGGACTTCAAAATCTACACAACGTGACCTACATGGACCCCACCCTCCGCGTCACAGCCA	
		661 GCACCCTGAAGTCCAGGGCTACGTACAGCGCACGGGTGAAGGCCAGGGCTCAGAACTACA	
		721 ACAGCACCTGGAGTGAGTGGAGCCCCAGCACCACGTGGCATAACTACTACGAGCAGCCCT	
		781 TGGAGCAGCGCCTCCCGCTTGGTGTCAGCATCTCCTGCGTTGTCATCCTGGCCATCTGCC	
		841 TGTCCTGCTATTTCAGCATCATCAAGATTTAAGAAAGAATGGTGGGACCAGATTCCCAACC	
		901 CAGCGCACAGCCCCCTCGTGGCTATCGTCCTCCAGGATTCTCAGGTGTCACTGTGGGGGA	
		961 AGCAGTCCCGAGGCCAGGAGCCAGCCAAGTGCCCACGCTGGAAGACTTGTCTTACCAAGC	
		1021 TCCTGCCCTGTTTACTGGAGCATGGCCTGCAAAAGGAGGAGGATTCCTCCAAGACTGTCA	
		1081 GAAATGGGCCTTTCCAGAGTCCTGGAAAATCAGCATGGCACACTGTGGAGGTCAACCACA	
		1141 CGATCCTCCGGCCAGAGATCATCAGCGTGGTGTGCCGTGTGTGGAGCTGTGTGAGGCCCAGG	
		1201 TGGAGAGCGAGGAGGAGGAAGTGGAGGAGATAGAGGGAGCTTCTGCCCGTCGCCTGAGA	
		1261 GCAGCGGGAGCGGCTTCCAGGAAGGCAGGGAGGGCGTCGCGGCCCGGCTGACAGAGAGCC	
		1321 TGTTCCTGGGCCTCCTCGGGGCTGAGAATGGGGCCTTGGGGGAGTCATGCCTTCTTCCCC	
		1381 CTTTAGGAAGTGCTCACATGCCCTGGGCCAGGATCTCAAGTGCAGGGCCCCAGGAGGCAG	
		1441 CGTCCCAGGGTGAGGAGCAGCCTCTCAACCCAGAGTCAAATCCTCTGGCCACTCTGACCC	
		1501 AGAGCCCAGGCAGCCTGGCTTTCACAGAGGCGCCTGCTGTGGTTGCAGACAACCCCGCCT	
		1561 ACCGCAGCTTCAGCAACTCCCTGAGCCAGCCCCGAGGTCCTGGAGAGCTTGACTCAGACC	
		1621 CACAGCTGGCCGAACACCTGGGCCAAGTGGACCCCAGCATCCCCTCCGCCCCCCAGCCCT	
		1681 CTGAACCACCCACTGCACTCCAGCCTGAACCAGAAACCTGGGAGCAGATGCTCCGCCAGA	
		1741 GTGTCCTCCAGCAGGGGGCAGCCCCAGCCCCTCGGCCCCACTGGCGGCTACCGGG	
		1801 AGTTTGCGCAGGTGGTGAAGCAGGGTGGCGGGGCGCGGGCTCCGGCCCTTCTGGGGAGG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1861 CTGGGTACAAGGCCTTCTCCAGCCTGCTCGCTGGCAGTGCCGTCTGCCCAGGGCAATCTG 1921 GGGTTGAGGCCAGCAGTGGGGAGGGGGGCTACAGGCCCTATGAGAGCCCCGACCCTGGAG 1981 CCCCTGCCCCGGTCCCCGTCCCCTGTTCACCTTTGGACTGGATGTGGAGCCACCTCACA 2041 GCCCTCAGAACTCCCTCCTCCTGCCAGGCGGCTCCCCAGAGCTCCCTGGCCCAGAGCCGACGG 2101 TGAAGGGAGAGGACCCACGGAAGCCCCCTGCTTTCCGCACAGCCACAGACTCCCTCA 2161 GGGACGACCTGGCAGCGGCATTGTCTACTCGGCCCTCACCTGCCACCTTTGTGGCCACC 2221 TGAAGCAGTGTCATGGCCAGGAGGAGCATGGCGAGGCCCACACTGTGGCCAGCCCCTGCT 2281 GTGGCTGCTGTTGTGGGGACAGGTCCTCCCCCCCCAGTGAGCCCCGTGAGGGCCCTGGACC 2341 CCCCGCCAGGTGGGGTTCCCCTGGAGGCGGGCCTCTCTCTTGCCTCCCCTGGGATCCTTGG 2401 GGCTCTCTGAGGAGCGCAAACCCTCCCTCTTCTTCCAGCCTGCTCCCGGCAATGCTCAGA 2461 GCTCGAGCCAGACCCCTCTCACGGTGGCCATGCTCTCCACAGGGCCCACATGCACGAGCG 2521 CTTCCTAGGGGCGTGCCCTCTGGTTGCTGCGGTCCACAGGTGAGGACCGGGTCTTCGAAA 2581 TGCCTCCCCCCCACATTTTGGGGCAGCCAGGCTGGCAGACTTCTGAAAGACTCAGAGAACC 2641 CTGGTAGGAAGCTGTGAGGTTGTCCAACCTGGGGCTACAGAGACTGGACCCCCTTGCTCCC 2701 CAGCCGTGGCCCAAGCTCCCCCCATCCCACGGGAGTGGAGCCTGCAGGGCAGCCATGCCCC 2761 ACGGCAGGCACCTGCGGGCATCGGGAGGTCCCTGGGCAGCTGAGCTTGTGAACGAGCCGT 2821 TGGCCGCTTCGTTGGTGCACAGCTTCTCCAGCATGCTGTCCCTGTCACGCCTGCCCAAGG 2881 CTTGTTTTGTCCACCTAATCTCTCTGTTACCCGAGTCTGACCCAGTCCTGGGTTAGCTGC 2941 CGCCATATCACTGGATTGGATGCTGAGCCTAGAAACTGATCAAGCTCATGGGGGAATGAC 3001 TTAGGAGGCCCCAGGAAATTCAAGGGAAGTCGGGTCCAGGAGGATAGGATTTGCCTAGA 3061 GAGGCCCGTTCCTTCAACAGAGCTTCATCTAGCTGGCACCAGAGGCAGGATTGCACCTGT 3121 GGTGGGTGCTTAGCCAAGTCGGGGTCACAGAGAAGGACATGAGAAATTGTGATTAGCCGG 3181 TAGTGACAGTTTGCTGTCAGGTCCCCCCACAACTGTAGGCCTGGGCCTCCTCTTAGGCAT 3241 GGGATCCCCAGAGTGGACCTGCCCAGCTACCCAGGGCCAGTTTGTGCACCCATGGAGAGC 3301 GTTGCTGGCAGCCATAGAGACCAGAGGGAGTGGGTCACAGCCCATGACCCAGCCGAATGG 3361 GGCATTCCAGACAGCTGACCCGGCACGTTTTGCCTGCACATGGCTCAGACCTTGGGTCGA 3421 GTAACGCTTGTTTGTTGTGTATCTCAAAGATATATTTTATCTCACTGGTATTTGTGTTTGC 3481 TGAGGACGGTGGAATGGGGGGGTCTGGAGTCTTGTATGAATAAAGATTCTTTCTCTCAAA 3541 AAAAAAAAAAAAAAA 1 M G C L C P G L T L P V S C L I L V W A 1 ATGGGGTGCCTTTGCCCCGGGCTCACGCTCCCTGTGAGCTGCCTGATCCTGGTGTGGGCG 21 A G S G S V K V L R L T A C F S D Y I S 61 GCAGGCTCTGGGAGCGTTAAGGTCCTGCGTCTCACCGCCTGCTTCTCCGACTACATCAGC 41 A S T C E W K M D R P T N C S A Q L R L 121 GCCTCCACCTGTGAGTGGAAGATGGACCGTCCCACCAACTGCAGTGCCCAGCTCCGTCTG 61 S Y Q L N D E F S D N L T C I P E N R E 181 TCCTACCAGCTGAACGACGAGTTCTCTGACAACCTCACGTGTATCCCCGAGAACAGAGAA 81 D E V C V C R M L M D N I V S E D V Y E	SEQ ID NO:230

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		241 GATGAAGTGTGCGTGTGCCGTATGCTGATGGACAACATCGTCAGCGAGGACGTCTATGAG	
		101 L D L W A G N Q L L W N S S F K P S R H	
		301 CTGGACCTGTGGGCTGGGAACCAACTGCTGTGGAACAGCTCCTTCAAGCCCAGCCGGCAC	
		121 V K P R A P Q N L T V H A I S H T W L L	
		361 GTGAAACCCAGGGCCCCTCAAAACCTCACGGTTCACGCCATCTCCCACACGTGGCTGCTG	
		141 T W S N P Y P L K N H L W S E L T Y L V	
		421 ACGTGGAGCAACCCGTACCCTTTGAAGAATCACCTGTGGTCTGAGCTTACCTACCTGGTC	
		161 N I S K E D D P T D F K I Y N V T T Y M D	
		481 AACATCTCCAAGGAGGACGACCCCACGGACTTCAAAATCTACAACGTGACCTACATGGAC	
		181 P T L R V T A S T L K S R A T Y S A R V	
		541 CCCACCCTCCGCGTCACAGCCAGCACCCTGAAGTCCAGGGCTACGTACAGCGCACGGGTG	
		201 K A R A Q N Y N S T W S E W S P S T T W	
		601 AAGGCCAGGGCTCAGAACTACAACAGCACCTGGAGTGAGTGGAGCCCCAGCACCACGTGG	
		221 H N Y Y E Q P L E Q R L P L G V S I S C	
		661 CATAACTACTACGAGCAGCCCTTGGAGCAGCGCCTCCCGCTTGGTGTCAGCATCTCCTGC	
		241 V V I L A I C L S C Y F S I I K I K K E	
		721 GTTGTCATCCTGGCCATCTGCCTGTCCTATTTCAGCATCATCAAGATTAAGAAAGAA	
		261 W W D Q I P N P A H S P L V A I V L Q D	
		781 TGGTGGGACCAGATTCCCAACCCAGCGCACACAGCCCCCTCGTGGCTATCGTCCTCCAGGAT	
		281 S Q V S L W G K Q S R G Q E P A K C P R	
		841 TCTCAGGTGTCACTGTGGGGGAAGCAGTCCCGAGGCCAGGAGCCAGCCAAGTGCCCACGC	
		301 W K T C L T K L L P C L L E H G L Q K E	
		901 TGGAAGACTTGTCTTACCAAGCTCCTGCCCTGTTTACTGGAGCATGGCCTGCAAAGGAG	
		321 E D S S K T V R N G P F Q S P G K S A W	
		961 GAGGATTCCTCCAAGACTGTCAGAAATGGGCCTTTCCAGAGTCCTGGAAAATCAGCATGG	
		341 H T V E V N H T I L R P E I I S V V P C	
		1021 CACACTGTGGAGGTCAACCACACGATCCTCCGGCCAGAGATCATCAGCGTGGTGCCGTGT	
		361 V E L C E A Q V E S E E E E E V E E D R G	
		1081 GTGGAGCTGTGTGAGGCCCAGGTGGAGAGCGAGGAGGAGGAAGTGGAGGAAGATAGAGGG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		381 S F C P S P E S S S G G F Q E G R E G V 1141 AGCTTCTGCCCGTCGCCTGAGAGCAGCGGGAGCGGCTTCCAGGAAGGCAGGGAGGGCGTC	
		401 A A R L T E S L F L G L L G A E N G A L 1201 GCGGCCCGGCTGACAGAGAGCCTGTTCCTGGGCCTCCTCGGGGCTGAGAATGGGGCCTTG	
		421 G E S C L L P P L G S A H M P W A R I S 1261 GGGGAGTCATGCCTTCTTCCCCCTTTAGGAAGTGCTCACATGCCCTGGGCCAGGATCTCA	
		441 S A G P Q E A A S Q G E E Q P L N P E S 1321 AGTGCAGGGCCCCAGGAGGCAGCGTCCCAGGGTGAGGAGCAGCCTCTCAACCCAGAGTCA	
		461 N P L A T L T Q S P G S L A F T E A P A 1381 AATCCTCTGGCCACTCTGACCCAGAGCCCAGGCAGCCTGGCTTTCACAGAGGCGCCTGCT	
		481 V V A D N P A Y R S F S N S L S Q P R G 1441 GTGGTTGCAGACAACCCCGCCTACCGCAGCTTCAGCAACTCCCTGAGCCAGCCCCGAGGT	
		501 P G E L D S D P Q L A E H L G Q V D P S 1501 CCTGGAGAGCTTGACTCAGACCCACAGCTGGCCGAACACCTGGGCCAAGTGGACCCCAGC	
		521 I P S A P Q P S E P P T A L Q P E P E T 1561 ATCCCCTCCGCCCCCAGCCCTCTGAACCACCCACTGCACTCCAGCCTGAACCAGAAACC	
		541 W E Q M L R Q S V L Q Q G A A P A P A S 1621 TGGGAGCAGATGCTCCGCCAGAGTGTCCTCCAGCAGGGGGCAGCCCCAGCCCCGCCTCG	
		561 A P T G G Y R E E F A Q V V K Q G G G A A 1681 GCCCCCACTGGCGGCTACCGGGAGTTTGCGCAGGTGGTGAAGCAGGGTGGCGGGGGCGGCG	
		581 G S G P S G G E A G Y K A F S S L L A G S 1741 GGCTCCGGCCCTTCTGGGGAGGCTGGGTACAAGGCCTTCTCCAGCCTGCTCGCTGGCAGT	
		601 A V C P G Q S G G V E A S S G E G G Y R P 1801 GCCGTCTGCCCAGGGCAATCTGGGGTTGAGGCCAGCAGTGGGGAGGGGGGCTACAGGCCC	
		621 Y E S P D P G A P A P V P P V P L F T F G 1861 TATGAGAGCCCCGACCCTGGAGCCCCTGCCCCGGTCCCCGTCCCCCTGTTCACCTTTGGA	
		641 L D V E P P H S P Q N S L L P G G S P E 1921 CTGGATGTGGAGCCACCTCACAGCCCTCAGAACTCCCTCCTGCCAGGCGGCTCCCCAGAG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		661 L P G P E P T V K G E D P R K P L L S A 1981 CTCCCTGGCCCAGAGCCGACGGTGAAGGGAGAGGACCCACGGAAGCCCCTGCTTTCCGCA 681 Q Q A T D S L R D D L G S G I V Y S A L 2041 CAGCAGGCCACAGACTCCCTCAGGGACGACCTGGGCAGCGGCATTGTCTACTCGGCCCTC 701 T C H L C G H L K Q C H G Q E E H G E A 2101 ACCTGCCACCTTTGTGGCCACCTGAAGCAGTGTCATGGCCAGGAGGAGCATGGCGAGGCC 721 H T V A S P C C G C C C G D R S S P P V 2161 CACACTGTGGCCAGCCCCTGCTGTGGCTGCTGTTGTGGGGACAGGTCCTCCCCCCCAGTG 741 S P V R A L D P P P G G V P L E A G L S 2221 AGCCCCGTGAGGGCCCTGGACCCCCCGCCAGGTGGGGTTCCCCTGGAGGCGGGCCTCTCT 761 L A S L G S L G L S E E R K P S L F F Q 2281 CTTGCCTCCCTGGGATCCTTGGGGCTCTCTGAGGAGCGCAAACCCTCCCTCTTCTTCCAG 781 P A P G N A Q S S S Q T P L T V A M L S 2341 CCTGCTCCCGGCAATGCTCAGAGCTCGAGCCAGACCCCTCTCACGGTGGCCATGCTCTCC 801 T G P T C T S A S - 2401 ACAGGGCCCACATGCACGAGCGCTTCCTAG	
B1961941	Fibroblast mRNA for aldolase A	1 GGGGAACCACACTCCGTCCACGGACTCTCCGTTATTTTAGGAGGTCCCTGGCCAAAGATT 61 TATTTCTCTTGACAACCAAGGGCCTCCGTCTGGATTTCCAAGGAAGAATTTCCTCTGAAG 121 CACCGGAACTTGCTACTACCAGCACCATGCCCTACCAATATCCAGCACTGACCCCGGAGC 181 AGAAGAAGGAGCTGTCTGACATCGCTCACCGCATCGTGGCACCTGGCAAGGGCATCCTGG 241 CTGCAGATGAGTCCACTGGGAGCATTGCCAAGCGGCTGCAGTCCATTGGCACCGAGAACA 301 CCGAGGAGAACCGGCGCTTCTACCGCCAGCTGCTGCTGACAGCTGACGACCGCGTGAACC 361 CCTGCATTGGGGGTGTCATCCTCTTCCATGAGACACTCTACCAGAAGGCGGATGATGGGC 421 GTCCCTTCCCCCAAGTTATCAAATCCAAGGGCGGTGTTGTGGGCATCAAGGTAGACAAGG 481 GCGTGGTCCCCCTGGCAGGGACAAATGGCGAGACTACCACCCAAGGGTTGGATGGGCTGT 541 CTGAGCGCTGTGCCCAGTACAAGAAGGACGGAGCTGACTTTGCCAAGTGGCGCTGTGTGC 601 TGAAGATTGGGGAGCACACTCCCTCATCCCTTGCCATCATGGAAAATGCCAATGTTCTGG 661 CCCGTTATGCCAGCATCTGCCAGCAGAATGGCATTGTGCCCATCGTGGAGCCTGAGATCC 721 TCCCTGATGGGGACCATGACTTGAAGCGCTGTCAGTATGTAACCGAGAAGGTGCTGGCTG 781 CTGTTTACAAGGCTCTGAGTGACCACCACATCTACCTGGAAGGCACCTTGCTGAAGCCCA 841 ATATGGTAACCCCAGGCCACGCCTGCACCCACAAATATTCTCATGAGGAGATTGCCATGG 901 CAACTGTCACGGCACTGCGTCGCACGGTGCCCCCTGCTGTCACTGGGATCACCTTCCTAT 961 CTGGAGGCCAGAGTGAGGAGGAGGCATCCATCAACCTCAACGCCATCAACAAGTGCCCCC 1021 TGCTGAAGCCGTGGGCCCTGACCTTCTCCTATGGCCGAGCCCTGCAGGCCTCTGCCCTGA	SEQ ID NO:231

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1081 AGGCCTGGGGTGGGAAGAAGGAGAACCTGAAGGCTGCCCAGGAGGAATATGTCAAGCCAG 1141 CCCTGGCCAACAGCCTCGCCTGCCAAGGAAAATACACCCCAAGTGGTCACGCTGGGGCTG 1201 CAGCCAGCGAGTCCCTCTTCATCTCTAACCATGCCTACTAAGTGGAGGTATTCTAAGGCT 1261 GCCCCCTCAACACTCCAGGCCCTGCCTCCTCCCACTCTCACTCTTGAAGAGGGGGCCTCA 1321 TCCAGGGCTTTAGGCTGTTCTTTCCCATTCTCCTTGCCTCCCTGGTGACATTGGTCTGTG 1381 GTATTGTCTGTGTATGCTAACTCCATCACCCTTTCGAGCCCACTGCCAAATAAACAGCTA 1441 TTTAAGGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1501 AAAAAAAAAAAAAAA 1 M P Y Q Y P A L T P E Q K K E L S D I A 1 ATGCCCTACCAATATCCAGCACTGACCCCGGAGCAGAAGAAGGAGCTGTCTGACATCGCT 21 H R I V A P G K G I L A A D E S T G S I 61 CACCGCATCGTGGCACCTGGCAAGGGCATCCTGGCTGCAGATGAGTCCACTGGGAGCATT 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 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 GGCGAGACTACCACCCAAGGGTTGGATGGCTGTCTGAGCGCTGTGCCCAGTACAAGAAG 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 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 CGCTGTCAGTATGTAACCGAGAAGGTGCTGGCTGTTTACAAGGCTCTGAGTGACCAC 221 H I Y L E G T L L K P N M V T P G H A C	SEQ ID NO:232

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		661 CACATCTACCTGGAAGGCACCTTGCTGAAGCCCAATATGGTAACCCCAGGCCACGCCTGC 241 T H K Y S H E E I A M A T V T A L R R T 721 ACCCACAAATATTCTCATGAGGAGATTGCCATGGCAACTGTCACGGCACTGCGTCGCACG 261 V P P A V T G I T F L S G G Q S E E E A 781 GTGCCCCCTGCTGTCACTGGGATCACCTTCCTATCTGGAGGCCAGAGTGAGGAGGAGGCA 281 S I N L N A I N K C P L L K P W A L T F 841 TCCATCAACCTCAACGCCATCAACAAGTGCCCCCTGCTGAAGCCGTGGGCCCTGACCTTC 301 S Y G R A L Q A S A L K A W G G K K E N 901 TCCTATGGCCGAGCCCTGCAGGCCTCTGCCCTGAAGGCCTGGGGTGGGAAGAAGGAGAAC 321 L K A A Q E E Y V K R A L A N S L A C Q 961 CTGAAGGCTGCCCAGGAGGAATATGTCAAGCGAGCCCTGGCCAACAGCCTCGCCTGCCAA 341 G K Y T P S G H A G A A A S E S L F I S 1021 GGAAAATACACCCCAAGTGGTCACGCTGGGCTGCAGCCAGCGAGTCCCTCTTCATCTCT 361 N H A Y - 1081 AACCATGCCTACTAA	
BM734452	Equus caballus adenosine A2A receptor mRNA	1 gtgccccggg tgctgacgct gagctgagcc aagatgccgc gggagccgct agagagggcc 61 tggtttctgg agactcggag ttggctgtga aaaaaccctt ggggagcccc ccactcccca 121 gcacggacgc tcttggctcc tgtgagaagg gggctccggg gcctgggcag ggccggctgc 181 gctgcagcta tggaccgtga gctggcctgg ccccgctcct tgctgaccct gcccgtcttc 241 agccatgccc accgtgggct ccttggtgta catcatggtg gagctggcca tcgctctgct 301 ggccatcctg ggcaacatgc tggtgtgctg ggccgtgtgg ctgaacagca acctgcagaa 361 cgtcaccaac tactttgtgg tgtcactggc agcggccgac atcgctgtgg gggtccttgc 421 catccccttc gccatcacca tcagcacagg gttctgtgcc gcctgccacg gctgcctctt 481 catcgcctgc ttcgtgctgg tcctcacgca gagctccatc ttcagcctcc tggccatcgc 541 cattgaccgc tacatcgcca tccgcatccc actccgatac aatggcttgg tgaccggcac 601 gagggccaag ggcgtcattg cagtctgctg ggtgctgtcg ttcgccatcg gcctgacgcc 661 catgctgggc tggaacaact gccatcactg ggggagggcc gagaaccagt cgcagggctg 721 cggcgagggc caggtggcct gcctctttga ggacgtggtc cccatgaact acatggtgta 781 ctacaacttc tttgcttgcg ttctggtgcc cctgctgctc atgctgggcg tctacttgcg 841 catcttcctg gcggcgcggc gacagctgaa gcagatggag acccagcctc tgccgggga 901 gcgggctccgg tccacgctgc agaaggaggt ccacgccgcc aagtcgctgg ccatcatcgt 961 ggggctcttc gccctctgct ggctgcccct gcacatcatc aactgcttca cttcttctg 1021 cccgagtgc ccgcacgccc cgctctggct catgtacccg gccatcatcc tctcccactt 1081 caattccgtc gtgaacccct tcatctacgc ctaccgcatc cgcgagttcc gccacacctt	SEQ ID NO:233

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1141 ccacaagatc attcgcagtc acatcctgag gcggcaggag cccttcaagg caggggcac 1201 cagtgcccgg gccttggcag ctcatggcag cgatgcagag caggtcagcc tccgcctcaa 1261 cggccaccct tctgggtgt gccccaatgg cagcgccccc catcctgagc ggcggcccaa 1321 tggctatgcc ctgggctgg tgagtcgggc gagtgcccgc gagtcccctg gagacacagg 1381 cctcccagat gtggaactcc tcagccacga gctccatggg gcgagcccag agtcccctgg 1441 cctcgagggg ccccttggccc aagacggagc gggagtgtcc tgacgactcc ccgtgtctgc 1501 ccctcctaa gggaaggggg ccttttcttt tctggttgga ggaacgctc acgttgggag 1561 atgagtgcat gtgccgggag actcttctcg aggccagttc ctgccgcgga ctgagagaag 1621 ggagccccgg ctggagcagc atgaggtcca gcaggaaggt ctggcatcca aggagtgga 1681 cgcatcatgc tgggagggcc tgcacgaggc cagggccgcg gcaccagggc atcttggctg 1741 ggtaggcccg gtccccgact ccagcagcac gtagaagtgc ccctggtct ctgcagagca 1801 gccgtggcgg agcaggctgg ccggccctga ggctgggggag tggcccccgaa ggccccccgc 1861 cacacacgca ccaccctccc cagactttcc caggttcggg agctgtctgg tccagaggtg 1921 gcatttgact attttgacc aggagaaaat gtaaggcgca ggaaatcctt tttattgtat 1981 tatcttccct ccctggctgc tgggtctgtt gtcagtcctg ctgctaacct ggcaccagga 2041 gtggccaggg agtcccaggc agccctctcc ggctgccgtg agctgccatg tgcttctcac 2101 ccgtcagtcc tgaggccacc tcttgggggtg acaaagctgg gcttggtgac aggaagttgt 2161 aatggagcgg tgccagagtg cgggctcagg gagcaggttg gggctggctg gcatgggtg 2221 tgcctgggcg gctcagagct gcccaagtgg aggctcttagc tgactgcctt tccttctgag 2281 gggaatgttt ttttctgaga tacaataaaa atgagccaca ttgtgtttta aaaaaaaaaa 2341 aaaaaaaaaa aa 1 M P T V G S L V Y I M V E L A I A L L A 1 ATGCCCACCGTGGGCTCCTTGGTGTACATCATGGTGGAGCTGGCCATCGCTCTGCTGGCC 21 I L G N M L V C W A V W L N S N L Q N V 61 ATCCTGGGCAACATGCTGGTGTGGGCCGTGTGGCTGAACAGCAACCTGCAGAACGTC 41 T N Y F V V S L A A A D I A V G V L A I 121 ACCAACTACTTTGTGGTGTCACTGGCAGCGGCCGACATCGCTGTGGGGGTCCTTGCCATC 61 P F A I T I S T G F C A A C H G C L F I 181 CCCTTCGCCATCACCATCAGCACAGGTTCTGTGCCGCCTGCCACGGCTGCCTCTTCATC 81 A C F V L V L T Q S S I F S L L A I A I 241 GCCTGCTTCGTGCTGGTCCTCACGCAGAGCTCCATCTTCAGCCTCCTGGCCATCGCCATT 101 D R Y I A I R I P L R Y N G L V T G T R 301 GACCGCTACATCGCCATCCGCATCCCACTCCGATACAATGGCTTGGTGACCGGCACGAGG 121 A K G V I A V C W V L S F A I G L T P M 361 GCCAAGGGCGTCATTGCAGTCTGCTGGGTGCTGTCGTTCGCCATCGGCCTGACGCCCATG	SEQ ID NO:234

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		141 L G W N N C H H W G E G E N Q S Q G C G 421 CTGGGCTGGAACAACTGCCATCACTGGGGGGAGGGCGAGAACCAGTCGCAGGGCTGCGGC 161 E G Q V A C L F E D V V P M N Y M V Y Y 481 GAGGGCCAGGTGGCCTGCCTCTTTGAGGACGTGGTCCCCATGAACTACATGGTGTACTAC 181 N F F A C V L V P L L L M L G V Y L R I 541 AACTTCTTTGCTTGCGTTCTGGTGCCCCTGCTCATGCTGGGCGTCTACTTGCGCATC 201 F L A A R R Q L K Q M E T Q P L P G E R 601 TTCCTGGCGGCGCGGCAGCTGAAGCAGATGGAGACCCAGCCTCTGCCGGGGAGCGG 221 A R S T L Q K E V H A A K S L A I I V G 661 GCTCGGTCCACGCTGCAGAAGGAGGTCCACGCCGCCAAGTCGCTGGCCATCATCGTGGGG 241 L F A L C W L P L H I I N C F T F F C P 721 CTCTTCGCCCTCTGCTGGCTGCCCCTGCACATCATCAACTGCTTCACCTTCTTCTGCCCC 261 E C P H A P L W L M Y P A I I L S H F N 781 GAGTGCCCGCACGCCCCGCTCTGGCTCATGTACCCGGCCATCATCCTCTCCCACTTCAAT 281 S V V N P F I Y A Y R I R E F R H T F H 841 TCCGTCGTGAACCCCTTCATCTACGCCTACCGCATCCGCGAGTTCCGCCACACCTTCCAC 301 K I I R S H I L R R Q E P F K A G G T S 901 AAGATCATTCGCAGTCACATCCTGAGGCGGCAGGAGCCCTTCAAGGCAGGGGGCACCAGT 321 A R A L A A H G S D A E Q V S L R L N G 961 GCCCGGGCCTTGGCAGCTCATGGCAGCGATGCAGAGCAGGTCAGCCTCCGCCTCAACGGC 341 H P S G V C P N G S A P H P E R R P N G 1021 CACCCTTCTGGGGTGTGCCCCAATGGCAGCGCCCCCCATCCTGAGCGGCGCGGCCCAATGGC 361 Y A L G L V S R A S A R E S P G D T G L 1081 TATGCCCTGGGGCTGGTGAGTCGGCGAGTGCCCGCGAGTCCCCTGGAGACACAGGCCTC 381 P D V E L L S H E L H G A S P E S P G L 1141 CCAGATGTGGAACTCCTCAGCCACGAGCTCCATGGGGCGAGCCCAGAGTCCCCTGGCCTC 401 E G P L A Q D G A G V S - 1201 GAGGGGCCCCTGGCCCAAGACGGAGCGGGAGTGTCCTGA	
BM734511	No Homology		

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1 GTGGTCCTCCTCATCTCTTTCCTCATTTTCCTGATAGTGGGATGAGGATGGCCTTCCTGT 61 TTCACCATCTTCTCAATCTTTCTTTACCGGGTTGGGGAAGGGCTGTCTACCTGCGGCCCT 121 TTCAGTGGTGGTGTCTCCTTGCTTCTCTCTTCACCCGTAGGCTAATACGCTTGGCACT 181 GATGGGCACTGGGGAATGCAGAGCAGACCCCGGATGCTATTTATTCAAGCCCTGTTTGAA 241 TGAGTCCTTCGTGGCCAGTGCTGGGCTGGGAAGAGGGTAACAGCAAATAATCATTGGTT 301 GAGCTAGGCTTATCTTTTTGTCTAGTGCAACAGATTGAGGGTAAAACAGTTCTCAAAACA 361 GCCTTCAAATACCTTTACCTAAATACTTCCAGCTCCTTCTTCCAGCTAAAGCTCAGTACA 421 CTAATGCCTCATCTTAGCAGTGATTTTTGTAGCAATTCGAAGAAATTTTCTCATCCGTTTT 481 AAGAAAACCTGACTGAGTTTTCCTGTCTAAACAGCATTTCTGCCAAACTTAAAAGGAGGC 541 CCACATGATACCCATTC	SEQ ID NO:235
BM734531	No Homology	1 TCCTCATCAGAGTCACCCAAGGAACTTATGCAGATGCCATGTCCTCACTCCGAATCCTCA 61 CTCTGGGAGTGGAGCCAGGTGTCTGCATTTGAACAGGGTGAGGGGGTGGGTTGCCTGCTG 121 GACAAGGGAGCTGAGCCAGCAGCTCCGGACTCTGTCCTGTGGCTTTTGTGTGTCTCCCC 181 ATGTTCTCCCTCCCAGGGGCCCACCACTTCATGTTCTCTACAGAGCTAAGATGATGGCCT 241 TGCTTGAGAGAGGTCCATCCCCCGTGGTTGGGGTCACTTAGCAGCGACTTCTTGGACTGC 301 CATCCAGCCACAGTGGCCCCACAGAGCTGTCCAGAGCCGAGGCTGTGGGCTGCAGTCCCA 361 GTGAGCAGGGACGTTGCCCGCTGTTGGTCATGACAACCAAACGAGTCCGAGGGCACAGCC 421 AGGTGTCTTCCACCAGCCCATGAGCTGAGAATGCTAAGTCACCAGACAACCAGAAATTGA 481 GTCTCTGTCAGGATCCTTTTGAAGTGTAAGGAGAGAGAAACTTACACTTTGAAAGGTTTT 541 GAGCCTCATCCAGGACAATAAAAATAACTGT	SEQ ID NO:236
BM734632	Homo sapiens AT rich interactive domain 5A (MRF1-like), mRNA (cDNA clone MGC:75508 IMAGE:30409017)	1 cggacagccg cgcgctgagg gtctcggggc gggcgccgcg ggacctctcc gggccatggc 61 agccccctgtc aaagggaaca ggaagcagtc cacggagggt gacgcctag acccacctgc 121 atcccccaaa cctgctggca agcagaacgg aatccagaac cccatctcgc tggagttaac 181 ctgtggaaga tctacaaagc agtggagaag ctgggggcct atgagctggt gaccgggcgc 241 cgcctctgga agaacgtgta cgacgagctg gggggcagcc caggcagcac cagcgcggcc 301 acgtgcacgc gccgccacta cgaggagctg gtcctgccat acgtgcggca cctgaagggg 361 gaggatgaca agccgctgcc cacctccaag cccaggaaac agtacaagat ggctaaggag 421 aacagggggg atgatgcggc caccgagagg ccgaagaagg ccaaggagga gcggcgcatg 481 gaccagatga tgccaggaaa gaccaaagca gatgctgctg accagcacc acttcccagc 541 caggagcccc ccaggaacag cacagaacag cagggcctgg cctctgggtc ttctgtgtcc 601 ttgtgggtg ccagcggctg tcctgaggcc tacaagcggc tcctatccag cttctactgc 661 aaggggacac acggcatcat gtcaccactg gccaaaaaga agctcctggc ccaggtgagc 721 aagtggagg cctgcagtg ccaggaggag ggctgccgcc atgggcaga gccccaggcg 781 tcccagctg ttcacctccc agagagtccc cagagcccca aagggctgac tgagaactcc 841 aggcaccggc tgaccctca ggagggattg caggccccag gtggcagcct cagaggagag 901 gcgcaggcag gcccctgccc ggcagccccc atcttcaagg gtgcttcta cacccacccc 961 accgaggtgc tgaagcctgt cagccagcac cccagggact tcttctctag acttaaagat 1021 gggtgctat tgggcctcc tggcaaagag gggctgtcag tgaaagagcc ccagctggtg 1081 tgggcggag acgctaaccg ccttctgcg ttccataaag gtggctccag aaagggcatc	SEQ ID NO:237

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1141 ctctacccca agcccaaagc ctgctgggtg tccccatgg ccaaggtccc agccgagagc 1201 cccacgctcc cgcccacctt ccccagtagc ccaggcctgg gcagcaagcg cagcctggag 1261 gaagagggtg ctgcccacag tgggaagaga ctgcgggccg tgtctccctt tcttaaggag 1321 gcggatgcca agaagtgtgg ggccaaacct gcagggtccg gcctggtctc ctgcttctg 1381 ggcccagccc tggggcctgt gccccagag gcctacaggg gcaccatgct gcactgcccg 1441 ctgaacttca ctggcacccc gggcccctg aaggccagg ctgcactccc cttcagcccc 1501 ctggtcatcc cggccttccc ggcccacttc ctggccaccg caggcccctc gcccatggcc 1561 gctggcctga tgcacttccc cccaacgtcc ttcgacagtg ccctccgcca cagactttgc 1621 ccggcctcat ctgcctggca cgcaccacca gtcacaacct atgcagcgcc ccacttcttc 1681 cacctcaaca ccaagctgta ggccagccca tggtgttgtg tacactgtgg agtcgacagg 1741 ggcctacaac aggcaggtac tgctgccagg gggctctgaa ctagtgcctg ctacccagga 1801 cacccgggcc atgcccctgg ctgggcagcc tggcacaagt gaagaagaag gcagtgggaa 1861 aactgggttt atctcaaggc agcagcctga gcccaggagc agaggaccca gttgttataa 1921 ggcgctggga gaggatgggc agctcccact gccccagagc ggagctcgaa gcacccaggt 1981 tgcccacgga aaatccaata aaaagacacc agtgtgaatc caaaaaaaaa aaaaaaaaaa 2041 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2101 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1 M A K E N R G D D G A T E R P K K A K E 1 ATGGCTAAGGAGAACAGGGGGGATGATGGGGCCACCGAGAGGCCGAAGAAGGCCAAGGAG 21 E R R M D Q M M P G K T K A D A A D P A 61 GAGCGGCGCATGGACCAGATGATGCCAGGAAGACCAAAGCAGATGCTGCTGACCCAGCA 41 P L P S Q E P P R N S T E Q Q G L A S G 121 CCACTTCCCAGCCAGGAGCCCCCCAGGAACACAGCAGAACACAGGGCCTGGCCTTGGG 61 S S V S F V G A S G C P E A Y K R L L S 181 TCTTCTGTGTCCTTTGTGGGTGCCAGCGGCTGTCCTGAGGCCTACAAGCGGCTCCTATCC 81 S F Y C K G T H G I M S P L A K K K L L 241 AGCTTCTACTGCAAGGGGACACACGGCATCATGTCACCACTGGCCAAAAAGAAGCTCCTG 101 A Q V S K V E A L Q C Q E E G C R H G A 301 GCCCAGGTGAGCAAGGTGGAGGCCTTGCAGTGCCAGGAGGAGGGCTGCCGCCATGGGCA 121 E P Q A S P A V H L P E S P Q S P K G L 361 GAGCCCCAGGCGTCCCCAGCTGTTCACCTCCCAGAGAGTCCCCAGAGCCCCAAAGGCTG 141 T E N S R H R L T P Q E G L Q A P G G S 421 ACTGAGAACTCCAGGCACCGGCTGACCCCTCAGGAGGGATTGCAGGCCCCAGGTGGCAGC 161 L R E E A Q A G P C P A A P I F K G C F	SEQ ID NO:238

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		481 CTCAGAGAGGAGGCGCAGGCAGGCCCCTGCCCGGCAGCCCCCATCTTCAAGGGCTGCTTC	
		181 Y T H P T E V L K P V S Q H P R D F F S	
		541 TACACCCACCCCACCGAGGTGCTGAAGCCTGTCAGCCAGCACCCCAGGGACTTCTTCTCT	
		201 R L K D G V L L G P P G K E G L S V K E	
		601 AGACTTAAAGATGGGGTGCTATTGGGGCCTCCTGGCAAAGAGGGGCTGTCAGTGAAAGAG	
		221 P Q L V W G G D A N R P S A F H K G G S	
		661 CCCCAGCTGGTGTGGGCGGAGACGCTAACCGCCCTTCTGCGTTCCATAAAGGTGGCTCC	
		241 R K G I L Y P K P K A C W V S P M A K V	
		721 AGAAAGGGCATCCTCTACCCCAAGCCCAAAGCCTGCTGGGTGTCCCCCATGGCCAAGGTC	
		261 P A E S P T L P P T F P S S P G L G S K	
		781 CCAGCCGAGAGCCCCACGCTCCCGCCCACCTTCCCCAGTAGCCCAGGCCTGGGCAGCAAG	
		281 R S L E E E G A A H S G K R L R A V S P	
		841 CGCAGCCTGGAGGAAGAGGGTGCTGCCCACAGTGGGAAGAGACTGCGGGCCGTGTCTCCC	
		301 F L K E A D A K K C G A K P A G S G L V	
		901 TTTCTTAAGGAGGCGGATGCCAAGAAGTGTGGGGCCAAACCTGCAGGGTCCGGCCTGGTC	
		321 S C L L G P A L G P V P P E A Y R G T M	
		961 TCCTGCCTTCTGGGCCCAGCCCTGGGGCCTGTGCCCCCAGAGGCCTACAGGGGCACCATG	
		341 L H C P L N F T G T P G P L K G Q A A L	
		1021 CTGCACTGCCCGCTGAACTTCACTGGCACCCCGGGCCCCTTGAAGGGCCAGGCTGCACTC	
		361 P F S P L V I P A F P A H F L A T A G P	
		1081 CCCTTCAGCCCCCTGGTCATCCCGGCCTTCCCGGCCCACTTCCTGGCCACCGCAGGCCCC	
		381 S P M A A G L M H F P P T S F D S A L R	
		1141 TCGCCCATGGCCGCTGGCCTGATGCACTTCCCCCCAACGTCCTTCGACAGTGCCCTCCGC	
		401 H R L C P A S S A W H A P P V T T Y A A	
		1201 CACAGACTTTGCCCGGCCTCATCTGCCTGGCACGCACCACCAGTCACACAACCTATGCAGCG	
		421 P H F F H L N T K L -	
		1261 CCCCACTTCTTCCACCTCAACACCAAGCTGTAG	
BM734654	No homologies	1 AGGGCGTCACGCTGACCGTGATGGTCAACACCAGCCAAACGCAGGTTTCGGAGAAGCTCG	SEQ ID NO:239

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		61 TCTACACCAACCCAGGTGGTGAGGCACCGCCGCCCAGAACTTCTCATGCTTCATCTACA 121 TCGTGCACTTCATGATCTGCACTTGGGCCCCGGCCGCGGCCCCCGACGACGTCCAGT 181 ATTTCCTGTATATACGAGACTCCAAGAAGCGGGAGAGGGAATGTCCCCGTTACATGAGCG 241 ACTCGGGGACCCACGTGGGCTGCCACCTAGACGACCTCTCGGGATTGACCTCTTACAATT 301 ACTTCGTGGTGAACGGGACCAGCCAAACGACGGGATCCAGTTCTTCGATTCCGTTATGC 361 GGTCCAAGCAAATAGAGAGGTACAGCCCGCCCGCCAACATCAGCGTGCAGGTAAAC	
BM734661	Human UbA52 adrenal mRNA for ubiquitin-52 amino acid fusion protein.	1 GACGCAGACATGCAGATCTTTGTGAAGACCCTGACGGGCAAGACCATCACCCTCGAGGTT 61 GAGCCCAGTGACACCATTGAGAATGTTAAAGCTAAAATCCAAGACAAGGAGGGCATCCCA 121 CCTGACCAGCAGCGTTTGATTTTTGCCGGCAAACAGCTGGAGGACGGCCGCACTCTCTCA 181 GACTACAATATCCAGAAAGAGTCCACCCTGCACTTGGTGCTCCGCCTGCGGGGCGGCATC 241 ATTGAGCCTTCCCTCCGCCAGCTCGCCCAGAAATACAACTGCGACAAGATGATTTGCCGC 301 AAGTGTTATGCTCGCCTGCACCCTCGTGCTGTCAACTGCCGCAAGAAGTGCGGCCAC 361 ACCAACAACCTGCGCCCCAAGAAGAAGGTCAAATAAGGTTGTTCTTTCCTTGAAGGGCAG 421 CCTCCTGCCCAGGCCCCATGGCCCTGGGGCCTCAATAAAGTTTCCCTTTCATTGACTGGA 481 AAAAAAAAAAAAAAA 1 M Q I F V K T L T G K T I T L E V E P S 1 ATGCAGATCTTTGTGAAGACCCTGACGGGCAAGACCATCACCCTCGAGGTTGAGCCCAGT 21 D T I E N V K A K I Q D K E G I P P D Q 61 GACACCATTGAGAATGTTAAAGCTAAAATCCAAGACAAGGAGGGCATCCCACCTGACCAG 41 Q R L I F A G K Q L E D G R T L S D Y N 121 CAGCGTTTGATTTTTGCCGGCAAACAGCTGGAGGACGGCCGCACTCTCTCAGACTACAAT 61 I Q K E S T L H L V L R L R G G I I E P 181 ATCCAGAAAGAGTCCACCCTGCACTTGGTGCTCCGCCTGCGGGGCGGCATCATTGAGCCT 81 S L R Q L A Q K Y N C D K M I C R K C Y 241 TCCCTCCGCCAGCTCGCCCAGAAATACAACTGCGACAAGATGATTTGCCGCAAGTGTTAT 101 A R L H P R A V N C R K K K C G H T N N 301 GCTCGCCTGCACCCTCGTGCTGTCAACTGCCGCAAGAAGAAGTGCGGCCACACCAACAAC 121 L R P K K K V K - 361 CTGCGCCCCAAGAAGAAGGTCAAATAA	SEQ ID NO:240 SEQ ID NO:241
BM734694	Human hemopoietic cell protein-tyrosine kinase (HCK) gene.	1 GAATTCCTTTCTAAAATCCAACCATTCCAGGAAATAGAAATATCAACTTGGGGCTTCCT 61 GAGAATGTCAGATTGATGGGTGCATGAAGTCCAAGTTCCTCAGGTCGGAGGCAATACA 121 TTCTCAAAAACTGAAACCAGCGCCAGCCCACACTGTCCTGTGTACGTGCCGGATCCCACA	SEQ ID NO:242

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		181 TCCACCATCAAGCCGGGGCCTAATAGCCACAACAGCAACACCAGGAATCAGGGAGGCA 241 GGCTCTGAGGACATCATCGTGGTTGCCCTGTATGATTACGAGGCCATTCACCACGAAGAC 301 CTCAGCTTCCAGAAGGGGGACCAGATGGTGGTCCTAGAGGAATCCGGGGAGTGGTGGAAG 361 GCTCGATCCCTGGCCACCCGGAAGGAGGCTACATCCCAAGCAACTATGTCGCCCGCGTT 421 GACTCTCTGGAGACAGAGGAGTGGTTTTTCAAGGGCATCAGCCGGAAGGACGCAGAGCGC 481 CAACTGCTGGCTCCCGGCAACATGCTGGGCTCCTTCATGATCCGGGATAGCCGAGACCACT 541 AAAGGAAGCTACTCTTTGTCCGTGCGAGACTACGACCCTCGGCAGGGAGATACCGTGAAA 601 CATTACAAGATCCGGACCCTGGACAACGGGGCTTCTACATATCCCCCCGAAGCACCTTC 661 AGCACTCTGCAGGAGCTGGTGGACCACTACAAGAAGGGGAACGACGGGCTCTGCCAGAAA 721 CTGTCGGTGCCCTGCATGTCTTCCAAGCCCCAGAAGCCTTGGGAGAAAGATGCCTGGGAG 781 ATCCCTCGGGAATCCCTCAAGCTGGAGAAGAAACTTGGAGCTGGCAGTTTGGGGAAGTC 841 TGGATGGCCACCTACAACAAGCACACCAAGGTGGCAGTGAAGACGATGAAGCCAGGGAGC 901 ATGTCGGTGGAGGCCTTCCTGGCAGAGGCCAACGTGATGAAAACTCTGCAGCATGACAAG 961 CTGGTCAAACTTCATGCGGTGGTCACCAAGGAGCCCATCTACATCATCACGGAGTTCATG 1021 GCCAAAGGAAGCTTGCTGGACTTTCTGAAAAGTGATGAGGGCAGCAAGCCATTGCCA 1081 AAACTCATTGACTTCTCAGCCCAGATTGCAGAAGGCATGGCCTTCATCGAGCAGAGGAAC 1141 TACATCCACCGAGACCTCCGAGCTGCCAACATCTTGGTCTCTGCATCCCTGGTGTGTAAG 1201 ATTGCTGACTTTGGCCTGGCCCGGGTCATTGAGGACAACGAGTACACGGCTCGGGAAGGG 1261 GCCAAGTTCCCCATCAAGTGGACAGCTCNTGAGGCCATCAACTTTGGCTCCTTCACCATC 1321 AAGTCGGATGTCTGGTCCTTTGGTGTCCTGCTGATGGAGATTGTCACCTATGGCAGGATC 1381 CCTTACCCAGGGATGTCGAACCCCGAGGTGATCCGAGCCCTGGAGCACGGATACAGGATG 1441 CCTCGACCAGAGCACTGCCCCGAGGAGCTTTACAACATCATGACCCGCTGCTGGAAGAAC 1501 AGCCCCGAGGAGCGGCCCACCTTCGAGTACATCCAGAGTGTGCTGGAGGACTTCTACACC 1561 GCCACCGAGAGCCAGTACCAACAGCAGCCGTGATGGGTGGGACCAGGGCAGGGCAGGGGG 1621 TGCCCAGGTGGTGGCTGCAAGGTGGCTCCAGCACCATCTGCCCCGGGGCCCACTCACCT 1681 TCCCACTCCCAGACACCCACTCTCGCTCCAGCCACAGTTCCTCATCTGTCAAGGGGGTGG 1741 GTTGGACTGGACAATCTCTTTTTGACTCTAGCAATCCACAATCTGCCATTCTCAGGAGAC 1801 CCCCAAGTTGACATTTCTATGGCCTGGGAGAGTGTGGATTCCACTCACAGCTGTGGTTTGG 1861 ATGGGAAACTTTAAAAATAATGAAATAAATATTTAAATAAAGATATAAATGCCAAAGTC 1921 TTTACC 1 M G C M K S K F L Q V G G N T F S K T E SEQ ID NO:243 1 ATGGGGTGCATGAAGTCCAAGTTCCTCCAGGTCGGAGGCAATACATTCTCAAAAACTGAA 21 T S A S P H C P V Y V P D P T S T I K P 61 ACCAGCGCCAGCCCACACTGTCCTGTGTACGTGCCGGATCCCACATCCACCATCAAGCCG 41 G P N S H N S N T P G I R E A G S E D I 121 GGGCCTAATAGCCACAACAGCAACACCAGGAATCAGGGAGGCAGGCTCTGAGGACATC 61 I V V A L Y D Y E A I H H E D L S F Q K 181 ATCGTGGTTGCCCTGTATGATTACGAGGCCATTCACCACGAAGACCTCAGCTTCCAGAAG

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		81 G D Q M V V L E E S G E W W K A R S L A 241 GGGGACCAGATGGTGGTCCTAGAGGAATCCGGGGAGTGGTGGAAGGCTCGATCCCTGGCC 101 T R K E G Y I P S N Y V A R V D S L E T 301 ACCCGGAAGGAGGGCTACATCCCAAGCAACTATGTCGCCCGCGTTGACTCTCTGGAGACA 121 E E W F F K G I S R K D A E R Q L L A P 361 GAGGAGTGGTTTTTCAAGGGCATCAGCCGAAGGACGCAGACGCCAACTGCTGGCTCCC 141 G N M L G S F M I R D S E T T K G S Y S 421 GGCAACATGCTGGGCTCCTTCATGATCCGGATAGCGAGACCACTAAAGGAAGCTACTCT 161 L S V R D Y D P R Q G D T V K H Y K I R 481 TTGTCCGTGCGAGACTACGACCCTCGGCAGGGAGATACCGTGAAACATTACAAGATCCGG 181 T L D N G G F Y I S P R S T F S T L Q E 541 ACCCTGGACAACGGGGGCTTCTACATATCCCCCGAAGCACCTTCAGCACTCTGCAGGAG 201 L V D H Y K K G N D G L C Q K L S V P C 601 CTGGTGGACCACTACAAGAAGGGGAACGACGGGCTCTGCCAGAAACTGTCGGTGCCCTGC 221 M S S K P Q K P W E K D A W E I P R E S 661 ATGTCTTCCAAGCCCCAGAAGCCTTGGGAGAAAGATGCCTGGGAGATCCCTCGGGAATCC 241 L K L E K K L G A G Q F G E V W M A T Y 721 CTCAAGCTGGAGAAGAAACTTGGAGCTGGGCAGTTTGGGGAAGTCTGGATGGCCACCTAC 261 N K H T K V A V K T M K P G S M S V E A 781 AACAAGCACACCAAGGTGGCAGTGAAGACGATGAAGCCAGGGAGCATGTCGGTGGAGGCC 281 F L A E A N V M K T L Q H D K L V K L H 841 TTCCTGGCAGAGGCCAACGTGATGAAAACTCTGCAGCATGACAAGCTGGTCAAACTTCAT 301 A V V T K E P I Y I I T E F M A K G S L 901 GCGGTGGTCACCAAGGAGCCCATCTACATCATCACGGAGTTCATGGCCAAAGGAAGCTTG 321 L D F L K S D E G S K Q P L P K L I D F 961 CTGGACTTTCTGAAAAGTGATGAGGGCAGCCAAGCAGCCATTGCCAAAACTCATTGACTTC 341 S A Q I A E G M A F I E Q R N Y I H R D 1021 TCAGCCCAGATTGCAGAAGGCATGGCCTTCATCGAGCAGAGGAACTACATCCACCGAGAC 361 L R A A N I L V S A S L V C K I A D F G	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1081 CTCCGAGCTGCCAACATCTTGGTCTCTGCATCCCTGGTGTGTAAGATTGCTGACTTTGGC 381 L A R V I E D N E Y T A R E G A K F P I 1141 CTGGCCCGGGTCATTGAGGACAACGAGTACACGGCTCGGGAAGGGGCCAAGTTCCCCATC 401 K W T A X E A I N F G S F T T I K S D V W 1201 AAGTGGACAGCTCNTGAGGCCATCAACTTTGGCTCCTTCACCATCAAGTCGGATGTCTGG 421 S F G V L L M E I V T Y G R I P Y P G M 1261 TCCTTTGGTGTCCTGCTGATGGAGATTGTCACCTATGGCAGGATCCCTTACCCAGGGATG 441 S N P E V I R A L E H G Y R M P R P E H 1321 TCGAACCCCGAGGTGATCCGAGCCCTGGAGCACGGATACAGGATGCCTCGACCAGAGCAC 461 C P E E L Y N I M T R C W K N S P E E R 1381 TGCCCCGAGGAGCTTTACAACATCATGACCCGCTGCTGGAAGAACAGCCCCGAGGAGCGG 481 P T F E Y I Q S V L E D F Y T A T E S Q 1441 CCCACCTTCGAGTACATCCAGAGTGTGCTGGAGGACTTCTACACCGCCACCGAGAGCCAG 501 Y Q Q Q P - 1501 TACCAACAGCAGCCGTGA	
BM734719	No Homology	1 AGTCCTCTCGATGAAGCTTCTTCCCACCTAGAAAGAAGTCCTCTCTGAGACTCAAGGGCT 61 AAGGCAAGGTCTTCCAGAAAACAAGGCTTTGACTCCAAGAACAGAGGTGATGGGAGACT 121 TCTTGGCTCGGCGGGAAAGGAGACGCCAATGGTCAAACTAACTCTGAATCCCTCCCT 181 CCATCTCTCTTTTTCCACTGTCGTCAGAGCCAACAAGAAATGACAGCCTCCAAGCCTTCC 241 TAAAAGCACACTTGCCCCCGCCTGCCACCTCTCCTCAGGCTGCTGCCCTCCCAGGCGCTC 301 CACAGCGAAGGGGTGTGGTGTTTCCTGCAGGCCAGGCCAGCTGCCTCAGCCCCGCCAAAA 361 CTGTGTTCCCAGCCCAGCGCTCTGGAGCAGGGATGACGTGTGGCCAGCCCTTCTCAGGTCT 421 CAGCTCTGCTGGGATGGGAGGAGAGGCCAGGGAGAAAGGTTAGGGGCCCAGGGGTGGGTG 481 ACAACGCTGGCTGCTGAAAGCCCATGAGCTGCTTCTTTGTTCTCTGTCACGGGACAAAAA 541 TCTCTCATCCTATTCTGCTTTCAGTTCATTAAGAGGAGCACATTTTACTCATACACAAATA 601 AAAGTTTTCCCTTGTGGAAACAACAGCTTTAAAAGAAAGG	SEQ ID NO:244
BM734722	No Homology	1 ACCGCGACTTCCAGTACGAGCTGGTCATCCAGAGACAGAGGATCGAGGTGCCGGGCGACT 61 CGCAGAATCAATACATTTTCCCGAGTCTGGAGCCCAGACCGAAGCACACGGTGAAGATCA 121 GGACGGGGGACGCCCGGGACGCCCAGGAGACCCCCGCTGGGGCGCCTGGAGCCGGCCCGTCG 181 AGTTCGGCTCCGAGGACCCGGATGCGGGGGTCGTGCACGTGTACGTGCTCGTCGTGCTGG 241 GGACCCTGGGCTGCGCGCTGGCGCTCGGCTGCCTGGTGAAGAGGTTCCTCCGGAGACACA 301 GTCTGTTCCAGCCGGTCCCGCGCATCAAAGACAAACTGAACGATAACCATCCGACCGACC	SEQ ID NO:245

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		361 TCCAGGACGTCTGGGAGGAATTCCCGGCGGGGGCCGGAAAAGCCGAGCACGAAGAGGTGG 421 TGACCGTCCAGGAGGTCGACAGAGCCCCGGTCAGCGGGTGAAAGGTCACGGGCACCTCCG 481 GCCCCCAGACACCCCGGAAGCCGCCCGGTTTTCTCAAAACCGTTTTAAGCGTTTCTGCA 541 GCTATTTTTCTACTTTTTATTAAAAAAATAAATGTGAAGTTTGGCCAAGAGGCTTCCCGA 601 CGGGGGGCCGGAAAAAGGCCCAAAGCTT	
BM734780	Homo sapiens STAT4 mRNA.	1 GCTTTCTCCTAGGGACTGTGAGGGGCGCTTCTGACTTTGGACTTGAGCACTGCCTGGGAC 61 CTGTGCTGAGAGAGCGCTAGCATGTCTCAGTGGAATCAAGTCCAACAGTTAGAAATCAAG 121 TTTTTGGAGCAGGTGGATCAATTCTATGATGACAACTTTCCCATGGAAATTCGGCATCTG 181 TTGGCCCAATGGATTGAAAATCAAGACTGGGAGGCAGCTTCTAACAATGAAACCATGGCA 241 ACGATTCTTCTTCAAAACTTGTTAATACAACTGGATGAACAGTTAGGTCGTGTTTCCAAA 301 GAGAAAAACCTACTCTTGATACACAATCTAAAAAGAATTAGGAAGGTCTTCAGGGAAAA 361 TTTCATGGAAATCCAATGCATGTAGCTGTGGTTATTTCAAACTGTTTAAGGGAAGAGAGG 421 AGAATATTGGCTGCAGCCAACATGCCTGTCCAGGGGCCTCTAGAGAAATCCTTACAAAGT 481 TCTTCAGTTTCAGAAAGACAGAGGAATGTGGAGCACAAAGTGGCTGCCATTAAAAACAGT 541 GTGCAGATGACAGAACAAGATACCAAATACTTAGAAGATCTGCAAGACGAATTTGACTAC 601 AGGTATAAAACAATTCAGACAATGGATCAGAGTGACAAGAATAGTGCCATGGTGAATCAG 661 GAAGTTTTGACACTGCAGGAAATGCTTAACAGCCTCGATTTCAGAGAAAGGAGGCTCTC 721 AGTAAAATGACCCAAATCATCCATGAGACAGACCTGTTAATGAACACCATGCTCATAGAA 781 GAGCTGCAAGACTGGAAGCGGCGGCAGCAAATCGCCTGCATCGGGGGTCCACTCCACAAT 841 GGGCTCGACCAGCTTCAGAACTGCTTTACACTATTGGCAGAAAGTCTTTTCCAACTGAGA 901 AGGCAATTGGAGAAACTAGAGGAGCAATCTACCAAAATGACATATGAAGGTGATCCCATT 961 CCAATGCAAAGAACTCACATGCTAGAAAGAGTCACCTTCTTGATCTACAACCTTTTCAAG 1021 AACTCATTTGTGGTTGAGCGACAGCCATGTATGCCAACCCACCCTCAGAGGCCGTTGGTA 1081 CTTAAAACCCTAATTCAGTTCACTGTAAAACTAAGGCTACTATATAAAATTGCCAGAACTA 1141 AACTATCAGGTAAAGTTAAGGCATCAATTGACAAGAATGTTTCAACTCTAAGCAACCGA 1201 AGATTTGTACTTTGTGGAACTAATGTCAAAGCCATGTCTATTGAAGAATCTTCCAATGGG 1261 AGTCTCTCAGTAGAATTTCGACATTTGCAACCAAAGGAAATGAAGTCCAGTGCTGGAGGT 1321 AAAGGAAATGAGGGCTGTCACATGGTGACTGAAGAACTTCATTCCATAACGTTTGAAACA 1381 CAGATCTGCCTCTATGGCCTGACCATAGATTTGGAGACCAGCTCATTGCCTGTGGTGATG 1441 ATTTCCAATGTCAGTCAGTTACCTAATGCTTGGGCATCCATCATTGGTACAACGTGTCA 1501 ACCAACGATTCCCAGAACTTGGTTTCTTTAATAATCCTCCACCTGCCACATTGAGTCAA 1561 CTACTGGAGGTGATGAGCTGGCAGTTTTCATCGTACGTTGGTCGTGGTCTTAACTCAGAT 1621 CAACTCCATATGCTGGCAGAGAAGCTTACAGTCCAATCTAGCTACAGTGATGGTCACCTC 1681 ACCTGGGCCAAGTTCTGCAAGGAACATTTACCTGGTAAATCATTTACCTTTTGGACATGG 1741 CTTGAAGCAATATTGGATCTAATTAAGAAACACATTCTTCCCCTTTGGATTGATGGTAT 1801 GTCATGGGGCTTTGTTAGCAAAGAGAAGGAACGGCTGTTGCTAAAGGATAAAATGCCTGGC 1861 ACCTTTTTATTAAGATTCAGTGAAAGCCATCTCGGAGGAATAACTTTCACCTGGGTGGAC 1921 CATTCTGAAAGTGGGGAAGTGAGATTCCACTCTGTAGAGCCCTACAATAAAGGCCGCTTG 1981 TCTGCTTTGCCGTTTGCTGACATCCTTCGAGACTACAAGGTTATTATGGCTGAAAACATT 2041 CCTGAAAACCCTCTGAAGTACCTGTATCCTGACATTCCCAAAGACAAAGCCTTCGGTAAA 2101 CACTACAGCTCCCAGCCGTGCGAAGTTTCAAGACCAACAGAAAGAGGAGACAAAGGTTAT	SEQ ID NO:246

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2161 GTTCCTTCTGTTTTTATCCCCATCTCAACAATCCGAAGCGATTCCACTGAGCCGCAGTCT 2221 CCATCAGACCTTCTTCCCATGTCTCCAAGCGTATACGCAGTGCTGAGAGAAAACCTGAGT 2281 CCCACGACCATCGAAACTGCGATGAAGTCTCCATATTCTGCCGAATGACAGGATGACCTC 2341 TTGACACTCAAAAAATGGAAGCAAATGGAAACTTTAAGGACTGATCTTTGCCAACAGTC 2401 ATCTCTTATTCTTCATCTTTGTATATACGGATTTCCAGGAAACGGTTGAAGTCTGAAGCT 2461 CTGCTCTCACTGGCATGACACTCCCAATTGGGTGTGTTGACTGAAATGTTAAACCAA 2521 AGCTTCAGATAAACTTGCAAGATAAGACACTTTAAAAAATTAGTGTTAATATAATAACAA 2581 TATTAACAG 1 M S Q W N Q V Q Q L E I K F L E Q V D Q 1 ATGTCTCAGTGGAATCAAGTCCAACAGTTAGAAATCAAGTTTTTGGAGCAGGTGGATCAA 21 F Y D D N F P M E I R H L L A Q W I E N 61 TTCTATGATGACAACTTTCCCATGGAAATTCGGCATCTGTTGGCCCAATGGATTGAAAAT 41 Q D W E A A S N N E T M A T I L L Q N L 121 CAAGACTGGGAGGCAGCTTCTAACAATGAAACCATGGCAACGATTCTTCTTCAAAACTTG 61 L I Q L D E Q L G R V S K E K N L L L I 181 TTAATACAACTGGATGAACAGTTAGGTCGTGTTTCCAAAGAGAAAAACCTACTCTTGATA 81 H N L K R I R K V L Q G K F H G N P M H 241 CACAATCTAAAAAGAATTAGGAAGGTCCTTCAGGGAAAATTTCATGGAAATCCAATGCAT 101 V A V V I S N C L R E E R R I L A A A N 301 GTAGCTGTGGTTATTTCAAACTGTTTAAGGGAAGAGAGGAGAATATTGGCTGCAGCCAAC 121 M P V Q G P L E K S L Q S S S V S E R Q 361 ATGCCTGTCCAGGGGCCTCTAGAGAAATCCTTACAAAGTTCTTCAGTTTCAGAAAGACAG 141 R N V E H K V A A I K N S V Q M T E Q D 421 AGGAATGTGGAGCACAAAGTGGCTGCCATTAAAAACAGTGTGCAGATGACAGAACAAGAT 161 T K Y L E D L Q D E F D Y R Y K T I Q T 481 ACCAAATACTTAGAAGATCTGCAAGACGAATTTGACTACAGGTATAAAACAATTCAGACA 181 M D Q S D K N S A M V N Q E V L T L Q E 541 ATGGATCAGAGTGACAAGAATAGTGCCATGGTCAATCAGGAAGTTTTGACACTGCAGGAA 201 M L N S L D F K R K E A L S K M T Q I I 601 ATGCTTAACAGCCTCGATTTCAAGAGAAAGGAGGCTCTCAGTAAAATGACCCAAATCATC 221 H E T D L L M N T M L I E E L Q D W K R	SEQ ID NO:247

Gene Name	GenBank HomoLogy	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		661 CATGAGACAGACCTGTTAATGAACACCATGCTCATAGAAGAGCTGCAAGACTGGAAGCGG	
		241 R Q Q I A C I G G P L H N G L D Q L Q N 721 CGGCAGCAAATCGCCTGCATCGGGGGTCCACTCCACAATGGGCTCGACCAGCTTCAGAAC	
		261 C F T L L A E S L F Q L R R Q L E K L E 781 TGCTTTACACTATTGGCAGAAAGTCTTTTCCAACTGAGAAGGCAATTGGAGAAACTAGAG	
		281 E Q S T K M T Y E G D P I P M Q R T H M 841 GAGCAATCTACCAAAATGACATATGAAGGTGATCCCATTCCAATGCAAGAACTCACATG	
		301 L E R V T F L I Y N L F K N S F V V E R 901 CTAGAAAGAGTCACCTTCTTGATCTACAACCTTTTCAAGAACTCATTTGTGGTTGAGCGA	
		321 Q P C M P T H P Q R P L V L K T L I Q F 961 CAGCCATGTATGCCAACCCACCCTCAGAGGCCGTTGGTACTTAAAACCCTAATTCAGTTC	
		341 T V K L R L L I K L P E L N Y Q V K V K 1021 ACTGTAAAACTAAGGCTACTAATAAAATTGCCAGAACTAAACTATCAGGTAAAGGTTAAG	
		361 A S I D K N V S T L S N R R F V L C G T 1081 GCATCAATTGACAAGAATGTTTCAACTCTAAGCAACCGAGATTTGTACTTTGTGGAACT	
		381 N V K A M S I E E S S N G S L S V E F R 1141 AATGTCAAAGCCATGTCTATTGAAGAATCTTCCAATGGGAGTCTCTCAGTAGAATTTCGA	
		401 H L Q P K E M K S S A G G K G N E G C H 1201 CATTTGCAACCAAAGGAAATGAAGTCCAGTGCTGGAGGTAAAGGAAATGAGGGCTGTCAC	
		421 M V T E E L H S I T F E T Q I C L Y G L 1261 ATGGTGACTGAAGAACTTCATTCCATAACGTTTGAAACACAGATCTGCCTCTATGGCCTG	
		441 T I D L E T S S L P V V M I S N V S Q L 1321 ACCATAGATTTGGAGACCAGCTCATTGCCTGTGGTGATGATTTCCAATGTCAGTCAGTTA	
		461 P N A W A S I I W Y N V S T N D S Q N L 1381 CCTAATGCTTGGGCATCCATCATTTGGTACAACGTGTCAACCAACGATTCCCAGAACTTG	
		481 V F F N N P P P A T L S Q L L E V M S W 1441 GTTTTCTTTAATAATCCTCCACCTGCCACATTGAGTCAACTACTGGAGGTGATGAGCTGG	
		501 Q F S S Y V G R G L N S D Q L H M L A E 1501 CAGTTTTCATCGTACGTTGGTCGTGGTCTTAACTCAGATCAACTCCATATGCTGGCAGAG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		521 K L T V Q S S Y S D G H L T W A K F C K 1561 AAGCTTACAGTCCAATCTAGCTACAGTGATGGTCACCTCACCTGGGCCAAGTTCTGCAAG	
		541 E H L P G K S F T F W T W L E A I L D L 1621 GAACATTTACCTGGTAAATCATTTACCTTTTGGACATGGCTTGAAGCAATATTGGATCTA	
		561 I K K H I L P L W I D G Y V M G F V S K 1681 ATTAAGAAACACATTCTTCCCCTTTGGATTGATGGGTATGTCATGGGCTTTGTTAGCAAA	
		581 E K E R L L L K D K M P G T F L L R F S 1741 GAGAAGGAACGGCTGTTGCTAAAGGATAAAATGCCTGGCACCTTTTTATTAAGATTCAGT	
		601 E S H L G G I T F T W V D H S E S G E V 1801 GAAAGCCATCTCGGAGGAATAACTTTCACCTGGGTGGACCATTCTGAAAGTGGGGAAGTG	
		621 R F H S V E P Y Y N K G R L S A L P F A D 1861 AGATTCCACTCTGTAGAGCCCTACAATAAAGGCCGCTTGTCTGCTTTGCCGTTTGCTGAC	
		641 I L R D Y K V I M A E N I P E N P L K Y 1921 ATCCTTCGAGACTACAAGGTTATTATGGCTGAAAACATTCCTGAAAACCCTCTGAAGTAC	
		661 L Y P D I P K D K A F G K H Y S S Q P C 1981 CTGTATCCTGACATTCCCAAAGACAAAGCCTTCGGTAAACACTACAGCTCCCAGCCGTGC	
		681 E V S R P T E R G D K G Y V P S V F I P 2041 GAAGTTTCAAGACCAACAGAAAGAGGAGACAAAGGTTATGTTCCTTCTGTTTTTATCCCC	
		701 I S T I R S D S T E P Q S P S D L L P M 2101 ATCTCAACAATCCGAAGCGATTCCACTGAGCCGCAGTCTCCATCAGACCTTCTTCCCATG	
		721 S P S V Y A V L R E N L S P T T I E T A 2161 TCTCCAAGCGTATACGCAGTGCTGAGAGAAAACCTGAGTCCCACGACCATCGAAACTGCG	
		741 M K S P Y S A E - 2221 ATGAAGTCTCCATATTCTGCCGAATGA	
BM734795	Homo sapiens granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine	1 cagatttcca ggttgattga tgtgggacag cagccacaat gaggaactcc tatagatttc 61 tggcatcctc tctctcagtt gtcgtttctc tcctgctaat tcctgaagat gtctgtgaaa 121 aaattattgg aggaatgaa gtaactcctc attcaagacc ctacatggtc ctacttagtc 181 ttgacagaaa aaccatctgt gctgggctt tgattgcaaa agactgggtg ttgactgcag 241 ctcactgtaa cttgaacaaa aggtcccagg tcattcttgg ggctcactca ataccaggg	SEQ ID NO:248

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
	esterase 3) (GZMA)	301 aagagccaac aaaacagata atgcttgtta agaaagagtt tccctatcca tgctatgacc 361 cagccacacg cgaaggtgac cttaaacttt tacagctgac ggaaaaagca aaaattaaca 421 aatatgtgac tatccttcat ctacctaaaa aggggatga tgtgaaacca ggaaccatgt 481 gccaagttgc agggtggggg aggactcaca atagtgcatc ttggtccgat actctgagag 541 aagtcaatat caccatcata gacagaaaag tctgcaatga tcgaaatcac tataatttta 601 accctgtgat tggaatgaat atggtttgtg ctggaagcct ccgaggtgga agagactcgt 661 gcaatggaga ttctggaagc cctttgttgt gcgagggtgt tttccgaggg gtcacttcct 721 ttggccttga aaataaatgc ggagaccctc gtgggcctgg tgtctatatt cttctctcaa 781 agaaacacct caactggata attatgacta tcaagggagc agtttaaata accgtttcct 841 ttcatttact gtggcttctt aatctttcca caaataaa 1 M R N S Y R F L A S S L S V V V S L L L 1 ATGAGGAACTCCTATAGATTTCTGGCATCCTCTTCTCAGTTGTCGTTTCTCTCCTGCTA 21 I P E D V C E K I I G G N E V T P H S R 61 ATTCCTGAAGATGTCTGTGAAAAAATTATTGGAGGAAATGAAGTAACTCCTCATTCAAGA 41 P Y M V L L S L D R K T I C A G A L I A 121 CCCTACATGGTCCTACTTAGTCTTGACAGAAAAACCATCTGTGCTGGGGCTTTGATTGCA 61 K D W V L T A A H C N L N K R S Q V I L 181 AAAGACTGGGTGTTGACTGCAGCTCACTGTAACTTGAACAAAAGGTCCCAGGTCATTCTT 81 G A H S I T T R E E P T K Q I M L V K K E 241 GGGGCTCACTCAATAACCAGGGAAGAGCCACACAAAACAGATAATGCTTGTTAGAAAGAG 101 F P Y P C Y D P A T R E G D L K L L Q L 301 TTTCCCTATCCATGCTATGACCCAGCCACACGCGAAGGTGACCTTAAACTTTTACAGCTG 121 T E K A K I N K Y V T I L H L P K K G D 361 ACGGAAAAAGCAAAAATTAACAAATATGTGACTATCCTTCATCTACCTAAAAAGGGGGAT 141 D V K P G T M C Q V A G W G R T H N S A 421 GATGTGAAACCAGGAACCATGTGCCAAGTTGCCAGGGTGGGGGAGGACTCACACAATAGTGCA 161 S W S D T L R E V N I T I I D R K V C N 481 TCTTGGTCCGATACTCTGAGAGAAGTCAATATCACCATCATAGACAGAAAAGTCTGCAAT 181 D R N H Y N F N P V I G M N M V C A G S 541 GATCGAAATCACTATAATTTTAACCCTGTGATTGGAATGAATATGGTTTGTGCTGGAAGC 201 L R G G R D S C N G D S G S P L L C E G 601 CTCCGAGGTGGAAGAGACTCGTGCAATGGAGATTCTGGAAGCCCTTTGTTGTGCGAGGGT	SEQ ID NO:249

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		221 V F R G V T S F G L E N K C G D P R G P 661 GTTTTCCGAGGGGTCACTTCCTTGGCCTTGAAAATAAATGCGGAGACCCTCGTGGCCT 241 G V Y I L L S K K H L N W I I M T I K G 721 GGTGTCTATATTCTTCTCTCAAGAAACACCTCAACTGGATAATTATGACTATCAAGGGA 261 A V - 781 GCAGTTTAA	
BM734844	Homo sapiens phosphate cytidylyltransfera se 1, choline, alpha isoform, mRNA (cDNA clone MGC:49915 IMAGE:5744747),	1 cccgggcgtc tccccgcaac ctcctcaact tccctagtca gtgacgcggc gccggccaga 61 aatccgaccg gaccgggctc ggggagcgt gagttgcagc atgtgccgaa gcgccacctc 121 agaagataaa aagaaatgag tctcatattt ggcattcttt tagttaaaag aagatggatg 181 cacagtgttc agccaaggtc aatgcaagga agaggagaaa agaggcgccc ggaccaacg 241 gggcaacaga agaagatggg gttccttcca aagtgcagcg ctgtgcagtg ggcttacggc 301 aaccagctcc ttttctgat gaaattgaag ttgactttag taagccctat gtcaggctaa 361 ctatggaaga agccagcaga ggaactcctt gtgagcgacc tgtgagagtt tatgccgatg 421 gaatatttga cttatttcac tctggtcacg ccgagctct gatgcaagcg aagaaccttt 481 tccctaatac gtacctcatt gtgggagttt gcagtgatga gctcacacac aacttcaaag 541 gcttcacggt gatgaacgag aatgagcgct atgacgcagt ccagcactgc cgctacgtgg 601 atgaggtggt gaggaatgcg cctggacgc tgacacccga gttcctggcc gaacaccgga 661 ttgattttgt agcccatgat gatattcctt attcatctgc tggcagtgat gatgtttata 721 agcatcaaa ggaggcaggc atgtttgctc caacacagag gacagaaggt atctccacat 781 cagacatcat caccgaatt gtgcgggatt atgatgtgta tgcgaggcgg aacctgcaga 841 gggctacac agcaaaggag ctcaatgtca gctttatcaa cgagaagaaa taccacttgc 901 aggagagggt tgacaaagta aagaagaaag tgaaagatgt ggaggaaaag tcaaaagaat 961 ttgttcagaa ggtggaggaa aaaagcattg acctcattca gaagtgggag gagaagtccc 1021 gagaattcat tggaagtttt ctggaaatgt ttggtccgga aggagcactg aaacatatgc 1081 tgaaagaggg gaagggccgg atgctgcagg ccatcagccc gaagcagagc cccagcagca 1141 gccctactcg cgagcgctcc ccctcccct ctttccgatg gccttctccc ggcaagactt 1201 ccccaccttg ctccccagca aatctctcca ggcacaaggc tgcagcctat gatatcagtg 1261 aggatgaaga agactaatgt ttcctccctc ctttcctgtc ctccctttct gtcccattac 1321 cttcagaagc tcttgttga attccaaatt gtgacccaa cactaaacct aaggacagct 1381 acaaaggaaa gacaactggg gaaagaagac ctaggactgg gggaacccaa acagcctgtc 1441 ctgcaagtga catcactcac ccacacgaag gaggggact gcaccttaga agcctgctct 1501 gcatccattt acccccccc aagggcttg tttcactgtt tatgttcacg tgatctcaac 1561 agggaattg tcatttttctt taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1621 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1 M D A Q C S A K V N A R K R R K E A P G 1 ATGGATGCACAGTGTTCAGCCAAGGTCAATGCAAGGAAGAGGAGAAAAGAGGCGCCCGGA	SEQ ID NO:250 SEQ ID NO:251

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		21 P N G A T E E D G V P S K V Q R C A V G 61 CCCAACGGGGCAACAGAAGAAGATGGGGGTTCCTTCCAAAGTGCAGCGCTGTGCAGTGGGC 41 L R Q P A P F S D E I E V D F S K P Y V 121 TTACGGCAACCAGCTCCTTTTTCTGATGAAATTGAAGTTGACTTTAGTAAGCCCTATGTC 61 R V T M E E A S R G T P C E R P V R V Y 181 AGGGTAACTATGGAAGAAGCCAGCAGAGGAACTCCTTGTGAGCGACCTGTGAGAGTTTAT 81 A D G I F D L F H S G H A R A L M Q A K 241 GCCGATGGAATATTTGACTTATTTCACTCTGGTCACGCCCGAGCTCTGATGCAAGCGAAG 101 N L F P N T Y L I V G V C S D E L T H N 301 AACCTTTTCCCTAATACGTACCTCATTGTGGGAGTTTGCAGTGATGAGCTCACACACAAC 121 F K G F T V M N E N E R Y D A V Q H C R 361 TTCAAAGGCTTCACGGTGATGAACGAGAATGAGCGCTATGACGCAGTCCAGCACTGCCGC 141 Y V D E V V R N A P W T L T P E F L A E 421 TACGTGGATGAGGTGGTGAGGAATGCGCCCTGGACGCTGACACCCGAGTTCCTGGCCGAA 161 H R I D F V A H D D I P Y S S A G S D D 481 CACCGGATTGATTTTGTAGCCCATGATGATATTCCTTATTCATCTGCTGGCAGTGATGAT 181 V Y K H I K E A G M F A P T Q R T E G I 541 GTTTATAAGCACATCAAGGAGGCAGGCATGTTTGCTCCAACACAGAGGACAGAAGGTATC 201 S T S D I I T R I V R D Y D V Y A R R N 601 TCCACATCAGACATCATCACCCGAATTGTGCGGGATTATGATGTGTATGCGAGGCGGAAC 221 L Q R G Y T A K E L N V S F I N E K K Y 661 CTGCAGAGGGGCTACACAGCAAAGGAGCTCAATGTCAGCTTTATCAACGAGAAGAAATAC 241 H L Q E R V D K V K K K V K D V E E K S 721 CACTTGCAGGAGAGGGTTGACAAAGTAAAGAAGAAAGTGAAAGATGTGGAGGAAAAGTCA 261 K E E F V Q K V E E K S I D L I Q K W E E 781 AAAGAATTTGTTCAGAAGGTGGAGGAAAAAAGCATTGACCTCATTCAGAAGTGGGAGGAG 281 K S R E E F I G S F L E M F G P E G A L K 841 AAGTCCCGAGAATTCATTGGAAGTTTTCTGGAAATGTTTGGTCCGAAGGAGCACTGAAA 301 H M L K E G K G R M L Q A I S P K Q S P	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		901 CATATGCTGAAAGAGGGAAGGGCCGGATGCTGCAGGCCATCAGCCCGAAGCAGAGCCCC	
		321 S S S P T T R E R S P S P S F R W P F S G	
		961 AGCAGCAGCCCTACTCGCGAGCGCTCCCCCTCCCCCTCTTTCCGATGGCCCTTCTCCGGC	
		341 K T S P P C S P P A N L S R H K A A A Y D	
		1021 AAGACTTCCCCACCTTGCTCCCCAGCAAATCTCTCCAGGCACAAGGCTGCAGCCTATGAT	
		361 I S E D E E D -	
		1081 ATCAGTGAGGATGAAGAAGACTAA	
BM734862	Homo sapiens triggering receptor expressed on myeloid cells 1, mRNA.	1 GTCCCGGGAGCCCTCAGCAGCAGTTGGAGCTGTGTGCACAGGAAGGATGAGGAAGACCAGG	SEQ ID NO:252
		61 CTCTGGGGGCTGCTGTGGATGCTCTTTGTCTCAGAACTCCGAGCTGCAACTAAATTAACT	
		121 GAGGAAAAGTATGAACTGAAAGAGGGCAGACCCTGGATGTGAAATGTGACTACACGCTA	
		181 GAGAAGTTTGCCAGCAGCCAGAAAGCTTGGCAGATAATAAGGGACGGAGAGATGCCCAAG	
		241 ACCCTGGCATGCACAGAGAGGCCTTCAAAGAATTCCCATCCAGTCCAAGTGGGGAGGATC	
		301 ATACTAGAAGACTACCATGATCATGGTTTACTGCGCGTCCGAATGGTCAACCTTCAAGTG	
		361 GAAGATTCTGGACTGTATCAGTGTGTGATCTACCAGCCTCCCAAGGAGCCTCACATGCTG	
		421 TTCGATCGCATCCGCTTGGTGGTGACCAAGGGTTTTTCAGGGACCCCTGGCTCCAATGAG	
		481 AATTCTACCCAGAATGTGTATAAGATTCCTCCTACCACCACTAAGGCCTTGTGCCCACTC	
		541 TATACCAGCCCCCAGAACTGTGACCCAACCCCCACCCCAAGTCAACTGCCGGTGTCTCCCGC	
		601 CCTGGACTTGAAGTCAACCCCACACATGTGACACAGACGTCACCAGGATCTCTGTGTTCAGC	
		661 ATTGTCATTCCTGTGGCGTGCGCACTCGTGACTAAGAGCCTGGTCCTTACTGTCCTGTTT	
		721 GCTGTCACACAGAAGTCATTTGGATCCTAGGCCCATGGACCCATGAGGATGACCTCTGAT	
		781 CTCCATCTACATCCATCTGGCAGTTGTGCCAAGGGAGGAGGGAGGTAAAAGGCAGGG	
		841 AGTTAATAACATGAATTAAATCTGTAATCACCGCCAAAAAAAAAAAAAAAAAAAAAA	
		901 AAAAA	
		1 M R K T T R L W G L L W M L F V S E L R A	SEQ ID NO:253
		1 ATGAGGAAGACCAGGCTCTGGGGGCTGCTGTGGATGCTCTTTGTCTCAGAACTCCGAGCT	
		21 A T K L T E E K 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	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		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 GCCTTGTGCCCACTCTATACCAGCCCCAGAACTGTGACCCAACCCCACCCAAGTCAACT 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	SEQ ID NO:254
BM734891	No Homology	1 AACGAAGTCATGTTCCTGGCCCCACTGGTATTCTCAGCTTCGTATGCTGCAGTACCTGTG 61 GACAAACACAGGTGGAGAGGTGTCCAGGGTGGGGCTGGGGAAGGATCCTCCTTCTGGACT 121 TGTTTCCTGTCAGACCCCCAAGCCCCTTAGACCCAAAGCCAGAGGAGCTTGCCACTGCCT 181 TTGGGATATAGGGACTGCAGCCTTTGTTCTGTGTTCCCCAGAATTTGGGTGACTTTTGG 241 TTACCTGGGCACACTCCCTTGTGGCCATAATGGGTCCCTTCAGTCAGTGGCATGGACAT 301 CTGGATGTCCGCACCTCTCTAGAACCTCAGGCCAGCGAGATCAGCAAGGCCTTTTCTCTC 361 TATGTCCAGAAGTCAGTCAAGAGCTGCTTGACCTGAATGTGTTACAAGGATTGGGATAGG 421 GCAGAGGGAAGTCTGGGGTCACATCCTGAGCTGGGGCGGCCCTCCTTCCCTCTGCCCTG 481 GAGTGGTCTCTGCATGGGCAGCAACCCACCTGGTGGGCTGCCAGTTTTAGCTGGGATGG 541 TCAATGTGCATGTTTCAGACCTTCTGCTCTCTCTGGAATGGGTAGTGTTGGATCTCAGCC 601 ACCCATCAGACTGTGTCCGGCATTCTTTGCAATAAATACTT	SEQ ID NO:255
BM734900	Homo sapiens matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase), mRNA (cDNA clone	1 tcaccatgag cctctggcag cccctggtcc tggtgctcct ggtgctgggc tgctgctttg 61 ctgcccccag acagcgccag tccacccttg tgctcttccc tggagacctg agaaccaatc 121 tcaccgacag gcagctggca gaggaatacc tgtaccgcta tggttacact cgggtggcag 181 agatgcgtgg agagtcgaaa tctctggggc ctgcgctgct gcttctccag aagcaactgt 241 ccctgcccga gaccggtgag ctggatagcg ccacgctgaa ggccatgcga acccacggt 301 gcgggtccc agacctgggc agattccaaa cctttgaggg cgacctcaag tggcaccacc 361 acaacatcac ctattggatc caaaactact cggaagactt gccgcgggcg gtgattgacg	SEQ ID NO:255

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
	MGC:12688 IMAGE:4054882)	421 acgcctttgc ccgcgccttc gcactgtgga gcgcggtgac gccgctcacc ttcactcgcg 481 tgtacagccg ggacgcagac atcgtcatcc agtttggtgt cgcggagcac ggagacgggt 541 atcccttcga cgggaaggac gggctcctgg cacacgcctt tcctcctggc ccggcattc 601 agggagacgc ccatttcgac gatgacgagt tgtggtccct gggcaagggc gtcgtggttc 661 caactcggtt tggaaacgca gatggcgcgg cctgccactt cacctttcatc ttcgagggcc 721 gctcctactc tgcctgcacc accgacggtc gctccgacgg cttgccctgg tgcagtacca 781 cggccaacta cgacaccgac gaccggtttg gcttctgccc cagcgagaga ctctacaccc 841 gggacggcaa tgctgatggg aaaccctgcc agtttccatt catcttccaa ggccaatcct 901 actccgcctg caccacggac ggtcgctccg acggctaccg ctggtgcgcc accaccgcca 961 actacgaccg ggacaagctc ttcggcttct gcccgacccg agctgactcg acggtgatgg 1021 ggggcaactc ggcgggggag ctgtgcgtct tcccttcac tttcctgggt aaggagtact 1081 cgacctgtac cagcgagggc cgcggagatg ggcgcctctg gtgcgctacc acctcgaact 1141 ttgacagcga caagaagtgg ggcttctgcc cggaccaagg atacagtttg ttcctcgtgg 1201 cggcgcatga gttcggccac gcgctgggct tagatcattc ctcagtgccg gaggcgctca 1261 tgtacctat gtaccgcttc actgaggggc ccccttgca taaggacgac gtgaatggca 1321 tccggcacct ctatggtcct cgccctgaac ctgagccacg gcctccaacc accaccacac 1381 cgcagcccac ggctccccg acggtctgcc ccaccggacc ccccactgtc caccctcag 1441 agcgccccac agctggcccc acaggtcccc cctcagctgg ccccacaggt ccccccactg 1501 ctggccttc tacggccact actgtgcctt tgagtccggt ggacgatgcc tgcaacgtga 1561 acatcttcga cgccatcgcg gagattggga accagctgta tttgttcaag gatgggaagt 1621 actggcgatt ctctgagggc aggggagcc ggccgcaggg ccccttcctt atcgccgaca 1681 agtggcccgc gctgccccgc aagctggact cggtctttga ggagccgctc tccaagaagc 1741 tttcttctct ctctgggcgc caggtgtggg tgtacacagg cgcgtcggtg ctgggcccga 1801 ggcgtctgga caagctgggc ctgggagccg acgtggccca ggtgaccggg gccctccgga 1861 gtggcagggg gaagatgctg ctgttcagcg ggcggcgcct ctggaggttc gacgtgaagg 1921 cgcagatggt ggatccccgg agcgccagcg aggtggaccg gatgttcccc gggtgcctt 1981 tggacacgca cgacgtcttc cagtaccgag agaaagccta tttctgccag gaccgcttct 2041 actggcgcgt gagttcccgg agtgagttga accaggtgga ccaagtgggc tacgtgacct 2101 atgacatcct gcagtgccct gaggactagg gctcccgtcc tgctttggca gtgccatgta 2161 aatcccact gggaccaacc ctgggaagg agccagtttg ccggatacaa actggtattc 2221 tgttctggag gaaagggagg agtggaggtg ggctgggccc tctcttctca cctttgtttt 2281 ttgttggagt gtttctaata aacttggatt ctctaacctt taaaaaaaaa aaaaaaaaaa 2341 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1 M S L W Q P L V L V L L V L G C C F A A 1 ATGAGCCTCTGGCAGCCCCTGGTCCTGGTGCTCCTGGTGCTGGCTGCTTTGCTGCC 21 P R Q R Q S T L V L F P G D L R T N L T 61 CCCAGACAGCGCCAGTCCACCCTTGTGCTCTTCCCTGGAGACCTGAGAACCAATCTCACC 41 D R Q L A E E Y Y L Y R Y G Y T R V A E M 121 GACAGGCAGCTGGCAGAGGAATACCTGTACCGCTATGGTTACACTCGGGTGGCAGAGATG	SEQ ID NO:256

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		61 R G E S K S L G P A L L L L Q K Q L S L 181 CGTGGAGAGTCGAAATCTCTGGGGCCTGCGCTGCTTCTCCAGAAGCAACTGTCCCTG	
		81 P E T G E L D S A T L K A M R T P R C G 241 CCCGAGACCGGTGAGCTGGATAGCGCCACGCTGAAGGCCATGCGAACCCCACGGTGCGGG	
		101 V P D L G R F Q T F E G D L K W H H H N 301 GTCCCAGACCTGGGCAGATTCCAAACCTTTGAGGGCGACCTCAAGTGGCACCACCACAAC	
		121 I T Y W I Q N Y S E D L P R A V I D D A 361 ATCACCTATTGGATCCAAAACTACTCGGAAGACTTGCCGCGGGCGGTGATTGACGACGCC	
		141 F A R A F A L W S A V T P L T F T R V Y 421 TTTGCCCGCGCCTTCGCACTGTGGAGCGCGGTGACGCCGCTCACCTTCACTCGCGTGTAC	
		161 S R D A D I V I Q F G V A E H G D G Y P 481 AGCCGGGACGCAGACATCGTCATCCAGTTTGGTGTCGCGGAGCACGGAGACGGGTATCCC	
		181 F D G K D G L L A H A F P P G P G I Q G 541 TTCGACGGGAAGGACGGGCTCCTGGCACACGCCTTTCCTCCTGGCCCCGGCATTCAGGGA	
		201 D A H F D D D E L W S L G K G V V V P T 601 GACGCCCATTTCGACGATGACGAGTTGTGGTCCCTGGGCAAGGGCGTCGTGGTTCCAACT	
		221 R F G N A D G A A C H F P F I F E G R S 661 CGGTTTGGAAACGCAGATGGCGCGGCCTGCCACTTCCCCTTCATCTTCGAGGGCCGCTCC	
		241 Y S A C T T D G R S D D G L P W C S T T A 721 TACTCTGCCTGCACCACCGACGGTCGCTCCGACGGCTTGCCCTGGTGCAGTACCACGGCC	
		261 N Y D T D D R F G F C P S E R L Y T R D 781 AACTACGACACCGACGACCGGTTTGGCTTCTGCCCCAGCGAGAGACTCTACACCCGGGAC	
		281 G N A D G K P C Q F P F I F Q G Q S Y S 841 GGCAATGCTGATGGGAAACCCTGCCAGTTTCCATTCATCTTCCAAGGCCAATCCTACTCC	
		301 A C T T D G R S D G Y R W C A T T A N Y 901 GCCTGCACCACGGACGGTCGCTCCGACGGCTACCGCTGGTGCGCCACCACCGCCAACTAC	
		321 D R D K L F G F C P T R A D S T V M G G 961 GACCGGGACAAGCTCTTCGGCTTCTGCCCGACCCGAGCTGACTCGACGGTGATGGGGGC	
		341 N S A G E L C V F P F T F L G K E Y S T	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1021 AACTCGGCGGGGGAGCTGTGCGTCTTCCCCTTCACTTTCCTGGGTAAGGAGTACTCGACC	
		361 C T T S E G R G D G R L W C A T T S N F D	
		1081 TGTACCAGCGAGGGCCGCGGAGATGGGCGCCTCTGGTGCGCTACCACCTCGAACTTTGAC	
		381 S D K K W G F C P D Q G G Y S L F L V A A	
		1141 AGCGACAAGAAGTGGGGCTTCTGCCCGGACCAAGGATACAGTTTGTTCCTCGTGGCGGCG	
		401 H E F G H A L G L D H S S V P E A L M Y	
		1201 CATGAGTTCGGCCACGCGCTGGGCTTAGATCATTCCTCAGTGCCGGAGGCGCTCATGTAC	
		421 P M Y R F T E G P P L H K D D V N G I R	
		1261 CCTATGTACCGCTTCACTGAGGGCCCCCCTTGCATAAGGACGACGTGAATGGCATCCGG	
		441 H L Y G P R P E E P P R P P T T T T P Q	
		1321 CACCTCTATGGTCCTCGCCCTGAACCTGAGCCACGGCCTCCAACCACACCACACCGCAG	
		461 P T A P P T V C P T G P P T V H P S E R	
		1381 CCCACGGCTCCCCCCGACGGTCTGCCCCACCGGACCCCCCCACTGTCCACCCCTCAGAGCGC	
		481 P T A G P T G P P S A G P P T G P P P T A G	
		1441 CCCACAGCTGGCCCCACAGGTCCCCCCTCAGCTGGCCCCACAGGTCCCCCCCACTGCTGGC	
		501 P S T A T T V P L S P V D D A C N V N N I	
		1501 CCTTCTACGGCCACTACTGTGCCTTTGAGTCCGGTGGACGATGCCTGCAACGTGAACATC	
		521 F D A I A E I G N Q L Y L F K D G K Y W	
		1561 TTCGACGCCATCGCGGAGATTGGGAACCAGCTGTATTTGTTCAAGGATGGGGAAGTACTGG	
		541 R F S E G R G S R P P Q G P F L I A D K W	
		1621 CGATTCTCTGAGGGCAGGGGGAGCCGGCCGCAGGGCCCCTTCCTTATCGCCGACAAGTGG	
		561 P A L P R K L D S V F E E P L S K K L F	
		1681 CCCGCGCTGCCCCGCAAGCTGGACTCGGTCTTTGAGGAGCCGCTCTCCAAGAAGCTTTTC	
		581 F F S G R Q V W V Y T G A S V L G P R R	
		1741 TTCTTCTCTGGGCGCCAGGTGTGGGTGTACACAGGCGCGTCGGTGCTGGGCCCGAGGCGT	
		601 L D K L G L G A D V A Q V T G A L R S G	
		1801 CTGGACAAGCTGGGCCTGGGAGCCGACGTGGCCCAGGTGACCGGGGCCCTCCGGAGTGGC	
		621 R G K M L L F S G R R L W R F D V K A Q	
		1861 AGGGGGAAGATGCTGCTGTTCAGCGGCGGCGCCTCTGGAGGTTCGACGTGAAGGCGCAG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		641 M V D P R S A S E V D D R M F P G V P L D 1921 ATGGTGGATCCCCGGAGCGCCAGCGAGGTGGACCGGATGTTCCCCGGGGTGCCTTTGGAC 661 T H D V F Q Y Y R E E K A Y F C Q D R F Y W 1981 ACGCACGACGTCTTCCAGTACCGAGAGAAAGCCTATTTCTGCCAGGACCGCTTCTACTGG 681 R V S S R S E L N Q V D D Q V G Y Y V T Y D 2041 CGCGTGAGTTCCCGGAGTGAGTTGAACCAGGTGGACCAAGTGGGCTACGTGACCTATGAC 701 I L Q C P E D - 2101 ATCCTGCAGTGCCCTGAGGACTAG	
BM734933	Homo sapiens S100 calcium binding protein P, mRNA.	1 GCCTTATAAAGCACCAAGAGGCTGCCATGGGACATTTCCTCGGCCACGCCAGCCCCCAGC 61 AGGAAGGTGGGTCCACGCCAGCCCCCAGCAGGAAGGTGGGTCCAAATCCAGCACCATGAC 121 GGAACTGGAGACAGCCATGAGCATGATCATCGACGTCTTTGCCCGGTACTCGGGTGCCGA 181 GGGCAGCAAGCAGAGCCTGACCAAGGGGGAGCTGAAGACGCTCATGGAGAAGGAGCTCCC 241 GGGCTTCCTGCAGACCGGAAGGACAAGGGTGCCGTGGACAAACTGCTCAAGGACCTGGA 301 CGCCAACGGAGACGCCGAGGTGGACTTCAGCGAGTTCATCGTGTTTGTGGCCGCGCTCAC 361 GTCTACCTGCCACAAGTACTTTGAGAAGGCAGGACTCAAATGATGCCCTGGAGATGTCAC 421 AGATTCCTGGCAGAGCCATGGTCCCAGGCTTCCCAAAAGTGTTTGTGGCAATTATTCCCC 481 TAGGCTGAGCCTGCTCATGTACCTCTGATTAATAAATGCTTATGAAATGAAAAAAAAAA 541 AAAA	SEQ ID NO:257
		1 M T E L E T A M S M I I D V F A R Y S G 1 ATGACGGAACTGGAGACAGCCATGAGCATGATCATCGACGTCTTTGCCCGGTACTCGGGT 21 A E G S K Q S L T K G E L K T L M E K E 61 GCCGAGGGCAGCAAGCAGAGCCTGACCAAGGGGGAGCTGAAGACGCTCATGGAGAAGGAG 41 L P G F L Q T G R N K G A V D K L L K D 121 CTCCCGGGCTTCCTGCAGACCGGAAGGAACAAGGGTGCCGTGGACAAACTGCTCAAGGAC 61 L D A N G D A E V D F S E F I V F V A A 181 CTGGACGCCAACGGAGACGCCGAGGTGGACTTCAGCGAGTTCATCGTGTTTGTGGCCGCG 81 L T S T C H K Y F E K A G L K - 241 CTCACGTCTACCTGCCACAAGTACTTTGAGAAGGCAGGACTCAAATGA	SEQ ID NO:258
BM734943	No Homoloy	1 AACTCAGGGAGGGAGCGGAGGTCCCTGGGAGCAGTTGCACATGGAGTAGGCACCGGGAAAG 61 GCTAGAGAGGAGCAGAGCCATGTAAGCAGAGGGCTCAGGACTCCCCAGACAGAGTCCTGC	SEQ ID NO:259

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		121 TCCCAAGGGGGCTACTGGCCCTTCGCTCAGCATTCCTGTTTCCCTTATATCCAAAATAAA 181 CTTTCCTGAGCTTGTCTGAGTCTTGAATCGTTACCACGGAACAGCTTTATTTCCTGGTAA 241 TCTCAATTCCTGCCTCTTGCCATACGATGCCGTATGATCTGGCCACAAGGCTCTTCAGT 301 CCTGGCCTGAGTGTCAGCCCCCGAGCTCTGTGCCCAGACCTTGCTGTGCGTCCTGGAGCA 361 AACAAGGAACCCTTTCTGCAAGTCAGTTTCCACTTTGAAAAGTTCCGGGGAGGGTGACAT 421 TGCTCAAGCCATGGTCATTTGTGTTACGTATATATTTTTAATGATCTGTGTGTACTATCTTT 481 GCTGTTGTTTACTTAATATTTTTCTTTAAGCCAATTCACTTTAAAAAATATTTTTATTTTA 541 AAGAAAAATCTTTATATTGCTTTTGTAAATGGAAAAATGGATATTCACTATAAATAAAAA 601 GTAACTGTAAAAAGTAAATACAATAAAACAAAATGTTTCAACTC	
BM734975	Human mRNA for coupling protein G(s) alpha-subunit (alpha-S1) (stimulatory regulatory component Gs of adenylyl cyclase).	1 GCCGCCGCCGCCATGGGCTGCCTCGGGAACAGTAAGACCGAGGACCAGCGCAACGAGGAG 61 AAGGCGCAGCGTGAGGCCAACAAAAGATCGAGAAGCAGCTGCAGAAGGACAAGCAGGTC 121 TACCGGGCCACGCACCGCCTGCTGTGCTGGGTCTGGAGAATCTGGTAAAAGCACCATT 181 GTGAAGCAGATGAGGATCCTGCATGTTAATGGGTTTAATGGAGACAGTGAGAAGGCAACC 241 AAAGTGCAGGACATCAAAAACAACCTGAAAGAGGCGATTGAAACCATTGTGGCCGCCATG 301 AGCAACCTGGTGCCCCCCGTGGAGCTGGCCAACCCCGAGAACCAGTTCAGAGTGGACTAC 361 ATCCTGAGTGTGATGAACGTGCCTGACTTTGACTTCCCTCCCGAATTCTATGAGCATGCC 421 AAGGCTCTGTGGGAGGATGAAGGAGTGCGTGCCTGCTACGAACGCTCCAACGAGTACCAG 481 CTGATTGACTGTGCCCAGTACTTCCTGGACAAGATCGACGTGATCAAGCAGGCTGACTAT 541 GTGCCGAGCGATCAGGACCTGCTTCGCTGCCGTGTCCTGACTTCTGGAATCTTTGAGACC 601 AAGTTCCAGGTGGACAAAGTCAACTTCCACATGTTTGACGTGGGTGGCCAGCGCGATGAA 661 CGCCGCAAGTGGATCCAGTGCTTCAACGATGTGACTGCCATCATCTTCGTGGTGGCCAGC 721 AGCAGCTACAACATGGTCATCCGGGAGGACAACCAGACCAACCGCCTGCAGGAGGCTCTG 781 AACCTCTTCAAGAGCATCTGGAACAACAGATGGCTGCGCACCATCTCTGTGATTCTGTTC 841 CTCAACAAGCAAGACCTGCTCGCTGAGAAAGTCCTTGCTGGAAAATCGAAAATTGAGGAC 901 TACTTTCCAGAATTTGCTCGCTACACTACTCCTGAGGATGCTACTCCCGAGCCCGGAGAG 961 GACCCACGCGTGACCCGGGCCAAGTACTTCATCCGTGACGAATTTCTGAGAATCAGCCCC 1021 GCTAGTGGGGACGGGCGCCACTACTGCTACCCCCACTTCACCTGCGCTGTGGTCACCGAG 1081 AACATCCGCCGGGTGTTCAACGACTGCCGGGACATCATCCAGCGCATGCACCTCCGTCAG 1141 TATGAGCTGCTCTAAGAAGGGAACGCCCAGTTTAATTAAGCCTTAAGCACAATTAATTA 1201 AAAGTGAAACGTAATTGTTCACGCAGTTAATCACCCACCATAGGGCATGATTAACAAAGC 1261 CACCTTTCCCTTCCCCCTTGAGTGATTTGGCGAAACCCCCCTGCTCCCTTCAGCTTGGTTA 1321 AATATATTCCAAATTTAGAAAGCTTAAGGCGGCCTACAGAAAAAGAAACAGGCCACAAAA 1381 GTTCCCTCTCTCTTTCAGTAAAAATAAATAAACAGCAGCAGCAAACAATAAAATGAAA 1441 TAAAAGAAACAAATGAAATAAATATTGTTGTGCAGCATTAAAAAAAATCAAAATAAAA 1501 ATTAAATGTGAGCAAAG 1 M G C L G N S K T E D Q R N E E K A Q R 1 ATGGGCTGCCTCGGAACAGTAAGACCGAGGACCAGCGCAACGAGGAGAAGGCGCAGCGT 21 E A N K K I E K Q L Q K D K Q V Y R A T 61 GAGGCCAACAAAAAGATCGAGAAGCAGCTGCAGAAGGACAAGCAGGTCTACCGGGCCACG	SEQ ID NO:260 SEQ ID NO:261

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		41 H R L L L L G A G E S G K S T I V K Q M 121 CACCGCCTGCTGCTGCTGGGTGCTGGAGAATCTGGTAAAAGCACCATTGTGAAGCAGATG 61 R I L H V N G F N G D S E K A T K V Q D 181 AGGATCCTGCATGTTAATGGTTTAATGGAGACAGTGAGAAGGCAACCAAAGTGCAGGAC 81 I K N N L K E A I E T I V A A M S N L V 241 ATCAAAAACAACCTGAAAGAGGCGATTGAAACCATTGTGGCCGCCATGAGCAACCTGGTG 101 P P V E L A N P E N Q F R V D Y I L S V 301 CCCCCCGTGGAGCTGGCCAACCCGAGAACCAGTTCAGAGTGGACTACATCCTGAGTGTG 121 M N V P D F D F P P E F Y E H A K A L W 361 ATGAACGTGCCTGACTTTGACTTCCCTCCCGAATTCTATGAGCATGCCAAGGCTCTGTGG 141 E D E G V R A C Y E R S N E Y Q L I D C 421 GAGGATGAAGGAGTGCGTGCCTGCTACGAACGCTCCAACGAGTACCAGCTGATTGACTGT 161 A Q Y F L D K I D V I K Q A D Y V P S D 481 GCCCAGTACTTCCTGGACAAGATCGACGTGATCAAGCAGGCTGACTATGTGCCGAGCGAT 181 Q D L L R C R V L T S G I F E T K F Q V 541 CAGGACCTGCTTCGCTGCCGTGTCCTGACTTCTGGAATCTTTGAGACCAAGTTCCAGGTG 201 D K V N F H M F D V G G Q R D E R R K W 601 GACAAAGTCAACTTCCACATGTTTGACGTGGGTGGCCAGCGCGATGAACGCCGCAAGTGG 221 I Q C F N D V T A I I F V V A S S Y N 661 ATCCAGTGCTTCAACGATGTGACTGCCATCATCTTCGTGGTGGCCAGCAGCTACAAC 241 M V I R E D N Q T N R L Q E A L N L F K 721 ATGGTCATCCGGGAGGACAACCAGACCAACCGCCTGCAGGAGGCTCTGAACCTCTTCAAG 261 S I W N N R W L R T I S V I L F L N K Q 781 AGCATCTGGAACAACAGATGGCTGCGCACCATCTCTGTGATTCTGTTCCTCAACAAGCAA 281 D L L A E K V L A G K S K I E D Y F P E 841 GACCTGCTCGCTGAGAAAGTCCTTGCTGGAAAATCGAAAATTGAGGACTACTTTCCAGAA 301 F A R Y T T P E D A T P E E P G E D P R V 901 TTTGCTCGCTACACTACTCCTGAGGATGCTACTCCCGAGCCCGGAGAGGACCCACGCGTG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		321 T R A K Y F I R D E F L R I S P A S G D 961 ACCCGGGCCAAGTACTTCATCCGTGACGAATTTCTGAGAATCAGCCCCGCTAGTGGGGAC 341 G R H Y C Y P H F T C A V V T E N I R R 1021 GGGCGCCACTACTGCTACCCCCACTTCACCTGCGCTGTGGTCACCGAGAACATCCGCGG 361 V F N D C R D I I Q R M H L R Q Y E L L 1081 GTGTTCAACGACTGCCGGGACATCATCCAGCGCATGCACCTCCGTCAGTATGAGCTGCTC 381 - 1141 TAA	
BM735057	Human mRNA for macrophage inflammatory protein-2alpha (MIP2alpha)	1 ctctcctcct cgcacagccg ctcgaaccgc ctgctgagcc ccatggcccg cgccacgctc 61 tccgccgccc ccagcaatcc ccggctcctg cgggtggcgc tgctgctcct gctcctggtg 121 gccgccagcc ggcgcgcagc aggagcgccc ctggccactg aactgcgctg ccagtgcttg 181 cagaccctgc agggaattca cctcaagaac atccaaagtg tgaagtgtaa gtcccccgga 241 ccccactgcg cccaaaccga agtcatagcc acactcaaga atgggcagaa agcttgtctc 301 aacccgcgat cgcccatggt taagaaaatc atcgaaaaga tgctgaaaaa tggcaaatcc 361 aactgaccag aaggaaggag gaagcttatt ggtggctgtt cctgaaggag gccctgccct 421 tacaggaaca gaaggaggaa gagagcacca gctgcagagg ccacctggat tgcgcctaat 481 gtgtttgagc atcacttagg agaagtcttc tatttattta tttatttatt tatttgtttg 541 tttagaaga ttctatgtta atattttatg tgtaaaataa ggttatgatt gaatctactt 601 gcacactctc ccattatatt tattgtttat tttagtcaa acccaagtta gttcaatcct 661 gattcatatt taatttgaag atagaaggtt tgcagatatt ctctagtcat ttgttaatat 721 ttcttcgtga tgacatatca catgtcagcc actgtgatag aggctgagga atccaagaaa 781 atggccagtg agatcaatgt gacggcaggg aaatgtatgt gtgtctattt tgtaactgta 841 aagatgaatg tcagttgtta tttattgaaa tgatttcaca gtgtgtggtc aacatttctc 901 atgttgaagc tttaagaact aaaatgttct aaatatccct tggacatttt atgtctttct 961 tgtaaggcat actgccttgt ttaatgttaa ttatgcagtg tttccctctg tgttagagca 1021 gagaggtttc gatatttatt gatgttttca caaagaacag gaaaataaaa tatttaaaaa 1081 t 1 M A R A T L S A A P S N P R L L R V A L 1 ATGGCCCGCGCCACGCTCTCCGCCGCCCCCAGCAATCCCCGGCTCCTGCGGGTGGCGCTG 21 L L L L L V A A S R R A A G A P L A T E 61 CTGCTCCTGCTCCTGGTGGCCGCCAGCCGGCGCGCAGCAGGAGCGCCCCTGGCCACTGAA 41 L R C Q C L Q T L Q G I H L K N I Q S V 121 CTGCGCTGCCAGTGCTTGCAGACCCTGCAGGGAATTCACCTCAAGAACATCCAAGTGTG 61 K V K S P G P H C A Q T E V I A T L K N	SEQ ID NO:262 SEQ ID NO:263

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		181 AAGGTGAAGTCCCCCGGACCCCACTGCGCCCAAACCGAAGTCATAGCCACACTCAAGAAT 81 G Q K A C L N P A S P M V K K I I E K M 241 GGGCAGAAAGCTTGTCTCAACCCCGCATCGCCCATGGTTAAGAAAATCATCGAAAAGATG 101 L K N G K S N - 301 CTGAAAAATGGCAAATCCAACTGA	
BM735091	Horse serpin mRNA.	1 CCCCCGCCGCCGGGACCGTCAGCCGCGCCGCCTTCGCCATGGAGCAGCTGAGCACAGC 61 CAACACCCACTTTGCGGTGGACTTGTTCCGCGCTTTGAATGAGAGCGATCCTACTGGAAA 121 CATCTTCATCTCTCCCTTAAGCATTTCCTCAGCGCTGGCCATGATCTTTCTGGGGACCAG 181 AGGCAACACAGCGGCACAGGTGTCCAAGGCACTTTATTTTGATACTGTTGAGGATATTCA 241 TTCAAGATTTCAGAGTCTGAATGCTGATATCAACAAACCTGGAGCTCCCTATATTCTGAA 301 ACTCGCTAATAGATTATATGGAGAGAAAACCTATAAATTTCCTCGCTGATTTCTTAGCTTC 361 AACTCAGAAAATGTATGGTGCTGAATTGGCCAGTGTGGATTTTCAGCAAGCCCCTGAAGA 421 TGCAAGAAAGGAGATAAATGAATGGGTCAAAGGACAGACAGAGGGAAAATTCCGGAACT 481 GTTGGTCAAGGGTATGGTTGATAACATGACTAAACTTGTACTGGTGAATGCCATCTACTT 541 CAAGGGAAACTGGCAGGAGAAATTCATGAAAGAGGCCACCAGAGACGCCCCATTCCGATT 601 GAATAAGAAAGACACAAAAACCGTGAAAATGATGTATCAGAAGAAGAAATTTCCATACAA 661 CTACATCGAGGACCTCAAGTGCCGTGTGCTGGAGCTGCCTTACCAAGGCAAAGAGCTCAG 721 CATGATCATCCTCTGCTGCCAGACGACATTGAGGATGAGTCCACGGGCCTGGAGAAGATTGA 781 GAAACAGTTGACTTTGGAAAAACTGCGTGAGTGGACCAAACCTGAGAATCTGTATCTCGC 841 TGAAGTCAATGTCCACTTGCCCAGGTTCAAGCTGGAAGAGAGCTACGATCTCACCTCCCA 901 TCTAGCCCGCCTAGGTGTACAAGACCTCTTTAACAGGGGCAAAGCTGATCTGTCTGGCAT 961 GTCAGGGGCCAGAGATCTTTTCGTATCGAAAATTATCCACAAATCCTTTGTGACCTGAA 1021 TGAGGAGGGTACAGAGGCTGCGGCAGCCACAGCACGATCATGCTTGCCATGCTGAT 1081 GCCAGAGGAAAATTTCAATGCCGACCATCCATTCATTTTCTTCATTCGGCACAATCCCTC 1141 AGCTAACATCCTGTTCTTAGGCAGATTTTCTTCCCTTAGAGAAGGTGGAAGTACAAGGT 1201 GAAGCTTAGAGCTTTATTACCTGCTAGTATTATTACCATTACTTTTAATAGTGACAGTTT 1261 TCATATATCTTTTACCAATAAAACTACTATCCAAAAACAAATCTTTAATTTCCTTTGTAAG 1321 TTCAGCTCTATTGGCTGTTGCACCCCTTAACTTTGGCGTGGGTAGCTATTTTCCTTTTTT 1381 ATGTTGAAAAAATCTAGTTATTGCTTTTGGATGCATCAAGTTAAAAAATAAAAAGACTAA 1441 ATCAAATTTATAGATTCTTGATAATGCAGTAAGCTATGAAACTACTATACTCTCCTGATA 1501 GTGTGGAACATTATAGTACTGTAATTATTTACTAGATAGATTTCAATGAAATATAGTAAAG 1561 GACGCTCTGATTGTTGAAGGAAGGGCTTAAAAACAGATATTCAATTGAAATATAGTAAAG 1621 CACCCCAATTAAGCCTGGGTTGTGCAGACAAACTCTGTCTTGGCCGTTGTTTCTAACCCT 1681 TTGTTCCACAGGGTTAGTGTCCTAGGCAGCACTCCAATTTCAAACTGTTAGCCACCTGGT 1741 GATACCCCGCCTTCTCTTTTTTGTTCTCCTTTATCCTACCTGACATGTATTTTGTGTAGG 1801 ATCACATGGGGTCAGAAAGTAGGTGTTCTATCATAAAAGATACCAAGAACGACAAAAGGA 1861 AATGCGTAGGAGACTGTAGCAAGGCACAAGATCTCACTGTTACCCAGCTTCTTGCGT 1921 TTTCTGATGAAGGCTCTTGCCTTCCATTGTCTGGTAAGGTTGTTACACCAGTGCGATGGC 1981 TTTATGCAATGTTGTGGTGGGAGATGGGGGGGTTCTTTTATTAATATAAACCTTTGTCAA	SEQ ID NO:264

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2041 ATGTTTGAATGGGGCTGAAAATGCTGCATTTTCTTGCTCCCACAAAGCTGGTATGCTGGT 2101 TAATAAAGTTTCCTAAGATTCTGCA	
		1 M E Q L S T A N T H F A V D L F R A L N 1 ATGGAGCAGCTGAGCACAGCCAACACCCACTTTGCGGTGGACTTGTTCCGCGCTTTGAAT	SEQ ID NO:265
		21 E S D P T G N I F I S P L S I S S A L A 61 GAGAGCGATCCTACTGGAAACATCTTCATCTCCCTTAAGCATTTCCTCAGCGCTGGCC	
		41 M I F L G T R G N T A A Q V S K A L Y F 121 ATGATCTTTCTGGGACCAGAGGCAACACAGCGGCACAGGTGTCCAAGGCACTTTATTTT	
		61 D T V E D I H S R F Q S L N A D I N K P 181 GATACTGTTGAGGATATTCATTCAAGATTTCAGAGTCTGAATGCTGATATCAACAAACCT	
		81 G A P Y I L K L A N R L Y G E K T Y N F 241 GGAGCTCCCTATATTCTGAAACTCGCTAATAGATTATATGGAGAGAAAACCTATAATTTC	
		101 L A D F L A S T Q K M Y G A E L A S V D 301 CTCGCTGATTTCTTAGCTTCAACTCAGAAAATGTATGGTGCTGAATTGGCCAGTGTGGAT	
		121 F Q Q A P E D A R K E I N E W V K G Q T 361 TTTCAGCAAGCCCCTGAAGATGCAAGAAAGGAGATAAATGAATGGGTCAAAGGACAGACA	
		141 E G K I P E L L V K G M V D N M T K L V 421 GAGGGGAAAATTCCGGAACTGTTGGTCAAGGGTATGGTTGATAACATGACTAAACTTGTA	
		161 L V N A I Y F K G N W Q E K F M K E A T 481 CTGGTGAATGCCATCTACTTCAAGGGAAACTGGCAGGAGAAATTCATGAAAGAGGCCACC	
		181 R D A P F R L N K K D T K T V K M M Y Q 541 AGAGACGCCCCATTCCGATTGAATAAGAAAGACACAAAAACCGTGAAAATGATGTATCAG	
		201 K K K F P Y N Y I E D L K C R V L E L P 601 AAGAAGAAATTTCCATACACTACAACTACATCGAGGACCTCAAGTGCCGTGTGCTGGAGCTGCCT	
		221 Y Q G K E L S M I I L L P D D I E D E S 661 TACCAAGGCAAAGAGCTCAGCATGATCATCCTGCTGCCAGACGACATTGAGGATGAGTCC	
		241 T G L E K I E K Q L T L E K L R E W T K 721 ACGGGCCTGGAGAAGATTGAGAAACAGTTGACTTTGGAAAAACTGCGTGAGTGGACCAAA	
		261 P E N L Y L A E V N V H L P R F K L E E	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		781 CCTGAGAATCTGTATCTCGCTGAAGTCAATGTCCACTTGCCCAGGTTCAAGCTGGAAGAG 281 S Y D L T S H L A R L G V Q D L F N R G 841 AGCTACGATCTCACCTCCCATCTAGCCCGCCTAGGTGTACAAGACCTCTTTAACAGGGGC 301 K A D L S G M S G A R D L F V S K I I H 901 AAAGCTGATCTGTCTGGCATGTCAGGGGCCAGAGATCTTTTCGTATCGAAAATTATCCAC 321 K S F V D L N E E G T E A A A A T A G T 961 AAATCCTTTGTGGACCTGAATGAGGAGGGTACAGAGGCTGCGGCAGCCACAGCAGGCACG 341 I M L A M L M P E E N F N A D H P F I F 1021 ATCATGCTTGCCATGCTGATGCCAGAGGAAAATTTCAATGCCGACCATCCATTCATTTTC 361 F I R H N P S A N I L F L G R F S S P - 1081 TTCATTCGGCACAATCCCTCAGCTAACATCCTGTTCTTAGGCAGATTTTCTTCCCCTTAG	
BM735286	Equus caballus mRNA for ferritin light chain.	1 ATGAGCTCCCAGATTCGTCAGAATTATTCTACTGAAGTGGAGGCCGCCGTCAACCGCCTG 61 GTCAACCTGTACCTGCGGGCCTCCTACACCTACCTCTCTGGCTTCTATTTCGACCGC 121 GACGATGTGGCTCTGGAGGGCGTATGCCACTTCTTCCGCGAGTTGGCGGAGGAGAAGCGC 181 GAGGGTGCCGAGCGTCTCTTGAAGATGCAAAACCAGCGCGGCGCGCTCTCTTCCAG 241 GACTTGCAGAAGCCGTCCCAGGATGAATGGGGTACAACCCTGGATGCCATGAAAGCCGCC 301 ATTGTCCTGGAGAAGAGCCTGAACCAGGCCCTTTTGGATCTGCATGCCCTGGGTTCTGCC 361 CAGGCAGACCCCCATCTCTGTGACTTCTTGGAGAGCCACTTCCTAGACGAGGAGGTGAAA 421 CTCATCAAGAAGATGGGCGACCATCTGACCAACATCCAGAGGCTCGTTGGCTCCCAAGCT 481 GGGCTGGGCGAGTATCTCTTTGAAAGGCTCACCCTCAAGCACGACTAA 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 GTCAACCTGTACCTGCGGGCCTCCTACACCTACCTCTCTGGCTTCTATTTCGACCGC 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 GAGGGTGCCGAGCGTCTCTTGAAGATGCAAAACCAGCGCGGCGGCGCTCTCTTCCAG 81 D L Q K P S Q D E W G T T L D A M K A A 241 GACTTGCAGAAGCCGTCCCAGGATGAATGGGGTACAACCCTGGATGCCATGAAAGCCGCC	SEQ ID NO:266 SEQ ID NO:267

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		101 I V L E K S L N Q A L L D L H A L G S A 301 ATTGTCCTGGAGAAGAGCCTGAACCAGGCCTTTTGGATCTGCATGCCCTGGGTTCTGCC 121 Q A D P H L C D F L E S H F L D E E V K 361 CAGGCAGACCCCCATCTCTGTGACTTCTTGGAGACCACTTCCTAGACGAGGAGGTGAAA 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	
BM735386	No Homology	1 TTTCCTTCATGTTCCATTGGAATAGTATGTGGTTCCTTCTCAGAACCAAGGGCAA 61 TCCTGCTTCACTGGTGTGCCATTTGCTGACCTTGTGGTGCTCTCAGGGGCCGCCTGGGCC 121 CAGGGCGAGGCCTCGACGCCTGCCGGGCTCGTGAGATGCTCCAGGTCCTCTCCCCTCCCT 181 GGGCGGTTCTGGGCTGAGGGTTCAGGGAGCGTTTCCTTTACCTGGAAGTTGTCACCATGA 241 AGTTGTCACGTGCAGTGTCTTTCTCTCTTTCTCCGTCCCGTTGCTGGTGCCCCTGTAA 301 AGAGGCTTTTGGGAACGAGTAGAGGGCAGAGGTGGCACAGGAGGGTAAAGGATGTCCTGG 361 TGCTGGCTCAGCCTGGCAGGGCTCTGCTGACCTCAGGGCCGGCACAGCCAGGATGGCT 421 GTTTTCCTGTCCCAGAGACCTGTTGTGCTGTGTTATTTTGATTTCCCATTTATTCAAATG 481 TATGTATTTACAATTGTAAAGGGGGGGGATGTCTGACCTTAGTGTTCCAAACAGAACTGT 541 ATTTTTGCCTTTAAAATCCAGTGATATAACTGGAAGGTGAATAAATGACCTTATCTTTT	SEQ ID NO:268
BM735402	No Homology	1 CCAGACTGGCAGACAGTCGCGCCCTGGGGCTTTTCTCACTTACTTTCCCTTTAGGAGGAC 61 AGTGAGTGAGCAAGAGCAGTGCTCTGGTACTCACCCATGGAGATGCTTAGAGAATCTTTT 121 CTCCATGCATGTAAATTTGTTTAATTCCGTTTTCACAGAAGGGCTCAATTTGTTCCTTAT 181 CGTCTCCCCATTGAAGTGTCGATGAAGAGTTCCTGGAAGATGGATCTCTCAGAACTCAAT 241 TAGGTGAAATGCCAGAAAGTGAGAAAGACAGAGACTCAACAGATAGGACAAGAATGTTTG 301 GTGCATTTGGATGTATCTGTAGAAACTCTGACCAACCTCAAAGTGACCAATTTGCTGAAT 361 AACCAGTCCTCTCCTTTTCTGTGAAACTAACTGCTGCGCCCCCACCTCCATAACCCCACA 421 GCTTGAGTACTTACTGCTTGGCGGTCACCTTCACACTGCTGCTCCCACCCAGTTGAGTT 481 ATTTGCTTATTATTACTATATAAAGCTTTTCTGTTGTCTC	SEQ ID NO:269
BM735452	No Homology	1 TGAGAGAAGGGGGACAGGGGCGCCTCCGCCAGCCTCCCGAGGCCTCAGTGCAGTGCCTT 61 CCCGGCCGTGCCTGCCTGGGCAGACCCCCAAGAAGCTGCCGGCCCTGCGGGGTGCCCCCG 121 GGCCCTGCCTTGGGGGCTGCCGCGTGCGCAGGTCCCACTCAGGATGACTCGGGTCCAGTG 181 GCCCAGGCGGGGGCCTGCGAGTGGGGACCGCCCTCTCTGTGCCTCTCTTCTCCTGCTGCCCT 241 CCAGGCCTGGGGGGGGCACCAGGCCCGAACCCCCGGAAGTCTGCAAAATTGGGTGCCCCAAG 301 AGCTGGAAACTCAGGAAACCCCAGGTGCTCAGGGCCCCGCCGTGTCTGGGGGGGCTCCGC 361 GGGGCAGACCCCCCGTTAATATATGCAATTCCCCATCCCTGCTCTCTGCTCCCTAAATTAT	SEQ ID NO:270

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		421 TGCCCGGCCGCCTCTCCCAGGCCCCAGAATCTGCCCCAGGAGTCGGTGGGGCACGGCAGC 481 GCCCCCGGTTTCATATCTGTATTTATAATTATGTCTAAGTGTATATATGTAAAGAGATCT 541 TTCT	
BM735487	No Homology	1 CTGGCCATAGCATTAACCCCTCGCCCGGCCCGGACACAAGGAGGAAGCTCCTAGGGGCCA 61 GGGGCAGGACTGTGGAGGGACAGGCTTCCCCTCACNCCACCCACTCCCTCCTTCTGCCCC 121 CTCCCACATGCCCGCCTCGCCTCCCACCAGGACTCTAGCCCCAGAGTGGCTCCAGAAGGT 181 CCCCCGGGCGTCTGACCCCAGCGAAGGCCAGCCTTGCTTGGTTCAGCTGGGGGTGCTTG 241 CTTGGGAGTTCGAAGTCACCCTAATCACGTAAATGGAACTCTCCTTTTCGAGCATCTCTC 301 CCTTCCCACACCTTCCTCCGTTAGCTTCCCCAAAAGAATTGTGTTATTAAACTTATTCTC 361 AATGAGTCCTCCTGC	SEQ ID NO:271
BM735494	Homo sapiens T-cell receptor beta (TCRB) mRNA.	1 ATGGGCACCAGCCTCCTCTGCTGGATGGCCCTGTGTCTCCTGGGGGCAGATCACGCAGAT 61 ACTGGAGTCTCCCAGAACCCCAGACACAAGATCACAAAGAGGGGACAGAATGTAACTTTC 121 AGGTGTGATCCAATTTCTGAACACAACCGCCTTTATTGGTACCGACAGACCCTGGGGCAG 181 GGCCCAGAGTTTCTGACTTACTTCCAGAATGAAGCTCAACTACTAGAAAAATCAGGCTGCTC 241 AGTGATCGGTTCTCTGCAGAGAGGCCTAAGGGATCTTTCTCCACCTTGGAGATCCAGCGC 301 ACAGAGCAGGGGGACTCGGCCATGTATCTCTGTGCCAGCAGCCCAGGGACTAGCTACGAG 361 CAGTACTTTGGGCCCGGCACCAGGCTCACTGTCACAGAGAACCTGAACCAGGTGACCCTA 421 CCCAAGGTGGCTGTGTTTGAACCTTCGGAAGCAGAGATCTCCCGCACCGAGAAGGCCACG 481 CTCGTGTGCCTGGCCACAGGCTTCTACCCCGACCACGTGGAGCTGAGCTGGTGGGTGAAT 541 GGGAAGGAAGTCCAGACTGGGGTCAGCACGGACCCTCAGCCCCTCAAGGAGCAGCCCGCC 601 CTCAATGACTCCAGCTACTGTCTGAGCAGCCGGCTGAGGGTCTCTGCTGCCTTCTGGCAC 661 AACCCCCGCAACCACTTCCGCTGCCAAGTCCAGTTCTACGGGCTCTCGGAGAATGACGAG 721 TGGACCCAGGATAGGGCCAAACCCGTCACCCAGATCGTCAGCGCCGAGGCCTGGGGTAGA 781 GCAGACTGTGGCTTCACCTCCGAGTCTTACCAGCAAGGGGTCCTGTCTGCCACCATCCTC 841 TATGAGATCTTGCTAGGGAAGGCCACCTTGTATGCCGTGCTGGTCAGTGCCCTCGTGCTG 901 ATGGCCATGGTCAAGAGAAAGGATTCCAGAGGCTAG	SEQ ID NO:272
		1 M G T S L L C W M A L C L L G A D H A D 1 ATGGGCACCAGCCTCCTCTGCTGGATGGCCCTGTGTCTCCTGGGGGCAGATCACGCAGAT 21 T G V S Q N P R H K I T K R G Q N V T F 61 ACTGGAGTCTCCCAGAACCCCAGACACAAGATCACAAAGAGGGGACAGAATGTAACTTTC 41 R C D P I S E H N R L Y W Y R Q T L G Q 121 AGGTGTGATCCAATTTCTGAACACAACCGCCTTTATTGGTACCGACAGACCCTGGGGCAG 61 G P E F L T Y F Q N E A Q L E K S R L L 181 GGCCCAGAGTTTCTGACTTACTTCCAGAATGAAGCTCAACTAGAAAAATCAGGCTGCTC	SEQ ID NO:273

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		81 S D R F S A E R P K G S F S T L E I Q R 241 AGTGATCGGTTCTCTGCAGAGAGGCCTAAGGGATCTTTCTCCACCTTGGAGATCCAGCGC 101 T E Q G D S A M Y L C A S S P G T S Y E 301 ACAGAGCAGGGGACTCGGCCATGTATCTCTGTGCCAGCAGCCCAGGGACTAGCTACGAG 121 Q Y F G P G T R L T V T E N L N Q V T L 361 CAGTACTTTGGGCCCGGCACCAGGCTCACTGTCACAGAGAACCTGAACCAGGTGACCCTA 141 P K V A V F E P S E A E I S R T E K A T 421 CCCAAGGTGGCTGTGTTTGAACCTTCGGAAGCAGAGATCTCCCGCACCGAGAAGGCCACG 161 L V C L A T G F Y P D H V E L S W W V N 481 CTCGTGTGCCTGGCCACAGGCTTCTACCCCGACCACGTGGAGCTGAGCTGGTGGGTGAAT 181 G K E V Q T G V S T D P Q P L K E Q P A 541 GGGAAGGAAGTCCAGACTGGGGTCAGCACGGACCCTCAGCCCCTCAAGGAGCAGCCCGCC 201 L N D S S Y C L S S R L R V S A A F W H 601 CTCAATGACTCCAGCTACTGTCTGAGCAGCCGGCTGAGGGTCTCTGCTGCCTTCTGGCAC 221 N P R N H F R C Q V Q F Y G L S E N D E 661 AACCCCCGCAACCACTTCCGCTGCCAAGTCCAGTTCTACGGGCTCTCGGAGAATGACGAG 241 W T Q D R A K P V T Q I V S A E A W G R 721 TGGACCCAGGATAGGGCCAAACCCGTCACCCAGATCGTCAGCGCCGAGGCCTGGGGTAGA 261 A D C G F T S E S Y Q Q G V L S A T I L 781 GCAGACTGTGGCTTCACCTCCGAGTCTTACCAGCAAGGGGTCCTGTCTGCCACCATCCTC 281 Y E I L L G K A T L Y A V L V S A L V L 841 TATGAGATCTTGCTAGGGAAGGCCACCTTGTATGCCGTGCTGGTCAGTGCCCTCGTGCTG 301 M A M V K R K D S R G - 901 ATGGCCATGGTCAAGAGAAAGGATTCCAGAGGCTAG	
BM735519	Homo sapiens ring finger protein 10, mRNA (cDNA clone MGC:35311 IMAGE:5177665)	1 cgactcgtcg ccattcccgg agcaggtcgg cctcggccca ggggcgagta tccgttgctg 61 tgtcggagac actagtcccc gacaccgaga cagccagccc tctcccctgc ctcgcggcgg 121 gagagcgtgt ccggccggcc ggccggcggg gctcgcgcaa cctccctcgc ctccccttcc 181 ccccgagcct ccgccccgcc aggcccggcc cggactcccg agccccggcc tcctcgtcct 241 cggtcgccgc tgccgccggg cttaacagcc ccgtccgccg cttctcttcc tagtttgaga 301 agccaaggaa ggaaacaggg aaaaatgtcg ccatgaaggc cgagaaccgc tgccgccgcc	SEQ ID NO:274

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		361 gacccccgcc ggccctgaac gccatgagcc tgggtccccg ccgcgcccgc tccgctccga	
		421 ctgccgtcgc cgccgaggcc cccgttgatg ccgctgagct cccccaacgc cgccgccacc	
		481 gcctcccgaca tggacaagaa cagcggctcc aacagctcct ccgcctcttc gggcagcagc	
		541 aaagggcaac agccgccccg ctccgcctcg gcggggccag ccggcgagtc taaacccaag	
		601 agcgatggaa agaactccag tggatccaag cgttataatc gcaaacgtga actttcctac	
		661 cccaaaaatg aaagttttaa caaccagtcc cgtcgctcca gttcacagaa aagcaagact	
		721 tttaacaaga tgcctcctca aaggggcggc ggcagcagca aactctttag ctcttctttt	
		781 aatggtggaa gacgagatga ggtagcagag gctcaacggg cagagtttag ccctgcccag	
		841 ttcttctggtc ctaagaagat caacctgaac cacttgttga atttcacttt tgaaccccgt	
		901 ggccagacgg gtcacttga aggcagtgga catggtagct gggaaaagag gaacaagtgg	
		961 ggacataagc cttttaacaa ggaactcttt ttacaggcca actgccaatt tgtggtgtct	
		1021 gaagaccaag actacacagc tcatttttgct gatcctgata cattagttaa ctgggacttt	
		1081 gtggaacaag tgcgcatttg tagccatctt gtgccatctt gcccaatatg cctctatcca	
		1141 cctactgcag ccaagataac ccgttgtgga cacatcttct gctgggcatg catcctgcac	
		1201 tatctttcac tgagtgagaa gacgtggagt aaatgtccca tctgttacag ttctgtgcat	
		1261 aagaaggatc tcaagagtgt tgttgccaca gagtcacatc agtatgttgt tggtgatacc	
		1321 attacgatgc agctgatgaa gagggagaaa ggggtgttgg tggctttgcc caaatccaaa	
		1381 tggatgaatg tagaccatcc cattcatcta ggagatgaac agcacagcca gtactccaag	
		1441 tttctgctgg cctctaagga gcaggtgctg caccgggtag ttctggagga gaaagtagca	
		1501 ctagagcagc agctggcaga ggagaagcac actcccgagt cctgctttat tgaggcagct	
		1561 atccaggagc tcaagactcg ggaagaggct ctgtcgggat tggccggaag cagaagggag	
		1621 gtcactggtg ttgtggctgc tctggaacaa ctggtgctga tggctccctt ggcgaaggag	
		1681 tctgttttttc aacccaggaa gggtgtgctg gagtatctgt ctgccttcga tgaagaaacc	
		1741 acggaagttt gttctctgga cactcctttt agacctcttg ctctccctct ggtagaagag	
		1801 gaggaagcag tgtctgaacc agagcctgag gggttgccag aggcctgtga tgacttggag	
		1861 ttagcagatg acaatcttaa agaggggacc atttgcactg agtccagcca gcaggaaccc	
		1921 atcaccaagt caggcttcac acgcctcagc agctctcctt gttactactt ttaccaagcg	
		1981 gaagatggac agcatatgtt cctgcacctt gtgaatgtgc gctgcctcgt gcgggagtac	
		2041 ggcagcctgg agaggagccc cgagaagatc tcagcaactg tggtggagat tgctggctac	
		2101 tccatgtctg 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 gggcctctcc catttctcct	
		2461 ctcagcagaa gtccaggttc ccatgcagac tttctgctga ccccttctgtc acccactgcc	
		2521 agtcagggca gtccctcatt ctgcgttggg agtctggaag aagactctcc cttcctttcc	
		2581 tttgcccaga tgctgagggt 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 acctttctcca tctggttttt gttttgttt ttttttcccc	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2941 catgcttttg tttggctgct gtaatttta agtatttgag tttgaacaga ttagcttctgg 3001 ggggaggggg tttccacaat gtgaggggga accaagaaaa ttttaaatac agtgtatttt 3061 ccagctttcct gtctttacac caaaataaag tattgacaca agagaaaaaa 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 ATGCCGCTGAGCTCCCCCAACGCCGCCGCCACCGCCTCCGACATGGACAAGAACAGCGGC 21 S N S S S A S S S G S S K G Q Q P P R S A 61 TCCAACAGCTCCTCCGCCTCTTCGGGCAGCAGCAAGGGCAACAGCCGCCCCGCTCCGCC 41 S A G P A G E S S K P K S D G K N S S S G S 121 TCGGCGGGCCAGCCGGCGAGTCTAAACCCAAGAGCGATGGAAAGAACTCCAGTGGATCC 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 S S S Q K S K T F N K M P P Q R G 241 TCCCGTCGCTCCAGTTCACAGAAAAGCAAGACTTTTAACAAGATGCCTCCTCAAAGGGGC 101 G G S S S K L F S S S F N G G R R D E V A 301 GGCGGCAGCAGCAAACTCTTTAGCTCTTCTTTTAATGGTGGAAGACGAGATGAGGTAGCA 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 R G Q T G H F E G S 421 AACCACTTGTTGAATTTCACTTTTGAACCCCGTGGCCAGACGGTCACTTTGAAGGCAGT 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 GGACACATCTTCTGCTGGGCATGCATCCTGCACTATCTTTCACTGAGTGAGAAGACGTGG	SEQ ID NO:275

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		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 AAAGGGGGTGTTGGTGGCTTTGCCCAAATCCAATGGATGAATGTAGACCATCCCATTCAT	
		321 L G D E Q H S Q Y S K L L L A S K E Q V 961 CTAGGAGATGAACAGCACACAGCCAGTACTCCAAGTTGCTGCTGGCCTCTAAGGAGCAGGTG	
		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 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 CAACTGGTGCTGATGGCTCCCTTGGCGAAGGAGTCTGTTTTTCAACCCAGGAAGGGTGTG	
		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 P E P 1321 TCTAGACCTCTTGCTCTCCCTCTGGTAGAAGAGGAAGCAGTGTCTGAACCAGAGCCT	
		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 ACCATTTGCACTGAGTCCAGCCAGCAGGAACCCATCACCAAGTCAGGCTTCACACGCCTC	
		501 S S S P C Y Y F Y Q A E D G Q H M F L H 1501 AGCAGCTCTCCTTGTTACTACTTTTACCAAGCGGAAGATGGACAGCATATGTTCCTGCAC	
		521 P V N V R C L V R E Y G S L E R S P E K 1561 CCTGTGAATGTGCGCTGCCTCGTGCGGGAGTACGGCGAGCCTGGAGAGGAGCCCCGAGAAG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		541 I S A T V V E I A G Y S M S E D V R Q R 1621 ATCTCAGCAACTGTGGTGGAGATTGCTGGCTACTCCATGTCTGAGGATGTTCGACAGCGT 561 H R Y L S H L P L T C E F S I C E L A L 1681 CACAGATATCTCTCTCACTTGCCACTCACCTGTGAGTTCAGCATCTGTGAACTGGCTTTG 581 Q P P V V S K E T L E M F S D D I E K R 1741 CAACCTCCTGTGGTCTCTAAGGAAACCCTAGAGATGTTCTCAGATGACATTGAGAAGAGG 601 K R Q R Q K K A R 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 CAGTTTCCTGCCTTCAATTCTTATACCTGCTCCTCTGATTCTGCTTTGGGTCCCACCAGC 661 T E G H G A L S I S P L S R S P G S H A 1981 ACCGAGGGCCATGGGGCCCTCTCCATTTCTCCTCTCAGCAGAAGTCCAGGTTCCCATGCA 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 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	
BM735585	Human Fc-epsilon-		

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
	receptor gamma-chain mRNA.	1 CAGAACGGCCGATCTCCAGCCCAAGATGATTCCAGCAGTGGTCTTGCTCTTACTCCTTTT 61 GGTTGAACAAGCAGCGGCCCTGGGAGAGCCTCAGCTTTGCTATATTCTGGATGCCATCCT 121 GTTCTTGTATGGTATTGTCCTCACCCTGCTCTACTGTCGACTCAAGATCCAGGTGCGAAA 181 GGCAGCTATAGCCAGCTATGAGAAATCAGATGCCGTTTACACGGGCTTGAGTACCCGGAC 241 CCAGGAGACTTATGAGACTCTGAAGCATGAGAAACCGCCCACAGTAACTTTAGAATAGATG 301 CGGTCATATTCTTCTTTGGCTTCTGGTTCTTCCAGCCCTCATGGTTGGCATCACACATGT 361 CTCCCTGCCATTAATGCTAGCTGACCCTACCCCTGTAATGATGCTATTCATTAATGT 421 GGACATCAGTGGTTCCTCTTCCCTGTTAAACACCTATGCTCAGATGCTATTCATTAATGT 481 TTATATTCTAGTCTCACTCTCTTGTCCCACCCTTCTTCTTCCCCATTCCCAACTCCAG 541 CTAAAATATGGGAAGGGAGAACCCCCAATAAAACTGCCATGGACTGGACTC 1 M I P A V V 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:276 SEQ ID NO:277
BM780906	No homology	1 GGGGTTTCTCCCCCTCCTTTCCCTTTACCCGCAGTATCAAGCACAAGAATTGTTGGATTAA 61 AAAAAGAACTGATATCTTAGAACCCGAAAGAATCAATTGAATAGGATAAATCAGTACGTC 121 AGTGGTGGAGCTTTTGCCTGTAGCTTGAGAGGGGAAAGGTGGGAGGGAAAGGAGAAAACG 181 AAAGCTGAAACACATCTCTTGGGTCCTCCTGTTCCGTTTTCAAGGACCAGTCAGCTTCCC 241 ATCATAGTTTTGCCG	SEQ ID NO:278
BM780914	No homologies	1 GGCACGAGAGGTACAGGACTTTGAAACGTTCTACGGGATGCCCAATCCCGGGACCTACAC 61 CGTAAGGATAAGAGCCCGTGGGTACTTCACCGGAATCGTGAGCGAGTGGAGCGCCCCCAA 121 GAACTTTGTGTGCGACCCCGAGGAGGAGGGCGCGCGCCTCCGCGTCCGGCTGACCGCCTC 181 GCTGACCGCGCTGGGCCCGCTGCTCGCTGGGGCTCCTCGTCCTCGATCTGCAGAAAGTA 241 CTCGCTGATGCGGAA	SEQ ID NO:279
BM780999	Homo sapiens male-specific lethal 3-	1 GGCTGCCCCGGAGCCTCGCCCTCCGCCACGATGAGCAAATGAGCGCGAGCGAGGGCATGA	SEQ ID NO:280

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
	like 1 (Drosophila), transcript variant 1, mRNA	61 AATTTAAATTCCACTCAGGGGAGAAAGTGCTGTGCTTCGAGCCTGACCCCACCAAGGCGC 121 GAGTGCTGTACGATGCCAAGATTGTTGATGTTATTGTTGGGAAAGACGAAAAAGGCAGAA 181 AGATCCCAGAATATCTGATCCATTTTAATGGTTGGAACAGAAGCTGGGATAGATGGGCAG 241 CAGAAGATCATGTGCTTCGTGATACCGATGAAAATCGTAGATTACAGCGTAAATTGGCAA 301 GAAAAGCTGTAGCTCGCCTGAGGAGCACAGGAAGAAAGAAGAAGCGCTGCAGGTTGCCTG 361 GTGTGGACTCTGTCTTAAAAGGCCTCCCCACTGAAGAAAAAGATGAAAATGATGAAAACT 421 CATTAAGCAGTTCCTCTGACTGTAGTGAAAACAAGGATGAAGAAATAAGTGAAGAAAGTG 481 ATATTGAAGAAAAGACTGAAGTGAAAGAAGAACCAGAGCTTCAAACAAGAAGGGAAATGG 541 AAGAAAGAACAATAACTATAGAAATCCCTGAAGTTCTGAAGAAGCAGCTGGAGGATGATT 601 GTTACTACATTAACAGGAGGAAACGGTTAGTGAAACTTCCATGCCAGACCAACATCATAA 661 CGATTTTGGAATCCTATGTGAAGCATTTTGCTATCAATGCAGCCTTTTCAGCCAATGAGA 721 GGCCTCGTCACCATCACGTTATGCCACATGCCAACATGAACGTGCATTATATCCCAGCAG 781 AAAAGAATGTTGACCTTTGTAAGGAGATGGTGGATGGATTAAGAATAACCTTTGATTACA 841 CTCTCCCGTTGGTTTTACTCTATCCATATGAACAAGCTCAGTATAAAAAGGTGACTTCGT 901 CTAAATTTTTTCTTCCAATTAAGGAAAGTGCCACAAGCACTAACAGGAGCCAGGAGGAAC 961 TCTCTCCCAGTCCGCCTTTGTTGAATCCATCCACGCCACAGTCCACAGAGAGTCAGCCGA 1021 CCACCGGTGAACCAGCCACCCCCAAAAGGCGCAAAGCTGAGCCAGAAGCATTGCAGTCTC 1081 TGAGGCGGTCCACGCGCCACAGTGCCAACTGTGACAGGCTTTCTGAGAGCAGCGCTTCAC 1141 CTCAGCCCAAGCGCCGGCAGCAGGACACATCCGCCAGCATGCCCAAGCTCTTCCTGCACC 1201 TGGAAAAGAAGACACCTGTGCATAGCAGATCATCTTCACCTATTCCTCTGACTCCTAGCA 1261 AGGAAGGGAGTGCTGTGTTTGCTGGCTTTGAAGGGAGAAGAACTAATGAAATAAACGAGG 1321 TCCTCTCCTGGAAGCTTGTGCCTGACAATTACCCCCCAGGTGACCAGCCGCCTCCACCCT 1381 CTTACATTTATGGGGCACAACATTTGCTGCGATTGTTTGTGAAACTTCCAGAAATCCTTG 1441 GAAAGATGTCCTTTTCTGAGAAGAATCTGAAGGCTTTATTGAAGCACTTTGATCTCTTTT 1501 TGAGGTTTTTAGCAGAATACCACGATGACTTCTTCCCAGAGTCGGCTTATGTCGCTGCCT 1561 GTGAGGCACATTACAGCACCAAGAACCCCCGGGCAATTTATTAAAATGTTGTTGGTTCTG 1621 TAAGAGCAACTGCTCTGTCTAGTTTGGCGCTCTGGGTTCCAGGTGAATAACTAACAAGGT 1681 GGTGGGTCTTTACCCACAGCGCAAACACAATGCCCACCTTGGGGCTCTGTTGTTTGAGTT 1741 GCCCACATACTGCAGTTATTCTGTTAGGAATGATTCCCTGGGTGCCTGAAAGTGCTCTGA 1801 CACGACACTTGTTACTTTGCAGGCCATCTGTGATGGCAAGGAAAAAGCAACTATGTTCAC 1861 AGTGAAATATTCGTGGAATAGGTTAGGCCATTTCAGTAGACATTGCAGTTAGTTAGCAAG 1921 AACCACATTGTCTCTTTATTTGTTAGCATTAAACAAATTTTTTTTTTGCAAATTGGTTTT 1981 ATTTTTTTGATGAGGCCGAGCAACTCTGTCCAACAGATTTTAGTTTTGCTTGGAAACCGC 2041 AAGGTAGTCCCAGAATATTTTAGAGGAATTGATATTGATGGCAAAAGAAAATTTGCAGCT 2101 ATACATTTGCTTGTTACAGTTCATTTTCTCTAAAACCTTATTTTTGGTGATCTAAATAAA 2161 GCATTTCCTGTCTTGTTTGAGATTTTACAGCTGTACTTTGTTGTGTAATGTTATGGTTCC 2221 CTTTCTGTAAACCTTATTTNTGGTGATCTAAATAAAGCCTGTCTTGTTTGAAAGAAAAAA 2281 AAAAAAAAAA 1 M S A S E G M K F K F H S G E K V L C F 1 ATGAGCGCGAGCGAGGGCATGAAATTTAAATTCCACTCAGGGGAGAAAGTGCTGTGCTTC 21 E P D P T K A R V L Y D A K I V D V I V	SEQ ID NO:281

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		61 GAGCCTGACCCCACCAAGGCGCGAGTGCTGTACGATGCCAAGATTGTTGATGTTATTGTT	
		41 G K D E K G R K I P E Y L I H F N G W N	
		121 GGGAAAGACGAAAAAGGCAGAAAGATCCCAGAATATCTGATCCATTTTAATGGTTGGAAC	
		61 R S W D R W A A E D H V L R D T D E N R	
		181 AGAAGCTGGGATAGATGGGCAGCAGAAGATCATGTGCTTCGTGATACCGATGAAAATCGT	
		81 R L Q R K L A R K A V A R L R S T G R K	
		241 AGATTACAGCGTAAATTGGCAAGAAAAGCTGTAGCTCGCCTGAGGAGCACAGGAAGAAG	
		101 K K R C R L P G V D S V L K G L P T E E	
		301 AAGAAGCGCTGCAGGTTGCCTGGTGTGGACTCTGTCTTAAAAGGCCTCCCCACTGAAGAA	
		121 K D E N D E N S L S S S S D C S E N K D	
		361 AAAGATGAAAATGATGAAAACTCATTAAGCAGTTCCTCTGACTGTAGTGAAAACAAGGAT	
		141 E E I S E E S D I E E K T E V K E E P E	
		421 GAAGAAATAAGTGAAGAAAGTGATATTGAAGAAAAGACTGAAGTGAAAGAAGAACCAGAG	
		161 L Q T R R E M E E E R T I T I E I P E V L	
		481 CTTCAAACAAGAAGGGAAATGGAAGAAAGAACAATAACTATAGAAATCCCTGAAGTTCTG	
		181 K K Q L E D D C Y Y I N R R K R L V K L	
		541 AAGAAGCAGCTGGAGGATGATTGTTACTACATTAACAGGAGGAAACGGTTAGTGAAACTT	
		201 P C Q T N I I T T I L E S Y V K H F A I N	
		601 CCATGCCAGACCAACATCATAACGATTTTGGAATCCTATGTGAAGCATTTTGCTATCAAT	
		221 A A F S A N E R P R H H H V M P H A N M	
		661 GCAGCCTTTTCAGCCAATGAGAGGCCTCGTCACCATCACGTTATGCCACATGCCAACATG	
		241 N V H Y I P A E K N V D L C K E M V D G	
		721 AACGTGCATTATATCCCAGCAGAAAAGAATGTTGACCTTTGTAAGGAGATGGTGGATGGA	
		261 L R I T F D Y T L P L V L L Y P Y E Q A	
		781 TTAAGAATAACCTTTGATTACACTCTCCCGTTGGTTTTACTCTATCCATATGAACAAGCT	
		281 Q Y K K V T S S K F F L P I K E S A T S	
		841 CAGTATAAAAAGGTGACTTCGTCTAAATTTTTTCTTCCAATTAAGGAAAGTGCCACAAGC	
		301 T N R S Q E E L S P S P P L L N P S T P	
		901 ACTAACAGGAGCCAGGAGGAACTCTCCCAGTCCGCCTTTGTTGAATCCATCCACGCCA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		321 Q S T E S S Q P T T T G E P P A T P K R R R K A 961 CAGTCCACAGAGAGTCAGCCGACCACCGGTGAACCAGCCACCCCCAAAAGGCGCAAAGCT 341 E P E A L Q S L R R S T R H S A N C D R 1021 GAGCCAGAAGCATTGCAGTCTCTGAGGCGGTCCACGCGCCACAGTGCCAACTGTGACAGG 361 L S E S S A S P Q P K R R R Q Q D T S A S 1081 CTTTCTGAGAGCAGCGCTTCACCTCAGCCCAAGCGCCGGCAGCAGGACACATCCGCCAGC 381 M P K L F L H L E K K T P V H S R S S S 1141 ATGCCCAAGCTCTTCCTGCACCTGGAAAAGAAGACACCTGTGCATAGCAGATCATCTTCA 401 P I P L T P S K E G S A V F A G F E G R 1201 CCTATTCCTCTGACTCCTAGCAAGGAAGGGAGTGCTGTGTTTGCTGGCTTTGAAGGAGA 421 R T N E I N E V L S W K L V P D N Y P P 1261 AGAACTAATGAAATAAACGAGGTCCTCTCCTGGAAGCTTGTGCCTGACAATTACCCCCCA 441 G D Q P P P S Y I Y G A Q H L L R L F 1321 GGTGACCAGCCGCCTCCACCCTCTTACATTTATGGGGCACAACATTTGCTGCGATTGTTT 461 V K L P E I L G K M S F S E K N L K A L 1381 GTGAAACTTCCAGAAATCCTTGGAAAGATGTCCTTTTCTGAGAAGAATCTGAAGGCTTTA 481 L K H F D L F L R F L A E Y H D D F F P 1441 TTGAAGCACTTTGATCTCTTTTTGAGGTTTTTAGCAGAATACCACGATGACTTCTTCCCA 501 E S A Y V A A C E A H Y S T K N P R A I 1501 GAGTCGGCTTATGTCGCTGCCTGTGAGGCACATTACAGCACCAAGAACCCCCGGGCAATT 521 Y - 1561 TATTAA	
BM781033	Homo sapiens replication protein A1, 70kDa, mRNA	1 GGAGCTGTTGCGGGGTCCGCGGGGAAGTCTTGGCGGTGGAGCCATGGTCGGCCAACTGAG 61 CGAGGGGGCCATTGCGGCCATCATGCAGAAGGGGGATACAAACATAAAGCCCATCCTCCA 121 AGTCATCAACATCCGTCCCCATTACTACGGGGAATAGTCCGCCGCGTTATCGACTGCTCAT 181 GAGTGATGGATTGAACACTCTATCCTCTTTCATGTTGGCGACACAGTTGAACCCCTCGT 241 GGAGGAAGAACAATTGTCCAGCAACTGTGTATGCCAGATTCACAGATTTATTGTGAACAC 301 TCTGAAAGACGGAAGGAGAGTAGTTATCTTGATGGAATTAGAAGTTTTGAAGTCAGCTGA 361 AGCAGTTGGAGTGAAGATTGGCAATCCAGTGCCCTATAATGAAGGACTCGGGCAGCCGCA 421 AGTAGCTCCTCCAGCGCCAGCAGCCAGCCCAGCAGCAAGCAGCAGGCCCCAGCCGCAGAA	SEQ ID NO:282

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		481 TGGAAGCTCGGGAATGGGTTCTACTGTTTCTAAGGCTTATGGTGCTTCAAAGACATTTGG 541 AAAAGCTGCAGGTCCCAGCCTGTCACACACTTCTGGGGGAACACAGTCCAAAGTGGTGCC 601 CATTGCCAGCCTCACTCCTTACCAGTCCAAGTGGACCATTTGTGCTCGTGTTACCAACAA 661 AAGTCAGATCCGTACCTGGAGCAACTCCCGAGGGGAAGGGAAGCTTTTCTCCCTAGAACT 721 GGTTGACGAAAGTGGTGAAATCCGAGCTACAGCTTTCAATGAGCAAGTGGACAAGTTCTT 781 TCCTCTTATTGAAGTGAACACAAGGTGTATTATTTCTCGAAAGGCACCCTGAAGATTGCTAA 841 CAAGCAGTTCACAGCTGTTAAAAATGACTACGAGATGACCTTCAATAACGAGACTTCCGT 901 CATGCCCTGTGAGGACGACCATCATTTACCTACGGTTCAGTTTGATTTCACGGGGATTGA 961 TGACCTCGAGAACAAGTCGAAAGACTCACTTGTAGACATCATCGGGATCTGCAAGAGCTA 1021 TGAAGACGCCACTAAAATCACAGTGAGGTCTACAACAGAGAAGTTGCCAAGAGGAATAT 1081 CTACTTGATGGACACATCTGGGAAGGTGGTGACTGCTACACTGTGGGGGGAAGATGCTGA 1141 TAAATTTGATGGTTCTAGACAGCCCGTGTTGGCTATCAAAGGAGCCCGAGTCTCTGATTT 1201 CGGTGGACGGAGCCTCTCCGTGCTGTCTTCAAGCACTATCATTGCGAATCCTGACATCCC 1261 AGAGGCCTATAGCTTCGTGGATGTTTGACGCAGAAGGACAGCCTTAGATGGTGTTTC 1321 CATCTCTGATCTAAAGAGCGGCGGAGTCGGAGGGAGTAACACCAACTGGAAAACCTTGTA 1381 TGAGGTCAAATCCGAGAACCTGGGCCAAGGCGACAAGCCGGACTACTTTAGTTCTGTGGC 1441 CACAGTGGTGTATCTTCGCAAAGAGAACTGCATGTACCAAGCCTGCCCGACTCAGGACTG 1501 CAATAAGAAAGTGATTGATCACAGAATGGATTGTACCGCTGTGAGAAGTGCGACACCGA 1561 ATTTCCCAATTTCCAAGTACCGCATGATCCTGTCAGTAAATATTGCAGATTTTCAAGAGAA 1621 TCAGTGGGTGACTTGTTTCCAGGAGTCTGCTGAAGCTATCCTTGGACAAAATGCTGCTTA 1681 TCTTGGGGAATTAAAAGACAGAATGAACAGGCATTTGAAGAAGTTTTCCAGAATGCCAA 1741 CTTCCGATCTTTTCATATTCAGAGTCAGGGTCAAAGTGGAGACCTACAACGACGAGTCTCG 1801 AATTAAGGCCACTGTGATGGACGTGAAGCCCGTGGACTACAGAGAGTATGGCCGAAGGCT 1861 GGTCATGAGCATCAGGAGAAGTGCATTGATGTGAGAGGAGCAGTGCCAATCGGGCAGAAG 1921 TTTGCAAATAGGCAGAATGGAATCGATTTCCTCCCACCTCCGTGTGACGATCCCATGTTA 1981 GCTACACAGTGCAGAGGCTCTTGATGGTGGACTAAGCAATTTCCTCCCTTGTGCGCATCT 2041 CAGAACCCATCGGTAGGCAAAGGAAAAATACGCTCAGGTGGTTGTGGTGTAGACTGTGTCA 2101 GGCCTACGGAGTCAGCCAGTGGCTAGCGCAAGACCAGTCACTCCCTCTGCCTTCAGGCTT 2161 CTGTCAATTTCATTATCTTCAAGCAGGAATTATGTTGCAAGTAAATTGACCCTAAATCTG 2221 CAGACAGTGAAATAAATTATGTAACTAGGTTTCTGCTTCTCCAGTGGTGACCACCCCCCC 2281 CCCATCCCCGCTCACAACTTGGGTTCTTCTCAGCGGGGCGAGCTGAGAAGCGGTCATGAG 2341 CACCTGGGTGTTTTAGTAAGCGCGTCTTCCTAGAATTCAAGGCGCTCTCTTCTAGAGG 2401 TGCCACATAGTTGTTAATGCTCAGAATGGCAATAGGTAGAATTATTAATCAAAGACATA 2461 TCTTTTATATCTGAAGATAGCCTTCCTTCAGGGTTTAATAGACTGAGTCAGATGGGTCTG 2521 ATATTAATCAAAATTGTCTCTTCTGAGGAAGGCTGATAAGCATTGACTTGCTGTCCCCCA 2581 GGGACATCCACGCAACTACAAAGCCTTGCTTTAGTTTCACTTCAATTAATGTTGCATTTT 2641 GGTTGGTGAATGCACACTTTTTCTACCTGTACACATTCCTGCATTCATGTATTTTGTTTTT 2701 TTTTGACTAAAGCTATGTTTACATGGAAAGGATTTTGAAGCCCTTTGTTTCTCTTGCTTTG 2761 TTTTAATAAACAGTATATTCTTTGGTTGTGAATCCTAAAAAAAAAAAAAAAAAAAAAAAA 2821 AAAAA 1 M V G Q L S E G G A I A A I M Q K G D T N 1 ATGGTCGGCCAACTGAGCGAGGGGGCCATTGCGGCCATCATGCAGAAGGGGGATACAAAC	SEQ ID NO:283

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		21 I K P I L Q V I N I R P I T T G N S P P 61 ATAAAGCCCATCCTCCAAGTCATCAACATCCGTCCCATTACTACGGGAATAGTCCGCCG	
		41 R Y R L L M S D G L N T L S S F M L A T 121 CGTTATCGACTGCTCATGAGTGATGGATTGAACACTCTATCCTCTTTCATGTTGGCGACA	
		61 Q L N P L V E E E Q L S S N C V C Q I H 181 CAGTTGAACCCTCTCGTGGAGGAAGAACAATTGTCCAGCAACTGTGTATGCCAGATTCAC	
		81 R F I V N T L K D G R R V V I L M E L E 241 AGATTTATTGTGAACACTCTGAAAGACGGAAGGAGAGTAGTTATCTTGATGGAATTAGAA	
		101 V L K S A E A V G V K I G N P V P Y N E 301 GTTTTGAAGTCAGCTGAAGCAGTTGGAGTGAAGATTGGCAATCCAGTGCCCTATAATGAA	
		121 G L G Q P Q V A P P A P A A S P A A S S 361 GGACTCGGGCAGCCGCAAGTAGCTCCTCCAGCGCCAGCCAGCCCAGCCAGCAAGCAGC	
		141 R P Q P Q N G S S G M G S T V S K A Y G 421 AGGCCCCAGCCGCAGAATGGAAGCTCGGGAATGGGTTCTACTGTTTCTAAGGCTTATGGT	
		161 A S K T F G K A A G P S L S H T S G G T 481 GCTTCAAAGACATTTGGAAAAGCTGCAGGTCCCAGCCTGTCACACACTTCTGGGGGAACA	
		181 Q S K V V P I A S L T P Y Q S K W T I C 541 CAGTCCAAAGTGGTGCCCATTGCCAGCCTCACTCCTTACCAGTCCAAGTGGACCATTTGT	
		201 A R V T N K S Q I R T W S N S R G E G K 601 GCTCGTGTTACCAACAAAAGTCAGATCCGTACCTGGAGCAACTCCCGAGGGGAAGGGAAG	
		221 L F S L E L V D D E S G E I R A T A F N E 661 CTTTTCTCCCTAGAACTGGTTGACGAAAGTGGTGAAATCCGAGCTACAGCTTTCAATGAG	
		241 Q V D K F F P L I E V N K V Y Y F S K G 721 CAAGTGGACAAGTTCTTTCCTCTTATTGAAGTGAACAAGGTGTATTATTTCTCGAAAGGC	
		261 T L K I A N K Q F T A V K N D Y E M T F 781 ACCCTGAAGATTGCTAACAAGCAGTTCACAGCTGTTAAAAATGACTACGAGATGACCTTC	
		281 N N E T S V M P C E D D H H L P T V Q F 841 AATAACGAGACTTCCGTCATGCCCTGTGAGGACGACCATCATTTACCTACGGTTCAGTTT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		301 D F T G I D D L E N K S K D S L V D I I 901 GATTTCACGGGATTGATGACCTCGAGAACAAGTCGAAAGACTCACTTGTAGACATCATC	
		321 G I C K S Y E D A T K I T V R S N N R E 961 GGGATCTGCAAGAGCTATGAAGACGCCACTAAAATCACAGTGAGGTCTAACAACAGAGAA	
		341 V A K R N I Y L M D T S G K V V T A T L 1021 GTTGCCAAGAGGAATATCTACTTGATGGACACATCTGGGAAGGTGGTGACTGCTACACTG	
		361 W G E D A D K F D G S R Q P V L A I K G 1081 TGGGGGGGAAGATGCTGATAAATTTGATGGTTCTAGACAGCCCGTGTTGGCTATCAAAGGA	
		381 A R V S D F G G R S L S V L S S S T I I 1141 GCCCGAGTCTCTGATTTCGGTGGACGGAGCCTCTCCGTGCTGTCTTCAAGCACTATCATT	
		401 A N P D I P E A Y K L R G W F D A E G Q 1201 GCGAATCCTGACATCCCAGAGGCCTATAAGCTTCGTGGATGGTTTGACGCAGAAGGACAA	
		421 A L D G V S I S D L K S G G V G G S N T 1261 GCCTTAGATGGTGTTTCCATCTCTGATCTAAAGAGCGGCGGAGTCGGAGGGAGTAACACC	
		441 N W K T L Y E V K S E N L G Q G D K P D 1321 AACTGGAAAACCTTGTATGAGGTCAAATCCGAGAACCTGGCCAAGGCGACAAGCCGGAC	
		461 Y F S S V A T V V Y L R K E N C M Y Q A 1381 TACTTTAGTTCTGTGGCCACAGTGGTGTATCTTCGCAAAGAGAACTGCATGTACCAAGCC	
		481 C P T Q D C N K K V I D Q Q N G L Y R C 1441 TGCCCGACTCAGGACTGCAATAAGAAAGTGATTGATCAACAGAATGGATTGTACCGCTGT	
		501 E K C D T E F P N F K Y R M I L S V N I 1501 GAGAAGTGCGACACCGAATTTCCCAATTTCAAGTACCGCATGATCCTGTCAGTAAATATT	
		521 A D F Q E N Q W V T C F Q E S A E A I L 1561 GCAGATTTTCAAGAGAATCAGTGGGTGACTTGTTTCCAGGAGTCTGCTGAAGCTATCCTT	
		541 G Q N A A Y L G E L K D K N E Q A F E E 1621 GGACAAAATGCTGCTTATCTTGGGGAATTAAAAGACAAGAATGAACAGGCATTTGAAGAA	
		561 V F Q N A N F R S F I F R V R V K V E T 1681 GTTTTCCAGAATGCCAACTTCCGATCTTTCATATTCAGAGTCAGGGTCAAAGTGGAGACC	
		581 Y N D E S R I K A T V M D V K P V D Y R	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1741 TACAACGACGAGTCTCGAATTAAGGCCACTGTGATGGACGTGAAGCCCGTGGACTACAGA 601 E Y G R R L V M S I R R S A L M - 1801 GAGTATGGCCGAAGGCTGGTCATGAGCATCAGGAGAAGTGCATTGATGTGA	
BM781067	Human mRNA for T3 epsilon chain (20K) of T-cell receptor (from peripheral blood lymphocytes).	1 GTAAGTCTGCTGGCCTCCGCCATCTTAGTAAAGTAACAGTCCCATGAAACAAAGATGCAG 61 TCGGGCACTCACTGGAGAGTTCTGGGCCTCTGCCTCTTATCAGTTGGCGTTTGGGGGCAA 121 GATGGTAATGAAGAAATGGGTGGTATTACACAGACACCATATAAAGTCTCCATCTCTGGA 181 ACCACAGTAATATTGACATGCCCTCAGTATCCTGGATCTGAAATACTATGGCAACACAAT 241 GATAAAAACATAGGCGGTGATGAGGATGATAAAAACATAGGCAGTGATGAGGATCACCTG 301 TCACTGAAGGAATTTTCAGAATTGGAGCAAAGTGGTTATTATGTCTGCTACCCCAGAGGA 361 AGCAAACCAGAAGATGCGAACTTTTATCTCTACCTGAAAGCCAGAGTGTGTGAGAACTGC 421 ATGGAGGTGGATCTGACGGCAGTGGCCACAATCATCGTAGTCGACCTCTGCATCACTCTG 481 GGCTTACTGCTGCTGGTGTATTACTGGAGCAAGTCTAAAAAGGCCAGGGCCAAGCCTGTG 541 ACGAGGGGAGCAGATGTTGGCGGCAGGCCCCGGGGACAAAACAAGGAGAGACCCCCGCCT 601 GTTCCCAATCCAGATTATGAGCCCATCCGGAAAGGCCAGCGGGACCTGTACGCTGGCCTG 661 AATCAGAGAGCCGTCTGACAGTTCCTGAGGACACTGCCTCCTGCTGGCCCAGCTCTCCTC 721 TCCAGTCCCCCTGCGACTCCCTGTTTCCTGGGCTAGTCTTGGACCCCACGAGAGAGAATC 781 GTTCCTCAGCCTCATGGTGAACTCGCGCCCTCCAGCCTGATCCCCCGCTCCCTCCTCCCT 841 GCCTTCTCTGCTGGTACCCAGTCCTAAAATATTGCTGCTTCCTCTTCCTTTGAAGCATCA 901 TCAGTAGTCACACCCTCACAGCTGGCCTGCCCTCTTGCCAGGATATTTATTTGTGCTATT 961 CACTCCCTTCCCTTTGGATGTAACTTCTCCGTTCAGTTCCCTCCTTTTCTTGCATGTAAG 1021 TTGTCCCCCATCCCAAAGTATTCCATCTACTTTTCTATCGCCGTCCCCTTTTGCAGCCCT 1081 CTCTGGGGATGGACTGGGTAAATGTTGACAGAGGCCCTGCCCCGTTCACAGATCCTGGCC 1141 CTGAGCCAGCCCTGTGCTCCTCCCTCCCCCAACACTCCCTACCAACCCCCTAATCCCCTA 1201 CTCCCTCCAACCCCCCCTCCCACTGTAGGCCCCTGGATGTTCGTTTGCATCTCCATGAAT 1261 GTGCTAGGCTCCTTGTCAGCTGAGAGAGAAAAGAAATAAAGTGTATTTGGCTGC 1 M Q S G T H W R V L G L C L L S V G V W 1 ATGCAGTCGGGCACTCACTGGAGAGTTCTGGGCCTCTGCCTCTTATCAGTTGGCGTTTGG 21 G Q D G N E E M G G I T Q T P Y K V S I 61 GGGCAAGATGGTAATGAAGAAATGGGTGGTATTACACAGACACCATATAAAGTCTCCATC 41 S G T T V I L T C P Q Y P G S E I L W Q 121 TCTGGAACCACAGTAATATTGACATGCCCTCAGTATCCTGGATCTGAAATACTATGGCAA 61 H N D K N I G G D E D D K N I G S D E D 181 CACAATGATAAAAACATAGGCGGTGATGAGGATGATAAAAACATAGGCAGTGATGAGGAT 81 H L S L K E F S E L E Q S G Y Y V C Y P 241 CACCTGTCACTGAAGGAATTTTCAGAATTGGAGCAAAGTGGTTATTATGTCTGCTACCCC	SEQ ID NO:284 SEQ ID NO:285

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		101 R G S K P E D A N F Y L Y L K A R V C E 301 AGAGGAAGCAAACCAGAAGATGCGAACTTTTATCTCTACCTGAAAGCCAGAGTGTGTGAG 121 N C M E V D L L T A V A T I I V V D L C I 361 AACTGCATGGAGGTGGATCTGACGGCAGTGGCCACAATCATCGTAGTCGACCTCTGCATC 141 T L G L L L L V Y Y W S K S K K A R A K 421 ACTCTGGGCTTACTGCTGCTGGTGTATTACTGGAGCAAGTCTAAAAAGGCCAGGGCCAAG 161 P V T R G A D V G G R P R G Q N K E R P 481 CCTGTGACGAGGGGAGCAGATGTTGGCGGCAGGCCCCGGGGACAAAACAAGGAGAGACCC 181 P P V P N P D Y E P I R K G Q R D L Y A 541 CCGCCTGTTCCCAATCCAGATTATGAGCCCATCCGGAAAGGCCAGCGGGACCTGTACGCT 201 G L N Q R A V - 601 GGCCTGAATCAGAGAGCCGTCTGA	
BM781103	Human mRNA for cathepsin H	1 TTGCCGGCGCAAGAGCCAAGCCGCCAGCGCTGCTATGTGGGCCACGCTGCCGCTGCTCTG 61 CGCCGGGGCCTGGCTCCTGGGAGTCCCCGTCTGCGGTGCCGCCGAACTGTCCGTGAACTC 121 CTTAGAGAAGTTTCACTTCAAGTCATGGATGTCTAAGCACCGTAAGACCTACAGTACGGA 181 GGAGTACCACCACAGGCTGCAGACGTTTGCCAGCAACTGGAGGAAGATAAACGCCCACAA 241 CAATGGGAACCACACATTTAAAATGGCACTGAACCAATTTTCAGACATGAGCTTTGCTGA 301 AATAAAACACAAGTATCTCTGGTCAGAGCCTCAGAATTGCTCAGCCACCAAAGTAACTA 361 CCTTCGAGGTACTGGTCCCTACCCACCTTCCGTGGACTGGCGGAAAAAGGAAATTTTGT 421 CTCACCTGTGAAAAATCAGGGTGCCTGCGGCAGTTGCTGGACTTTCTCCACCACTGGGGC 481 CCTGGAGTCTGCAATCGCCATCGCAACCGGAAAGATGCTGTCCTTGGCGGAACAGCAGCT 541 GGTGGACTGCGCCCAGGACTTCAATAATTACGGCTGCCAAGGGGGTCTCCCCAGCCAGGC 601 TTTCGAGTATATCCTGTACAACAAGGGGATCATGGTGAAGACACCTACCCCTACCAGGG 661 CAAGGATGGTTATTGCAAGTTCCAACCTGGAAAGGCCATCGGCTTTGTCAAGGATGTAGC 721 CAACATCACAATCTATGACGAGGAAGCGATGGTGGAGGCTGTGTGGCCCTCTACAACCCTGT 781 GAGCTTTGCCTTTGAGGTGACTGAAGACTTTATGATGTACAGAAAGGGCATCTACTCCAG 841 TACTTCCTGTCATAAAACTCCAGATAAAGTAAACCACGCAGTACTGGCTGTTGTGGGTATGG 901 AGAAGAAAATGGGATACCCTACTGGATCGTGAAAAACTCTTGGGGTCCCCACTGGGGCAT 961 GAACGGGTACTTCCTCATTGAGCGTGGGAAGAACATGTGTGGTCTGGCCGCCTGTGCCTC 1021 CTACCCCATCCCTCTGGTGTGAGCCGTGGCAGCCGCAGCGCAGACTGGCGGAGAAGGAGA 1081 GGAACGGGCAGCCTGGCCATTGGTGGAAGTCCTGCCCTGGAGGAAGTTGTGGGGAGATCC 1141 ACTGGGACCCCCAACATTCTGCCCTCACCTCTGTGCCCAGCCTGGAAACCTACAGACAAG 1201 GAGGAGTTCCACCATGAGCTCACCCGTGTCTATGACGCAAAGATCACCAGCCATGTGCCT 1261 TAGTGTCCTTCTTAACTGACTCAAACCCACGTGGACCAAGAATATTCTTTCCTTCCTGAA 1321 GGGCTACTTTTCACATATAGAGCTCCAGGGACTGTCTTTCTGTATTCGCTGTTCAATAA	SEQ ID NO:286

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1381 ACATTGAGTGAGCACCTCCA	
		1 M W A T L P L L C A G G A W L L G V P V C	SEQ ID NO:287
		1 ATGTGGGCCACGCTGCCGCTGCTCTGCGCCGGGCCTGGCTCCTGGGAGTCCCCGTCTGC	
		21 G A A A E L S V N S L E E K F H H F K S W M S	
		61 GGTGCCGCCGAACTGTCCGTGAACTCCTTAGAGAAGTTTCACTTCAAGTCATGGATGTCT	
		41 K H R R K T Y S T E E E Y H H R R L Q T T F A S	
		121 AAGCACCGTAAGACCTACAGTACGGAGGAGTACCACCACACAGGCTGCAGACGTTTGCCAGC	
		61 N W R R K I N N A H N N G N N H T T F K M A L N	
		181 AACTGGAGGAAGATAAACGCCCACACAACAATGGGAACCACACATTTAAAATGGCACTGAAC	
		81 Q F S D M S F A E E I K H H K Y L W S E P P Q	
		241 CAATTTTCAGACATGAGCTTTGCTGAAATAAAACACAAGTATCTCTGGTCAGAGCCTCAG	
		101 N C S A T K S N Y L R G T G P Y P P S V	
		301 AATTGCTCAGCCACCAAAAGTAACTACCTTCGAGGTACTGGTCCCTACCCACCTTCCGTG	
		121 D W R R K K G N F V S P V K N Q G A C G S	
		361 GACTGGCGGAAAAAGGAAATTTTGTCTCACCTGTGAAAAATCAGGGTGCCTGCGGCAGT	
		141 C W T F S T T G A L E S A I A I A T G K	
		421 TGCTGGACTTTCTCCACCACTGGGGCCCTGGAGTCTGCAATCGCCATCGCAACCGGAAAG	
		161 M L S L A E Q Q L V D D C A Q D F N N Y G	
		481 ATGCTGTCCTTGGCGGAACAGCAGCTGGTGGACTGCGCCCAGGACTTCAATAATTACGGC	
		181 C Q G G L P S Q A F E Y I L Y N K G I M	
		541 TGCCAAGGGGGTCTCCCCAGCCAGGCTTTCGAGTATATCCTGTACAACAAGGGGATCATG	
		201 G E D T Y P Y Q G G K D G Y C K F Q P G K	
		601 GGTGAAGACACCTACCCCTACCAGGGCAAGGATGGTTATTGCAAGTTCCAACCTGGAAAG	
		221 A I G F V K D V A N N I T I Y D E E A M V	
		661 GCCATCGGCTTTGTCAAGGATGTAGCCAACATCACAATCTATGACGAGGAAGCGATGGTG	
		241 E A V A L Y N P V S F A F E V T E D F M	
		721 GAGGCTGTGGCCCTCTACAACCCTGTGAGCTTTGCCTTTGAGGTGACTGAAGACTTTATG	
		261 M Y R K G I Y S S T S C H K T P D K V N	
		781 ATGTACAGAAAGGGCATCTACTCCAGTACTTCCTGTCATAAAACTCCAGATAAAGTAAAC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		281 H A V L A V G Y G E E N G I P Y W I V K 841 CACGCAGTACTGGCTGTTGGGTATGGAGAAGAAAATGGGATACCCTACTGGATCGTGAAA 301 N S W G P H W G M N G Y F L I E R G K N 901 AACTCTTGGGGTCCCCACTGGGGCATGAACGGGTACTTCCTCATTGAGCGTGGGAAGAAC 321 M C G L A A C A S Y P I P L V - 961 ATGTGTGGTCTGGCCGCCTGTGCCTCCTACCCCATCCCTCTGGTGTGA	
BM781186	Homo sapiens membrane-spanning 4-domains, subfamily A, member 6A, transcript variant 1, mRNA (cDNA clone MGC:22650 IMAGE:3934920).	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 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	SEQ ID NO:288 SEQ ID NO:289

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		121 CTAAAGGCAGAGGTCAAAGTTCTCGGGACTATCCAGATCCTGTGTGGGATGATGGTGTTG	
		61 S L G G I I L L A S A S F S Q H F T Q A F S 181 AGTTTGGGAATTATTTTGGCATCGGCTTCCTTCTCTCAGCATTTACCCAAGCGTTTCT	
		81 I L L L K A 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 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 AACATTCTGAGCTCTCTATCAGCTCTGGTGGGTTTCATCCTCCTTCTGTCAAACAGGCC	
		141 T L N P A S L Q C E L D K N N I P T R S 421 ACCTTAAATCCTGCCTCACTGCAGTGTGAGTTGGACAAAAATAATATACCAACAGAAGT	
		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 AGTCTGGCTGGATCCCTCTCTCTGATGCTGATTTGCACTCTGCTGGAATTCTGCCTAGCT	
		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	
BM781233	H.sapiens mRNA for elongation factor 1-beta.	1 GCCTCGAGGCGGCGTCTTCGGTCATCTCCGGCGCTTCTAGGGCTGGTTCCCGTCATCTT 61 CGGGAGCCGTGGAGCTCTCGGATACAGCCGACACCATGGGTTTCGGAGACCTGAAAAGCC 121 CTGCCGGCCTCCAGGTGCTCAACGATTACCTGGCGGACAAGAGCTACATCGAGGGTATG 181 TGCCATCACAAGCAGATGTGGCAGTATTTGAAGCCGTGTCCAGCCCACCGCCTGCCGACT 241 TGTGTCATGCCCTACGTTGGTATAATCACATCAAGTCTTACGAAAAGGAGAAGGCCAGTC 301 TGCCAGGAGTGAAGAAAGCTTTGGGCAAGTATGGTCCTGCGGATGTGGAAGACACCACAG 361 GAAGTGGAGCTACCGATAGTAAAGACGACGATGACATAGATCTCTTTGGGTCTGATGACG 421 AGGAGGAAAGTGAAGAAGCGAAGAGGCTAAGAGAAGAAGAACGCCTTGCACAGTATGAGTCAA 481 AGAAAGCCAAGAAACCTGCACTTGTTGCCAAGTCTTCCATCTTACTAGATGTGAAACCTT 541 GGGATGACGAGACAGATATGGCAAAGCTGGAGGAGTGCGTCAGAAGCATTCAAGCAGACG	SEQ ID NO:290

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		601 GCTTGGTCTGGGGCTCCTCTAAACTAGTTCCAGTGGGTATGGAATTAAAAAACTTCAAA 661 TACAGTGTGTAGTTGAAGACGATAAAGTTGGAACTGATATGCTGGAGGAGCGGATCACTG 721 CTTTTGAGGACTATATGTGCAGTCCATGGATGTGGCCGCTTTCAACAAGATCTAAAACCCGT 781 CGTGGATCATGGCATTTAAATAAAAGATTGAAAGATTA 1 M G F G D L K S P A G L Q V L N D Y L A 1 ATGGGTTTCGGAGACCTGAAAAGCCCTGCCGGCCTCCAGGTGCTCAACGATTACCTGGCG 21 D K S Y I E G Y V P S Q A D V A V F E A 61 GACAAGAGCTACATCGAGGGGTATGTGCCATCACAAGCAGATGTGGCAGTATTTGAAGCC 41 V S S P P P A D L C H A L R W Y N H I K 121 GTGTCCAGCCCACCGCCTGCCGACTTGTGTCATGCCCTACGTTGGTATAATCACATCAAG 61 S Y E K E K A S L P G V K K A L G K Y G 181 TCTTACGAAAAGGAGAAGGCCAGTCTGCCAGGAGTGAAGAAAGCTTTGGGCAAGTATGGT 81 P A D V E D T T G S G A T D S K D D D D D 241 CCTGCGGATGTGGAAGACACCACAGGAAGTGGAGCTACCGATAGTAAAGACGACGATGAC 101 I D L F G S D D E E E S E E A K R L R E 301 ATAGATCTCTTTGGGTCTGATGACGAGGAGGAAAGTGAAGAAGCGAAGAGGCTAAGAGAA 121 E R L A Q Y E S K K A K K P A L V A K S 361 GAACGCCTTGCACAGTATGAGTCAAAGAAAGCCAAGAAACCTGCACTTGTTGCCAAGTCT 141 S I L L D V K P W D D E T D M A K L E E 421 TCCATCTTACTAGATGTGAAACCTTGGGATGACGAGACAGATATGGCAAAGCTGGAGGAG 161 C V R S I Q A D G L V W G S S K L V P V 481 TGCGTCAGAAGCATTCAAGCAGACGGCTTGGTCTGGGGCTCCTCTAAACTAGTTCCAGTG 181 G Y G I K K L Q I Q C V V E D D K V G T 541 GGGTATGGAATTAAAAAACTTCAAATACAGTGTGTAGTTGAAGACGATAAAGTTGGAACT 201 D M L E E R I T A F E D Y V Q S M D V A 601 GATATGCTGGAGGAGCGGATCACTGCTTTTGAGGACTATGTGCAGTCCATGGATGTGGCC 221 A F N K I - 661 GCTTTCAACAAGATCTAA	SEQ ID NO:291
BM781237	Homo sapiens transforming	1 ggcggcggta gcagccaggc ttggcccccg gcgtggagca gacgcggacc cctccttcct	SEQ ID NO:292

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
	acidic coiled-coil containing protein 3 (TACC3) mRNA	61 ggcggcggcg gcgcgggctc agagcccggc aacgggcggg cgggcagaat gagtctgcag 121 gtcttaaacg acaaaaatgt cagcaatgaa aaaaatacag aaaattgcga cttcctgttt 181 tcgccaccag aagttaccgg aagatcgtct gttcttcgtg tgtcacagaa agaaaatgtg 241 ccacccaaga acctggccaa agctatgaag gtgacttttc agacacctct gcgggatcca 301 cagacgcaca ggattctaag tcctagcatg gccagcaaac ttgaggctcc tttcactcag 361 gatgcaccc ttggactgga aaactcacac ccggtctgga cacagaaaga gaaccaacag 421 ctcatcaagg aagtggatgc caaaactact catggaattc tacagaaacc agtggaggct 481 gacaccgacc tcctgggga tgcaagccca gcctttggga gtggcagctc cagcgagtct 541 ggcccaggtg ccctggctga cctggactgc tcaagctctt cccagagccc aggaagttct 601 gagaaccaaa tggtgtctcc aggaaaagtg tctggcagcc ctgagcaagc cgtggaggaa 661 aaccttagtt cctattcctt agacagaaga gtgacacccg cctctgagac cctagaagac 721 ccttgcagga cagagtccca gcacaaagcg gagactccgc acggagccga ggaagaatgc 781 aaagcggaga ctccgcacgg agccgaggag gaatgccggc acggtgaggt ctgtgctccc 841 gcagcagtgg ccacttcgcc tcctggtgca atcctaagg aagcctgcgg aggagcaccc 901 ctgcagggtc tgcctggcga agccctgggc tgccctgcgg gtgtgggcac ccccgtgcca 961 gcagatggca ctcagaccct tacctgtgca cacacctctg ctcctgagag cacagcccca 1021 accaaccacc tggtggctgg cagggccatg acctgagtc ctcaggaaga agtggctgca 1081 ggccaaatgg ccagctcctc gaggagcgga cctgtaaaac tagaatttga tgtatctgat 1141 ggcgccacca gcaaaagggc accccacca aggagactgg gagagaggtc cggcctcaag 1201 cctcccttga ggaaagcagc agtgaggcag caaaaggccc cgcaggaggt ggaggaggac 1261 gacggtagga gcggagcagg agaggacccc cccatgccag ctcctcgggg ctcttaccac 1321 ctcgactggg acaaaatgga tgacccaaac ttcatccccgt tcggaggtga caccaagtct 1381 ggttgcagtg aggccagcc cccagaaagc cctgagacca ggctgggcca gccagcggct 1441 gaacagttgc atgctgggcc tgccacggag gagccaggtc cctgtctgag ccagcagctg 1501 cattcagcct cagcggagga cacgcctgtg gtgcagttgg cagccgagac cccaacagca 1561 gagagcaagg agagagcctt gaactctgcc agcacctcgc ttcccacaag ctgtccaggc 1621 agtgagccag tgcccaccca tcagcagggg cagcctgcct tggagctgaa agaggagagc 1681 ttcagagacc ccgtgaggt tctaggcacg ggcgcggagg tggattacct ggagcagttt 1741 ggaacttcct cgtttaagga gtcggccttg aggaagcagt ccttatacct caagttcgac 1801 cccctcctga gggacagtcc tggtagacca gtgcccgtgg ccaccgagac cagcagcatg 1861 cacggtgcaa atgagactcc ctcaggacgt ccgcgggaag ccaagcttgt ggagttcgat 1921 ttcttgggag cactggacat tcctgtgcca ggcccacccc caggtgttcc cgcgcctggg 1981 ggcccacccc tgtccaccgg acctatagtg gacctgctcc agtacagcca gaaggacctg 2041 gatgcagtgg taaaggcgac acaggaggag aaccgggagc tgaggagcag gtgtgaggag 2101 ctccacgggga agaacctgga actggggaag atcatggaca ggttcgaaga ggttgtgtac 2161 caggccatgg aggaagttca gaagcagaag gaactttcca aagctgaaat ccagaaagtt 2221 ctaaaagaaa aagaccaact taccacagat ctgaactcca tggagaagtc cttctccgac 2281 ctcttcaagc gttttgagaa acagaaagag gtgatcgagg gctaccgcaa gaacgaagag 2341 tcactgaaga agtgcgtgga ggattacctg gcaaggatca cccaggaggg ccagaggtac 2401 caagccctga aggcccacgc ggaggagaag ctgcagctgg caaacgagga gatcgcccag 2461 gtccggagca aggcccaggc ggaagcgttg gccctccagg ccagcctgag gaaggagcag 2521 atgcgcatcc agtcgctgga gaagacagtg gagcagaaga ctaaagagaa cgaggagctg 2581 accaggatct gcgacgacct catctccaag atggagaaga tctgacctcc acggagccgc	SEQUENCE IDENTIFIER:

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2641 tgtccccgcc cccctgctcc cgtctgtctg tcctgtctga ttctctttagg tgtcatgttc 2701 ttttttctgt cttgtcttca acttttttta aaactagatt gctttgaaaa catgactcaa 2761 taaaagtttc ctttcaattt aaaaaaaa 1 M S L Q V L N D K N V S N E K N T E N C 1 ATGAGTCTGCAGGTCTTAAACGACAAAAATGTCAGCAATGAAAAAATACAGAAAATTGC 21 D F L F S P P E V T G R S S V L R V S Q 61 GACTTCCTGTTTTCGCCACCCAGAAGTTACCGGAAGATCGTCTGTTCTTCGTGTGTCACAG 41 K E N V P P K N L A K A M K V T F Q T P 121 AAAGAAAATGTGCCACCCAAGAACCTGGCCAAAGCTATGAAGGTGACTTTTCAGACACCT 61 L R D P Q T H R I L S P S M A S K L E A 181 CTGCGGGATCCACAGACGCACAGGATTCTAAGTCCTAGCATGGCCAGCAAACTTGAGGCT 81 P F T Q D D T L G L E N S H P V W T Q K 241 CCTTTCACTCAGGATGACACCCTTGGACTGGAAAACTCACACCCGGTCTGGACACAGAAA 101 E N Q Q L I K E V D A K T T H G I L Q K 301 GAGAACCAACAGCTCATCAAGGAAGTGGATGCCAAAACTACTCATGGAATTCTACAGAAA 121 P V E A D T D L L G D A S P A F G S G S 361 CCAGTGGAGGCTGACACCGACCTCCTGGGGGATGCAAGCCCAGCCTTTGGGAGTGGCAGC 141 S S E S G P G A L A D L D C S S S S Q S 421 TCCAGCGAGTCTGGCCCAGGTGCCCTGGCTGACCTGGACTGCTCAAGCTCTTCCCAGAGC 161 P G S S E N Q M V S P G K V S G S P E Q 481 CCAGGAAGTTCTGAGAACCAAATGGTGTCTCCAGGAAAAGTGTCTGGCAGCCCTGAGCAA 181 A V E E N L S S Y S L D R R V T P A S E 541 GCCGTGGAGGAAAACCTTAGTTCCTATTCCTTAGACAGAAGAGTGACACCCGCCTCTGAG 201 T L E D P C R T E S Q H K A E E T P H G A 601 ACCCTAGAAGACCCTTGCAGGACAGAGTCCCAGCACAAAGCGGAGACTCCGCACGGAGCC 221 E E E C K A E E T P H G A E E E E C R H G G 661 GAGGAAGAATGCAAAGCGGAGACTCCGCACGGAGCCGAGGAGGAATGCCGGCACGGTGGG 241 V C A P A A V A T S P P P G A I P K E A C 721 GTCTGTGCTCCCGCAGCAGTGGCCACTTCGCCTCCTCCTGGTGCAATCCCTAAGGAAGCCTGC	SEQ ID NO:293

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		261 G G A P L Q G L P G E A L G C P A G V G 781 GGAGGAGCACCCCTGCAGGGTCTGCCTGGCGAAGCCCTGGGCTGCCCTGCGGGTGTGGGC	
		281 T P V P A D G T Q T L T C A H T S A P E 841 ACCCCCGTGCCAGCAGATGGCACTCAGACCCTTACCTGTGCACACACCTCTGCTCCTGAG	
		301 S T A P T N H L V A G R A M T L S P Q E 901 AGCACAGCCCCAACCAACCACCTGGTGGCTGGCAGGGCCATGACCCTGAGTCCTCAGGAA	
		321 E V A A G Q M A S S S R S G P V K L E F 961 GAAGTGGCTGCAGGCCAAATGGCCAGCTCCTCGAGGAGCGGACCTGTAAAACTAGAATTT	
		341 D V S D G A T S K R A P P P R R L G E R 1021 GATGTATCTGATGGCGCCACCAGCAAAAGGGCACCCCCACCAAGGAGACTGGGAGAGAGG	
		361 S G L K P P L R K K A A V R Q Q K A P Q E 1081 TCCGGCCTCAAGCCTCCCTTGAGGAAAGCAGCAGTGAGGCAGCAAAAGGCCCCGCAGGAG	
		381 V E E D D G R S G G A G E D P P M P P A S R 1141 GTGGAGGAGGACGACGGTAGGAGCGGAGCAGGAGAGGACCCCCCCATGCCAGCTTCTCGG	
		401 G S Y H L D W D K M D D P N F I P P F G G 1201 GGCTCTTACCACCTCGACTGGGACAAAATGGATGACCCAAACTTCATCCCGTTCGGAGGT	
		421 D T K S G C S E A Q P P E S P E T R L G 1261 GACACCAAGTCTGGTTGCAGTGAGGCCCAGCCCCCAGAAAGCCCTGAGACCAGGCTGGGC	
		441 Q P A A E Q L H A G P P A T E E P G P C L 1321 CAGCCAGCGGCTGAACAGTTGCATGCTGGGCCTGCCACGGAGGAGCCAGGTCCCTGTCTG	
		461 S Q Q L H S A S A E D T P V V Q L A A E 1381 AGCCAGCAGCTGCATTCAGCCTCAGCGGAGGACACGCCTGTGGTGCAGTTGGCAGCCGAG	
		481 T P T A E S K E R A L N S A S T S L P T 1441 ACCCCAACAGCAGAGAGCAAGGAGAGAGAGCCTTGAACTCTGCCAGCACCTCGCTTCCCACA	
		501 S C P G S E P V P T H Q Q G Q P A L E L 1501 AGCTGTCCAGGCAGTGAGCCAGTGCCCACCCATCAGCAGGGGCAGCCTGCCTTGGAGCTG	
		521 K E E S F R D P A E V L G T G A E V D Y 1561 AAAGAGGAGAGCTTCAGAGACCCCGCTGAGGTTCTAGGCACGGCGCGGAGGTGGATTAC	
		541 L E Q F G T S S F K E S A L R K Q S L Y	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1621 CTGGAGCAGTTTGGAACTTCCTCGTTTAAGGAGTCGGCCTTGAGGAAGCAGTCCTTATAC	
		561 L K F D P L L R D S P G R P V P V A T E	
		1681 CTCAAGTTCGACCCCCTCCTGAGGGACAGTCCTGGTAGACCAGTGCCCGTGGCCACCGAG	
		581 T S S M H G A N E T P S G R P R E A K L	
		1741 ACCAGCAGCATGCACGGTGCAAATGAGACTCCCTCAGGACGTCCGCGGGAAGCCAAGCTT	
		601 V E F D F L G A L D I P V P G P P P G V	
		1801 GTGGAGTTCGATTTCTTGGGAGCACTGGACATTCCTGTGCCAGGCCCACCCCCAGGTGTT	
		621 P A P G G P P L S T G P I V D L L Q Y S	
		1861 CCCGCGCCTGGGGGCCCACCCCTGTCCACCGGACCTATAGTGGACCTGCTCCAGTACAGC	
		641 Q K D L D A V V K A T Q E E N R E L R S	
		1921 CAGAAGGACCTGGATGCAGTGGTAAAGGCGACACAGGAGGAGAACCGGGAGCTGAGGAGC	
		661 R C E E L H G K N L E L G K I M D R F E	
		1981 AGGTGTGAGGAGCTCCACGGGAAGAACCTGGAACTGGGGAAGATCATGGACAGGTTCGAA	
		681 E V V Y Q A M E E V Q K Q K E L S K A E	
		2041 GAGGTTGTGTACCAGGCCATGGAGGAAGTTCAGAAGCAGAAGGAACTTTCCAAAGCTGAA	
		701 I Q K V L K E K D Q L T T D L N S M E K	
		2101 ATCCAGAAAGTTCTAAAGAAAAAGACCAACTTACCACAGATCTGAACTCCATGGAGAAG	
		721 S F S D L F K K R F E E K Q K E V I E G Y R	
		2161 TCCTTCTCCGACCTCTTCAAGCGTTTTGAGAAACAGAAAGAGGTGATCGAGGGCTACCGC	
		741 K N E E S L K K K C V E D Y L A R I T Q E	
		2221 AAGAACGAAGAGTCACTGAAGAAGTGCGTGGAGGATTACCTGGCAAGGATCACCCAGGAG	
		761 G Q R Y Q A L K A H A E E K L Q L A N E	
		2281 GGCCAGAGGTACCAAGCCCTGAAGGCCCACGCGGAGGAGAAGCTGCAGCTGGCAAACGAG	
		781 E I A Q V R S K A Q A E E A L A L Q A S L	
		2341 GAGATCGCCCAGGTCCGGAGCAAGGCCCAGGCGGAAGCGTTGGCCCTCCAGGCCAGCCTG	
		801 R K E Q M R I Q S L E K K T V E Q K T K E	
		2401 AGGAAGGAGCAGATGCGCATCCAGTCGCTGGAGAAGACAGTGGAGCAGAAGACTAAAGAG	
		821 N E E L T R I C D D L I S K M E K K I -	
		2461 AACGAGGAGCTGACCAGGATCTGCGACGACCTCATCTCCAAGATGGAGAAGATCTGA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
BM781269	Equus caballus IL-1RII mRNA for interleukin-1 receptor type II.	1 TGAAGGTCAGGCCTGGCAGCCGTCCCCAGGCGAGAAGCGACAAGGAGAAAGAATGCAGAG 61 CTACAGGCTACAGGGTGCTGGCCCTGAGATCTCCACTTTCTGCATCCTCCAGAAGTTGTC 121 GAGAACAATGCCCATTTTGTACATGTTGATATTGGGTGTTCCCGCCTTCACCATTCAGCC 181 TGAGGAGCGCACAGTGACTGCAGGAAACTGCCAATTTCTTGGCAAGCATTTCAAAACCGA 241 CCTCATGGTGGAAAGGGAGCCTGTGGTCCTGAGGTGCCCCCAGGCATGGTATAGGTGGTT 301 GGACTCTGCCAGCTCACATGTCAACGTGACGTGGCGTAAAAACGATTCTACTAGGATGGT 361 TCCAGAGGAAGAAGAGACGCGAATGTGGGTCCAGGACAATGCTCTCTGGATTTTGCCGGC 421 CTTGCAGGGGGACTCTGGCACCTACATCTGCACTGTCAGAAACGCCTCGTACTGCTATGA 481 AATGTCCACTGAGCTCAGGGTTTTTGAGAAGACAGAAGCTGCCCTGACTTACATCTCATA 541 CCCGCAGATCCTAACCTTGTCAACCTCTGGCTTACTAGTTTGCCCTGAGCTGAGTGAATT 601 CACCCGGAACAAAACTGACGTGGAGGTTCAATGGTACAAGGATTCTGTCCTTTTGGATCA 661 AGACAACGAGAAGTTTCTAAGTGTGGCAGGACCCCCTCGTTTACTTGTACAAAATGTGTC 721 TATGGAGGATGCGGGCTATTACAGCTGTGTCATGACCTTGATCCACAATGGCACACGAGT 781 CAACATCACTAGAAATATCGAACTCCGTGTCCAGAAAAGAAGAGAGGAGACTGTTCCTGT 841 GATTGTCTCCCCCCGCCAGACCATACTGGCTTCACTGGGGTCAAGACTGATAATCCCGTG 901 TAAGGTGTTTCTGGGAGCCGGCACACAGTGGACCACCGATCTGTGGTGGATGGCCAACAA 961 CACCAACATAGACATTGCCTACCGGGGAGGTCGCGTGACGGAGGGGCAGCGCCAGGAGTA 1021 CTCAGAAAATAATGAGAACTACATCGAAGTGCCATTGATTTTTGATCCAGTCATAAGAGA 1081 GGATTTGAACACGGATTTTAAATGTGTTACCTATAACACACGGAGTTTTCAGACGCTACA 1141 TACCACAGTCAAAGAAGCCGCCACGTTCCCCTGGGGGACTGTACTGGCCCCTCTTTTGCT 1201 GGTCTTCTTGGTTTTGGGAGGAATATGGATGCGCAATCGGTGCAAACACAGACGTGGAAA 1261 AGCGTATGGTTTGACTGCATTAAAGATTGAGCGTCAAGTTTTTCAATCTTATCCAAGTAA 1321 AATAAAGGAAATAAAATAATTCAAATA 1 M P I L Y M L I L G V P A F T I Q P E E 1 ATGCCCATTTTGTACATGTTGATATTGGGTGTTCCCGCCTTCACCATTCAGCCTGAGGAG 21 R T V T A G N C Q F L G K H F K T D L M 61 CGCACAGTGACTGCAGGAAACTGCCAATTTCTTGGCAAGCATTTCAAAACCGACCTCATG 41 V E R E P V V L R C P Q A W Y R W L D S 121 GTGGAAAGGGAGCCTGTGGTCCTGAGGTGCCCCCAGGCATGGTATAGGTGGTTGGACTCT 61 A S S H V N V T W R K N D S T R M V P E 181 GCCAGCTCACATGTCAACGTGACGTGGCGTAAAAACGATTCTACTAGGATGGTTCCAGAG 81 E E E T R M W V Q D N A L W I L P A L Q 241 GAAGAAGAGACGCGAATGTGGGTCCAGGACAATGCTCTCTGGATTTTGCCGGCCTTGCAG 101 G D S G T Y I C T V R N A S Y C Y E M S 301 GGGGACTCTGGCACCTACATCTGCACTGTCAGAAACGCCTCGTACTGCTATGAAATGTCC	SEQ ID NO:294 SEQ ID NO:295

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		121 T E L R V F E K T E A A L T Y I S Y P Q 361 ACTGAGCTCAGGGTTTTTGAGAAGACAGAAGCTGCCCTGACTTACATCTCATACCCGCAG	
		141 I L T L S T S G L L V C P E L S E F T R 421 ATCCTAACCTTGTCAACCTCTGGCTTACTAGTTTGCCCTGAGCTGAGTGAATTCACCCGG	
		161 N K T D V E V Q W Y K D S V L L D Q D N 481 AACAAAACTGACGTGGAGGTTCAATGGTACAAGGATTCTGTCCTTTTGGATCAAGACAAC	
		181 E K F L S V A G P P R L L V Q N V S M E 541 GAGAAGTTTCTAAGTGTGGCAGGACCCCCTCGTTTACTTGTACAAAATGTGTCTATGGAG	
		201 D A G Y Y S C V M T L I H N G T R V N I 601 GATGCGGCTATTACAGCTGTGTCATGACCTTGATCCACAATGGCACACGAGTCAACATC	
		221 T R N I E L R V Q K R R E E T V P V I V 661 ACTAGAAATATCGAACTCCGTGTCCAGAAAAGAAGAGAGGAGACTGTTCCTGTGATTGTC	
		241 S P R Q T I L A S L G S R L I I P C K V 721 TCCCCCCGCCAGACCATACTGGCTTCACTGGGGTCAAGACTGATAATCCCGTGTAAGGTG	
		261 F L G A G T Q W T T D L W W M A N N T N 781 TTTCTGGGAGCCGGCACACAGTGGACCACCGATCTGTGGTGGATGGCCAACAACACCAAC	
		281 I D I A Y R G G R V T E G Q R Q E Y S E 841 ATAGACATTGCCTACCGGGGAGGTCGCGTGACGGAGGGCAGCGCCAGGAGTACTCAGAA	
		301 N N E N Y I E V P L I F D P V I R E D L 901 AATAATGAGAACTACATCGAAGTGCCATTGATTTTTGATCCAGTCATAAGAGAGGATTTG	
		321 N T D F K C V T Y N T R S F Q T L H T T 961 AACACGGATTTTAAATGTGTTACCTATAACACACGGAGTTTTCAGACGCTACATACCACA	
		341 V K E A A T F P W G T V L A P L L L V F 1021 GTCAAAGAAGCCGCCACGTTCCCCTGGGGACTGTACTGGCCCCTCTTTTGCTGGTCTTC	
		361 L V L G G I W M R N R C K H R R G K A Y 1081 TTGGTTTTGGGAGGAATATGGATGCGCAATCGGTGCAAACACAGACGTGGAAAAGCGTAT	
		381 G L T A L K I E E R Q V F Q S Y P S K I K 1141 GGTTTGACTGCATTAAAGATTGAGCGTCAAGTTTTTCAATCTTATCCAAGTAAAATAAAG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		401 E I K - 1201 GAAATAAAATAA	
BM781278	Homo sapiens chromosome 6 open reading frame 166, mRNA	1 GTTGACGTGTTCGCTTGGGTTCCTGCTGCGGCAGCCACCTCGCAATCTCTCTGCATCGA 61 TCGCCGCTCGCAAGCTACTGACCGTACTCGGGCGTATTAGGAGCCGCGTTCCAGCCTCAC 121 ACCCCACGGTGCTGTTTTCGACTTCAGAAAGGATCTAGCCTCAGCACAGAAGCGCCTCAG 181 GCGCGGCGCAAAGCTCGAGCGGACGGCGGGGGCGGCCGGAGCCTCTCTCGGGGGAGCCGC 241 GCCTGAGGAGGCGGAAGAACCCCCCTGACGCGACTGGCGTGTGCTTCTGCCCGCCACCGC 301 CCCTCCCGCTCTCACCCGGGCCGTCCCTGGCCACTGCCCCTGCCGCGGAGGCAGCGGCGG 361 CAGCGGCTCTCCTTTCCACAGCCGGCGCTCCGCGACCCGCTTGGCTCCTGAGCCCGTCGG 421 GTAGGCTCTCCTCGAGTTCCCGCTCTTCACCCCTTCCCTCACCCTCTTCTTTCGTCACCC 481 GTCCCCGACCCCACCCGAGCCCGGCGCCTCAGCTGCCCCCGGCCATGGCGTGCGGAGCCA 541 CTCTGAAAAGGACTCTGGATTTCGACCCGCTGTTGAGCCCGGCGTCCCCGAAGCGCAGGC 601 GATGTGCGCCATTGTCGGCGCCCACCTCGGCCGCTGCCTCCCCGTTGTCGGCGGCCGCGG 661 CCACCGCCGCCTCCTTCTCCGCTGCGGCCGCCTCGCCGCAGAAGTATCTCCGAATGGAGC 721 CATCCCCCTTCGGCGACGTCTCCTCCCGCCTCACCACAGAACACAAATTCTGTACAACATAA 781 AACAAGAGTATATAACGAATGCAGAGAGAAGACATTTAGAAACGAGTTTCCAACAGACAG 841 ATCCGTGTTGTACTTTTGATGCACAGCCACATGCATTCTTCCTCAGTGGACCAGCTTCGC 901 CAGGGGCTTCATCTGCAACATCCTCACCATTAAAAAAGAACAGCCCTTATTCACTCTAC 961 GGCAGGTTGGGATGATCTGTGAACGTTTGTTGAAAGAACGTGAAGAGAAGGTTCGAGAAG 1021 AGTATGAAGAAATATTAAACACAAAACTTGCAGAACAATATGATGCATTTGTGAAGTTTA 1081 CGCATGATCAAATAATGCGACGATATGGAGAACAGCCTGCTAGTTATGTTTCATGAATCA 1141 CGTTTTCTGCATTTGTGGGCTGCCTTGTTCTTTGTTGAATTGTTGCAAGAGGTCCCAATT 1201 ATGACATGCAGCAATGCCAATACCCCCCTATGAATACAGGTTATTTCAAGCTTTCGTCAG 1261 TGGCAACCACTTTAGGCAGCAACTGGTTTTGGAAATTTCCCTGATGTCAATACCACCGG 1321 ATGTGGACCTTTGCTACCTGTATTAATACCAGTGGCCTCATTTGCTGTATCATTACAATT 1381 TGGCTTCTTACATTAATGTTTGAAAAGGATTAAATCTGGTATTCTAAGAACATGCCCTTC 1441 ACTGGTTGTGTAAATAAAACTGTAGAATGACAAAAAAAAAAAAAAAAAAAAAA 1 M A C G A A T L K K R R T L L D F D D P L L S P A 1 ATGGCGTGCGGAGCCACTCTGAAAAGGACTCTGGATTTCGACCCGCTGTTGAGCCCGGCG 21 S P K R R R C A P L S S A P P T S A A A A S P 61 TCCCCGAAGCGCAGGCGATGTGCGCCATTGTCGGCGCCCACCTCGGCCGCTGCCTCCCCG 41 L S A A A A T A A S F S A A A A S P Q K 121 TTGTCGGCGCCGCGGCCACCGCCGCCTCCTTCTCCGCTGCGGCCGCCTCGCCGCAGAAG 61 Y L R M E P S P F G D V S S R L T T E Q 181 TATCTCCGAATGGAGCCATCCCCCTTCGGCGACGTCTCCTCCCGCCTCACCACAGAACAA 81 I L Y N I K Q E Y K K R M Q K R R H L E T	SEQ ID NO:296 SEQ ID NO:297

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		241 ATTCTGTACAACATAAAACAAGAGTATAAACGAATGCAGAAGAGAAGACATTTAGAAACG	
		101 S F Q Q Q T D D P C C C T F D A Q Q P P H A F F F L	
		301 AGTTTCCAACAGACAGATCCGTGTTGTACTTTGATGCACAGCCACATGCATTCTTCCTC	
		121 S G P P A S P G A S S S A T S S S P L K K K E E Q	
		361 AGTGGACCAGCTTCGCCAGGGGCTTCATCTGCAACATCCTCACCATTAAAAAAAGAACAG	
		141 P L F F T L R R Q V G G M I C C E E R L L L K K E E R E	
		421 CCCTTATTCACTCTACGGCAGGTTGGGATGATCTGTGAACGTTTGTTGAAAGAACGTGAA	
		161 E K V R E E E Y E E E I L L N T K L A E E Q Y D	
		481 GAGAAGGTTCGAGAAGAGTATGAAGAAATATTAAACACAAAACTTGCAGAACAATATGAT	
		181 A F V K K F T H D Q Q I M R R R Y Y G E E Q P P A S	
		541 GCATTTGTGAAGTTTACGCATGATCAAATAATGCGACGATATGGAGAACAGCCTGCTAGT	
		201 Y V S -	
		601 TATGTTTCATGA	
BM781319	Homo sapiens KIAK0002 mRNA.	1 AGAGCGAGCAGGGGAGAGCGAGACCAGTTTTAAGGGGAGGACCGGTGCGAGTAAGGCAGC	SEQ ID NO:298
		61 CCCGAGGCTCTGCTCGCCCACCACCCAATCCTCGCCTCCCTTCTGCTCCACCTTCTCTCT	
		121 CTGCCCTCACCTCTCCCCCGAAAACCCCCTATTTAGCCAAAGGAAGGAGGTCAGGGGAAC	
		181 GCTCTCCCCTCCCCTTCCAAAAAACACAAAAACAGAAAAACCCTTTTCCAGGCCGGGGAAAG	
		241 CAGGAGGGAGAGGGGCCGCCGGGCTGGCCATGGAGCTGCTGTGCCACGAGGTGGACCCGG	
		301 TCCGCAGGCCGTGCGGGACCGCAACCTGCTCCGAGACGACCGCGTCCTGCAGAACCTGC	
		361 TCACCATCGAGGAGCGCTACCTTCCGCAGTGCTCCTACTTCAAGTGCGTGCAGAAGGACA	
		421 TCCAACCCTACATGCGCAGAATGGTGGCCACCTGGATGCTGGAGGTCTGTGAGGAACAGA	
		481 AGTGCGAAGAAGAGGTCTTCCCTCTGGCCATGAATTACCTGGACCGTTTCTTGGCTGGGG	
		541 TCCCGACTCCGAAGTCCCATCTGCAACTCCTGGGTGCTGTCTGCATGTTCCTGGCCTCCA	
		601 AACTCAAAGAGACCAGCCCGCTGACCGCGGAGAAGCTGTGCATTTACACCGACAACTCCA	
		661 TCAAGCCTCAGGAGCTGCTGGAGTGGGAACTGGTGGTGCTGGGAAGTTGAAGTGGAACC	
		721 TGGCAGCTGTCACTCCTCATGACTTCATTGAGCACATCTTGCGCAAGCTGCCCCAGCAGC	
		781 GGGAGAAGCTGTCTCTGATCCGCAAGCATGCTCAGACCTTCATTGCTCTGTGTGCCACCG	
		841 ACTTTAAGTTTGCCATGTACCCACCGTCGATGATCGCAACTGGAAGTGTGGGAGCAGCCA	
		901 TCTGTGGGCTCCAGCAGGATGAGGAAGTGAGCTCGCTCACTTGTGATGCCCTGACTGAGC	
		961 TGCTGGCTAAGATCACCAACACAGACGTGGATTGTCTCAAAGCTTGCCAGGAGCAGATTG	
		1021 AGGCGGTGCTCCTCAATAGCCTGCAGCAGTACCGTCAGGACCAACGTGACGGATCCAAGT	
		1081 CGGAGGATGAACTGGACCAAGCAGCACCCCTACAGACGTGCGGGATATCGACCTGTGAG	
		1141 GATGCCAGTTGGCCGAAAGAGAGAAGACGCGTCCATAATCTGGTCTCTTCTTTCTTCTGG	
		1201 TTGTTTTTGTTCTTTGTGTTTTAGGGTGAAACTTAAAAAAAAAAATTCTGCCCCCCACCTAG	
		1261 ATCATATTTAAAGATCTTTTAGAAGTGAGAGAAAAAGGTCCTACGAAAACGGAATAATAA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1321 AAAGCATTTGGTGTGCCTATTTGAAGTACAGCATAAGGGAATCCCTTGTATATGCGAACAGT	
		1381 TATTGTTTGATTATATGTAAAAGTAATAGTAAAATGCTTACAGGAAAACCTGCAGAGTAGTTT	
		1441 AGAGAATATGTATGCCTGCAATATGGGAACAAATTAGAGGAGACTTTTTTTTTCATGTTA	
		1501 TGAGCTAGCACATACACCCCCTTGTAGTATAATTTCAAGGAACTGTGTACGCCATTTATG	
		1561 GCATGATTAGATTGCAAAGCAATGAACTCAAGAAGGAATTGAAATAAGGAGGGACATGAT	
		1621 GGGGAAGGAGTACAAAACAATCTCTCAACATGATTGAACCATTTGGGATGGAAGAAGCACC	
		1681 TTTGCTCTCAGCCACCTGTTACTAAGTCAGGAGTGTAGTTGGATCTCTACATTAATGTCC	
		1741 TCTTGCTGTCTACAGTAGCTGCTACCTAAAAAAAAGATGTTTTTATTTTGCCAGTTGGACAC	
		1801 AGGTGATTGGCTCCTGGGTTTCATGTTCTGTGACATCCTGCTTCTTCTTCCAAATGCCAGT	
		1861 TCATTGCAGACACCACCATATTGCTATCTAATGGGGAAATGTAGCTATGGGCCATAACCA	
		1921 AAACTCACATGAAACGGAGGCAGATGGAGACCAAGGGTGGGATCCAGAATGGAGTCTTTT	
		1981 CTGTTATTGTATTTAAAAGGGTAATGTGGCCTTGGCATTTCTTCTTAGAAAAAACTAAT	
		2041 TTTTGGTGCTGATTGGCATGTCTGGTTCACAGTTTAGCATTGTTATAAACCATTCCATTC	
		2101 GAAAAGCACTTTGAAAAATTGTTCCCGAGCGATAGATGGGATGGTTTATGCAAGTCATGC	
		2161 TGAATACTCCTCCCCTCTTCTCTTTGCCCCCTCCCTTCCTGCCCCCAGTCTGGGTTACT	
		2221 CTTCGCTTCTGGTATCTGGCGTTCTTTGGTACACAGTTCTGGTGTTCCTACCAGGACTCA	
		2281 AGAGACACCCCTTCCTGCTGACATTCCCATCACAACATTCCTCAGACAAGCCTGTAAACT	
		2341 AAAATCTGTTACCATCTGATGGCACAGAAGGATCTTAATTCCCATCTCTATACTTCTCCT	
		2401 TTGGACATGGAAAGAAAAGTTATTGCTGGTGCAAAGATAGATGGCTGAACATCAGGGTGT	
		2461 GGCATTTTGTTCCCTTTCCGTTTTTTTTTTTTTTATTGTTGTTGTTAATTTTATTGCAA	
		2521 AGTTGTATTCAGCGTACTTGAATTTTCTTCCTCTCCACTTCTTAGAGGCATTCAGTTAG	
		2581 CAAAGAGGTTGGAGCAACAACTTTTTTTTTTTTTTTTGCACAATTGTAATTGACAGGTA	
		2641 ATGAAGCTATTTGTTAAAATATTTGCCTTTTTAAGTAAAAAAAGAAAAATCAGAACAGGGC	
		2701 TATTTGAAGAATTATTTTATACACAGATTCTGCCTTGTTTCATAGTATGAGGGTTGAAGA	
		2761 CGGAAAACAATCTAAGGGTCTCTCATTTTTTTAATTTTGTTTTGTTCAGTTTGGTTTTT	
		2821 TTTTTTTTTGCGCTGCTAAGAAGCTAAAGTCATCCATCCTTATTCACGTTGACAGTACCT	
		2881 AGCTGTAATGTTTCACAGAGTGTGCTGCTATTTTATAAACATTTTTATATAATATTATTT	
		2941 TACTGCTTAAATTCCAAGTCCTGAAGTAGATGGTTGAGATATGAGTTCTTCGTACTGGAA	
		3001 AAGCCCTTCCGTAGTTTGTTTTCTTCTGGTAGCATATTCATGGTTGTTTTTTTTTTCTT	
		3061 TTTTGGTTTTTTGGTTTTTTTTTTTCCTCTGATCACATTCTTCTTCAAAGACGGAGTATTCT	
		3121 TACCTCAGGTTTACTGGACAAAATCAATAACTACACAAAAGGCAATGATTCACGCTTTTGTT	
		3181 TTCATAATACCTCACAACCGTACAGTTTCTGCTTGGGAGCCCATTCGCATGAGGAATACA	
		3241 GAAGCAGTGTGAGCAGGGCTGACTCCCTCTCAGGTGGAAGGCAGGGCGGTCTCACTCCCA	
		3301 GGGACCTTTTTGGTCATGGAGGCCATCGGGCTCCCAGTTAGACCCTGGTATCCTCATCAT	
		3361 GATGGAAAAAATACATTGAACCAAGGGATCCTCCCTCCCCTTCAAGGCAGACGTTCAGTA	
		3421 CAAACATTTATGCGGTAGGCTCAGATGTCGTAATTTGCACTTAGGTACCAGGTGTCAGGA	
		3481 AACAGACTAAAAAGAATTCCACCAGGCTGTTTGGAGATCCTCATCTTGGAGCTTTTTCAA	
		3541 AAGCGGGGCTTCATCTGCAAAGGGCCCTTTCATCTTGAAGTTTTTCCCCTCCGTCTTTCC	
		3601 CCTCCCCTGGCATGGACACCTTGTGTTTAGGATCATCTCTGCAGGTTTCCTAGGTCTGAA	
		3661 TCTGCGAGTAGATGAACCTGCAGCAAGCAGCGTTTATGGTGCTTCCTTCTCCCTCCTCTG	
		3721 TCTCAAACTGCGCAGGCAAGCACTATGCAAGCCCAGGCCCTCTGCTGAGCGGTACTAAAC	
		3781 GGTCGGGTTTTCAATCACACTGAATTGGCAGGATAAGAAAAATAGGTCAGATAAGTATGG	
		3841 GATGATAGTTGAAGGGAGGTGAAGAGGCTGCTTCTCTACAGAGGTGAAATTCCAGATGAG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		3901 TCAGTCTCTTGGGAAGTGTGTTTAGAAGGGTTCAGGACTTTGTGAGTTTAGCATGACCCTA	
		3961 AAATTCTAGGGGATTTCTGGTGGGACAATGGGTGGTGAATTTTGAAGTTTTGGAGAGGGA	
		4021 AGTGGAGCAGCCAGCAAGTAAGCTAGCCAGAGTTTTCTCAAGAGCCAGCTTTGCTCAGCA	
		4081 CACTCTCCTGGGCCCCAAGGAGTCCCACGGAATGGGGAAAGTGGGAACCCTGGAGTTCTT	
		4141 GGGAATCTTGGAGCCTAAAGAGAAACCGAGGTGCAAATTCATTTCATGGTGACTGACCCT	
		4201 TGAGCTTAAACAGAAGCAGCAAATGAAGAACCGGACACAAATAAGGAAGGGCACAAGCCTA	
		4261 CCCGACTCTATTTACAGTCTGTAACTTTCCACTCTTCCTGTAGTCCCGAGGCCCCTGGGT	
		4321 CCTTCTAGCTTTTCTCTTTCCCATCCTTGGGGCCTTGTGTGATGATGGGTGTGGGCTGC	
		4381 CGATGGGAAAGTCGGGGGTTGTTAGGCTTTTCTGCCTGCTCCTCGCTTAAACACAAGAAGG	
		4441 AATCCTGGATTTTGCCCTCTCCTTAGTCTCTTTGGTAGGAGTTTTGTTCCAGA	
		4501 GGAGCTCTCCCCCTTGGATTTGAACTTGCTCTTTTTGTTGTTGTTCTTTCTCTTCTT	
		4561 TTTCTTACCTCCCACTAAAGGGTTTCCAAATTATCCTGGTCTTTTTCTACCTTGTTGTGT	
		4621 TTCTATCTCGTCTTTACTTCCATCTGTTTGTTTTTTTCTCCATCAGTGGGGGCCGAGTTG	
		4681 TTCCCCCAGCCTGCCAAATTTTGATCCTTCCCCTCTTTTGGCCAAATCCTAGGGGGAAGA	
		4741 AATCCTAGTATGCCAAAAATATATGCTAAGCATAATTAAACTCCATGCGGGTCCATAACA	
		4801 GCCAAGAAGCCTGCAGGAGAAAGCCAAGGGCAGTTCCCTCCTCCGCAGAACACCCCATGCGTG	
		4861 CTGAGAGGCGAGCTCCTTGAAGAAGGGGCTGTTCTTCCAGGAGGCCTTATTTTGAACTGC	
		4921 CTCAGGACCCCACTGGAGAGCACAGCATGCCTTACTACTGGGTCATCCTTGGTCTATGTG	
		4981 CTCTGTACTGGAGGCTCTGTTCTGCCTCTTATCAGCCAGGTCAGGGGCACACATGGCTTA	
		5041 AGTGACAAAGCCAGAGGAGAAGACAACCCTGACACAGCATCACGCTGCATCCCATTGCTAGC	
		5101 AGGATTGGCAACTCTTCAGACGGAGCTGCGCTTCCCTGCAGTCTAGCACCTCTAGGGCCT	
		5161 CTCCAGACTGTGCCCTGGGAGCTCTGGGACTGAAAGGTTAAGAACATAAGGCAGGATCAG	
		5221 ATGACTCTCTCCAAGAGGGCAGGGGAATTTTCTCTCCATGGGCCACAGGGGACAGGGCTG	
		5281 GGAGAAGAAATAGACTTGCACCTTATGTCATGTAAATAATTGATTTTCTAGTTCAAGAAG	
		5341 ATAATATTGGTAGTGTGGGAATTGGAGGTAGGAAGGGGAGGAAGTCTGAGTAAGCCAGTT	
		5401 GGCTTCTAAGCCAAAAGGATTCCTCTTTGTTTATCTCTGAGACAGTCCAACCTTGAGAAT	
		5461 AGCTTTAAAAGGGAAATTAATGCTGAGATGATAAAGTCCCCTTAAGCCAACACAAACCCTCT	
		5521 GTAGCTATAGAATGAGTGCAGGTTTCTATTGGTGTGGACTCAGAGCAATTTACAAGAGCT	
		5581 GTTCATGCAGCCATCCATTTGTGCAAAATAGGGTAAGAAGATTCAAGAGGATATTTATTA	
		5641 CTTCCTCATACCACATGGCTTTGATGATTCTGGATTCTAAACAACCCAGAATGGTCATT	
		5701 TCAGGCACAACGATACTACATTCGTGTGTGTCTGCTTTTAAACTTGGCTGGGCTATCAGA	
		5761 CCCTATTCTCGGCTCAGGTTTTGAGAAGCCATCAGCAAATGTGTACGTGCATGCTGTAGC	
		5821 TGCAGCCTGCATCCCTTCGCCTGCAGCCTACTTTGGGGAAATAAAGTGCCTTACTGACTG	
		5881 TAGCCATTACAGTATCCAATGTATTTTGACAGGTGCCTGTCCTTGAAAAACAAAGTTTCT	
		5941 ATTTTTATTTTTAATTGGTTTTAGTTCTTACTGGCCAACTCTCTTAAATCCCCAGCAAATCA	
		6001 CTGGGCCATTGGATTTTTTCCATTATGTTCATTACCCTTGTACCATGTACCTCAGATCTC	
		6061 TCTCTCTCCTCTCTCTCAGTTATATAGTTTCTTGTCTTGGACTTTTTTTTTTTTCTTTCT	
		6121 TTTTCTTTTTTTTTTTGCTTTAAAACAAGTGTGATGCCATATCGAGTCAATGTTATTCTC	
		6181 TCACAATGTACTCTATAAGAGGTGTGGGTGTTTATTTGGTCGGGATGCTAGCAAGTGCTA	
		6241 AAGTAGCATGATCAGTATAAACAAAAGGTTTTTAGGAAGTATGGAAAAAATGTTTTATTG	
		6301 GCTATGATGGTGACATGGTATAGTCAGCTACCTTTTAAGAGGTCCTATCTGTTCAGTGTT	
		6361 AAGTGATTTAAAAAAAATAATAACCTGTTATTCTGACTAGCTTAAAGATGGATTTGAAAA	
		6421 TGGTTTTGGATGCAATTAGGTTATGCTATTTGGACAATAAACTCACCTTGACCT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1 M E L L C H E V D P V R R A V R D R N L 1 ATGGAGCTGCTGTGCCACGAGGTGGACCCGGTCCGCAGGGCCGTGCGGGACCGCAACCTG 21 L R D D R V L Q N L L T I E E R Y L P Q 61 CTCCGAGACGACCGCGTCCTGCAGAACCTGCTCACCATCGAGGAGCGCTACCTTCCGCAG 41 C S Y F K C V Q K D I Q P Y M R R M V A 121 TGCTCCTACTTCAAGTGCGTGCAGAAGGACATCCAACCCTACATGCGCAGAATGGTGGCC 61 T W M L E V C E E Q K C E E E V F P L A 181 ACCTGGATGCTGGAGGTCTGTGAGGAACAGAAGTGCGAAGAGAGGTCTTCCCTCTGGCC 81 M N Y L D R F L A G V P T P K S H L Q L 241 ATGAATTACCTGGACCGTTTCTTGGCTGGGGTCCCGACTCCGAAGTCCCATCTGCAACTC 101 L G A V C M F L A S K L K E T S P L T A 301 CTGGGTGCTGTCTGCATGTTCCTGGCCTCCAAACTCAAAGAGACCAGCCCGCTGACCGCG 121 E K L C I Y T D N S I K P Q E L L E W E 361 GAGAAGCTGTGCATTTACACCGACAACTCCATCAAGCCTCAGGAGCTGCTGGAGTGGGAA 141 L V V L G K L K W N L A A V T P H D F I 421 CTGGTGGTGCTGGGGAAGTTGAAGTGGAACCTGGCAGCTGTCACTCCTCATGACTTCATT 161 E H I L R K L P Q Q R E K L S L I R K H 481 GAGCACATCTTGCGCAAGCTGCCCCAGCAGCGGGAGAAGCTGTCTCTGATCCGCAAGCAT 181 A Q T F I A L C A T D F K F A M Y P P S 541 GCTCAGACCTTCATTGCTCTGTGTGCCACCGACTTTAAGTTTGCCATGTACCCACCGTCG 201 M I A T G S V G A A I C G L Q Q D E E V 601 ATGATCGCAACTGGAAGTGTGGGAGCAGCCATCTGTGGCTCCAGCAGGATGAGGAAGTG 221 S S L T C D A L T E L L A K I T N T D V 661 AGCTCGCTCACTTGTGATGCCCTGACTGAGCTGCTGGCTAAGATCACCAACACAGACGTG 241 D C L K A C Q E Q I E A V L L N S L Q Q 721 GATTGTCTCAAAGCTTGCCAGGAGCAGATTGAGGCGGTGCTCCTCAATAGCCTGCAGCAG 261 Y R Q D Q R D G S K S E D E L D Q A S T 781 TACCGTCAGGACCAACGTGACGGATCCAAGTCGGAGGATGAACTGGACCAAGCCAGCACC	SEQ ID NO:299

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		281 P T D V R D I D L - 841 CCTACAGACGTGCGGATATCGACCTGTGA	
BM781375	Homo sapiens EPK2 mRNA for serine/threonine kinase.	1 AAAGTTCATCCCCCCAGAATGAAAATGAGGACATTTGAGAAGGTGATTTAAGGTGTGGAC 61 ATTTGAGAAGGTGTCCTATCAAATTAGTAAACCAAAGGAAAAGTACTGAATAGATTAATC 121 CAAAACACTTACTGTGTTTTTAACGAAGAGGATTTCACCTTGACAGAAAAACACAACTTTTA 181 TTCAATATGTATTTCCTGAAATTAAAGAGACAAGTACAGACTGAAAGGAAAATAGATTCG 241 TAAATAAGCTACGTCAACTCTATCCTGCTGAGGATAGCTCAGTGATGTTAAATCCTTTAC 301 AAATCCCTGGTTGTCTTCCTACAGACAAGACTGCTTTTTGATGGGACTGATATTAAGAGA 361 AATAGGACCTTTGGGGCATTCAACTCCTTGATAAAACTTAAAAGTATCGGCATGAGTGGC 421 TTAACAGAGGAAATAAAGAAGTTTTCAACTAAATCCAAAAGTGCGGTCATTTTCTTTACT 481 GCTGTTATTTTAAAAACCTCTTCATAACCATTGAAAAAGAATCGACAACTATTTTAAAAG 541 ATTAAAGAAAGGCAGATGTCTGCAAATAATCCCCTCCATCAGCCCAGAAGTCTGTATTA 601 CCCACAGCTATTCCTGCTGTGCTTCCAGCTGCTTCTCCGTGTTCAAGTCCTAAGACGGGA 661 CTCTCTGCCCGACTCTCTAATGGAAGCTTCAGTGCACCATCACTCACCAACTCCAGAGGC 721 TCAGTGCATACAGTTTCATTTCTACTGCAAATTGGCCTCACACGGGAGAGTGTTACCATT 781 GAAGCCCAGGAACTGTCTTTATCTGCTGTCAAGGATCTTGTGTGCTCCATAGTTTATCAA 841 AAGTTTCCAGAGTGTGGATTCTTTGGCATGTATGACAAAATTCTTCTCTTTCGCCATGAC 901 ATGAACTCAGAAAACATTTTGCAGCTGATTACCTCAGCAGATGAAATACATGAAGGAGAC 961 CTAGTGGAAGTGGTCTCTTTCAGCTTTAGCCACAGTAGAAGACTTCCAGATTCGTCCACAT 1021 ACTCTCTATGTACATTCTTCTACAAAGCTCCTACTTTCTGTGATTACTGTGGTGAGATGCTG 1081 TGGGGATTGGTACGTCAAGGACTGAAATGTGAAGGCTGTGGATTAAATTACCATAAACGA 1141 TGTGCCTTCAAGATTCCAAATAACTGTAGTGGAGTAAGAAAGAGACGTCTGTCAAATGTA 1201 TCTTTACCAGGACCCGGCCTCTCAGTTCCAAGACCCCTACAGCCTGAATATGTAGCCCTT 1261 CCCAGTGAAGAGTCACATGTCCACCAGGAACCAGTAAGAGAATTCCTTCTTGGAGTGGT 1321 CGCCCAATCTGGATGGAAAAGATGGTAATGTGCAGAGTGAAAGTTCCACACACATTTGCT 1381 GTTCACTCTTACACCCGTCCCACGATATGTCAGTACTGCAAGCGGTTACTGAAAGGCCTC 1441 TTTCGCCAAGGAATGCAGTGTAAAGATTGCAAATTCAACTGCCATAAACGCTGTGCATCA 1501 AAAGTACCAAGAGACTGCCTTGGAGAGGTTACTTTCAATGGAGAACCTTCCAGTCTGGGA 1561 ACAGATACAGATATACCAATGGATATTGACATAAATAGTGATAGTAGTCGG 1621 GGTTTGGATGACACAGAAGAGCCATCACCCCCAGAAGATAAGATGTTCTTCTTGGATCCA 1681 TCTGATCTCGATGTGGAAAGAGATGAAGAAGCCGTTAAAACAATCAGTCCATCAACAAGC 1741 AATAATATTCCGCTAATGAGGGTTGTACAATCCATCAAGCACACACAAGAGGAAGAGCAGC 1801 ACAATGGTGAAGGAAGGGTGGATGGTCCATTACACCAGCAGGATAACCTGAGAAAGAGG 1861 CATTATTGGAGACTTGACAGCAAATGTCTAACATTATTTCAGAATGAATCTGGATCAAAG 1921 TATTATAAGGAAATTCCACTTTCAGAAATTCTCCGCATATCTTCACACGAGATTTCACA 1981 AACATTTCACAAGGCAGCAATCCACACTGTTTTGAAATCATTACTGATACTATGGTATAC 2041 TTCGTTGGTGAGAACAATGGGGACAGCTCTCATAATCCTGTTCTTGCTGCCACTGGAGTT 2101 GGACTTGATGTAGCACAGAGCTGGGAAAAAGCAATTCGCCAAGCCCTCATGCCTGTTACT 2161 CCTCAAGCAAGTGTTTGCACTTCTCCAGGGCAAGGAAATGTGGATATCAGTACTGTTTACCAG 2221 AGTATCTCTGTATCTAATTGTCAGATTCAGGAGAATGTGGATATCAGTACTGTTTATGGAGGAAAACAT 2281 ATCTTTGCAGATGAGGTGCTTGGTTCAGGCCAGTTTGGCATCGTTTATGGAGGAAAACAT	SEQ ID NO:300

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2341 AGAAAGACTGGGAGGGATGTGGCTATTAAAGTAATTGATAAGATGAGATTCCCCACAAAA	
		2401 CAAGAAAGTCAACTCCGTAATGAAGTGGCTATTTTACAGAATTTGCACCATCCTGGGATT	
		2461 GTAAACCTGGAATGTATGTTTGAAACCCCAGAACGAGTCTTTGTAGTAATGGAAAAGCTG	
		2521 CATGGAGATATGTTGGAAATGATTCTATCCAGTGAGAAAAGTCGGCTTCCAGAACGAATT	
		2581 ACTAAATTCATGGTCACACAGATACTTGTTGCTTTGAGGAATCTGCATTTTAAGAATATT	
		2641 GTGCACTGTGATTTAAAGCCAGAAAATGTGCTGCTTGCATCAGCAGAGCCATTTCCTCAG	
		2701 GTGAAGCTGTGTGACTTTGGATTTGCACGCATCATTGGTGAAAAGTCATTCAGGAGATCT	
		2761 GTGGTAGGAACTCCAGCATACTTAGCCCCTGAAGTTCTCCGGAGCAAAGGTTACAACCGT	
		2821 TCCCTAGATATGTGGTCAGTGGGAGTTATCATCTATGTGAGCCTCAGTGGCACATTTCCT	
		2881 TTTAATGAGGATGAAGATATAAATGACCAAATCCAAAATGCTGCATTTATGTACCCACCA	
		2941 AATCCATGGAGAGAAATTTCTGGTGAAGCAATTGATCTGATAAACAATCTGCTTCAAGTG	
		3001 AAGATGAGAAAACGTTACAGTGTTGACAAATCTCTTAGTCATCCCTGGCTACAGGACTAT	
		3061 CAGACTTGGCTTGACCTTAGAGAATTTGAAACTCGCATTGGAGAACGTTACATTACACAT	
		3121 GAAGTGATGATGCTCGCTGGGAAATACATGCATACACACATAACCTTGTATACCCAAAG	
		3181 CACTTCATTATGGCTCCTAATCCAGATGATATGGAAGAAGATCCCTTAATCACTGAGCTAA	
		3241 CCTAAATAAGGAAGGATTTCATTTTATGGACTGATATTTTGCTGTGTAACTTGTTCTTCG	
		3301 TAGATTGTCATCTGCAGTGCTGCAAAGATATGAAGAAATATGATAACGAATAAGTGACAC	
		3361 CAGTACTGTAGTTCATAAATGAGTAGGTACAGGCGGGAAACTGAATATATAAGAAGTCATAA	
		3421 TGGAATCAAGGTGAAGCTTTTTATAAACTTTTTTAGCCTAAGCAATAACTGGTTTTGTAT	
		3481 TTTTTCTTAATCCTTCACTTTAATACAATAGGCTCACTTAATTTGTCTTCCCATTTCTCT	
		3541 TTATATATATATATAAAAAAATATAAATATATGTTTGTTTGTTTTTTTTTTAA	
		3601 GGAAAAACAAGTCAAGCTAGCATCCAGTTACTATATAGCTTGGCTAAATTATACAAGACT	
		3661 TACAAGATTGATTACTCGACAGGCTTGTATTTAAGAGATAACTGTGAGGTTACCATTATG	
		3721 TGATGTTACTATAAGGACTTTTTAACATTGGTTTAACAAACCATAGAGGCATTGAAGGGTT	
		3781 TTTCTTAGATGCCTAGAAAAAGCACACTGGGCTGTTTTACCTTTCTTTTTTAGGTCAATC	
		3841 AAGACTCCAAAATAGTGATTCCTAACCTTTTTGGAGTTGCTCTGCTACTCTGAATATGTT	
		3901 CTATACAGCATAAGGATTGTCACCTTCTGTGTTGTTGCAACAGCTTCTAAGATAATTAGGG	
		3961 ACAAATGATGTTACAAAAGGAAGAGTACTGCTGGTCTAAGTGCTGAGTTGTATATGTCTTTG	
		4021 CATAGCTCCACTCTGCTGCTAAATATGCATGTTCTGACTGACACCATCTTGATGCCAGTA	
		4081 CTGGATTCCAGCATTCAGCAGGTGCAGATCTCGGCTTTACACAATTTATCTTTACCTAGG	
		4141 GTTCAGTCAGTAATTCTGCTTTTAGCCAGGGCCAGTGCAGGGTCAGTTAATGCTACAG	
		4201 TTACTGTATAGCAAACAGTATCCTTTTTCTCCTTCCCTAGCCTATTGGGCTTTGCAGA	
		4261 TATCTGGAGTGTTTTTAAAGTCAATTATTTTAAGCAGTTTGAGGGGATGTGTAGGAGTGGA	
		4321 GCATGAAACAGTTTATAAGGCTGGGGCTGTATTATCAGCACAGCAAATTAAAGAATGAAA	
		4381 GAAGTACTTCTTTTTACATTTCAGCTCCAGCAGCCAGCTATTTAAAAAATATTTTTAAAT	
		4441 ATCTTCCCCAAAGTTTAAGATGTGGGACCATCTACTTGTAAGAAACAGTGGCTTATTTCT	
		4501 TCATTTCTCAGTAATCATTGTAAACCTTTTTTTTTTTCTTCTCCACTCTAACAAAAGTAA	
		4561 AAGAACAAAACTTTTGCTGAGGTCTTGGACTCCACTACTTGTTTAGTTATGTTGGCCTGGA	
		4621 CAGATGGCAGGTCTGTCGGCAGTTCCTCAGTCTGTAAAATGAAGATTATCATTCTTGCCT	
		4681 CTCCCTTTGTCACAGTGTTGTCGTGAAGATCAGATATGTATGAATGCAGTCAAATAAACT	
		4741 AAAAACTAGGAAAGTGTTAACTATCGTTGCCCACCGAATTTGAGGTAGCAAAAAAAAAAA	
		4801 AGAATGTTCTGGTACATGAACAGACTGAGAAGGCCTTTCGACATCCCTGAAGCTAGTCTC	
		4861 CTGTCTAGACTAAAAATATCCTTGAAAGAATAGTAGCAAACAGTATGCAGTACTCCTGTG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		4921 TTCTAAGTTCTTTTATGTTTTAGTTTACCCTCACAGCAGCCATAGTGTTAAGTCATTATG 4981 AGCTTCATCTTAAAGATAAGAAAACTGAGGCAAGGGGAGATTAACTTACTGCCAAATTTC 5041 AAACAGTTAGTAGTATTTGAGACCAGTATGGCTCTAATCTTACCCTTAGCCCTCCCA 5101 ACCATTATGCTGTACTATCTACCCATAAATACCTCCAGGAAACATTCCCCTCTTGGTAAT 5161 TTGTCCTTCTATAGAAGCTTCAAAGATTAAATCAAATTAATTTTCAAAAAAAATTTTTTT 5221 TTAGAAATGTTATTTTCCCTGTGATAGAGGATGACTTCCCAGTTTCACCAAAGTCTGTTT 5281 ATATCAACGCGCAAAACAGAGTAATTCTGAGTCACTAGGCACCCTATTATGGTTTTACTG 5341 CATAAGGTGAAAATTAACTGGAATGATGTTTCTTTGCTATACTTAAATAATCAAACTTTA 5401 CAAGCCATGAAATTAATTGCACTCTTTTTGTTTTTATTGTTGAATGCCTAAGAAGTTTTC 5461 TAAAAAAATTTGCAGAGGCACTGTCAGATAATTTGGAGTTGAGTAACTACTCCAGATACT 5521 GTATAACTTTTTGTCTTTAAGTCGTGTTTGTATAAGAAATAATTGTTTAGAAACATTTGAT 5581 AATGTACAAAGTAGTCTATAATGACACTGTTCAGTACATTTTTATATTTTTTGTTACATC 5641 CCACTTTTTGTAAATATCCTCAGAGAAGCTTGATAATAAAATGTATTTCCTATCACCATA 5701 CTTTTCCATGTGAAAACCTGAGCCTATTTCTAGTATATAAGTATCCAAAGAAAAGTTTTACC 5761 TGGTTGTGTTATTTTACCAGAC	
		1 M S A N N S P P S A Q K S V L P T A I P 1 ATGTCTGCAAATAATTCCCCTCCATCAGCCCAGAAGTCTGTATTACCCACAGCTATTCCT	SEQ ID NO:301
		21 A V L P A A S P C S S P K T G L S A R L 61 GCTGTGCTTCCAGCTGCTTCTCCGTGTTCAAGTCCTAAGACGGGACTCTCTGCCCGACTC	
		41 S N G S F S A P S L T N S R G S V H T V 121 TCTAATGGAAGCTTCAGTGCACCATCACTCACCAACTCCAGAGGCTCAGTGCATACAGTT	
		61 S F L L Q I G L T R E S V T I E A Q E L 181 TCATTTCTACTGCAAATTGGCCTCACACGGGAGAGTGTTACCATTGAAGCCCAGGAACTG	
		81 S L S A V K D L V C S I V Y Q K F P E C 241 TCTTTATCTGCTGTCAAGGATCTTGTGTGCTCCATAGTTTATCAAAAGTTTCCAGAGTGT	
		101 G F F G M Y D K I L L L F R H D M N S E N 301 GGATTCTTTGGCATGTATGACAAAATTCTTCTCTTTCGCCATGACATGAACTCAGAAAAC	
		121 I L Q L I T S A D E I H E G D L V E V V 361 ATTTTGCAGCTGATTACCTCAGCAGATGAAATACATGAAGGAGACCTAGTGGAAGTGGTT	
		141 L S A L A T V E D F Q I R P H T L Y V H 421 CTTTCAGCTTTAGCCACAGTAGAAGACTTCCAGATTCGTCCACATACTCTCTATGTACAT	
		161 S Y K A P T F C D Y C G E M L W G L V R 481 TCTTACAAAGCTCCTACTTTCTGTGATTACTGTGGTGAGATGCTGTGGGGATTGGTACGT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		181 Q G L K C E G C G L N Y H K R C A F K I 541 CAAGGACTGAAATGTGAAGGCTGTGGATTAAATTACCATAACGATGTGCCTTCAAGATT	
		201 P N N C S G V R K R R L S N V S L P G P 601 CCAAATAACTGTAGTGGAGTAAGAAAGACGTCTGTCAAATGTATCTTTACCAGGACCC	
		221 G L S V P R P L Q P E Y V A L P S E E S 661 GGCCTCTCAGTTCCAAGACCCCTACAGCCTGAATATGTAGCCCTTCCCAGTGAAGAGTCA	
		241 H V H Q E P S K R I P S W S G R P I W M 721 CATGTCCACCAGGAACCAAGTAAGAGAATTCCTTCTTGGAGTGGTCGCCCAATCTGGATG	
		261 E K M V M C R V K K V P H T F A V H S Y T 781 GAAAAGATGGTAATGTGCAGAGTGAAAGTTCCACACACATTTGCTGTTCACTCTTACACC	
		281 R P T I C Q Y C K R L L K G L F R Q G M 841 CGTCCCACGATATGTCAGTACTGCAAGCGGTTACTGAAAGGCCTCTTTCGCCAAGGAATG	
		301 Q C K D C K F N C H K R C A S K V P R D 901 CAGTGTAAAGATTGCAAATTCAACTGCCATAAACGCTGTGCATCAAAGTACCAAGAGAC	
		321 C L G E V T F N G E P S S L G T D T D I 961 TGCCTTGGAGAGGTTACTTTCAATGGAGAACCTTCCAGTCTGGGAACAGATACAGATATA	
		341 P M D I D N N D I N S D S S R G L D D T 1021 CCAATGGATATTGACAATAATGACATAAATAGTGATAGTAGTCGGGGTTTGGATGACACA	
		361 E E P S P P E D K M F F L D P S D L D V 1081 GAAGAGCCATCACCCCCAGAAGATAAGATGTTCTTCTTGGATCCATCTGATCTCGATGTG	
		381 E R D E E A V K T I S P S T S N N I P L 1141 GAAAGAGATGAAGAAGCCGTTAAAACAATCAGTCCATCAACAAGCAATAATATTCCGCTA	
		401 M R V V Q S I K H T K R K S S T M V K E 1201 ATGAGGGTTGTACAATCCATCAAGCACACAAAGAGGAAGAGCAGCACAATGGTGAAGGAA	
		421 G W M V H Y T S R D N L R K R H Y W R L 1261 GGGTGGATGGTCCATTACACCAGCAGGGATAACCTGAGAAAGAGGCATTATTGGAGACTT	
		441 D S K C L T L F Q N E S G S K Y Y K E I 1321 GACAGCAAATGTCTTACATTATTTCAGAATGAATCTGGATCAAAGTATTATAAGGAAATT	
		461 P L S E I L R I S S P R D F T N I S Q G	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1381 CCACTTTCAGAAATTCTCCGCATATCTTCACCACGAGATTTCACAAACATTTCACAAGGC	
		481 S N P H C F E I I T D T M V Y F V G E N	
		1441 AGCAATCCACACTGTTTTGAAATCATTACTGATACTATGGTATACTTCGTTGGTGAGAAC	
		501 N G D S S H N P V L A A T G V G L D V A	
		1501 AATGGGGACAGCTCTCATAATCCTGTTCTTGCTGCCACTGGAGTTGGACTTGATGTAGCA	
		521 Q S W E K A I R Q A L M P V T P Q A S V	
		1561 CAGAGCTGGGAAAAAGCAATTCGCCAAGCCCTCATGCCTGTTACTCCTCAAGCAAGTGTT	
		541 C T S P G Q G K D H K D L S T S I S V S	
		1621 TGCACTTCTCCAGGGCAAGGGAAAGATCACAAAGATTTGTCTACAAGTATCTCTGTATCT	
		561 N C Q I Q E N V D I S T V Y Q I F A D E	
		1681 AATTGTCAGATTCAGGAGAATGTGGATATCAGTACTGTTTACCAGATCTTTGCAGATGAG	
		581 V L G S G Q F G I V Y G G K H R K T G R	
		1741 GTGCTTGGTTCAGGCCAGTTTGGCATCGTTTATGGAGGAAAACATAGAAAGACTGGGAGG	
		601 D V A I K V I D K M R F P T K Q E S Q L	
		1801 GATGTGGCTATTAAAGTAATTGATAAGATGAGATTCCCCACAAAACAAGAAAGTCAACTC	
		621 R N E V A I L Q N L H H P G I V N L E C	
		1861 CGTAATGAAGTGGCTATTTTACAGAATTTGCACCATCCTGGGATTGTAAACCTGGAATGT	
		641 M F E T P E R V F V V M E K L H G D M L	
		1921 ATGTTTGAAACCCCAGAACGAGTCTTTGTAGTAATGGAAAAGCTGCATGGAGATATGTTG	
		661 E M I L S S E K S R L P E R I T K F M V	
		1981 GAAATGATTCTATCCAGTGAGAAAAGTCGGCTTCCAGAACGAATTACTAAATTCATGGTC	
		681 T Q I L V A L R N L H F K N I V H C D L	
		2041 ACACAGATACTTGTTGCTTTGAGGAATCTGCATTTTAAGAATATTGTGCACTGTGATTTA	
		701 K P E N V L L A S A E P F P Q V K L C D	
		2101 AAGCCAGAAAATGTGCTGCTTGCATCAGCAGAGCCATTTCCTCAGGTGAAGCTGTGTGAC	
		721 F G F A R I I G E K S F R R S V V G T P	
		2161 TTTGGATTTGCACGCATCATTGGTGAAAAGTCATTCAGGAGATCTGTGGTAGGAACTCCA	
		741 A Y L A P E V L R S K G Y N R S L D M W	
		2221 GCATACTTAGCCCCTGAAGTTCTCCGGAGCAAAGGTTACAACCGTTCCCTAGATATGTGG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		761 S V G V I I Y V S L S G T F P F N E D E 2281 TCAGTGGGAGTTATCATCTATGTGAGCCTCAGTGGCACATTTCCTTTTAATGAGGATGAA 781 D I N D Q I Q N A A F M Y P P N P W R E 2341 GATATAAATGACCAAATCCAAAATGCTGCATTTATGTACCCACCAAATCCATGGAGAAA 801 I S G E A I D L I N N L L Q V K M R K R 2401 ATTTCTGGTGAAGCAATTGATCTGATAAACAATCTGCTTCAAGTGAAGATGAGAAAACGT 821 Y S V D K S L S H P W L Q D Y Q T W L D 2461 TACAGTGTTGACAAATCTCTTAGTCATCCCTGGCTACAGGACTATCAGACTTGGCTTGAC 841 L R E F E T R I G E R Y I T H E S D D A 2521 CTTAGAGAATTTGAAACTCGCATTGGAGAACGTTACATTACACATGAAAGTGATGATGCT 861 R W E I H A Y T H N L V Y P K H F I M A 2581 CGCTGGGAAATACATGCATACACACATAACCTTGTATACCCAAAGCACTTCATTATGGCT 881 P N P D D M E E D P - 2641 CCTAATCCAGATGATATGGAAGAAGATCCTTAA	SEQ ID NO:302
BM781379	Homo sapiens inhibitor of Bruton agammaglobulinemia tyrosine kinase (IBTK), mRNA.	1 attcctgtag tagcggctgt attgcagccg cctgccgaac tgacccgggt ctggggactg 61 gcccctctgg cgccgttcgg tttctcttat tgccttcact gaggatgagt cccttttgtgg 121 ctctatgtgg accctgcgga atccaccggc gcagtttcat ctagcgactg gtcaccctg 181 caattatgga tatttaaaag ggtcagacag tgtggagggg gagttcccct cctcactccc 241 ccttggtgct tgactccagg aataatttat aaactgtgga atttttttaa atgaagaact 301 tgtatttgat atgaacttta tagagctatt tataatttt ttgatttaag tgccaaaaaa 361 ttgtataaag atatatagtt ttatactatt gtcaggagga tttaaattat cctaaaaagg 421 taatttattc tctgtaactt cctcaatagc acctttgtgt cctggctttt tcatttttta 481 aaattagttt tcacgattct gaagtaagtg gtataaaaac agttaggatg agttcaccca 541 tgcctgactg cacatcaaag tgtcgatccc tgaagcatgc tttggatgtc ctttctgtgg 601 taacaaaggg gagcgaaaac cagattaagg cctttctctc cagtcattgt tacaatgctg 661 caactatcaa ggatgttttt ggcaggaatg ccctccacct tgtttcctcc tgtggaaaga 721 aaggagtgtt agattggctt attcagaaag gagtggatct gttggtgaaa gacaaagagt 781 ctggatggac agcattgcac agaagcattt tttatggaca tattgattgt gtttggtctc 841 tatgaagca tggtgttagt ctgtatattc aagataaaga aggcttgtca gctttggatc 901 ttgtaatgaa ggatagacca actcatgtag tattcaagaa tactgatcct acagatgttt 961 atacttgggg cgataataca aattttaccc tgggtcatgg aagccagaat agcaaacatc 1021 atccagagtt ggtggatctg ttctccagga gtgggattta tatcaagcag gtggtgcttt 1081 gtaaatttca ctccgtgttt ctgtctcaga aagggcaggt ttatacctgt ggtcatggtc 1141 ctggagggcg attaggacat ggagatgaac agacatgctt ggtccctcgg cttgtggaag

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1201 gactgaatgg tcataattgt tcccaagtgg cagctgctaa ggatcatact gttgtattaa 1261 ctgaagatgg atgtgtttat acatttggtc taaacatttt tcatcaatta ggaattattc 1321 caccgccttc cagttgtaat gtacccagac agatacaggc aaaatatctg aaaggaagga 1381 caatcattgg cgttgcagca ggcaggtttc atacagtcct atggactaga gaagctgttt 1441 acactatggg actaaatggt ggacaactgg gttgtttgct agatcccaat ggagaaaagt 1501 gtgtaactgc tcctcgtcag gtcctgccc ttcaccataa agacattgct ctgtctttgg 1561 ttgctgcaag tgatggagct acagtctgtg ttaccacaag gggagatatt tacttacttg 1621 cagactatca gtgcaagaag atggcttcta aacagttgaa cttgaaaaaa gttcttgtgt 1681 ctgggggtca tatggaatac aaggttgatc ctgaacattt gaaagaaaat gggggtcaaa 1741 aaatttgcat tcttgcaatg gatggagctg gaagggtgtt ttgctggaga tcagtcaaca 1801 gttctctgaa gcagtgtcga tgggcctatc cacgtcaggt cttcatttct gatattgctt 1861 taaatagaaa tgaaattcta ttgttacgc aagatggaga aggatttaga gggagatggt 1921 ttgaagagaa aagaaagagt tctgaaaaga aagagatttt atcaaacctt cacaattcct 1981 catcagatgt gtcttatgtc tctgatataa atagtgtgta tgaaagaatt cgacttgaga 2041 aacttacctt tgcacataga gctgttagtg tcagcacaga tccaagtgga tgcaactttg 2101 caatcctgca gtcagatcct aaaacaagcc tttatgaaat tccagctgtg tcctcatcat 2161 ccttttttga agagtttggc aaactgttga gggaagcaga tgaaatggac agcattcatg 2221 atgtgacatt tcaagttggc aatagactct tccctgcaca taaatatatt ttggcagtgc 2281 attctgattt tttcagaaa ttgtttcttt cagatggtaa tacttcagaa tttacagata 2341 ttaccagaa agatgaagat tctgcagggt gccatctctt tgtggtagag aaggttcatc 2401 ctgacatgtt tgaatacctt ttacaattta tatacacaga tacttgtgac tttttaactc 2461 atggcttcaa accaagaata cacttaaaca aaaacccaga agaatatcag ggaactctga 2521 attctcattt gaataaagtg aatttccatg aagatgataa ccagaagtct gcatttgaag 2581 tttacaaaag taatcaagct caaacagtta gtgagaggca gaagagcaaa cctaaatctt 2641 gtaaaaaagg aaaaaatatt agggaagatg atcctgtaag aatgttgcaa actgttgcaa 2701 agaaattcga cttcagtaat ttgagtagta ggttagatgg agtcagattt gaaaatgaaa 2761 aaattaatgt tattgccaag aacactggta ataaactgaa gctaagtcag aaaaaatgtt 2821 catttctgtg tgacgtgacc atgaaatcag tggatggaaa ggaatttcct tgtcataaat 2881 gtgttctttg tgctagactt gaatatttcc atagtatgct gagtagctca tggattgagg 2941 cttccagttg tgcagctctg gaaatgccaa tacattctga tatattaaaa gttatttggg 3001 actacctcta tactgatgaa gctgtggtga taaaagaatc tcaaaatgta gattttattt 3061 gtagtgttct tgtggtggct gatcaacttc tcataacccg gttgaaagag atttgtgaag 3121 tagcattaac tgaaaaacct accctgaaga atgctgctat gctactggaa tttgcagcaa 3181 tgtatagtgc aaaacagttg aaactgtctt gtttacagtt tataggattg aatatggcag 3241 ctttacttga agcaaggtct cttgatgttt taagcgatgg tgttttgaag gatcttctg 3301 agttttaccg gaaaatgatt ccagcaatgg atagaagagt cattacacca tatcaagatg 3361 gaccagatat tagctatttg gaagtagaag atggagatat ctccttgaaa gaagaaataa 3421 atatggaaca aaatcattcg gaaactatgt tcaagaaagc aaaaacaaaa gctaaaaaga 3481 agccacgtaa acgttcagat agttctggag gttataacct ttcagatatt attcagagtc 3541 catcattcac aggattatta aagtctggta agaccaattc tgtggaatct ctcccagaac 3601 tgttgacatc agactctgaa ggaagctatg caggagtggg tagtcctaga gatttacagt 3661 cccctgattt cacaacagga tttcattcag ataagattga ggcgaaagtc aaaccgtatg 3721 ttaatggtac atctcctgtg tattctaggg aagatttaaa accatgggaa aagtcaccaa	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		3781 tacttaaaat atctgctcca cagcctattc ccagtaacag aattgatact accagctctg 3841 ccagttgggt tgctggttct ttcagtcctg tcagccctcc tgttgtggat ctcagaacta 3901 tcatggaaat agaagaaagt agacaaaaat gtggagctac accaaagtca cattaggca 3961 aaacagtttc tcatggagtt aaactttctc agaagcaacg aaaaatgatt gcattgacta 4021 ccaaggaaaa caattcagga atgaatagca tggaaacagt tttattcact ccttcaaaag 4081 ccccaaacc agtgaatgca tgggcatctt ctctgcattc agtttcatcc aagtcattcc 4141 gggatttctt actagaagaa aaaaagtctg ttactagcca tagttcaggc gatcatgtca 4201 aaaaagtttc tttaaagga attgaaaatt ctcaggcacc aaaaattgtc agatgctcta 4261 cccatggtac cccaggacca gaaggcaacc atattttcaga tttacgactt ctagacagtc 4321 ccaatccctg gctatcttct tcagtgactg ctccatccat ggtagcccca gtcacttttg 4381 catctattgt agaagaagaa ctacaacaag aagcagctct tattagaagt cgagaaaaac 4441 cgttggctct gattcagatt gaggagcatg ccatacaaga tttattggtt ttctatgagg 4501 catttggcaa ccctgaagag tttgtcattg ttgaaaggac acgcagggga ccactggcag 4561 tacctatgtg gaataagcat ggatgctagt tcactgtgga gttgagatgc atttacata 4621 attatgagtt tgttcatata aagaaaagct gtggaaaaga gtcttagaga tttgtaata 4681 tcattctaaa tagattaaga aaagatataa tttctttact gcagttaaat catataatgt 4741 ttgtatgatt aaaaataaat ttctcagaat tgtgatttta gtaactttat ataaaatgtg 4801 tgagacaaaa acttattaag gttaaataga attgtttctt ctgaataatc taacaaagga 4861 aaatataagt gattgaatca taagatataa gggggtaaa gtattaaaaa taacttttt 4921 gtttgataac ttgagaattt agaagatttt gccaagtatg tgttgttgct tgacttctta 4981 aatatggcat tgatgaattt aaagtaggag catcagttat tacttctgat tcattaatgg 5041 ccagaatttt gtgtttggtg taatagttgt gtcaccattc ttgttgcttt ttaaaaatca 5101 ggctaatcat gtggtccatg tctcttcaaa gcttgacctg cacaaatgcc atatttctat 5161 ttggaccaca tattctccat tttgcattga gcagtagagt acagtggaaa gggaataaga 5221 atactgatta ttctgaacag tttagtccca agagaatagc gttttaaaaa agaaaaacaa 5281 gatttggagt cattgtgggt tatttttggt gggatggagg atcttaaaaa tgcctaattg 5341 tgagagaatc aattgctgaa agtgttaaaa tttctgaaaa taaatgctta attacatata 5401 caggaattaa atagtttgga agagggttgg attatcatta cctttacaat actgtataat 5461 cagaagttct ctgaacctca attgtatatc tagacataaa aattgttttc tgtataggat 5521 gttgtttggt ttgtttctga gtgtttaaat tttgcaaaaa caaatgttaa atttgtgctt 5581 cagtacctag ataaattgga aaggttaatg ttctagtttc tggaaggtaa gcctgggaga 5641 cacataagca attcactgct ataatttagt tgatgtaaaa tgacggaaac tgactcaata 5701 tgtcaggttt aactctgccc aaaagcagca gacatgtaag cagatgtgca ataaaaatg 5761 atcttgatcc atttc 1 M S S P M P D C T S K C R S L K H A L D 1 ATGAGTTCACCCATGCCTGACTGCACATCAAAGTGTCGATCCCTGAAGCATGCTTTGGAT 21 V L S V V T K G S E N Q I K A F L S S H 61 GTCCTTTCTGTGGTAACAAAGGGAGCGAAAACCAGATTAAGGCCTTTCTCTCCAGTCAT 41 C Y N A A T I K D V F G R N A L H L V S 121 TGTTACAATGCTGCAACTATCAAGGATGTTTTGGCAGGAATGCCCTCCACCTTGTTTCC	SEQ ID NO:303

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		61 S C G K K G V L D W L I Q K G V D L L V 181 TCCTGTGGAAAGAAAGGAGTGTTAGATTGGCTTATTCAGAAAGGAGTGGATCTGTTGGTG	
		81 K D K E S G W T A L H R S I F Y G H I D 241 AAAGACAAAGAGTCTGGATGGACAGCATTGCACAGAAGCATTTTTTATGGACATATTGAT	
		101 C V W S L L K H G V S L Y I Q D K E G L 301 TGTGTTTGGTCTCTATTGAAGCATGGTGTTAGTCTGTATATTCAAGATAAAGAAGGCTTG	
		121 S A L D L V M K K D R P T H V V F K N T D 361 TCAGCTTTGGATCTTGTAATGAAGGATAGACCAACTCATGTAGTATTCAAGAATACTGAT	
		141 P T D V Y T W G D N T N F T L G H G S Q 421 CCTACAGATGTTTATACTTGGGGCGATAATACAAATTTTACCCTGGGTCATGGAAGCCAG	
		161 N S K H H P E L V D L F S R S G I Y I K 481 AATAGCAAACATCATCCAGAGTTGGTGGATCTGTTCTCCAGGAGTGGGATTTATATCAAG	
		181 Q V V L C K F H S V F L S Q K G Q V Y T 541 CAGGTGGTGCTTTGTAAATTTCACTCCGTGTTTCTGTCTCAGAAAGGGCAGGTTTATACC	
		201 C G H G P G G R L G H G D E Q T C L V P 601 TGTGGTCATGGTCCTGGAGGGCGATTAGGACATGGAGATGAACAGACATGCTTGGTCCCT	
		221 R L V E G L N G H N C S Q V A A A K D H 661 CGGCTTGTGGAAGGACTGAATGGTCATAATTGTTCCCAAGTGGCAGCTGCTAAGGATCAT	
		241 T V V L T E D G C V Y T F G L N I F H Q 721 ACTGTTGTATTAACTGAAGATGGATGTGTTTATACATTTGGTCTAAACATTTTTCATCAA	
		261 L G I I P P P S S C N V P R Q I Q A K Y 781 TTAGGAATTATTCCACCGCCTTCCAGTTGTAATGTACCCAGACAGATACAGGCAAAATAT	
		281 L K G R T I I G V A A G R F H T V L W T 841 CTGAAAGGAAGGACAATCATTGGCGTTGCAGCAGGCAGGTTTCATACAGTCCTATGGACT	
		301 R E A V Y T M G L N G G Q L G C L L D P 901 AGAGAAGCTGTTTACACTATGGGACTAAATGGTGGACACACTGGGTTGTTTGCTAGATCCC	
		321 N G E K C V T A P R Q V S A L H H K D I 961 AATGGAGAAAAGTGTGTAACTGCTCCTCGTCAGGTCTCTGCCCTTCACCATAAAGACATT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		341 A L S L V A A S D G A T V C V T T R G D 1021 GCTCTGTCTTTGGTTGCTGCAAGTGATGGAGCTACAGTCTGTGTTACCACAAGGGGAGAT	
		361 I Y L L A D Y Q C K K M A S K Q L N L K 1081 ATTTACTTACTTGCAGACTATCAGTGCAAGAAGATGGCTTCTAAACAGTTGAACTTGAAA	
		381 K V L V S G G H M E Y K V D P E H L K E 1141 AAAGTTCTTGTGTCTGGGGGTCATATGGAATACAAGGTTGATCCTGAACATTTGAAAGAA	
		401 N G G Q K I C I L A M D G A G R V F C W 1201 AATGGGGGTCAAAAAATTTGCATTCTTGCAATGGATGGAGCTGGAAGGGTGTTTTGCTGG	
		421 R S V N S S L K Q C R W A Y P R Q V F I 1261 AGATCAGTCAACAGTTCTCTGAAGCAGTGTCGATGGGCCTATCCACGTCAGGTCTTCATT	
		441 S D I A L N R N E I L F V T Q D G E G F 1321 TCTGATATTGCTTTAAATAGAAATGAAATTCTATTTGTTACGCAAGATGGAGAAGGATTT	
		461 R G R W F E E K R R K S S E K K E I L S N 1381 AGAGGGAGATGGTTTGAAGAGAAAAGAAAGAGTTCTGAAAAGAAAGAGATTTTATCAAAC	
		481 L H N S S S D V S Y V S D I N S V Y E R 1441 CTTCACAATTCCTCATCAGATGTGTCTTATGTCTCTGATATAAATAGTGTGTATGAAAGA	
		501 I R L E K L T F A H R A V S V S T D P S 1501 ATTCGACTTGAGAAACTTACCTTTGCACATAGAGCTGTTAGTGTCAGCACAGATCCAAGT	
		521 G C N F A I L L Q S D P K T S L Y E I P A 1561 GGATGCAACTTTGCAATCCTGCAGTCAGATCCTAAACAAGCCTTTATGAAATTCCAGCT	
		541 V S S S S F F E E F G K L L R E A D E M 1621 GTGTCCTCATCATCCTTTTTTGAAGAGTTTGGCAAACTGTTGAGGGAAGCAGATGAAATG	
		561 D S I H D V T F Q V G N R L F P A H K Y 1681 GACAGCATTCATGATGTGACATTTCAAGTTGGCAATAGACTCTTCCCTGCACATAAATAT	
		581 I L A V H S D F F Q K L F L S D G N T S 1741 ATTTTGGCAGTGCATTCTGATTTTTTTCAGAAATTGTTTCTTCAGATGGTAATACTTCA	
		601 E F T D I Y Q K D E D S A G C H L F V V 1801 GAATTTACAGATATTTACCAGAAAGATGAAGATTCTGCAGGGTGCCATCTCTTTGTGGTA	
		621 E K V H P D M F E Y L L Q F I Y T D T C	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1861 GAGAAGGTTCATCCTGACATGTTTGAATACCTTTTACAATTTATATACACAGATACTTGT	
		641 D F L T H G F K P R I H L N K N P E E Y	
		1921 GACTTTTTAACTCATGGCTTCAAACCAAGAATACACTTAAACAAAACCCAGAAGAATAT	
		661 Q G T L N S H L N K V N F H E D D N Q K	
		1981 CAGGGAACTCTGAATTCTCATTTGAATAAAGTGAATTTCCATGAAGATGATAACCAGAAG	
		681 S A F E V V Y K S N Q A Q T V S E R Q K S	
		2041 TCTGCATTTGAAGTTTACAAAAGTAATCAAGCTCAAACAGTTAGTGAGAGGCAGAAGAGC	
		701 K P K S C K K G K N I R E D D P V R M L	
		2101 AAACCTAAATCTTGTAAAAAAGGAAAAAATATTAGGGAAGATGATCCTGTAAGAATGTTG	
		721 Q T V A K K F D F S N L S S R L D G V R	
		2161 CAAACTGTTGCAAAGAAATTCGACTTCAGTAATTTGAGTAGGTTAGATGGAGTCAGA	
		741 F E N E K I N V I A K N T G N K L K L S	
		2221 TTTGAAAATGAAAAAATTAATGTTATTGCCAAGAACACTGGTAATAAACTGAAGCTAAGT	
		761 Q K K C S F L C D V T M K S V D G K E F	
		2281 CAGAAAAAATGTTCATTTCTGTGTGACGTGACCATGAAATCAGTGGATGGAAAGGAATTT	
		781 P C H K C V L C A R L E Y F H S M L S S	
		2341 CCTTGTCATAAATGTGTTCTTTGTGCTAGACTTGAATATTTTCATAGTATGCTGAGTAGC	
		801 S W I E A S S C A A L E E M P I H S D I L	
		2401 TCATGGATTGAGGCTTCCAGTTGTGCAGCTCTGGAAATGCCAATACATTCTGATATATTA	
		821 K V I L D Y L Y T D E A V V I K E S Q N	
		2461 AAAGTTATTTTGGACTACCTCTATACTGATGAAGCTGTGGTGATAAAAGAATCTCAAAAT	
		841 V D F I C S V L V V A D Q L L I T R L K	
		2521 GTAGATTTTATTTGTAGTGTTCTTGTGGTGGCTGATCAACTTCTCATAACCCGGTTGAAA	
		861 E I C E V A L T E K L T L K N A A M L L	
		2581 GAGATTTGTGAAGTAGCATTAACTGAAAAACTTACCCTGAAGAATGCTGCTATGCTACTG	
		881 E F A A M Y S A K Q L K L S C L Q F I G	
		2641 GAATTTGCAGCAATGTATAGTGCAAAACAGTTGAAACTGTCTTGTTTACAGTTTATAGGA	
		901 L N M A A L L E A R S L D V L S D G V L	
		2701 TTGAATATGGCAGCTTTACTTGAAGCAAGGTCTCTTGATGTTTTAAGCGATGGTGTTTTG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		921 K D L S E F Y R K M I P A M D R R V I T 2761 AAGGATCTTTCTGAGTTTTACCGGAAAATGATTCCAGCAATGGATAGAAGAGTCATTACA	
		941 P Y Q D G P D I S Y L E V E D G D I F L 2821 CCATATCAAGATGGACCAGATATTAGCTATTTGGAAGTAGAAGATGGAGATATCTTCTTG	
		961 K E E I N M E Q N H S E T M F K K A K T 2881 AAAGAAGAAATAAATATGGAACAAAATCATTCGGAAACTATGTTCAAGAAAGCAAAAACA	
		981 K A K K K P R K R S D S S G G G Y N L S D 2941 AAAGCTAAAAAGAAGCCACGTAAACGTTCAGATAGTTCTGGAGGTTATAACCTTTCAGAT	
		1001 I I Q S P S S T G L L K S G K T N S V E 3001 ATTATTCAGAGTCCATCATCTACAGGATTATTAAAGTCTGGTAAGACCAATTCTGTGGAA	
		1021 S L P E L L T S D S E G S Y A G V G S P 3061 TCTCTTCCAGAACTGTTGACATCAGACTCTGAAGGAAGCTATGCAGGAGTGGGTAGTCCT	
		1041 R D L Q S P D F T T G F H S D K I E A K 3121 AGAGATTTACAGTCCCCTGATTTCACAACAGGATTTCATTCAGATAAGATTGAGGCGAAA	
		1061 V K P Y V N G T S P V Y S R E D L K P W 3181 GTCAAACCGTATGTTAATGGTACATCTCCTGTGTATTCTAGGGAAGATTTAAAACCATGG	
		1081 E K S P I L K I S A P Q P I P S N R I D 3241 GAAAAGTCACCAATACTTAAAATATCTGCTCCACAGCCTATTCCCAGTAACAGAATTGAT	
		1101 T T S S A S W V A G S F S P V S P P V V 3301 ACTACCAGCTCTGCCAGTTGGGTTGCTGGTTCTTTCAGTCCTGTCAGCCCTCCTGTTGTG	
		1121 D L R T I M E I E E S R Q K C G A T P K 3361 GATCTCAGAACTATCATGGAAATAGAAGAAAGTAGACAAAAATGTGGAGCTACACCAAAG	
		1141 S H L G K T V S H G V K L S Q K Q R K M 3421 TCACATTTAGGCAAAACAGTTTCTCATGGAGTTAAACTTTCTCAGAAGCAACGAAAAATG	
		1161 I A L T T K E N N S G M N S M E T V L F 3481 ATTGCATTGACTACCAAGGAAAACAATTCAGGAATGAATAGCATGGAAACAGTTTTATTC	
		1181 T P S K A P K P V N A W A S S L H S V S 3541 ACTCCTTCAAAAGCCCCCAAACCAGTGAATGCATGGGCATCTTCTCTGCATTCAGTTTCA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1201 S K S F R D F L L E E K K S V T S H S S 3601 TCCAAGTCATTCCGGGATTTCTTACTAGAAGAAAAAAAGTCTGTTACTAGCCATAGTTCA 1221 G D H V K K V S F K G I E N S Q A P K I 3661 GGCGATCATGTCAAAAAAGTTTCTTTTAAAGGAATTGAAAATTCTCAGGCACCAAAAATT 1241 V R C S T H G T P G P E G N H I S D L P 3721 GTCAGATGCTCTACCCATGGTACCCCAGGACCAGAAGGCAACCATATTTCAGATTTACCA 1261 L L D S P N P W L S S S V T A P S M V A 3781 CTTCTAGACAGTCCCAATCCCTGGCTATCTTCTTCAGTGACTGCTCCATCCATGGTAGCC 1281 P V T F A S I V E E E L Q Q E A A L I R 3841 CCAGTCACTTTTGCATCTATTGTAGAAGAAGAACTACAACAAGAAGCAGCTCTTATTAGA 1301 S R E K P L A L I Q I E E H A I Q D L L 3901 AGTCGAGAAAAACCGTTGGCTCTGATTCAGATTGAGGAGCATGCCATACAAGATTTATTG 1321 V F Y E A F G N P E E F V I V E R T P Q 3961 GTTTTCTATGAGGCATTTGGCAACCCTGAAGAGTTTGTCATTGTTGAAAGGACACCGCAG 1341 G P L A V P M W N K H G C - 4021 GGACCACTGGCAGTACCTATGTGGAATAAGCATGGATGCTAG	
BM781394	No Homology	1 GGCACGAGGGCCCCTACAAATGCAAAACCCAGGTTTCTAACTGTTCAAGATATAGTCAAG 61 AGTTCAGCTTCACGTTTGCCAACCCAGTGACCACACCAGTGCTGAACATTAGTGCCTTTC 121 AAACAGAAACAGCCCGATACATAACACTCCGCTGCATCTCATACAATGGCTCTCTGCCCA 181 TCAATTACACTTTCTTTGAAAAAGACGTCGCCATATCACCTGCTATTTCCAAGAATGTAA 241 GGGAACCTGCTGAATTTAACTTAACCGAGAGGATCACCGTGACAAAGGGAAGAATATAGG 301 TGTAAAGCCAAAAACAGATTGCCCAACCATGCAAAATACAGTCAACCCTTCACCATGCCC 361 TCAACAGGCGGAGACAGCTGTCCTTTCTGCCTGCAGCTACTGCTTCCGGGGTTATTACTG 421 CTGCTGATAGTAATAATCCTAATGCTGGCATTTTGGATACTACCAAAGTACAAAGCAAGA 481 AAAGCTATGAGAGATAATGCACCCAGAAACTATGGAAATAAACCCATGGAAGTTGGAATA 541 TATGCAAATGTCTGTCAAAACCAAGCAGATGACAAATCTGTGCCAGGCTTGGAACCAAGG 601 CAGTGTGTTTCCACAGCCCAA	SEQ ID NO:304
BM781409	No homology	1 GGCACGAGGAACTTTCATATATTGTGCCAGGTGCTAGGGATACAGTGATAAACAAAATTA 61 TCATGGTTCCTGCTCCTGGAGATCTTATGGTATAGTAGGATAAACAGAATTAAAAAAATA 121 AAAATAAATATTTAATGACAAATGACATGGAGGTTGTGAAAGAATAATAAGGGGATCCAT 181 TTTAGATGGAATGGTCTGAGAAGGTCTGTCTTCGAAGGTGACATATGTAAGCTGAGACCT	SEQ ID NO:305

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		241 AAAGAAAAGGAGGAACCAGGCAGGCAGAGGAAAGGCCTTGAGGCAGATGTAAAAACTGTG 301 ACATAGAGAACTCTTTCCTCTAACAGAGGAGCTGAAAGAAGCTCAGGGAGGCTAAATAGA 361 GATAGTGCGGGGAGAGTGATGATAGCTGAGGCTTGAGATGGGTCAGACCATCCAGGGCCA 421 GGGAGACTCAGTTTCATTCTGAGTGCACTGGGAAGTCTTGCAGCGTTTTAAGCAGACAAG 481 CGAAGGATCTGATTTATATTTAAAAATATTACTGTTGTAATATTGTCTTGTCTTGTGGAGA 541 ATGGATTGGAAGGAAAAACGAGCAACAGTTGCAGAGAGTTGTTCAGAATTTGTTGTAGTA 601 CTCCAGGTCAGCTCGTGC	
BM781416	No homology	1 TTTAATCGTTAATTGTTTTTTCCCTTGTCCGTTTTTATTTGGGCATCCACCACAGACAAT 61 TTAAATTTCGTAGATGCGCTCAGAACGCAGCAGGCGTACGTAGCAGAAATGCAAGGT 121 GGACAGGTAGTACAATTACTGGCTTTTCTGCTGTAAATAGAATGAAGGAAAATGACTCAA 181 ATCAAGTAAAACTAACACACATGATTTGATTGACAATAAAGTATTTGCCATCACATGCTG 241 CAGCTGTTTGTCAGGAACATGGTGTCATTCATTCATTCAGTAATCACGCTGCAGAAATTG 301 GCAGCCTGCACCTTATGCGTCACCATTACCTTTAGTCGTTTTTTTTGTATTAATTGTAGCC 361 AACTCGTGC	SEQ ID NO:306
BM781438	Homo sapiens cysteine-rich motor neuron 1 (CRIM1)	1 ggcccggctg cgaggaggag gcggcggcgg cgcaggagga tgtacttggt ggcgggggac 61 aggggttggg ccggctgcgg gcacctcctg gtctcgctgc tggggctgct gctgctgctg 121 gcgcgctccg gcacccgggc gctggtctgc ctgccctgtg acgagtccaa gtgcgaggag 181 cccaggaact gcccggggag catcgtgcag ggcgtctgcg gctgctgcta cacgtcgccc 241 agccagagga acgagagctg cggcggcacc ttcgggattt acggaacctg cgaccggggg 301 ctgcgttgtg tcatccgccc cccgctcaat ggcgactccc tcaccgagta cgaagcgggc 361 gtttgcgaag atgagaactg gactgatgac caactgcttg gttttaaacc atgcaatgaa 421 aaccttattg ctggctgcaa tataatcaat gggaaatgtg aatgtaacac cattcgaacc 481 tgcagcaatc cctttgagtt tccaagtcag gatatgtgcc tttcagcttt aaagagaatt 541 gaagaagaga agccagattg ctcccaaggcc cgctgtgaag tccagttctc tccacgttgt 601 cctgaagatt ctgttctgat cgagggttat gctcctcctg gggagtgctg tcccttaccc 661 agccgctgcg tgtgcaaccc cgcaggctgt ctgcgcaaag tctgccagcc gggaaacctg 721 aacatactag tgtcaaaagc ctcagggaag ccgggagagt gctgtgacct ctatgagtgc 781 aaaccagttt tcggcgtgga ctgcaggact gtggaatgcc ctcctgttca gcagaccgcg 841 tgtccccggg acagctatga aactcaagtc agactaactg cagatggttg ctgtactttg 901 ccaacaagat gcgagtgtct ctctggctta tgtggtttcc ccgtgtgtga ggtgggatcc 961 actccccgca tagtctctcg tggcgatggg acacctggaa agtgctgtga tgtctttgaa 1021 tgtgttaatg atacaaagcc agcctgcgta tttaacaatg tggaatatta tgatggagac 1081 atgtttcgaa tggacaactg tcggttctgt cgatgccaag gggcgttgc catctgcttc 1141 actgcccagt gtggtgagat aaactgcgag aggtactacg tgcccgaagg agagtgctgc 1201 ccagtgtgtg aagatccagt gtatcctttt aataatcccg ctggctgcta tgccaatggc 1261 ctgatccttg cccacggaga ccggtggcgg gaagacgact gcacattctg ccagtgcgtc 1321 aacggtgaac gccactgcgt tgcgaccgtc tgcggacaga cctgcacaaa ccctgtgaaa 1381 gtgcctgggg agtgttgccc tgtgtgcgaa gaaccaacca tcatcacagt tgatccacct 1441 gcatgtgggg agttatcaaa ctgcactctg acagggaagg actgcattaa tggtttcaaa	SEQ ID NO:307

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1501 cgcgatcaca atggttgtcg gacctgtcag tgcataaaca ccgaggaact atgttcagaa	
		1561 cgtaaacaag gctgcacctt gaactgtccc ttcggtttcc ttactgatgc ccaaaactgt	
		1621 gagatctgtg agtgccgccc aaggcccaag aagtgcagac ccataatctg tgacaagtat	
		1681 tgtccacttg gattgctgaa gaataagcac ggctgtgaca tctgtcgctg taagaaatgt	
		1741 ccagagctct catgcagtaa gatctgcccc ttggttttcc agcaggacag tcacggctgt	
		1801 cttatctgca agtgcagaga ggcctctgct tcagctgggc cacccatcct gtcgggcact	
		1861 tgtctcaccg tggatggtca tcatcataaa aatgaggaga gctggcacga tgggtgccgg	
		1921 gaatgctact gtctcaatgg acgggaaatg tgtgccctga tcacctgccc ggtgcctgcc	
		1981 tgtggcaacc ccaccattca ccctggacag tgctgcccat catgtgcaga tgactttgtg	
		2041 gtgcagaagc cagagctcag tactccctcc atttgccacg ccctggagg agaatacttt	
		2101 gtggaaggag aaacgtggaa cattgactcc tgtactcagt gcacctgcca cagcggacgg	
		2161 gtgctgtgtg agacagaggt gtgcccaccg ctgctctgcc agaacccctc acgcacccag	
		2221 gattcctgct gcccacagtg tacagatcaa cctttcggc cttccttgtc ccgcaataac	
		2281 agcgtaccta attactgcaa aaatgatgaa ggggatatat tcctggcagc tgagtcctgg	
		2341 aagcctgacg tttgtaccag ctgcatctgc attgatagcg taattagctg tttctctgag	
		2401 tcctgccctt ctgtatcctg tgaaagacct gtcttgagaa aaggccagtg ttgtccctac	
		2461 tgcatagaag acacaattcc aaagaaggtg gtgtgccact tcagtgggaa ggcctatgcc	
		2521 gacgaggagc ggtgggacct tgacagctgc acccactgct actgcctgca gggccagacc	
		2581 ctctgctcga ccgtcagctg ccccctctg ccctgtgttg agcccatcaa cgtggaagga	
		2641 agttgctgcc caatgtgtcc agaaatgtat gtcccagaac caaccaatat acccattgag	
		2701 aagacaaacc atcgaggaga ggttgacctg gaggttcccc tgtggcccac gcctagtgaa	
		2761 aatgatatcg tccatctccc tagagatatg ggtcacctcc aggtagatta cagagataac	
		2821 aggctgcacc caagtgaaga ttcttcactg gactccattg cctcagttgt ggttcccata	
		2881 attatatgcc tctctattat aatagcattc ctattcatca atcagaagaa acagtggata	
		2941 ccactgcttt gctggtatcg aacaccaact aagccttctt ccttaaataa tcagctagta	
		3001 tctgtggact gcaagaaagg aaccagagtc caggtggaca gttcccagag aatgctaaga	
		3061 attgcagaac cagatgcaag attcagtggc ttctacagca tgcaaaaaca gaaccatcta	
		3121 caggcagaca atttctacca aacagtgtga agaaaggcaa ctaggatgag gtttcaaaag	
		3181 acggaagacg actaaatctg ctctaaaaag taaactagaa tttgtgcact tgcttagtgg	
		3241 attgtattgg attgtgactt gatgtacagc gctaagacct tactgggatg ggctctgtct	
		3301 acagcaatgt gcagaacaag cattcccact tttcctcaag ataactgacc aagtgttttc	
		3361 ttagaaccaa agtttttaaa gttgctaaga tatatttgcc tgtaagatag ctgtagagat	
		3421 atttgggtg gggacagtga gtttggatgg ggaaatgggt gggagggtgg tgttgggaag	
		3481 aaaaattggt cagcttggct cggggagaaa cctggtaaca taaaagcagt tcagtggccc	
		3541 agaggttatt ttttcctat tgctctgaag actgcactgg ttgctgcaaa gctcaggcct	
		3601 gaatgagcag gaaacaaaaa aggccttgcg acccagctgc cataaccacc ttagaactac	
		3661 cagacgagca catcagaacc ctttgacagc catcccaggt ctaaagccac aagtttcttt	
		3721 tctatacagt cacaactgca gtaggcagtg aggaagccag agaaatgcga tagcggcatt	
		3781 tctctaaagc gggttattaa ggatatatac agttacactt tttgctgctt ttatttcttt	
		3841 ccaagccaat caatcagcca gttcctagca gagtcagcac atgaacaaga tctaagtcat	
		3901 ttctttgatgt gagcactgga gctttttttt ttttacaacg tgacaggaag aggagggaga	
		3961 gggtgacgaa caccaggcat ttccagggggc tatatttcac tgtttgttgt tgctttgttc	
		4021 tgttatattg ttggttgttc atagttttg ttgaagtctt agcttaagaa gaaacttttt	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		4081 ttaaaaagac tgtttgggga ttcttttttcc ttattatata ctgattctac aaaatagaaa 4141 ctacttcatt ttaattgtat attattcaag caccttgtgt gaagctcaaa aaaaatgatg 4201 cctcttttaaa ctttagcaat tataggagta tttatgtaac tatctttatgc ttcaaaaaac 4261 aaaagtattt gtgtgcatgt gtatatatata tatatatata catatatatt tatacacata 4321 caatttatgt tttcctgttg aatgtatttt tatgagattt taaccagaac aaaggcagat 4381 aaacaggcat tccatagcag tgcttttgat cacttacaaa ttttttgaat aacacaaaat 4441 ctcattctac ctgcagttta attggaaaga tgtgtgtgtg agagtatgta tgtgtgtgtg 4501 tgtgtgtgtg tgtgtgcgcg cgcacgcacg ccttgagcag tcagcattgc acctgctatg 4561 gagaagggta ttcctttatt aaaatccttcc tcatttggat ttgctttcag ttggttttca 4621 attgctcac tggccagaga cattgatggc agttcttatc tgcatcacta atcagctcct 4681 ggattttttt ttttttttt tcaaacaatg gtttgaaaca actactggaa tattgtccac 4741 aataagctgg aagttttgttg tagtatgcct caaatataac tgactgtata ctatagtggt 4801 aacttttcaa acagccctta gcacttttat actaattaac ccatttgtgc attgagtttt 4861 ctttaaaaa tgcttgttgt gaaagacaca gatacccagt atgcttaacg tgaaaagaaa 4921 atgtgttctg tttgtaaag gaactttcaa gtattgttgt aaatacttgg acagaggttg 4981 ctgaacttta aaaaaaatta atttattatt ataatgacct aatttattaa tctgaagatt 5041 aaccatttt ttgtcttaga atatcaaaaa gaaaaagaaa aaggtgtttct agctgtttgc 5101 atcaaaggaa aaaaagattt attatcaagg ggcaatattt ttatcttttc caaaataaat 5161 ttgttaatga tacattacaa aaatagattg acatcagcct gattagtata aattttgttg 5221 gtaattaatc catcctggc ataaaaagtc tttatcaaaa aaaattgtag atgcttgctt 5281 tttgtttttt caatcatggc catattatga aaatactaac aggatatagg acaaggtgta 5341 aatttttta ttattatttt aaagatatga tttatcctga gtgctgtatc tattactctt 5401 ttactttggt tcctgttgtg ctcttgtaaa agaaaaatat aattcctga agaataaaat 5461 agatatatgg cacttggagt gcatcatagt tctacagttt gttttgttt tcttcaaaaa 5521 agctgtaaga gaattatctg caacttgatt cttggcagga aataaacatt ttgagttgaa 5581 atcaaaaaaa aaaaaaaaaa a 1 M Y L V A G D R G L A G C G H L L V S L 1 ATGTACTTGGTGGCGGGGACAGGGGTTGGCCGGCTGCGGGCACCTCCTGGTCTCGCTG 21 L G L L L L L A R S G T R A L V C L P C 61 CTGGGGCTGCTGCTGCTGGCGCGCTCCGGCACCCGGGCGCTGGTCTGCCTGCCCTGT 41 D E S K C E E P R N C P G S I V Q G V C 121 GACGAGTCCAAGTGCGAGGAGCCCAGGAACTGCCCGGGAGCATCGTGCAGGGCGTCTGC 61 G C C Y T C A S Q R N E S C G G T F G I 181 GGCTGCTGCTACACGTGCGCCAGCCAGAGGAACGAGCTGCGGCGGCACCTTCGGGATT 81 Y G T C D R G L R C V I R P P L N G D S 241 TACGGAACCTGCGACCGGGGGCTGCGTTGTGTCATCCGCCCCCCGCTCAATGGCGACTCC 101 L T E Y E A G V C E D E N W T D D Q L L	SEQ ID NO:308

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		301 CTCACCGAGTACGAAGCGGGCGTTTGCGAAGATGAGAACTGGACTGATGACCAACTGCTT	
		121 G F K P C N E N L I A G C N I I N G K C	
		361 GGTTTTAAACCATGCAATGAAAACCTTATTGCTGGCTGCAATATAATCAATGGGAAATGT	
		141 E C N T I R T C S N P F E F P S Q D M C	
		421 GAATGTAACACCATTCGAACCTGCAGCAATCCCTTTGAGTTTCCAAGTCAGGATATGTGC	
		161 L S A L K R I E E E E K P D C S K A R C E	
		481 CTTTCAGCTTTAAAGAGAATTGAAGAAGAGAAGCCAGATTGCTCCAAGGCCCGCTGTGAA	
		181 V Q F S P R C P E D S V L I E G Y A P P	
		541 GTCCAGTTCTCTCCACGTTGTCCTGAAGATTCTGTTCTGATCGAGGGTTATGCTCCTCCT	
		201 G E C C P L P S R C V C N P A G C L R K	
		601 GGGGAGTGCTGTCCCTTACCCAGCCGCTGCGTGTGCAACCCCGCAGGCTGTCTGCGCAAA	
		221 V C Q P G N L N I L V S K A S G K P G E	
		661 GTCTGCCAGCCGGGAAACCTGAACATACTAGTGTCAAAAGCCTCAGGGAAGCCGGGAGAG	
		241 C C D L Y E C K P V F G V D C R T V E C	
		721 TGCTGTGACCTCTATGAGTGCAAACCAGTTTTCGGCGTGGACTGCAGGACTGTGGAATGC	
		261 P P V Q Q T A C P P D S Y E T Q V R L T	
		781 CCTCCTGTTCAGCAGACCGCGTGTCCCCCGGACAGCTATGAAACTCAAGTCAGACTAACT	
		281 A D G C C T L P T R C E C L S G L C G F	
		841 GCAGATGGTTGCTGTACTTTGCCAACAAGATGCCAGTGTCTCTCTGGCTTATGTGGTTTC	
		301 P V C E V G S T P R I V S R G D G T P G	
		901 CCCGTGTGTGAGGTGGGATCCACTCCCCCGCATAGTCTCTCGTGGCGATGGGACACCTGGA	
		321 K C C D V F E C V N D T K P A C V F N N	
		961 AAGTGCTGTGATGTCTTTGAATGTGTTAATGATACAAAGCCAGCCTGCGTATTTAACAAT	
		341 V E Y Y D G D M F R M D N C R F C R C Q	
		1021 GTGGAATATTATGATGGAGACATGTTTCGAATGGACAACTGTCGGTTCTGTCGATGCCAA	
		361 G G V A I C F T A Q C G E I N C E R Y Y	
		1081 GGGGGCGTTGCCATCTGCTTCACTGCCCAGTGTGGTGAGATAAACTGCGAGAGGTACTAC	
		381 V P E G E C C P V C E D P V Y P F N N P	
		1141 GTGCCCGAAGGAGAGTGCTGCCCAGTGTGTGAAGATCCAGTGTATCCTTTTAATAATCCC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		401 A G C Y A N G L I L A H G D R W R E D D 1201 GCTGGCTGCTATGCCAATGGCCTGATCCTTGCCCACGGAGACCGGTGGCGGGAAGACGAC	
		421 C T F C Q C V N G E R H C V A T V C G Q 1261 TGCACATTCTGCCAGTGCGTCAACGGTGAACGCCACTGCGTTGCGACCGTCTGCGGACAG	
		441 T C T N P V K V P G E C C P V C E E P T 1321 ACCTGCACAAACCCTGTGAAAGTGCCTGGGGAGTGTTGCCCTGTGTGCGAAGAACCAACC	
		461 I I T V D P P A C G E L S N C T L T G K 1381 ATCATCACAGTTGATCCACCTGCATGTGGGGAGTTATCAAACTGCACTCTGACAGGGAAG	
		481 D C I N G F K R D H N G C R T C Q C I N 1441 GACTGCATTAATGGTTTCAAACGCGATCACAATGGTTGTCGGACCTGTCAGTGCATAAAC	
		501 T E E L C S E R K Q G C T L N C P F G F 1501 ACCGAGGAACTATGTTCAGAACGTAAACAAGGCTGCACCTTGAACTGTCCCTTCGGTTTC	
		521 L T D A Q N C E I C E C R P R P K K C R 1561 CTTACTGATGCCCAAAACTGTGAGATCTGTGAGTGCCGCCCAAGGCCCAAGAAGTGCAGA	
		541 P I I C D K Y C P L G L L K N K H G C D 1621 CCCATAATCTGTGACAAGTATTGTCCACTTGGATTGCTGAAGAATAAGCACGGCTGTGAC	
		561 I C R C K K C P E L S C S K I C P L G F 1681 ATCTGTCGCTGTAAGAAATGTCCAGAGCTCTCATGCAGTAAGATCTGCCCCTTGGGTTTC	
		581 Q Q D S H G C L I C K C R E A S A S A G 1741 CAGCAGGACAGTCACGGCTGTCTTATCTGCAAGTGCAGAGAGGCCTCTGCTTCAGCTGGG	
		601 P P I L S G T C L T V D G H H H K N E E 1801 CCACCCATCCTGTCGGGCACTTGTCTCACCGTGGATGGTCATCATCATAAAAATGAGGAG	
		621 S W H D G C R E C Y C L N G R E M C A L 1861 AGCTGGCACGATGGGTGCCGGAATGCTACTGTCTCAATGGACGGGAAATGTGTGCCCTG	
		641 I T C P V P A C G N P T I H P G Q C C P 1921 ATCACCTGCCCGGTGCCTGCTGGCAACCCCACCATTCACCCTGGACAGTGCTGCCCA	
		661 S C A D D F V V Q K P E L S T P S I C H 1981 TCATGTGCAGATGACTTTGTGGTGCAGAAGCCAGAGCTCAGTACTCCCTCCATTTGCCAC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		681 A P G G E Y F V E G E T W N I D S C T Q 2041 GCCCCTGGAGGAGAATACTTTGTGGAAGGAGAACGTGGAACATTGACTCCTGTACTCAG	
		701 C T C H S G R V L C E T E V C P P L L C 2101 TGCACCTGCCACAGCGGACGGGTGCTGTGTGAGACAGAGGTGTGCCCACCGCTGCTCTGC	
		721 Q N P S R T Q D S C C P Q C T D Q P F R 2161 CAGAACCCCTCACGCACCCAGGATTCCTGCTGCCCACAGTGTACAGATCAACCTTTTCGG	
		741 P S L S R N N S V P N Y C K N D E G D I 2221 CCTTCCTTGTCCCGCAATAACAGCGTACCTAATTACTGCAAAAATGATGAAGGGATATA	
		761 F L A A E S W K P D V C T S C I C I D S 2281 TTCCTGGCAGCTGAGTCCTGGAAGCCTGACGTTTGTACCAGCTGCATCTGCATTGATAGC	
		781 V I S C F S E S C P S V S C E R P V L R 2341 GTAATTAGCTGTTTCTCTGAGTCCTGCCCTTCTGTATCCTGTGAAGACCTGTCTTGAGA	
		801 K G Q C C P Y C I E D T I P K K V V C H 2401 AAAGGCCAGTGTTGTCCCTACTGCATAGAAGACACAATTCCAAAGAAGGTGGTGTGCCAC	
		821 F S G K A Y A D E E R W D L D S C T H C 2461 TTCAGTGGGAAGGCCTATGCCGACGAGGAGCGGTGGGACCTTGACAGCTGCACCCACTGC	
		841 Y C L Q G Q T L C S T V S C P P L P C V 2521 TACTGCCTGCAGGGCCAGACCCTCTGCTCGACCGTCAGCTGCCCCCCTGCCCTGTGTT	
		861 E P I N V E G S C C P M C P E M Y V P E 2581 GAGCCCATCAACGTGGAAGGAAGTTGCTGCCCAATGTGTCCAGAAATGTATGTCCCAGAA	
		881 P T N I P I E K T N H R G E V D L E V P 2641 CCAACCAATATACCCATTGAGAAGACAAACCATCGAGGAGAGGTTGACCTGGAGGTTCCC	
		901 L W P T P S E N D I V H L P R D M G H L 2701 CTGTGGCCCACGCCTAGTGAAAATGATATCGTCCATCTCCCTAGAGATATGGGTCACCTC	
		921 Q V D Y R D N R L H P S E D S S L D S I 2761 CAGGTAGATTACAGAGATAACAGGCTGCACCCAAGTGAAGATTCTTCACTGGACTCCATT	
		941 A S V V V P I I C L S I I I A F L F I 2821 GCCTCAGTTGTGGTTCCCATAATTATATGCCTCTCTATTATAATAGCATTCCTATTCATC	
		961 N Q K K Q W I P L L C W Y R T P T K P S	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2881 AATCAGAAGAAACAGTGGATACCACTGCTTTGCTGGTATCGAACACCAACTAAGCCTTCT 981 S L N N Q L V S V D D C K K G G T R V Q V D 2941 TCCTTAAATAATCAGCTAGTATCTGTGGACTGCAAGAAAGGAACCAGAGTCCAGGTGGAC 1001 S S Q R M L R I A E P D D A R F S G G F Y S 3001 AGTTCCCAGAGAATGCTAAGAATTGCAGAACCAGATGCAAGATTCAGTGGCTTCTACAGC 1021 M Q K Q N H L Q A D N F Y Q T V - 3061 ATGCAAAAACAGAACCATCTACAGGCAGACAATTTCTACCAAACAGTGTGA	
Foe1075	H.sapiens initiation factor 4B cDNA.	1 TCTAGAGCCCTCTCCCAACATGGCGGCCTCAGCAAAAAGAAGAATAAGAAGGGGAAGAC 61 TATCTCCCTAACAGACTTTCTGGCTGAGGATGGGGGTACTGGTGGAGGAAGCACCTATGT 121 TTCCAAACCAGTCAGCTGGGCTGATGAAACGGATGACCTGGAAGGAGATGTTTCGACCAC 181 TTGGCACAGTAACGATGACGATGTGTATAGGGCGCCTCCAATTGACCGTTCCATCCTTCC 241 CACTGCTCCACGGGCTGCTCGGGAACCCAATATCGACCGGAGCCGTCTTCCCAAATCGCC 301 ACCCTACACTGCTTTTCTAGGAAACCTACCCTATGATGTTACAGAAGAGTCAATTAAGGA 361 ATTCTTTCGAGGATTAAATATCAGTGCAGTGCGTTTACCACGTGAACCCAGCAATCCAGA 421 GAGGTTGAAAGGTTTTGGTTATGCTGAATTTGAGGACCTGGATTCCCTGCTCAGTGCCCT 481 GAGTCTCAATGAAGAGTCTCTAGGTAACAGGAGAATTCGAGTGGACGTTGCTGATCAAGC 541 ACAGGATAAAGACAGGGATGATCCGTTCTTTTGGCCGTGATAGAAATCGGGATTCTGACAA 601 AACAGATACAGACTGGAGGGCTCGTCCTGCTACAGACAGCTTTGATGACTACCCACCTAG 661 AAGAGGTGATGATAGCTTTGGAGACAAGTATCGAGATCGTTATGATTCAGACCGGTATCG 721 GGATGGGTATCGGGATGGGTATCGGGATGGCCCACGCCGGGATATGGATCGATATGGTGG 781 CCGGGATCGCTATGATGACCGAGGCAGCAGAGACTATGATAGAGGCTATGATTCCCGGAT 841 AGGCAGTGGCAGAAGAGCATTTGGCAGTGGGTATCGCAGGGATGATGACTACAGAGGAGG 901 CGGGGACCGCTATGAAGACCGATATGACAGACGGGATGATCGGTCGTGGAGCTCCAGAGA 961 TGATTACTCTCGGGATGATTATAGGCGTGATGATAGAGGTCCCCCCCCAAAGACCCAAACT 1021 GAATCTAAAGCCTCGGAGTACTCCTGAAGAAGATGATTCCTCTGCTAGTACCTCCCAGTC 1081 CACTCGAGCTGCTTCTATCTTTGGAGGGGCAAAGCCTGTTGACACAGCTGCTAGAGAAAG 1141 AGAAGTAGAAGAACGGCTACAGAAGGAACAAGAGAAGTTGCAGCGTCAGTGGAATGAGCC 1201 AAAACTAGAACGACGGCCTCGGGAGAGACACCCAAGCTGGCGAAGTGAAGAAACTCAGGA 1261 ACGGGAACGGTCGAGGACAGGAAGTGAGTCATCACACAAACTGGGACCTCCACCACATCTAG 1321 CAGAAATGCACGAAGGAGAGGAGTGAGAAGTCTCTAGAAAATGAAACACTCAATAAGGA 1381 GGAAGATTGCCACTCTCCAACTTCTAAACCTCCCAAACCTGATCAGCCCCTAAAGGTAAT 1441 GCCAGCCCCCTCCACCAAAGGAGAATGCTTGGGTGAAGCGAAGTTCTAACCCTCCTGCTCG 1501 ATCTCAGAGCTCAGACACAGAGCAGCAGTCCCCTACAAGTGGTGGGGGAAAAGTAGCTCC 1561 AGCTCAACCATCTGAGGAAGGACCAGGAAGGAAAGATGAAAATAAAGTAGATGGGATGAA 1621 TGCCCCAAAAGGCCAAACTGGGAACTCTAGCCGTGGTCCAGGAGACGGGAGGGAACAGAGA 1681 CCACTGGAAGGAGTCAGATAGGAAAGATGGCAAAAAGGATCAAGACTCCAGATCTGCACC 1741 TGAGCCAAAGAAACCTGAGGAAAATCCAGCTTCTAAGTTCAGTTCTGCAAGCAAGTATGC 1801 TGCTCTCTCTGTTGATGGTGAAGATGAAAATGAGGGAGAAGATTATGCCGAATAGACCTC	SEQ ID NO:309

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1861 TACATCCTGTGCTTTTCTCCTAGTTTCTCCACCCTGGAACATTCGAGAGCAAATCAAA	
		1921 ACCTCTATCCAGACAAGACAAAATAAAACTCAACATCTCCTGAAGACCTTTCTTACCTTT	
		1981 TTTTAAAAACACAAAAANTGAAATTATTTTGCATGCTGCTGCAGCCTTTAAAGTATTGAAGT	
		2041 AACTGGAGAATTGCCAATACAGCCAGAGAAGGGACTACAGCTTTTTAGAGGAAAAGT	
		2101 TGTGGTGCGTTTATGTCACCATGCAGTTGCCAGTGTGATTAGTGCCTAGGGGTCTCATTTA	
		2161 GCAGAAATGGTAATGACAGTGATATAATGCCTGGTTGGGCAGTAGGGGAGGGA	
		2221 GGTAGAAGGAAAAGTGTGAGATTTCTACCTTTTAGTTTTCATCCTATTGTGGCATATATG	
		2281 AATTCTCAAACATTATCTGAATAAATTTTCCACTCTTGGAAAGGTAGATTTAGCCTCAAG	
		2341 TTGTTCTAGTCTCCAGGAGGCTGCCAGCCCCTCCTCTTATTTAATTCTGAGTTTTGGGGG	
		2401 CCAGCCTAGAGGGAATTCCTTTTTTTTTTTTTAACCCCCCAGGGGGGTAGTTGGGAGT	
		2461 GAGACTATAGGCCATAAAGAATGGGACTGCATTGGACCAAAATAAATGGGAAAATCGTGG	
		2521 TTTGAAAAGAAGCTTTTGGGAAGTGATGAGTCATTTTGCACCAGGTAATAGGGGAAAATT	
		2581 GTGTGACCTCCAGCAAACACATGAATGGTTATTTCCTGGAGCCGGAAGCACTTGGGGGTC	
		2641 GTGGTAATTCCCAGTGTTTTCTGTGTCCTAGTTTTACCCTTTCTCTAAACACTGTCCTTTTT	
		2701 GAAAGTTTTGAATATATCCACATTCTATTGAAACCTTGAAACTAAAAATTTAGACTCTTA	
		2761 TCGTCATCTTAAGTTCTTCATGCTACTCTTAACCTCCCAAAAAGCAGTATCTAAGTCACA	
		2821 TACATGATGTCTTGGGCATTTTCTGAGCCATGGAGAACTCTGAAAGGAAGAATCGCTGCT	
		2881 TTTCTCAAGCAAATCGGTTTCTTGATGTCTTTTGGTTCTCCTTGCCTGCTCCTGATGCTT	
		2941 GGACCCCTTTTATTGATCAGAGTGCTCTAGAATAATGGATGGTCTTGGATGATGGATAAA	
		3001 TAGGGACAGGGACAGTTAAATTGGGAGCCTTTCTTACAACCTTGATGGGATTTTTCCCCC	
		3061 CAAGTTTCCTTCTCCACTGAAATGCCACACTAATGCTTGTTGGATTCATGAGGTGGCCAG	
		3121 ACCAATGTGTTGTTTTGTTGTTTTTTTTTTAAGCTTCCCTTGAGAGAATAAGTGATA	
		3181 ATGGAGAGAGCTGTGTAACAAGATCCAGGTTTCTCTTGCAATACAGTAGCTAAACTTGCC	
		3241 TGCTTTTATATGCATTTTTGTAGGGATCAGCTTGGTAGACAGTATTAGCGGAGAAACACC	
		3301 TTGATCTTGGTTTGCAAGGCCTCCTCCGGTCAGTCCTAGGTTAGACCCTGTCCAGCCACG	
		3361 CGGGGCTGTTGGTGTTTGAGTGCTGCAGCAGTGGGCAGAATGAATCATTTACCCAGTGGA	
		3421 CAAAGGTGTGTACCAAGTGAATTTAAATAATTGGTGTGGATTGGCCAGTAGCTAAGAAGT	
		3481 GGGCTTTTAAAGAGTATTGAAGATTGAAAGGGTTTTTCTTTCTTTTTTAAAAAAGAAAAA	
		3541 CAAACTATTGATTGTAGATGATGAAAAGGTAGGGTTTGCCCTCTTCATGTCTACTCCTTC	
		3601 CAAATAGTTGTATCCAAAACTGTTTTTCCCTCTCCCCTACCTTGTCCCCCCTATTAAAAT	
		3661 AGAAACAGGGATTGATTTATGTCCCACTCCTCAATACGTGTAAAATTTGTACAAAAATAT	
		3721 CTTCTATGAAAATGATTTGTAATCTGTAGACAATACCTGGGAGATGTCTTGAGATGTAAA	
		3781 ATCCCATCCTTTCGGTTGTGGGATTTTTTGTTTTCTCCAAATAAATCTGATCTTTAAAGT	
		3841 TAAAAAAAAAAAAAAACTCTAGAGTCGAGGAATTC	
		1 M A A S A K K K K N K K G K T I S L T D F	SEQ ID NO:310
		1 ATGGCGGCCTCAGCAAAAAGAAGAATAAGAAGGGGAAGACTATCTCCCTAACAGACTTT	
		21 L A E D G G T G G G S T Y V S K P V S W	
		61 CTGGCTGAGGATGGGGGTACTGGTGGAGGAAGCACCTATGTTTCCAAACCAGTCAGCTGG	
		41 A D E T D D L E G D V S T T W H S N D D	
		121 GCTGATGAAACGGATGACCTGGAAGGAGATGTTTCGACCACTTGGCACAGTAACGATGAC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		61 D V Y R A P P I D R S I L P T A P R A A 181 GATGTGTATAGGGCGCCTCCAATTGACCGTTCCATCCTTCCCACTGCTCCACGGGCTGCT	
		81 R E P N I D R S R L P K S P P Y T A F L 241 CGGGAACCCAATATCGACCGGAGCCGTCTTCCCAAATCGCCACCCTACACTGCTTTTCTA	
		101 G N L P Y D V T E E S I K E F F R G L N 301 GGAAACCTACCCTATGATGTTACAGAAGAGTCAATTAAGGAATTCTTTCGAGGATTAAAT	
		121 I S A V R L P R E P S N P E R L K G F G 361 ATCAGTGCAGTGCGTTTACCACGTGAACCCAGCAATCCAGAGAGGTTGAAAGGTTTTGGT	
		141 Y A E E F E D L D S L L S A L S L N E E S 421 TATGCTGAATTTGAGGACCTGGATTCCCTGCTCAGTGCCCTGAGTCTCAATGAAGAGTCT	
		161 L G N R R I R V D V A D Q A Q D K D R D 481 CTAGGTAACAGGAGAATTCGAGTGGACGTTGCTGATCAAGCACAGGATAAAGACAGGGAT	
		181 D R S F G R D R N R D S D K T D T D W R 541 GATCGTTCTTTTGGCCGTGATAGAAATCGGGATTCTGACAAAACAGATACAGACTGGAGG	
		201 A R P A T D S F D D D Y P P R R G D D S F 601 GCTCGTCCTGCTACAGACAGCTTTGATGACTACCCACCTAGAAGAGGTGATGATAGCTTT	
		221 G D K Y R D R Y D S D R Y R D G Y R D G 661 GGAGACAAGTATCGAGATCGTTATGATTCAGACCGGTATCGGGATGGGTATCGGGATGGG	
		241 Y R D G P R R R D M D R Y G G G R D R Y D D 721 TATCGGGATGGCCCACGCCGGGATATGGATCGATATGGTGGCCGGGATCGCTATGATGAC	
		261 R G S R D D Y D R G G Y D D S R R I G S G G R R R A 781 CGAGGCAGCAGAGACTATGATAGAGGCTATGATTCCCGGATAGGCAGTGGCAGAAGAGCA	
		281 F G S G G Y R R R D D D D Y R G G G G D R R Y E D 841 TTTGGCAGTGGGTATCGCAGGGATGATGACTACAGAGGAGGCGGGGGACCGCTATGAAGAC	
		301 R Y D R R R D D D R S W S S R R D D D Y S R R D D 901 CGATATGACAGACGGGATGATCGGTCGTGGAGCTCCAGAGATGATTACTCTCGGGATGAT	
		321 Y R R R D D D R G P P Q R P P K L N L K P R S 961 TATAGGCGTGATGATAGAGGTCCCCCCCCAAAGACCCAAACTGAATCTAAAGCCTCGGAGT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		341 T P E E D D S S A S T S Q S T R A A S I 1021 ACTCCTGAAGAAGATGATTCCTCTGCTAGTACCTCCCAGTCCACTCGAGCTGCTTCTATC	
		361 F G G A K P V D T A A R E E R E V E E E R L 1081 TTTGGAGGGGCAAAGCCTGTTGACACAGCTGCTAGAGAAAGAGAAGTAGAAGAACGGCTA	
		381 Q K E Q E K L Q R Q W N E P K L E R R R P 1141 CAGAAGGAACAAGAGAAGTTGCAGCGTCAGTGGAATGAGCCAAAACTAGAACGACGGCCT	
		401 R E R H P S W R S E E E T Q E R E R S R T 1201 CGGGAGAGACACCCAAGCTGGCGAAGTGAAGAAACTCAGGAACGGGAACGGTCGAGGACA	
		421 G S E S S Q T G T S T T S S R N A R R R R 1261 GGAAGTGAGTCATCACAAACTGGGACCTCCACCACATCTAGCAGAAATGCACGAAGGAGA	
		441 E S E K S L E N E T L N K E E D C H S P 1321 GAGAGTGAGAAGTCTCTAGAAAATGAAACACTCAATAAGGAGGAAGATTGCCACTCTCCA	
		461 T S K P P K P D Q P L K V M P A P P P K 1381 ACTTCTAAACCTCCCAAACCTGATCAGCCCTAAAGGTAATGCCAGCCCCTCCACCAAAG	
		481 E N A W V K K R S S N P P A R R S Q S S D T 1441 GAGAATGCTTGGGTGAAGCGAAGTTCTAACCCTCCTGCTCGATCTCAGAGCTCAGACACA	
		501 E Q Q S P T S G G G K V A P A Q P S E E 1501 GAGCAGCAGTCCCCTACAAGTGGTGGGGGAAAAGTAGCTCCAGCTCAACCATCTGAGGAA	
		521 G P G R K D E N K V D G M N A P K G Q T 1561 GGACCAGGAAGGAAAGATGAAAATAAAGTAGATGGGATGAATGCCCCAAAAGGCCAAACT	
		541 G N S S R G P G D G G N R D H W K E S D 1621 GGGAACTCTAGCCGTGGTCCAGGAGACGGAGGGAACAGAGACCACTGGAAGGAGTCAGAT	
		561 R K D G K K D Q D S R S A P E P K K P E 1681 AGGAAAGATGGCAAAAAGGATCAAGACTCCAGATCTGCACCTGAGCCAAAGAAACCTGAG	
		581 E N P A S K F S S A S K Y A A L S V D G 1741 GAAAATCCAGCTTCTAAGTTCAGTTCTGCAAGCAAGTATGCTGCTCTCTCTGTTGATGGT	
		601 E D E N E G E D Y A E - 1801 GAAGATGAAAATGAGGGAGAAGATTATGCCGAATAG	
Foe1092	No homology		

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1 CCCCATTTTCACACCTGTCTTCCGATCTTCACACCTGCCTTCCCCATGTTCACACCTGCC 61 TCCCCATCTTCACGCCTGTCTTCCCTGTGTTCACACCTGTCTTCCCATATTCATACCTGC 121 ATTCCCCATGTTCACACTTGCCTCTCCATCTTCACAACTGCCTTCTCCATGTTTATACCT 181 GCCTTTCTCACCATTTTGGTTTGAAAGACAGTTTTCCATGGATGTTTTTTTTCCAGAAAGT 241 CAGTATTATTTTTTAAATAAGAAAAATACTCCTTAAAAGATCACAATTGTGAAAACTACT 301 GTGGCCTTTCTGCTTTTCCAGATTTTAGTCTCTTTCTCCCCATCCTCTGATCCAGCAAA 361 GATGGTGAGGACAAAGTGGTAAACTTCTCTGCACTCCCATGATGGTCTACACATGGTCTGA 421 CCTGCACTGTTTCTGGCACCCACTGAAAAAGAAGTTGAGTAGACAGTGTAGAGTACAGAA 481 ATGTGGCTTTTGCCTAACACTTTTGCATCTCCAAAGTCTTAAGAGTTGGTTCATCCCCATT 541 TGAGGACAATGTTCAGTTGTACATCTCAGAGTTGGAAATGGAAGAAAGCAGAGGGAGTCT 601 ATTTTCACTCATTCTTTCAATAAATATTTATTGAGCACCAAAAAAAAAAAA	SEQ ID NO:311
Foe1216	Homo sapiens RNF4 mRNA.	1 GAGGAGCTCTCCTGGGCGGCTGAAGAAGGAGCTTCTTCTCCGGAGTGCGAAGGCGGTGGC 61 GCCTGCGGACCTAACTAGCTCCAGGTTAGGCCGAGCTTTGCGGGAAAGCAGCGGACTTGA 121 AAATACTGGAAATCTGTCCGGATCCAAATTATTTTGCAAGCCAGATGAGTAACCAGAGGG 181 CATGAAAGGTTGAGAACATTTGACTTCCCTGCAAACCTTGGTATAGATCACTTCCTTTTC 241 TGTAGGAAAGGAAAGGCACCAAAGAGCACAATGAGTACAAGAAAGCGTCGTGGTGGAGCA 301 ATAAATTCTAGACAAGCTCAGAAGCGAACTCGGGAAGCACCTCCACCCCCGAGATCTCC 361 TTGGAAGCAGAACCCATAGAACTCGTGGAAACTGCTGGAGATGAAATTGTGGACCTCACT 421 TGTGAATCTTTAGAGCCTGTGGTGGTTGATCTGACTCACAATGACTCTGTTGTGATTGTT 481 GACGAAAGAAGAAGACCAAGGAGGAATGCTAGGAGGCTGCCCCAGGACCATGCTGACAGC 541 TGTGTGGTGAGCAGTGACGATGAGGAGTTGTCCAGGGACAGAGACGTATATGTGACTACC 601 CATACTCCCAGAAACGCCAGGGATGAGGGCGCTACAGGCCCTCAGGCCCTCAGGTACTGTC 661 AGTTGTCCCATCTGCATGGAGACGGATACTCAGAGATCGTGCAGAATGGACGTCTCATCGTT 721 TCCACAGAATGCGGCCATGTCTTCTGTAGCCAGTGCCTCCGTGATTCCCTGAAGAATGCT 781 AATACTTGCCCAACTTGTAGGAAAAAGATCAACCACACAAACGGTACCACCCCATTTATATA 841 TGAAGTATTCAGAGCCCCCCAGGAGACGGATGGACAGACAGCCAGGTTCTCCAG 901 TGGTATCTGCCTCCATTTCTCTGAGATCAAAAAGACTGTTTCGAAACCAACATCTGATAT 961 GTAAACTGCTCTTTTGTTTCCAACCCCTTCCTTTTGTTATCTCCAGTTTGATGCTATGGC 1021 GCTGGACCCAGGGCCCTCCCAGGCCATCTCTGTTCCTCTGGGGTGGTTCCAGTTCTAGAGT 1081 GGGAGAAAGGGAGTCAGGCGCATTGGGAATCGTGGTTCCAGTCTGGTTGCAGAATCTGCA 1141 CATTTGCCAAGAAATTTCCCTGTTTGGAAAGTTTGCCCCAGCTTTCCCGGGCACACCAC 1201 CTTTTGTCCCAAGTGTCTGCCGGTCGACCAATCTGCCTGCCACACATTGACCAAGCCAGA 1261 CCCGGTTCACCCAGCTCGAGGATCCCAGGTTGAAGAGTGGCCCCTTGAGGCCCTGGAAAG 1321 ACCAATCACTGGACTTCTTCCCTTGAGAGTCAGAGGTCACCGTGATTCTGCCTGCACCT 1381 TATCATTGATCTGCAGTGATTTCTGCAAATCAAGAGAAACTCTGCAGGGCACTCCCCCTGT 1441 TTCCTAAGAACGAAAAAGTGCAATAAAGGCCATTCGTTACCTACTTTTCAGCAGCCCACA 1501 AGATGTAGCACTATTAGTGTCCCCCTCAGAGGCTTAATGTTGCCTGTGGAGCAGTGCCCA 1561 TCCCAGCCCGTTTCTGCCCACCAGTTGTTCTCAGGAACCTTACCCATGCTCCAGCGTCCT 1621 TCACCTGGCACAGGACATGCAAGATAAATAGGGCAGGCACGTGTTTGGGTGTCCTCTTT 1681 TTCTGATAAAATCCATCCCCGTGTTTGCCACACGCCCTCCAGTCCTCAGTTCCCACTGCCT 1741 AACGTCTGCCCCCGTGTAGATACTGAGAGGTGGTGGCAGTAATTGTGGCCTTATCAGCCG	SEQ ID NO:312

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1801 CTCAGTTCCAGGCTTTTGCCCAGGTCACTGTTGCCCCATGTTCGGAGAACCTGGCCCACC 1861 TGTCTTGGCTTTCTCATCCTTCCCAACCCAGTGCCGTTTATTTCAGAAGCTTCCTGGCCA 1921 CTGGGCTTGGATGCTTCGGGCTTCTGACTGCTCCATAGGTTTTGACTGGTGAAACAGGGG 1981 CCCAGATGACAACCTCTCCTTCGCTCCACAGGTACGCGGAGCCTCAGGTTCTCTCAGGG 2041 GCAGCAAAGTGGCCCAAGCTGCCCCTGACAGCACAGGCCTGGGGGTGGCTAACGAGAGA 2101 GGCCTTACAGTGCCGGCATGCCTCCTCTTCCACTGTCGTCCTTCCTCAGAGGCCTCACG 2161 CCAAACAAACGGCCTTTTCGTGTGAAACATCTTCAGGGCGGGAAAGGGGCCACTTCTGGC 2221 TTTGTTAGCAATAACTGACCTTCAGTTTACCCTTCTGAAGGAGCAGGGACTCAGCACAGA 2281 ATTCACTTTAAACGGGGCTGAAGGAGTGTTCCTCCTTTATGTGAAAGAAAATCATTTTA 2341 CTCTTCATTTTGACTTTTGACTGTTGGGCTCACTTCCAGTTAGTTTGAATGAAGTACT 2401 AATTTTCTACTTGGAGTTGAGGAGGGCAGAATCCGCAGCTCTCATCATTGTGATGTGTAG 2461 CATGTCTGCCCTCTGACTGGACATCATTGCCATTAACTTTCTTCTGGGCATCACGGCAGT 2521 GTCACGATGCCCAGACTTGGAGCAAGGCAACCTTGGAGTCAGTCCACTCATAAAATATGG 2581 TAACACCCATTTTAAAATTTAAGTTTTGTCCTTAAAGACAACTTCAGTGGTTAATTATAA 2641 AAGTTGTGTTACTTCGTCCTAAATTAAATTGATAGAAGATTTAAAATGTGTTTTGTTT 2701 CTAGTATTCAGAAACTGCGAAGTAGGAAAAGGTTGATATGGAAACAATCCCTTTCCCTTC 2761 CTCAATGTACATAGTTCAAATCTTTCTTTGTTACATTTAAACTATATCCGTGTATGTCAG 2821 TCTGTTTTGGACTCCCTCTGCTAGTGTTACAGATGGAAATAAAACCATTAATTTGAACCAA 2881 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	
		1 M S T R K R R G G A I N S R Q A Q K R T 1 ATGAGTACAAGAAAGCGTCGTGGTGGAGCAATAAATTCTAGACAAGCTCAGAAGCGAACT 21 R E A T S T P E I S L E A E P I E L V E 61 CGGGAAGCAACCTCCACCCCCGAGATCTCCTTGGAAGCAGAACCCATAGAACTCGTGGAA 41 T A G D E I V D L T C E S L E P V V V D 121 ACTGCTGGAGATGAAATTGTGGACCTCACTTGTGAATCTTTAGAGCCTGTGGTGGTTGAT 61 L T H N D S V V I V D E R R R P R R N A 181 CTGACTCACAATGACTCTGTTGTGATTGTTGACGAAAGAAGAAGACCAAGGAGGAATGCT 81 R R L P Q D H A D S C V V S S D D E E L 241 AGGAGGCTGCCCCAGGACCATGCTGACAGCTGTGTGGTGAGCAGTGACGATGAGGAGTTG 101 S R D R D V Y V V T T H T P R N A R D E G 301 TCCAGGGACAGAGACGTATATGTGACTACCCATACTCCCAGAAACGCCAGGGATGAGGGC 121 A T G L R P S G T V S C P I C M D G Y S 361 GCTACAGGCCTCAGGCCCTCAGGTACTGTCAGTTGTCCCATCTGCATGGACGGATACTCA 141 E I V Q N G R L I V S T E C G H V F C S 421 GAGATCGTGCAGAATGGACGTCTCATCGTTTCCACAGAATGCGGCCATGTCTTCTGTAGC	SEQ ID NO:313

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		161 Q C L R D S L K N A N T C P T C R K K I 481 CAGTGCCTCCGTGATTCCCTGAAGAATGCTAATACTTGCCCAACTTGTAGGAAAAAGATC 181 N H K R Y H P I Y I - 541 AACCACACAAACGGTACCACACCCCATTTATATATGA	
Foe1263	No homology	1 TTCTTTACAACATGGTTTTAGTGGAGTAGATTTCTTAAGACAGGAAACATTTTCTTTTTT 61 TTCTTTACAACATGGTTTTAGTGGAGTAGATTTCTTAAGACAGGAAACATTTTCTTTTTT 121 AAAGGCATTGTTCCTTCCAGTCCATCTCGTTTCTTTATAAAGAAATAAAGTGACTTTATT 181 TTAAACATAGTTCCACTGTCATTTCTGAAAAATGTAATGCTCTTTAAGTCATAGCACCGG 241 TAAACAAAGTAAGTTATGTAAGGGGGAAATGGTTGCAGCAAACTTTTTAACTGATTTTGT 301 CAAACCAACTAATAGGTTACTGCTTCCCACACTACATTGGTTCAAAACACAAAAAAAGCT 361 CGACAGCACTCAGGTCCTAAAGAAGAAATTTAGCTCATAATAAGAACATCTGTTATGGA 421 ACTAAACAACTGAAATAGGCTTGGTTTTAAGAGTTCCGGTATCTAAGTCACAATTTGAAA 481 CATTTCTAATAAACAGTATCTCTTGGAGTTTCAGTACTGTCACAAGTAGTGAATAAGCA 541 TGTGCAGGGGTAAATGTAAGGATTGTTAACCTATATAAACAGAATTTTAAATTTCAGTGT 601 GTTTTATTCTGATTTTTAAGACAAGAGGTGGTCTGTAATGGATTCAAATGTTTCATTTGT 661 AGTATAATGAAATGTTTACAGAAAGAACTTTTTCATTAAAATATTTTTAGAAAAAAAAA 721 AAAAAGGCATTGTTCCTTCCAGTCCATCTCGTTTCTTTATAAAGAAATAAAGTGACTTTA 781 TTTTAAACATAGTTCCACTGTCATTTCTGAAAAATGTAATGCTCTTTAAGTCATAGCACC 841 GGTAAACAAAGTAAGTTATGTAAGGGGGAAATGGTTGCAGCAAACTTTTTAACTGATTTT 901 GTCAAACCAACTAATAGGTTACTGCTTCCCACACTACATTGGTTCAAAAACAAAAAAAG 961 CTCGACAGCACTCAGGTCCTAAAGAAGAAATTTAGCTCATAATAAGAACATCTGTTATG 1021 GAACTAAACAACTGAAATAGGCTTGGTTTTAAGAGTTCCGGTATCTAAGTCACAATTTGA 1081 AACATTTCTAATAAACAGTATCTCTTGGAGTTTCAGTACTGTCACAAAGTAGTGAATAAG 1141 CATGTGCAGGGGTAAATGTAAGGATTGTTAACCTATATAAACAGAATTTTAAATTTCAGT 1201 GTGTTTTATTCTGATTTTTAAGACAAGAGGTGGTCTGTAATGGATTCAAATGTTTCATTT 1261 GTAGTATAATGAAATGTTTACAGAAAGAACTTTTTCATTAAAATATTTTTAGAAAAAAAA 1321 AAAA	SEQ ID NO:314
Foe1288	No Homology	1 GCTTTCCTTCAGGGCTGTCAAGACTGCCGTGTGCCCGAGGTATGCAGGTTTACTTCAGAA 61 AACACGAGATGGTACCCAACGCATCACCTTTGGAAGCCAGCGGCAATGCCATTCTGCTAC 121 TATCCACTGACTTCCCACAGATTTGTTATCCTCAACAGAGGATGTAACACCACCTTGCCA 181 TGGTTGTCCAAATCTGGATTTTAGACATTTCAATTAATTGAGACTGTGATTTGGTTCTTC 241 CTTCCCATCATGCATTCTGGCATCAAGTCCCTTTCAGTGTTCTGAAGTTAGACTGAAGTT 301 TCTTTGACCCAAGACTACACAAGGTGAGACCCTGAAGTAAAGACAAGGTACACGTACATTA 361 TCTGAGTAACCATTTCCTTTGTGGCCAATCTGTGTATGCTTTTAGAAGTTTACAAGATGC 421 TTTATTTTTGTCTGTAACAGTCTCTGTCATTCATTTCTGTCGATAAAGTATTGGGACAGA 481 ATGAGGAAGTTTGCCTTGTATCTCCCTAGTGCTAACAACACACTCCAGTCACGAGCCGGGC 541 TTTACAAAATAAAGCACTTTGACGACTCAAAAAAAAAAAA	SEQ ID NO:315

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
Foe1317	Human 3-hydroxyacyl-CoA dehydrogenase, isoform 2 mRNA.	1 CGTGTATACCCGCTCAACGCTGGGACGTTACAGCCAGGGCCAATGGGCAGAGCGGGACTC 61 GAGGCCCCGCCCCCCGCCTTGTGGCGTCACGGGGACGCCCGGGGGCGCCGGGCTGCAGGGC 121 CGCGTAGGTCCCCCGCCCCCCAGAGTCTGGCTTTCCGCGGCTGCCTGCCTCGCGCGTCTTCC 181 CTGCCCGGGTCTCCTCGCTGTCGCCGCGCTGCCACACCATGGCCTTCGTCACCAGGCAG 241 TTCATGCGTTCCGTGTCCTCCTCGTCCACCGCCTCGGCCTCGGCCAAGAAGATAATCGTC 301 AAGCACGTGACGGTCATCGGCGGCGGCTGATGGCGCCGGCATTGCCCAGGTTGCTGCA 361 GCAACTGGTCACACAGTAGTGTTGGTAGACCAGACAGAGGACATCCTGGCAAAATCCAAA 421 AAGGGAATTGAGGAAAGCCTTAGGAAAGTGGCAAAGAAGAAGTTTGCAGAAAACCCTAAG 481 GCCGGCGATGAATTTGTGGAGAAGACCCTGAGCACCATAGCGACCAGCACGGATGCAGCC 541 TCCGTTGTCCACAGCACAGACTTGGTGGTGGAAGCCATCGTGGAGAATCTGAAGGTGAAA 601 AACGAGCTCTTCAAAAGGCTGGACAAGTTTGCTGCTGAACATACAATCTTTGCCAGCAAC 661 ACTTCCTCCTTGCAGATTACAAGCATAGCTAATGCCACCACAGACAAGACCGATTCGCT 721 GGCCTCCATTTCTTCAACCCAGTGCCTGTCATGAAACTTGTGGAGGTCATTAAAACACCA 781 ATGACCAGCCAGAAGACATTTGAATCTTTGGTAGACTTTAGCAAAGCCCTAGGAAAGCAT 841 CCTGTTTCTTGCAAGGACACTCCTGGGTTTATTGTGAACCGCCTCCTGGTTCCATACCTC 901 ATGGAAGCAATCAGGCTGTATGAACGAGACTTCCAAACGTGTGGTGATTCTAACTCGGGT 961 TTGGGCTTTTCTTTAAAAGGTGACGCATCCAAAGAAGACATTGACACTGCTATGAAATTA 1021 GGAGCCGGTTACCCCATGGGCCCATTTGAGCTTCTAGATTATGTCGGACTGGATACTACG 1081 AAGTTCATCGTGGATGGTGGCATGAAATGGATGCAGAGAACCCATTACATCAGCCCAGC 1141 CCATCCTTAAATAAGCTGGTAGCAGAGAACAAGTTCGGCAAGAAGACTGGAGAAGGATTT 1201 TACAAATACAAGTGATGTGCAGCTTCTCCGGCTCTGAGAAGAACACCTGAGAGCGCTTTC 1261 CAGCCAGTGCCCCGAGTGCCTGTGGGAATGCTCTTTGGTCAGACATTCCCTCACACAGTA 1321 CAGTTTAATAAATGTGCATTTTGATTGTAATCTATCGAAGTGATTATTACACCAGTTACA 1381 GCAGTAATAGATTCTCCATTGAGAACTAATTCCCTTTTTTAGTCTGTTTGTTTCTGTGTA 1441 TTTTCTAAAAAGCTTTACACCCTTGGTGCCTTGGAGCAAATATTTCTTCTGAACCTTGTC 1501 ATTTTCGTGAATAATGCCTAGATTCCTTCTCTCATCAACGGGAAAGTACTTCCTCTGAG 1561 AGTGCGAGTGCACCATGCTCACTGTTGCTGCGTGGGAGAGTCACAAGCCACTGGCAAGCA 1621 AGTGGTATAGTCTGTGAAGCACTGCAGCGAGCAGCACCTGGATCTTGCCTTTATAAGAAC 1681 ATTTTACTACCTGCAGCTTTGAGTCTTGCCCTACATTTT 1 M G R A G L E A P P P P C G V T G T P G 1 ATGGGCAGAGCGGGACTCGAGGCCCCGCCCCCGCCTTGTGGCGTCACGGGGACGCCGGGG 21 A R G L Q G R V G P R P P Q S L A F R G C 61 GCGCGCGGCTGCAGGGCCGCGTAGGTCCCCGCCCCCAGAGTCTGGCTTTCCGCGGCTGC 41 L P R A S S L P G S P R C R R R C H T M 121 CTGCCTCGCGCGTCTTCCCTGCCCGGGTCTCCTCGCTGTCGCCGCCGCTGCCACACCATG 61 A F V T R Q F M R S V S S S S T A S A S 181 GCCTTCGTCACCAGGCAGTTCATGCGTTCCGTGTCCTCCTCGTCCACCGCCTCGGCCTCG	SEQ ID NO:316 SEQ ID NO:317

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		81 A K K I I V K H V T V I G G G L M G A G 241 GCCAAGAAGATAATCGTCAAGCACGTGACGGTCATCGGCGGCGGGCTGATGGGCGCCGGC	
		101 I A Q V A A A T G H T V V L V D Q T E D 301 ATTGCCCAGGTTGCTGCAGCAACTGGTCACACAGTAGTGTTGGTAGACCAGACAGAGGAC	
		121 I L A K S K K G I E E S L R K V A K K K 361 ATCCTGGCAAAATCCAAAAAGGGAATTGAGGAAAGCCTTAGGAAAGTGGCAAAGAAGAAG	
		141 F A E N P K A G D E F V E K T L S T I A 421 TTTGCAGAAAACCCTAAGGCCGGCGATGAATTTGTGGAGAAGACCCTGAGCACCATAGCG	
		161 T S T D A A S V V H S T D L V V E A I V 481 ACCAGCACGGATGCAGCCTCCGTTGTCCACAGCACACAGACTTGGTGGTGGAAGCCATCGTG	
		181 E N L K V K N E L F K R L D K F A A E H 541 GAGAATCTGAAGGTGAAAAACGAGCTCTTCAAAAGGCTGGACAAGTTTGCTGCTGAACAT	
		201 T I F A S N T S S L Q I T S I A N A T T 601 ACAATCTTTGCCAGCAACACTTCCTCCTTGCAGATTACAAGCATAGCTAATGCCACCACC	
		221 R Q D R F A G L H F F N P V P V M K L V 661 AGACAAGACCGATTCGCTGGCCTCCATTTCTTCAACCCAGTGCCTGTCATGAAACTTGTG	
		241 E V I K T P M T S Q K T F E S L V D F S 721 GAGGTCATTAAAACACCAATGACCAGCCAGAAGACATTTGAATCTTTGGTAGACTTTAGC	
		261 K A L G K H P V S C K D T P G F I V N R 781 AAAGCCCTAGGAAAGCATCCTGTTTCTTGCAAGGACACTCCTGGGTTTATTGTGAACCGC	
		281 L L V P Y L M E A I R L Y E R D F Q T C 841 CTCCTGGTTCCATACCTCATGGAAGCAATCAGGCTGTATGAACGAGACTTCCAAACGTGT	
		301 G D S N S G L G F S L K G D A S K E D I 901 GGTGATTCTAACTCGGGTTTGGGCTTTTCTTTAAAGGTGACGCATCCAAAGAAGACATT	
		321 D T A M K L G A G Y P M G P F E L L D Y 961 GACACTGCTATGAAATTAGGAGCCGGTTACCCCATGGGCCCATTTGAGCTTCTAGATTAT	
		341 V G L D T T K F I V D G W H E M D A E N 1021 GTCGGACTGGATACTACGAAGTTCATCGTGGATGGGTGGCATGAAATGGATGCAGAGAAC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		361 P L H Q P S P S L N K L V A E N K F G K 1081 CCATTACATCAGCCCAGCCCATCCTTAAATAAGCTGGTAGCAGAGAACAAGTTCGGCAAG 381 K T G E G F Y K Y K - 1141 AAGACTGGAGAAGGATTTTACAAATACAAGTGA	
Foe1324	Homo sapiens mRNA; cDNA DKFZp434I0612 (from clone DKFZp434I0612).	1 GTAATTGTTAACTAATGTGCATTTTAAAATTCTCATTTGTCTTATGTACTGAGCCCTTAT 61 ACCAGTGCTAATTTATGTGACTCCTTTCTCCTGCAGCTAAGAGAAAAATACCTTTTTAAT 121 TCATTTATAGTACCCAGTTTTTAAAGAAGATTTATTTTGTAAAATTTTGCTTATGGTACA 181 TGTCATCTTAGCCTGTAAATAAATTAAAGCATTAATTTTTATCCCTCCCTGGTCTTTTCC 241 TCCTTCTGACTTTATACGTCTTTCTAGAGAGCTTATCTTCTATAATACAATTCTTTGTT 301 TTAAAGTGAGAAAGATCAGTCTAAAGAAAAGGAGAAGAAGTGAAAAAAACAATTCCTTC 361 CTGGGCTACCCTTTCTGCCAGCCAGCTAGCCAGGGCCCAGAACAAACACCGATGGCTTC 421 TTCCCCACGTCCCAAGATGGATGCAATCTTAACTGAGGCCATTAAGGCATGCTTCCAGAA 481 GAGTGGTGCATCAGTGGTTGCTATTCGAAAATACATCATCCATAAGTATCCTTCTCTGGA 541 GCTGGAGAGAAGGGGTTATCTCCTTAAACAAGCACTGAAAAGAGAATTAAATAGAGGAGT 601 CATCAAACAGGTTAAAGGAAAAGGTGCTTCTGGAAGTTTTGTTGTGGTTCAGAAATCAAG 661 AAAAACACCTCAGAAATCCAGAAACAGAAAGAATAGGAGCTCTGCAGTGGATCCAGAACC 721 ACAAGTAAAATTGGAGGATGTCCTCCCCACTGGCCTTTACTCGCCTTTGTGAACCTAAAGA 781 AGCTTCCTACAGTCTCATCAGGAAATATGTGTCTCAGTATTATCCTAAGCTTAGAGTGGA 841 CATCAGGCCTCAGCTGTTGAAGAACGCTCTGCAGAGAGCAGTAGAGAGGGGCCAGTTAGA 901 ACAGATAACTGGCAAAGGTGCTTCGGGGACATTCCAGCTGAAGAAATCAGGGGAGAAACC 961 CCTGCTTGGTGGAAGCCTGATGGAATATGCAATCTTGTCTGCCATTGCTGCCATGAATGA 1021 GCCGAAGACCTGCTCTACCACTGCTCTGAAGAAGTATGTCCTAGAGAATCACCCAGGAAC 1081 CAATTCTAACTATCAAATGCATTTGCTGAAAAAAAACCCTGCAGAAATGCGAAAAGAATGG 1141 GTGGATGGAACAGATCTCTGGGAAAGGGTTCAGTGGCACCTTCCAGCTCTGTTTTCCCTA 1201 TTATCCCAGCCCAGGAGTTCTGTTCCGAAGAAAGAGCCAGATGATTCTAGAGATGAGGA 1261 TGAAGATGAAGATGAGTCATCAGAAGAAGACTCTGAGGATGAAGAGCCGCCACCTAAGAG 1321 AAGGTTGCAGAAGAAAACCCCAGCCAGTCCCCAGGGAAGGCGCCGCATCTGTGAAGCAGAG 1381 AGGGTCCAAACCTGCACCTAAAGTCTCAGCTGCCCAGCGGGGGAAAGCTAGGCCCCTTGCC 1441 TAAGAAGCACCTCCTAAGGCCAAAACGCCTGCCAAGAAGACCAGACCCTCATCCACAGT 1501 CATCAAGAAACCTAGTGGTGGCTCCTCAAAGAAGCCTGCAACCAGTGCAAGAAAGGAAGT 1561 AAAATTGCCGGGCAAGGGCAAATCCACCATGAAGAAGTCTTTCAGAGTGAAAAAGTAAAT 1621 TTTATAGGAAAAAAAGGGTATCATGATGAAATTCAAAATCTTATTTTCTCCCCATGAACATTGTG 1681 CATTTGTTTAGTTTTGATGCTTTTCAAATTACATTATTTTCCTCCCCTATGAACATTGTG 1741 GGGAGGGACTCTAAATAAACCAGTTTAGGCATTTGCTAGCTTTAGGTGCTTTTATTGGTG 1801 CCTGCCCTTTTCCTTGTTCATTTTAATTTCTGCAATAATCCTGGACTTTCCTAAACTATG 1861 TAATGTATACTTGTCCTTTTTCTCTGCCTCCCCCAACCCCTGTTGTTTTTATGGTCAGC 1921 TTTGCCTTTTTTTTTTCTTCCAATTTTATCTAAACAGTTGCAGAGATTTTTATATTTGTA 1981 GAAAGCATCAAGAACGGTATGCCAGTCAGGTCCTGGAAGTAAAATGGAGGCACAATATAG 2041 CACTGACTGAGTTGTAAAGCCTCCTGCCTGGAGACTTCAGTTATAGCTGTAAATAATTAAT 2101 CTTATTTATAAAAGCCACTCCACTAACCTTTTCTCTCCAACTGTAAACACAGAGACAGCT	SEQ ID NO:318

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2161 TTGGGAATAAGCCAAAAACAGGGTGATCTCATTAGATTTTGAAGATATATGACTCCTTTG 2221 GGCTACATTTCATATTGATCAATTTCTAGGTATTTTTCACTGGCCCAAAGTATTGCATTC 2281 CCTTAACAGCAAGCACAAGTTCTCTATATCACTTGTTTTTTGTTGTTGTTGTTGTCG 2341 TCGTTGTTTTGAGACGGAGTCTTGCTCAGGTGCCCCGGAGTGCAGTGGTGCAATCTCAGC 2401 TCACTGCAACCTCCACCTCCTGGGTTCAAGCAATTCTCCTGCTTCAGCCTCCCGAGTAGC 2461 TGGGATTACAGGTGTGTACCACCACGCCTGGCAATTTTTTGTATTTTTAGTAGAGATGG 2521 GGTTTCGCCGTGTTGGTCAGGCTGGTCTCGAACTCCTGACCTCAGGTGATCCGCCTGCCT 2581 CGGCCTCCCAAAGTGCTGGGATTACAGGAGTGAGCCACTGTGCCTGGCCTATCCCACTTG 2641 GTTTTTGACTGCAAGGGGAAGTGTAGAAATATATTGATTTGTGATTTCTGGTGTCACCTGT 2701 GTTACCAAAAATCAAAACAAATCTTTTTTATTTTTTATTATTATTATTTTTGAGACA 2761 GAGTCTCGCTCTGTCGCCCAGTGTGGAGTGCAGTGGTGTGATCTTGGCTCACTGCAACT 2821 CCGCCTCCCAGGTTCAAGCGATTCTCCCACCTCAGCCTCCTGAGTTGGGTCCTACAGGCG 2881 CACACGACCACGCCCAGCTAATTTTTTGTATTTTTAGTAGAGTTGGGGTTTCACCATGTT 2941 AGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCACCTCACCTCAGCCTCCCAAAATCC 3001 TGGGGTTACAGATGTGAGCTACCACTCACGGCCCAAATCTTCTTGATCATATGTTTAAAT 3061 ATATTTTTTAATATTTGGAGCATGAGTTGTCACTTCTTGTTTGCCTTTTTTATAAGGAAA 3121 TGTTGGAGAGTTAAATCATTGCTAATGTAGAAATGTTAAGTGGAAAAACATACAATTTGC 3181 TAAAATAAACTAGATTCCAGATTCCATCTCTGGGTTTTTTTCCCCTCCTTTCTTTCCACAG 3241 CACTTTTGATATCAAACAAGTGGCTTCCTTTTTGAGATATTAAAAAAAAAAGAAAAGGA 3301 AAAAAGTAAATGAAGCCCAACTACCTAACCCTTTCTTATTTGTATTTGTTTTTAGTATTGT 3361 GAGGTTGTGTTAAATAGTACTAGCTAGAAATACAAATTTCTGGTTATCATTTATCCTCCC 3421 TGTGGCACTTGACATTTTAATTGTCTTAAACCTTTTGGTGTACATCCTCTGGCCCCTTAA 3481 GTGCTGCCAGAAGCAGAAGATATCTGTCTCATTCATTCCACTTGCACTGTCTCCTGGGAT 3541 CTTGTCTGCAGCCCGACGTGTGGCTGGGAAATGGACTCGAGAAGATTGGCTTCAATTAGA 3601 TCCATAATCATGTGTGATCCCATCATGAGTTCATTGGAATTTGTGTTGCATGTAAGGCAA 3661 TCTTTCCTGTTGTAAATCTTCCTTTTTTTATGTACATATATTTTGAAAAATATGAATAAA 3721 CATGAAATTTTAAAAAAAAAAAAAAAAAAAA 1 M A S S P R P K M D A I L T E A I K A C 1 ATGGCTTCTTCCCCACGTCCCAAGATGGATGCAATCTTAACTGAGGCCATTAAGGCATGC 21 F Q K S G A S V V A I R K Y I I H K Y P 61 TTCCAGAAGAGTGGTGCATCAGTGGTTGCTATTCGAAAATACATCATCCATAAGTATCCT 41 S L E L E R R G Y L L K Q A L K R E L N 121 TCTCTGGAGCTGGAGAGAAGGGGTTATCTCCTTAAACAAGCACTGAAAAGAGAATTAAAT 61 R G V I K Q V K G K G A S G S F V V V Q 181 AGAGGAGTCATCAAACAGGTTAAAGGAAAAGGTGCTTCTGGAAGTTTTGTTGTGGTTCAG 81 K S R K T P Q K S R N R K N R S S A V D 241 AAATCAAGAAAAACACCTCAGAAATCCAGAAACAGAAAGAATAGGAGCTCTGCAGTGGAT	SEQ ID NO:319

Gene Name / GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
	101 P E P Q V K K L E D V L P L A F T R L C E 301 CCAGAACCACAAGTAAAATTGGAGGATGTCCTCCCACTGGCCTTTACTCGCCTTTGTGAA	
	121 P K E A S Y S L I R K Y V S Q Y Y P K L 361 CCTAAAGAAGCTTCCTACAGTCTCATCAGGAAATATGTGTCTCAGTATTATCCTAAGCTT	
	141 R V D I R P Q L L K N A L Q R A V E R G 421 AGAGTGGACATCAGGCCTCAGCTGTTGAAGAACGCTCTGCAGAGACAGTAGAGAGGGGC	
	161 Q L E Q I T G K G A S G T F Q L K K S G 481 CAGTTAGAACAGATAACTGGCAAAGGTGCTTCGGGGACATTCCAGCTGAAGAAATCAGGG	
	181 E K P L L G G S L M E Y A I L S A I A A 541 GAGAAACCCCTGCTTGGTGGAAGCCTGATGGAATATGCAATCTTGTCTGCCATTGCTGCC	
	201 M N E P K T C S T T A L K K Y V L E N H 601 ATGAATGAGCCGAAGACCTGCTCTACCACTGCTCTGAAGAAGTATGTCCTAGAGAATCAC	
	221 P G T N S N Y Q M H L L K K T L Q K C E 661 CCAGGAACCAATTCTAACTATCAAATGCATTTGCTGAAAAAAACCCTGCAGAAATGCGAA	
	241 K N G W M E Q I S G K G F S G T F Q L C 721 AAGAATGGGTGGATGGAACAGATCTCTGGGAAAGGGTTCAGTGGCACCTTCCAGCTCTGT	
	261 F P Y Y P S P G V L F P K K E P D D S R 781 TTTCCCTATTATCCCAGCCCAGGAGTTCTGTTTCCGAAGAAAGAGCCAGATGATTCTAGA	
	281 D E D E D E D E S S E E D S E D E E P P 841 GATGAGGATGAAGATGAAGATGAGTCATCAGAAGAAGACTCTGAGGATGAAGAGCCGCCA	
	301 P K R R L Q K K T P A K S P G K A A S V 901 CCTAAGAGAAGGTTGCAGAAGAAAACCCCAGCCAAGTCCCCAGGGAAGGCCGCATCTGTG	
	321 K Q R G S K P A P K V S A A Q R G K A R 961 AAGCAGAGAGGTCCAAACCTGCACCTAAAGTCTCAGCTGCCCAGCGGGGGAAAGCTAGG	
	341 P L P K K A P P K A K T P A K K T R P S 1021 CCCTTGCCTAAGAAAGCACCTCCTAAGGCCAAAACGCCTGCCAAGAAGACCAGACCCTCA	
	361 S T V I K K P S G G S S K K P A T S A R 1081 TCCACAGTCATCAAGAAACCTAGTGGTGGCTCCTCAAAGAAGCCTGCAACCAGTGCAAGA	
	381 K E V K L P G K G K S T M K K S F R V K	

Gene Name	GenBank Homology	DNA SEQUENCE // DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1141 AAGGAAGTAAAATTGCCGGGCAAGGGCAAATCCACCATGAAGAAGTCTTTCAGAGTGAAA 401 K - 1201 AAGTAA	
Foe146	No homology	1 TTATTTATTTAGGATATAAATAGCAGAAAACCAATTACTATGTCAGAGTATGGACACTTG 61 ATACATAATGCCAAATTATTCTTCATAAGAGCTGTTGCCAAATCAGTGATAATATTCATT 121 TCACTGTACTCTTGCCAGCCATCACTCCAGTGATGGTTGTGGTGGTTGTCGTCATTT 181 GGGGGCAGGTGCCTAATGTGCGGTCTTTAATGAATATCTAATGAATGTTTGAAAAAAATG 241 ATTATTCTCTGTTTATCAGGTACAAAGGTATTTATGGTACATGTATATGGTATGTGTATA 301 TGACTTGTCAAATTACTATTAACATTTCTATAGCCTTAGATAATGCATGAAAAAGCATA 361 GTTCAGTGCCACTCACATAAGAAGTGCCCAATAAGTGTTAACTATTATTTTTGTCTACTT 421 GGTTTTACCACCTTCTAAAAGTATGTTGAAGTGTCTCTCTGTCATTGTGGATTTGTCAGT 481 TTCTCTCTGCATTTCTCAGAGTACTTGTTTTTATATATTTTGAAGCTATTGTTAGATGATA 541 GATTCATGATTTGTAGTGGAATGTTCTTTTATCAATTTTTGAAAATTGCCCTTGTCTCAT 601 AATGCTTTTCATATTGAATTCTATTTTGTCTGCTATTAAATATTTCCATACCTGCAAAAA 661 AAAAA	SEQ ID NO:320
Foe148	Homo sapiens fucosyltransferase 8 (alpha (1,6) fucosyltransferase) (FUT8), transcript variant 1	1 cgtttagtac agaaatctca tgggagagag catccatgca tttacaaatt gttattgaat 61 tatttattg aatgatgaca cccaaactga gctagaacat aattctggct ctgctagtac 121 atcttctgtg tgatcttgga caagtcactc tacttttctt tcaatttttct tttctcacag 181 ggagataatc ataaaaacga ctgtaaagta cagcacttca tagagtgctt tttgtttaaa 241 gagctgacaa taaatacgag tctcaaggtc taggaaagcc tccctcacaa cctgagctgc 301 ttgaggacaa gggattttct tttgaatcag cagtacctta tttgtgtatc tgtgatagag 361 ttcctggtac ataagaaggt ctcaataaat atgtgaattt atgaatatta ggcagattgc 421 aaccttgaca ggccactgcc tcttaaatct cctttctgtg atcttttaat atttaacatc 481 taaaaggccg ccgctacttg ctttgggata agtatcccccg gtatgtactt taaaatgccc 541 aagcctagag aaatgattct tgtcttaagg gcaccatttc gctctcccac cgtaaagcgc 601 cccaggcttg ggatctgggt cccaaggcta cagggaagag ttggaacgg gaagctcatc 661 ttccggccct ctgattggcc ggctcgcact ccactcacgc ggcgcgcagc tctgattggc 721 ctcggcggca ccctcgtcc cgcgactact ttgtgtgctg gggcggcgcg gctcggtcct 781 cccgctcagc tggcggtctg ggctgctctg gggcagccct tcggtccact gctctgcatc 841 gcgggcgccg ggaattttcc gagtccgagc gggttgctgc tttgctcag aggacatcca 901 tgaccctaat ggtcttttg ttcaagataa agtgatttt tgcctttgtt gattaactgg 961 acaaattcag catgtagagc gcatgaagta caggacaata aagcttccta cacatatcac 1021 caggaggatc tctttgaaag attcactgca ggactaccag agagaataat ttgtctgaag 1081 catcatgtgt tgaaacaaca gaagtcttatt cacctgtgca ctaactagaa acagagttac 1141 aatgttttca attcttgag ctccaggact ccagggaagt gagttgaaaa tctgaaaatg 1201 cggccatgga ctggttcctg gcgttggatt atgctcattc ttttgcctg ggggaccttg 1261 ctgttttata taggtggtca cttggtacga gataatgacc atcctgatca ctctagccga 1321 gaactgtcca agatttggc aaagcttgaa cgcttaaaac aacagaatga agacttgagg	SEQ ID NO:321

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1381 cgaatggccg aatctctccg gataccagaa ggccctattg atcagggccc agctatagga 1441 agagtacgcg tttagaaga gcagcttgtt aaggccaaag aacagattga aaattacaag 1501 aaacagacca gaaatggtct gaggaaggat catgaaatcc tgaggaggag gattgaaaat 1561 ggagctaaag agtctggttt ttcctacag agtgaattga agaaattaaa gaacttagaa 1621 ggaaatgaac tccaaagaca tgcagatgaa tttcttttgg atttaggaca tcatgaaagg 1681 tctataatga cggatctata ctacctcagt cagacagatg gagcaggtga ttggcgggaa 1741 aaagaggcca aagatctgac agaactggtt cagcggagaa taacatatct tcagaatccc 1801 aaggactgca gcaaagccaa aaagctggtg tgtaatatca acaaaggctg tggctatggc 1861 tgtcagctcc atcatgtggt ctactgcttc atgattgcat atggcaccca gcgaacactc 1921 atcttggaat ctcagaattg gcgctatgct actggtggat gggagactgt atttaggcct 1981 gtaagtgaga catgcacaga cagatctggc atctccactg gacactggtc aggtgaagtg 2041 aaggacaaaa atgttcaagt ggtcgagctt cccattgtag acagtcttca tcccgtcct 2101 ccatatttac ccttggctgt accagaagac ctcgcagatc gacttgtacg agtgcatggt 2161 gaccctgcag tgtggtgggt gtctcagttt gtcaaatact tgatccgccc acagccttgg 2221 ctagaaaaag aaatagaaga agccaccaag aagcttggct tcaaacatcc agttattgga 2281 gtccatgtca gacgcacaga caaagtggga acagaagctg ccttccatcc cattgaagag 2341 tacatggtgc atgttgaaga acatttcag cttcttgcac gcagaatgca agtggacaaa 2401 aaaagagtgt atttggccac agatgaccct tctttattaa aggaggcaaa aacaaagtac 2461 cccaattatg aatttattag tgataactct atttcctggt cagctggact gcacaatcga 2521 tacacagaaa attcacttcg tggagtgatc ctggatatac attttctctc tcaggcagac 2581 ttcctagtgt gtacttttc atcccaggtc tgtcgagttg cttatgaaat tatgcaaaca 2641 ctacatcctg atgcctctgc aaacttccat tctttagatg acatctacta ttttgggggc 2701 cagaatgccc acaatcaaat tgccatttat gctcaccaac cccgaactgc agatgaaatt 2761 cccatggaac ctggagatat cattggtgtg gctggaaatc attgggatgg ctattctaaa 2821 ggtgtcaaca ggaaatggg aaggacgggc ctatatccct cctacaaagt tcgagagaag 2881 atagaaacgg tcaagtaccc cacatatcct gaggctgaga aataaagctc agatggaaga 2941 gataaacgac caaactcagt tcgaccaaac tcagttcaaa ccatttcagc caaactgtag 3001 atgaagaggg ctctgatcta acaaaataag gttatatgag tagatactct cagcaccaag 3061 agcagctggg aactgacata ggcttcaatt ggtggaattc ctctttaaca agggctgcaa 3121 tgccctcata cccatgcaca gtacaataat gtactcacat ataacatgca aacaggttgt 3181 tttctacttt gccccttca gtatgtcccc ataagacaaa cactgccata ttgtgtaatt 3241 taagtgacac agacattttg tgtgagactt aaaacatggt gcctatatct gagagacctg 3301 tgtgaactat tgagaagatc ggaacagctc cttactctga ggaagttgat tcttatttga 3361 tggtggtatt gtgaccactg aattcactcc agtcaacaga ttcagaatga gaatggacgt 3421 ttggttttct ttttgttttg ttttgtcttt ttccttata agttgtctg ttttttttt 3481 tttaaataat tgcatcagtt cattgacctc atcattaata agtgaagaat acatcagaaa 3541 ataaaatatt cactctccat tagaaaattt tgtaaaacaa tgccatgaac aaattcttta 3601 gtactcaatg tttctggaca ttctctttga taacaaaaaa taaattttaa aaaggaattt 3661 tgtaaagttt ctagaatttt atatcattgg atgatatgtt gatcagcctt atgtggaaga 3721 actgtgataa aaagaggagc ttttagttt ttcagcttaa aaaaaaaaaa aaaaa 1 M R P W T G S W R W I M L I L F A W G T 1 ATGCGGCCATGGACTGGTTCCTGGCGTTGGATTATGCTCATTCTTTTGCCTGGGGGACC	SEQ ID NO:322

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		21 L L F Y I G G H L V R D N D H P D H S S 61 TTGCTGTTTTATATAGGTGGTCACTTGGTACGAGATAATGACCATCCTGATCACTCTAGC 41 R E L S K I L A K L E R L K Q Q N E D L 121 CGAGAACTGTCCAAGATTCTGGCAAAGCTTGAACGCTTAAACACAACAGAATGAAGACTTG 61 R R M A E S L R I P E G P I D Q G P A I 181 AGGCGAATGGCCGAATCTCTCCGGATACCAGAAGGCCCTATTGATCAGGGCCAGCTATA 81 G R V R V L E E Q L V K A K E Q I E N Y 241 GGAAGACTACGCGTTTTAGAAGAGCAGCTTGTTAAGGCCAAAGAACAGATTGAAAATTAC 101 K K Q T R N G L G K D H E I L R R R I E 301 AAGAAACAGACCAGAAATGGTCTGGGGAAGGATCATGAAATCCTGAGGAGGAGGATTGAA 121 N G A K E L W F F L Q S E L K K L K N L 361 AATGGAGCTAAAGAGCTCTGGTTTTTCCTACAGAGTGAATTGAAGAAATTAAAGAACTTA 141 E G N E L Q R H A D E F L L D L G H H E 421 GAAGGAAATGAACTCCAAAGACATGCAGATGAATTTCTTTTGGATTTAGGACATCATGAA 161 R S I M T D L Y Y L S Q T D D G A G D W R 481 AGGTCTATAATGACGGATCTATACTACCTCAGTCAGACAGATGGAGCAGGTGATTGGCGG 181 E K E A K D L T E L V Q R R I T Y L Q N 541 GAAAAAGAGGCCAAAGATCTGACAGAACTGGTTCAGCGGAGAATAACATATCTTCAGAAT 201 P K D C S K A K K L V C N I N K G C G Y 601 CCCAAGGACTGCAGCAAAGCCAAAAAGCTGGTGTGTAATATCAACAAAGGCTGTGGCTAT 221 G C Q L H H V V Y C F M I A Y G T Q R T 661 GGCTGTCAGCTCCATCATGTGGTCTACTGCTTCATGATTGCATATGGCACCCAGCGAACA 241 L I L E S Q N W R Y A T G G W E T V F R 721 CTCATCTTGGAATCTCAGAATTGGCGCTATGCTACTGGTGGATGGGAGACTGTATTTAGG 261 P V S E T C T D R S G I S T G H W S G E 781 CCTGTAAGTGAGACATGCACAGACAGATCTGGCATCTCCACTGGACACTGGTCAGGTGAA 281 V K D K N V Q V V E L P I V D S L H P R 841 GTGAAGGACAAAAATGTTCAGTGGTCGAGCTTCCCATTGTAGACAGTCTTCATCCCCGT	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		301 P P Y L P L A V P E D L A D R L V R V H 901 CCTCCATATTTACCCTTGGCTGTACCAGAAGACCTCGCAGATCGACTTGTACGAGTGCAT	
		321 G D P A V W W V S Q F V K Y L I R P Q P 961 GGTGACCCTGCAGTGTGGTGGGTGTCTCAGTTTGTCAAATACTTGATCCGCCCACAGCCT	
		341 W L E K E I E E A T K K L G F K H P V I 1021 TGGCTAGAAAAAGAAATAGAAGAAGCCACCAAGAAGCTTGGCTTCAAACATCCAGTTATT	
		361 G V H V R R T D K V G T E A A F H P I E 1081 GGAGTCCATGTCAGACGCACAGACAAAGTGGGAACAGAAGCTGCCTTCCATCCCATTGAA	
		381 E Y M V H V E E H F Q L L A R R M Q V D 1141 GAGTACATGGTGCATGTTGAAGAACATTTTCAGCTTCTTGCACGCAGAATGCAAGTGGAC	
		401 K K R V Y L A T D D P S L L K E A K T K 1201 AAAAAAAGAGTGTATTTGGCCACAGATGACCCTTCTTTATTAAAGGAGGCAAAAACAAAG	
		421 Y P N Y E F I S D N S I S W S A G L H N 1261 TACCCCAATTATGAATTTATTAGTGATAACTCTATTTCCTGGTCAGCTGGACTGCACAAT	
		441 R Y T E N S L R G V I L D I H F L S Q A 1321 CGATACACAGAAAATTCACTTCGTGGAGTGATCCTGGATATACATTTTCTCTCCAGGCA	
		461 D F L V C T F S S Q V C R V A Y E I M Q 1381 GACTTCCTAGTGTGTACTTTTTCATCCCAGGTCTGTCGAGTTGCTTATGAAATTATGCAA	
		481 T L H P D A S A N F H S L D D I Y Y F G 1441 ACACTACATCCTGATGCCTCTGCAAACTTCCATTCTTTAGATGACATCTACTATTTTGGG	
		501 G Q N A H N Q I A I Y A H Q P R T A D E 1501 GGCCAGAATGCCCACAATCAAATTGCCATTTATGCTCACCACCCCGAACTGCAGATGAA	
		521 I P M E P G D I I G V A G N H W D G Y S 1561 ATTCCCATGGAACCTGGAGATATCATTGGTGTGGCTGGAAATCATTGGGATGGCTATTCT	
		541 K G V N R K L G R T G L Y P S Y K V R E 1621 AAAGGTGTCAACAGGAAATTGGGAAGGACGGGCCTATATCCCTCCTACAAGTTCGAGAG	
		561 K I E T V K Y P T Y P E A E K - 1681 AAGATAGAAACGGTCAAGTACCCCACATATCCTGAGGCTGAGAAATAA	
Foe443	Homo sapiens		

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
	tripeptidyl peptidase II mRNA	1 gaattcccct ccatcctgcg tccatggcca ccgctgcgac tgaggagccc ttccctttcc 61 acggtctcct gccgaagaag gagaccggag ccgcctcctt cctctgccgc taccctggagt 121 atgatgggcg ggggtgctcc atcgcagtcc tggacacggg ggtcgacccg ggggctccgg 181 gcatgcaggt tacaactgat ggaaaaccaa aaatcgttga tatcattgat acaacaggaa 241 gtggcgatgt gaatactgct acagaagtag agccaaggga tggtgagatt gttggccttt 301 caggaagagt gcttaagatt cctgcaagct ggacaaatcc ctcaggcaaa tatcatattg 361 gcataaaaaa tggctatgac ttctatccta aggcactcaa ggaaaggata cagaaagaac 421 ggaaggaaaa aatctgggac cctgttcaca gagtggccct tgcagaagcc tgtagaaaac 481 aggaagaatt tgatgttgcc aacaacggct ctctcaagc aaataaacta atcaaggagg 541 aacttcaaag tcaagtggaa ttgctaaatt cttttgagaa gaaatacagc gatcctggcc 601 ctgtatatga ctgcttggta tggcatgatg gcgaagtctg gagagcctgc attgattcta 661 atgaagatgg ggacttgagt aaatctaccg tgttgagaaa ctacaaagaa gcccaagaat 721 atggctcttt tggcacagct gagatgttga attactccgt taatatatac gatgatagaa 781 acctgctctc cattgtgacc agtggaggag ctcatgggac acatgtagct agtatagctg 841 ctggacactt tccagaagaa cctgaacgga atgggtagc tcctggtgct caaattcttt 901 ccatcaagat tggtgataca agactaagca caatggaaac aggcacaggc ctcataagag 961 ctatgataga agttataaat cataagtgtg atcttgtcaa ctacagttac ggagaagcaa 1021 ctcactggcc aaattctggg agaatttgtg aagtaattaa tgaagcagta tggaagcata 1081 atataattta tgtttcaagt gctggaaata atggtccatg cctgttctaca gttggttgtc 1141 caggtggaac tacatcaagt gtgataggtg ttggtgctta tgtttctcct gatatgatgg 1201 ttgctgagta ttcactgaga gagaaattac ctgcaaatca atatacttgg tcttctagag 1261 gacctagtgc tgacggggcc cttggtgtga gtatcagtgc gccaggagga gccattgctt 1321 ctgttcctaa ctggacactg agagggacgc agctgatgaa tggaacatct atgtcttccc 1381 ccaatgcatg tggaggcatt gccctgatcc ttcaggtct gaaagctaat aacattgact 1441 acacagttca ttcagtcaga agagctctag aaaacactgc agtgaaggct gacaatatag 1501 aagtatttgc tcaaggacat ggtattattc agattgataa agcctatgac tacctcgttc 1561 agaatacatc atttgctaat aaattaggtt ttactgttac tgttggaaat aaccgtggca 1621 tctacctccg agatccttgt caggtggctg cacctcaga tcatggcgtt ggcattgaac 1681 ctgtatttcc ggagaacaca gaaaactctg aaaaatatc ccttcagctt catttagctc 1741 tgacttcaaa ttcatcttgg gttcagtgtc ccagccattt ggaactcatg aatcaatgta 1801 gacacataaa catacgtgtg gatcccaggg gcttaagaga aggattgcat tatacagagg 1861 tatgtggcta tgatatagca tcccctaacg caggtccgct cttcagagtt ccgatcactg 1921 cagttatagc agcaaaagta aatgaatcat cacattatga tctagccttt acagatgtac 1981 actttaaacc tggtcaaatt cgaaggcatt ttattgaggt tcctgagggt gcaacatggg 2041 ctgaagtgac agtgtgttcg tgttcttctg aggtgtcagc aaagtttgtt ctacatgcag 2101 tccagcttgt gaagcaaaga gcatatcgaa gccatgaatt ctataagttt tgttctcttc 2161 cagagaaagg aacactgact gaagctttc ctgtcctagg tggaaaagca attgaatttt 2221 gcattgctcg ttggtgggca agtctcagtg atgtcaacat tgattatacc atttctttcc 2281 atgggatagt gtgtactgct cctcagttaa acattcatgc atcggaagga atcaaccgct 2341 ttgatgttca gtcctccttg aaatacgaag atctggctcc ctgcataact ttgaagaact 2401 gggtccaaac actgcgccca gtgagtgcaa aaacaaaacc tttaggatca agagatgttt 2461 tgccaaataa ccgtcaactt tatgagatgg tcctgacata taactttcat caacccaaga 2521 gtggggaagt aactccaagc tgcccactac tttgtgaact attatatgaa tctgaatttg	SEQ ID NO:323

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2581 acagccaact gtggattatt tttgaccaga acaaaagaca gatgggttca ggcgatgcct 2641 atccacatca gtattctttg aaactggaga aaggagatta tacaattcga ctacagattc 2701 gccatgagca aatcagtgat ttggaacgcc ttaaagacct tccatttatt gtttctcata 2761 gattgtctaa tacttgagc ttagatattc atgaaaatca tagttttgca ctttaggga 2821 agaagaaatc aagcaatttg acattaccac ccaaatataa ccagccattc tttgttactt 2881 ccttacctga tgataaaata cctaaagggg caggacctgg atgctatctt gcaggatcct 2941 taacattgtc aaagactgaa ctaggaaaga aagctgatgt aatccctgtt cattactact 3001 taatacctcc accaacaaag actaagaatg gcagcaaaga taaggaaaaa gattcagaaa 3061 aagagaaaga tttaaaagaa gagtttactg aagcattacg agatcttaaa attcagtgga 3121 tgacaaagct ggattctagt gacatttata acgaattgaa agaacatat cctaattatc 3181 ttcctctgta cgttgcacga cttcatcaat tggatgctga aaaggaacga atgaaaagac 3241 ttaatgaaat tgttgatgcg gcaaatgctg ttatttctca tatagatcaa acagccctag 3301 cagtttatat tgcaatgaag actgatccca ggcctgatgc agctactata aaaaatgaca 3361 tggacaaaca aaaatccacc ctcgtagatg cccttgtag gaaaggttgt gccctggcag 3421 accatcttct tcacacccag gctcaagacg gagccatttc cactgatgca gaaggaaagg 3481 aggaggaagg agaaagtcct ttggattctc tggcagaaac attttgggaa actactaaat 3541 ggactgatct ctttgacaat aaggttttga catttgcata taaacatgca ttagtaaata 3601 aaatgtatgg gagaggcctt aaatttgcaa ctaaacttgt ggaagaaaaa ccaacaaaag 3661 aaaactggaa aaattgtatt caactgatga agttacttgg atggacccat tgtgcatctt 3721 ttactgaaaa ctggctcccc atcatgtatc ctcccgatta ttgcgtattc taaaatagga 3781 aacaagactt taaattttaa aaaaggaagt tttatagtga atgggtataa aaacaaattt 3841 gtggcatttt tagtctaatg catgttttca tccactatcc agtactgatt attaaaatga 3901 catgtattta tcagagaatt cactgacgtg tggcttaata catgtaaatc tagacctctg 3961 acatcatggt gttttcttaa tgcctcacat tgctggcacg gggatgtgcc ctgcctgcca 4021 gcacctagga cttcgagttg ggttgcagct tatgacatgc atgataggtt ttggaaggta 4081 acttttaact gcaaacctat aaagtactat ttttttattt ataaatgaac agggttttaa 4141 cgtgctcaac tttaatttct ttcaattgta tgaaggcctt aaaaaagcta cattaagcgt 4201 agctaaaatt atttattgga ctaaaaacta acagaacttc atttccagaa tttttttttt 4261 ttttttttct ttggcaaatg tttacattca attaagggga aaaagtagaa ccagcacaaa 4321 tgagtggcag ttgctggagc ataactgctt caataaatct tcatcttggg gtaattacag 4381 gcaagtcatt ttcacatcct cttgaggttc agagcatcag aatgaactct atgaatacat 4441 gtgtaagtgc cagacagctg aatctttatc aggtattgta aagatacaca tatgatatgt 4501 ttattaaaat tgaaataatg taaaacacat gaataaattt gcaaaaccaa gatcacagta 4561 caccatatgc actctggtac cttaatttct ttttataaat aataaaagtg aatattgaag 4621 cttctt 1 M A T A A T E E P P F P F H G L L P K K E 1 ATGGCCACCGCTGCGACTGAGGAGCCCTTCCCTTTTCACGGTCTCCTGCCGAAGAAGGAG 21 T G A A S F L C R Y P E Y D G R G V L I 61 ACCGGAGCCGCCTCCTTCCTCTGCCGCTACCCGGAGTATGATGGGCGGGGGGTGCTCATC 41 A V L D T G V D P G A P G M Q V T T D G	SEQ ID NO:324

Gene Name	GenBank HomoLogy	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		121 GCAGTCCTGGACACGGGGGTCGACCCGGGGGCTCCGGGCATGCAGGTTACAACTGATGGA	
		61 K P K I V D I I D T T G S G D V N N T A T	
		181 AAACCAAAAATCGTTGATATCATTGATACAACAGGAAGTGGCGATGTGAATACTGCTACA	
		81 E V E P K D G E I V G L S G R V L K I P	
		241 GAAGTAGAGCCAAAGGATGGTGAGATTGTTGGCCTTTCAGGAAGAGTGCTTAAGATTCCT	
		101 A S W T N P S G K Y H I G I K N G Y D F	
		301 GCAAGCTGGACAAATCCCTCAGGCAAATATCATATTGGCATAAAAAATGGCTATGACTTC	
		121 Y P K A L K E R I Q K E R K E K I W D P	
		361 TATCCTAAGGCACTCAAGGAAAGGATACAGAAAGAACGGAAGGAAAAAATCTGGGACCCT	
		141 V H R V A L A E A C R K Q E E F D V A N	
		421 GTTCACAGAGTGGCCCTTGCAGAAGCCTGTAGAAAACAGGAAGAATTTGATGTTGCCAAC	
		161 N G S S Q A N K L I K E E L Q S Q V E L	
		481 AACGGCTCTTCTCAAGCAAATAAACTAATCAAGGAGGAACTTCAAAGTCAAGTGGAATTG	
		181 L N S F E K K Y S D P G P V Y D C L V W	
		541 CTAAATTCTTTTGAGAAGAAATACAGCGATCCTGGCCCTGTATATGACTGCTTGGTATGG	
		201 H D G E V W R A C I D S N E D G D L S K	
		601 CATGATGGCGAAGTCTGGAGAGCCTGCATTGATTCTAATGAAGATGGGGACTTGAGTAAA	
		221 S T V L R N Y K E A Q E Y G S F G T A E	
		661 TCTACCGTGTTGAGAAACTACAAAGAAGCCCAAGAATATGGCTCTTTTGGCACAGCTGAG	
		241 M L N Y S V N I Y D D R N L L S I V T S	
		721 ATGTTGAATTACTCCGTTAATATATACGATGATAGAAACCTGCTCTCCATTGTGACCAGT	
		261 G G A H G T H V A S I A A G H F P E E P	
		781 GGAGGAGCTCATGGGACACATGTAGCTAGTATAGCTGCTGGACACTTTCCAGAAGAACCT	
		281 E R N G V A P G A Q I L S I K I G D T R	
		841 GAACGGAATGGGGTAGCTCCTGGTGCTCAAATTCTTTCCATCAAGATTGGTGATACAAGA	
		301 L S T M E T G T G L I R A M I E V I N H	
		901 CTAAGCACAATGGAAACAGGCACAGGCCTCATAAGAGCTATGATAGAAGTTATATAAATCAT	
		321 K C D L V N Y S Y G E A T H W P N S G R	
		961 AAGTGTGATCTTGTCAACTACAGTTACGGAGAAGCAACTCACTGGCCAAATTCTGGGAGA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		341 I C E V I N E A V W K H N I I Y V S S A 1021 ATTTGTGAAGTAATTAATGAAGCAGTATGGAAGCATAATATAATTTATGTTTCAAGTGCT	
		361 G N N G P C L S T V G C P G G T T S S V 1081 GGAAATAATGGTCCATGCCTGTCTACAGTTGGTTGTCCAGGTGGAACTACATCAAGTGTG	
		381 I G V G A Y Y V S P D M M V A E Y S L R E 1141 ATAGGTGTTGGTGCTTATGTTTCTCCTGATATGATGGTTGCTGAGTATTCACTGAGAGAG	
		401 K L P A N Q Y T W S S R G P S A D G A L 1201 AAATTACCTGCAAATCAATATACTTGGTCTTCTAGAGGACCTAGTGCTGACGGGGCCCTT	
		421 G V S I S A P G G A I A S V P N W T L R 1261 GGTGTGAGTATCAGTGCGCCAGGAGGAGCCATTGCTTCTGTTCCTAACTGGACACTGAGA	
		441 G T Q L M N G T S M S S P N A C G G I A 1321 GGGACGCAGCTGATGAATGGAACATCTATGTCTTCCCCAATGCATGTGGAGGCATTGCC	
		461 L I L S G L K A N N I D Y T V H S V R R 1381 CTGATCCTTTCAGGTCTGAAAGCTAATAACATTGACTACACAGTTCATTCAGTCAGAAGA	
		481 A L E N T A V K A D N I E V F A Q G H G 1441 GCTCTAGAAAACACTGCAGTGAAGGCTGACAATATAGAAGTATTTGCTCAAGGACATGGT	
		501 I I Q V D K A Y D Y L V Q N T S F A N K 1501 ATTATTCAGGTTGATAAAGCCTATGACTACCTCGTTCAGAATACATCATTTGCTAATAAA	
		521 L G F T V T V G N N R G I Y L R D P V Q 1561 TTAGGTTTTACTGTTACTGTTGGAAATAACCGTGGCATCTACCTCCGAGATCCTGTTCAG	
		541 V A A P S D H G V G I E P V F P E N T E 1621 GTGGCTGCACCTTCAGATCATGGCGTTGGCATTGAACCTGTATTTCCGGAGAACACAGAA	
		561 N S E K I S L Q L H L A L T S N S S W V 1681 AACTCTGAAAAAATATCCCTTCAGCTTCATTTAGCTCTGACTTCAAATTCATCTTGGGTT	
		581 Q C P S H L E L M N Q C R H I N I R V D 1741 CAGTGTCCCAGCCATTTGGAACTCATGAATCAATGTAGACACATAAACATACGTGTGGAT	
		601 P R G L R E G L H Y T E V C G Y D I A S 1801 CCCAGGGGCTTAAGAGAAGGATTGCATTATACAGAGGTATGTGGCTATGATATAGCATCC	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		621 P N A G P L F R V P I T A V I A A K V N 1861 CCTAACGCAGGTCCGCTCTTCAGAGTTCCGATCACTGCAGTTATAGCAGCAAAAGTAAAT	
		641 E S S H Y D L A F T D V H F K P G Q I R 1921 GAATCATCACATTATGATCTAGCCTTTACAGATGTACACTTTAAACCTGGTCAAATTCGA	
		661 R H F I E V P E G A T W A E V T V C S C 1981 AGGCATTTTATTGAGGTTCCTGAGGGTGCAACATGGGCTGAAGTGACAGTGTGTTCGTGT	
		681 S S E V S A K F V L H A V Q L V K Q R A 2041 TCTTCTGAGGTGTCAGCAAAGTTTGTTCTACATGCAGTCCAGCTTGTGAAGCAAAGAGCA	
		701 Y R S H E F Y K F C S L P E K G T L T E 2101 TATCGAAGCCATGAATTCTATAAGTTTTGTTCTCTTCCAGAGAAAGGAACACTGACTGAA	
		721 A F P V L G G K A I E F C I A R W W A S 2161 GCTTTTCCTGTCCTAGGTGGAAAAGCAATTGAATTTTGCATTGCTCGTTGGTGGGCAAGT	
		741 L S D V N I D Y T I S F H G I V C T A P 2221 CTCAGTGATGTCAACATTGATTATACCATTTCTTTCCATGGGATAGTGTGTACTGCTCCT	
		761 Q L N I H A S E G I N R F D V Q S S L K 2281 CAGTTAAACATTCATGCATCGGAAGGAATCAACCGCTTTGATGTTCAGTCCTCCTTGAAA	
		781 Y E D L A P C I T L K N W V Q T L R P V 2341 TACGAAGATCTGGCTCCCTGCATAACTTTGAAGAACTGGGTCCAAACACTGCGCCCAGTG	
		801 S A K T K P L G S R D V L P N N R Q L Y 2401 AGTGCAAAAACAAAACCTTTAGGATCAAGAGATGTTTTGCCAAATAACCGTCAACTTTAT	
		821 E M V L T Y N F H Q P K S G E V T P S C 2461 GAGATGGTCCTGACATATAACTTCATCAACCCAAGAGTGGGAAGTAACTCCAAGCTGC	
		841 P L L C E L L Y E S E F D S Q L W I I F 2521 CCACTACTTTGTGAACTATTATATGAATCTGAATTTGACAGCCAACTGTGGATTATTTTT	
		861 D Q N K R Q M G S G D A Y P H Q Y S L K 2581 GACCAGAACAAAAGACAGATGGGTTCAGGCGATGCCTATCCACATCAGTATTCTTTGAAA	
		881 L E K G D Y T I R L Q I R H E Q I S D L 2641 CTGGAGAAAGGAGATTATACAATTCGACTACAGATTCGCCATGAGCAAATCAGTGATTTG	
		901 E R L K D L P F I V S H R L S N T L S L	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		2701 GAACGCCTTAAAGACCTTCCATTTATTGTTTCTCATAGATTGTCTAATACCTTGAGCTTA	
		921 D I H E N H S F A L L L G K K K S S N L T	
		2761 GATATTCATGAAAATCATAGTTTTGCACTTCTAGGGAAGAAGAAATCAAGCAATTTGACA	
		941 L P P K Y N Q P F F V T S L P D D K I P	
		2821 TTACCACCCAAATATAACCAGCCATTCTTTGTTACTTCCTTACCTGATGATAAAATACCT	
		961 K G A G P G C Y L A G S L T L S K T E L	
		2881 AAAGGGGCAGGACCTGGATGCTATCTTGCAGGATCCTTAACATTGTCAAAGACTGAACTA	
		981 G K K A D V I P V H Y Y L I P P P T K T	
		2941 GGAAAGAAAGCTGATGTAATCCCTGTTCATTACTACTTAATACCTCCACCAACAAAGACT	
		1001 K N G S K D K E K D S E K E K D L K E E	
		3001 AAGAATGGCAGCAAAGATAAGGAAAAAGATTCAGAAAAAGAGAAAGATTTAAAAGAAGAG	
		1021 F T E A L R D L K I Q W M T K L D S S D	
		3061 TTTACTGAAGCATTACGAGATCTTAAAATTCAGTGGATGACAAAGCTGGATTCTAGTGAC	
		1041 I Y N E L K E T Y P N Y L P L Y V A R L	
		3121 ATTTATAACGAATTGAAAGAAACATATCCTAATTATCTTCCTCTGTACGTTGCACGACTT	
		1061 H Q L D A E K E R M K R L N E I V D A A	
		3181 CATCAATTGGATGCTGAAAAGGAACGAATGAAAAGACTTAATGAAATTGTTGATGCGGCA	
		1081 N A V I S H I D Q T A L A V Y I A M K T	
		3241 AATGCTGTTATTTCTCATATAGATCAAACAGCCCTAGCAGTTTATATTGCAATGAAGACT	
		1101 D P R P D A A T I K N D M D K Q K S T L	
		3301 GATCCCAGGCCTGATGCAGCTACTATAAAAATGACATGGACAAACAAAAATCCACCCTC	
		1121 V D A L C R K G C A L A D H L L H T Q A	
		3361 GTAGATGCCCTTTGTAGGAAAGGTTGTGCCCTGGCAGACCATCTTCTTCACACCCAGGCT	
		1141 Q D G A I S T D A E G K E E E G E S P L	
		3421 CAAGACGGAGCCATTTCCACTGATGCAGAAGGAAAGGAGGAAGGAGAAAGTCCTTTG	
		1161 D S L A E T F W E T T K W T D L F D N K	
		3481 GATTCTCTGGCAGAAACATTTTGGGAAACTACTAAATGGACTGATCTCTTTGACAATAAG	
		1181 V L T F A Y K H A L V N K M Y G R G L K	
		3541 GTTTTGACATTTGCATATAAACATGCATTAGTAAATAAAATGTATGGAGAGGCCTTAAA	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1201 F A T K L V E E K P T K E N W K N C I Q 3601 TTTGCAACTAAACTTGTGGAAGAAAAACCAACAAAGAAACTGGAAAAATTGTATTCAA 1221 L M K L L G W T H C A S F T E N W L P I 3661 CTGATGAAGTTACTTGGATGGACCCATTGTGCATCTTTTACTGAAAACTGGCTCCCCATC 1241 M Y P P D Y C V F - 3721 ATGTATCCTCCCGATTATTGCGTATTCTAA	
gi9717252	Equus caballus Toll-like receptor 4 mRNA, complete cds	1 GGCACGAGCGGCACGAGAGCAGCAGCTCCGAGGCTGCCCTGGCGGCAGGCTGTTACGGT 61 GCGTCATGCTTTCACAGGGCCCCTTCTGGGCACAGAAAATGCCAGGATGATGCCGCCCAC 121 CCGCCTGGCTGGGACTCTGATCCCAGCCATGGCCTTCCTCTCCTGCCTGAGACCCGAGAG 181 CTGGGACCCTTGCGTGCAGGTGGTTCCTAACACTACTTACCAATGCATGGACCTGAATCT 241 CTACAAAATCCCTGAGAACATCCCCACATCAACCAAGGAACTGGACCTGAGCTTTAACCC 301 CTTGAAGGAGTTAGGCAGCCATAGCTTCTCCAACTTCCCAGAACTGCAGGTGCTGGATTT 361 GTCCAGGTGTGAAATTGAGATGATTGAAGATGATGCATATCAGGGCCTCAACCATCTCTC 421 CACCTTGATATTGACAGGAAATCCTATCAGGAGCTTAGCCCTGGGAGCCTTTTCTGGACT 481 CTCCAGTTTACAGACGCTGGTGGCCGTGGAGACAAAGCTTTCATCTCTAGAGAAGTTCCC 541 CATTGGACATCTCAAGACCTTGAAGGAGCTTAATGTGGCTCATAATCTTATCCATTCCTT 601 CAAGTTACCCGAGTATTTTTCTAAAATGCCCAACCTGGAGCACTTGGACCTTTCCAATAA 661 CAAGATCCAAAATATTTCTCATGAAGACTTGCGTGTGCTACATCAAATGCCCTTACTCAA 721 CCTTTCTTTAGACTTGTCCCTGAATCCTTTAGAGTTTATCCAACCAGATGCCTTTAAAGA 781 AATTAAGCTCCATAAACTGACTTTGAGAAGTAATTTTGATAGTATAGATGTAATGAAATC 841 TTGTATTCAAGGACTGGCTGGTTTAAAAGTCAATCGGTTGGTTCTGGGAGAATTTAAAAA 901 TGAAAGGAAATTGGAAAGATTTGACACATCTGCCCTGCGCGGACTGCACAATTTGACGAT 961 TGAAGAATTCCGGTTAGCATACATTGATAATTACAGCTCAAAGGATTCTATTGATTTACT 1021 TAATTGTTTGGCAGATATTTCTAAAATTTCTCTGGTGAGTCTGGATTTAGGCAATCTAAA 1081 AGATTTTCCTAAAGGTTTCGGATGGCAAGACTTCGAATTGGTTAACTGTAGAATTGAAGG 1141 ATTTCCCACATTGGAGCTCACCTCTCTCAAAAGGTTGGTTTTCACTTCCAACAAAGATAT 1201 GAAATCTTTTAATGAAGTTAAGCTACCAAGCCTTGAGTTCTAGATCTCAGCAGAAATCG 1261 CTTGAGTTTCAAGTCCTGCTGTTCTGAGGCTGATTTGAAGACAACCAGACTGAAGCATTT 1321 AGATCTGAGCTTCAATGATGTTATTTCCATGAGTTCAAACTTCATGGGCTTAGAGCAACT 1381 AGAACATCTGGATTTCCAGCATTCCACTTTGAAACAGGCCAGTGATTTTCCAGTATTCTT 1441 ATCCCTCAAAAACCTCCGTTATCTTGATATTTCTTACACTAACACCCGAGTTGTCTTCCA 1501 TGGCATCTTTGATGGCTTGGTCAGCCTCCAAGTCTTGAAAATGGCTGGCAATTCTTTTAA 1561 GGACAACTTCCTTCCAAATATCTTCAGAGAGATGACTAACCTGACCACCCTGGACCTTTC 1621 TAAGTGTAACCTGGAACAGGTGTCCCAGGAGGCATTTTGCTTACTCCCTCGACTTCGGGT 1681 GTTAAATATGAGTCACAATAACCTCCTGTTCTTGGATATGCTTCCTTACAAACCTCTCCA 1741 TTCCCTCCAGATTCTGGATTGCAGTTTTAATCGTATTGTGGCCTTCAAGTGGCCAAGAACT 1801 GCAGCATTTTCCAAGTAGTCTAGCTTCCTTAAATCTTACTCAAAATGACTTTGCTTGTGT 1861 TTGTGAATACCAGAGTTTTCTGCAGTGGGTCAAGGACCAGAGGCAGCTCTTGGTGGAAGT	SEQ ID NO:325

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		1921 TGAACACTTGGTGTGTGCAATACCCTTACAGATGCGGGGCATGCCCGTGCTGGGTTTTAA 1981 CAATGCCACCTGTCAGATTAGCAAGACTATCGTTGGCGGGTCGGTTTTCAGTATACTCAT 2041 GGTTTCTGTCATAGCAGTTCTGGTCTATAAGTTCTATTTCCACCTGATGCTTCTTGCTGG 2101 CTGCAAAAAGTATGGGAGAGGTGAAAGCATCTATGATGCCTTTGTTATCTACTCAAGCCA 2161 GGACGAGACTGGGTGAGGAATGAATTGGTAAAGAACTTGGAGGAGGGGGTGCCCCCCTT 2221 TCAACTCTGCCTTCACTACAGAGACTTCATTCCTGGTGTGGCCATCGCCGCCAACATCAT 2281 CCAGGAAGGTTTCCACAAAAGCCGGAAAGTTATTGTCGTGGTGTCCCAGCACTTCATTCA 2341 GAGCCGATGGTGTATCTTTGAGTATGAGATTGCCCAGACCTGGCAGTTTCTGAGCAGTCG 2401 TGCTGGCATCATCTTCATCGTCCTGCACAAGCTGGAGAAGTCCCTGCTCCGGCAGCAGGT 2461 GGAGCTGTATCGCCTTCTCAACAGGAACACTTACCTGGAGTGGGAGGACACGTGTCCTGGG 2521 GCGGCACATCTTCTGGAGACGACTCAGGAAAGCCTTGCTGGATGGTAAACCGTGGAGTCC 2581 AGCAGGAACAGCAGATGCAGCAGAAAGCAGACAACATGATGCAGAAACCTCTACCTGAGG 2641 AGGAAAAACTCCTGAGGTGCTTCTTGCCCAGCTGGACCCAATACTTGTTCAGTTAACAAC 2701 TATTAAATGCTGCAACATACCAGGCATTGTGCTAGGGCCAGGTGATTCTGTCGTGCACAA 2761 GATACACAGGACTGCTAATCCCTTTGAGTTTACAGTGCAGAGGGAATAAATGCCGTGCTA 2821 AAATACAGAACCTCCAGGGGGATGTGTTTTAACCAAGTCAGCTAAGGAGTCCGTGCCAGGGA 2881 AAGTCAACTCAACTCTTACCCCATCAAAATGAATCAGAACTGAGAGACTGGGCCCCAGTG 2941 AGTTCAGAAAAGGACATCGTCTCCCAAGTCTTTTGAATGGAAACCATCTCATCTTTGACA 3001 TCTTAGCCATCCTAAACACAAACACAAGCAGTTTTGGTACTTTCAACTGAACAGCGTCTCT 3061 GTTCAATTTTCCCTTTTCTACTGAACACAATTTAAATTTTACTTGATGACTCAGAAGGCT 3121 CCTGATTCAGATCCTCCCTCTCTTTAGGCAGTTTCCTTATGAAGGTTAAACTCTTACG 3181 ACTAATTCCTAAGGAAATCTGATTGATACATTCACAAACATCCTGGTCATTCTTTAGC 3241 GTGCTCTATTTATTAATAAATAGCAGGTTCTATTTAAAAAAAAAAAAAAAAA 1 M M P P T R L A G T L I P A M A F L S C 1 ATGATGCCGCCCACCGCCTGGCTGGGACTCTGATCCCAGCCATGGCCTTCCTCCTGC 21 L R P E S W D P C V Q V V P N T T Y Q C 61 CTGAGACCCGAGAGCTGGGACCCTTGCGTGCAGGTGGTTCCTAACACTACTTACCAATGC 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	SEQ ID NO:326

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		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	
		721 GATGTAATGAAATCTTGTATTCAAGGACTGGCTGGTTTAAAGTCAATCGGTTGGTTCTG	
		261 G E F K N E R K L E R F D T S A L R G L	
		781 GGAGAATTTAAAAATGAAGGAAATTGGAAAGATTTGACACATCTGCCCTGCGCGGACTG	
		281 H N L T I E E F R L A Y I D N Y S S K D	
		841 CACAATTTGACGATTGAAGAATTCCGGTTAGCATACATTGATAATTACAGCTCAAAGGAT	
		301 S I D L L N C L A D I S K I S L V S L D	
		901 TCTATTGATTTACTTAATTGTTTGGCAGATATTTCTAAAATTTCTCTGGTGAGTCTGGAT	
		321 L G N L K D F P K G F G W Q D F E L V N	
		961 TTAGGCAATCTAAAAGATTTTCCTAAGGTTTCGGATGGCAAGACTTCGAATTGGTTAAC	
		341 C R I E G F P T L E L T S L K R L V F T	
		1021 TGTAGAATTGAAGGATTTCCCACATTGGAGCTCACCTCTCTCAAAGGTTGGTTTTCACT	
		361 S N K D M K S F N E V K L P S L E F L D	
		1081 TCCAACAAAGATATGAAATCTTTTAATGAAGTTAAGCTACCAAGCCTTGAGTTTCTAGAT	
		381 L S R N R L S F K S C C S E A D L K T T	
		1141 CTCAGCAGAAATCGCTTGAGTTTCAAGTCCTGCTGTTCTGAGGCTGATTTGAAGACAACC	
		401 R L K H L D L S F N D V I S M S S N F M	
		1201 AGACTGAAGCATTTAGATCTGAGCTTCAATGATGTTATTTCCATGAGTTCAAACTTCATG	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		421 G L E Q L E H L D F Q H S T L K Q A S D 1261 GGCTTAGAGCAACTAGAACATCTGGATTTCCAGCATTCCACTTTGAAACAGGCCAGTGAT	
		441 F P V F L S L K N L R Y L D I S Y T N T 1321 TTTCCAGTATTCTTATCCCTCAAAAACCTCCGTTATCTTGATATTTCTTACACTAACACC	
		461 R V V F H G I F D G L V S L Q V L K M A 1381 CGAGTTGTCTTCCATGGCATCTTTGATGGCTTGGTCAGCCTCCAAGTCTTGAAAATGGCT	
		481 G N S F K D N F L P N I F R E M T N L T 1441 GGCAATTCTTTTAAGGACAACTTCCTTCCAAATATCTTCAGAGATGACTAACCTGACC	
		501 T L D L S K C N L E Q V S Q E A F C L L 1501 ACCCTGGACCTTTCTAAGTGTAACCTGGAACAGGTGTCCCAGGAGGCATTTTGCTTACTC	
		521 P R L R V L N M S H N N L L F L D M L P 1561 CCTCGACTTCGGGTGTTAAATATGAGTCACAATAACCTCCTGTTCTTGGATATGCTTCCT	
		541 Y K P L H S L Q I L D C S F N R I V A F 1621 TACAAACCTCTCCATTCCCTCCAGATTCTGGATTGCAGTTTTAATCGTATTGTGGCCTTC	
		561 K W Q E L Q H F P S S L A S L N L T Q N 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 CTCTTGGTGGAAGTTGAACACTTGGTGTGTGCAATACCCTTACAGATGCGGGCATGCCC	
		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	

Gene Name	GenBank Homology	DNA SEQUENCE / DEDUCED AMINO ACID SEQUENCE	SEQUENCE IDENTIFIER:
		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 GACAGTGTCCTGGGGCGGCACATCTTCTGGAGACGACTCAGGAAAGCCTTGCTGATGGT	
		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	

TABLE 2

Probe Set Name	Sequence	Sequence Identifier
ILT11A mRNA for immunoglobulin-like transcript 11 protein		
B1961620.V1.3_at	AGGACGTGACCTACGCCCAGGTGAA	SEQ ID NO:327
B1961620.V1.3_at	AGGGACCCCAGAAGACATAGGAGCT	SEQ ID NO:328
B1961620.V1.3_at	AGGTGAACCACTTGACCCTCAGAGG	SEQ ID NO:329
B1961620.V1.3_at	AGTGGTACGCTGCTATGGCCATCCA	SEQ ID NO:330
B1961620.V1.3_at	AGCAGAGCCCAGTGGTACGCTGCTA	SEQ ID NO:331
B1961620.V1.3_at	CATAGGAGCTGCCTCCAGAGGACAC	SEQ ID NO:332
B1961620.V1.3_at	GAGACTGCAGGGACCCCAGAAGACA	SEQ ID NO:333
B1961620.V1.3_at	GATGCCACCCTCCATGGAGGGAGAC	SEQ ID NO:334
B1961620.V1.3_at	GTATGCACAGGCTGCTATATCTGAA	SEQ ID NO:335
B1961620.V1.3_at	TGGCCATCCACTAGCCCAGGAAGGA	SEQ ID NO:336
B1961620.V1.3_at	TAGCCCAGGAAGGACCCGGATGCCA	SEQ ID NO:337
No Homology		
B1961856.V1.3_at	ATGCTGGCAAAACCTCTAAGACTGT	SEQ ID NO:338
B1961856.V1.3_at	AGTTTCCCTTCTGCAGCTTGTTTTT	SEQ ID NO:339
B1961856.V1.3_at	ACCTGATTCTGCCTCTTTAATGAAT	SEQ ID NO:340
B1961856.V1.3_at	ACAGTTCCTATGCATGGTTTTTAAC	SEQ ID NO:341
B1961856.V1.3_at	CACGAGGGAAGAGGGTCTCCTTCCA	SEQ ID NO:342
B1961856.V1.3_at	GCTTGTTTTTTCTCACTATCTGTAT	SEQ ID NO:343
B1961856.V1.3_at	GAACAATTTAATTTCTTGGCCGTGT	SEQ ID NO:344
B1961856.V1.3_at	GGCCGTGTTTAGTAACAGTTCCTAT	SEQ ID NO:345
B1961856.V1.3_at	GAAAGTTGATTTGTCCTAGTGCAAA	SEQ ID NO:346
B1961856.V1.3_at	GAAACTCAATGCCTTATGTGCTCAC	SEQ ID NO:347
B1961856.V1.3_at	TTATGTGCTCACTCAGTTTCCCTTC	SEQ ID NO:348
Equus caballus tissue inhibitor of metalloproteinase-1 (TIMP-1) mRNA, complete cds		
B1961880.V1.3_at	AGACCACCTTACAGCGGCGTTATGA	SEQ ID NO:349
B1961880.V1.3_at	AGCTGAAGCTTGCACAGTGTTCACC	SEQ ID NO:350
B1961880.V1.3_at	ACAGGCTCTGACAAGGGCTTCCAGA	SEQ ID NO:351
B1961880.V1.3_at	GAATCCTGTCTCCAGCAGAAGCTGA	SEQ ID NO:352
B1961880.V1.3_at	GAATGCTCAGTGTTTCCCTGTTCAT	SEQ ID NO:353
B1961880.V1.3_at	GAACCGCAGCGAGGAGTTTCTCATC	SEQ ID NO:354
B1961880.V1.3_at	GGACGAGAAGCTGTACATCACCACC	SEQ ID NO:355
B1961880.V1.3_at	TGAGTTCGTCATCAGGGCCAAGTTC	SEQ ID NO:356
B1961880.V1.3_at	TGCGGATACTTCCACAGGTCGGAGA	SEQ ID NO:357
B1961880.V1.3_at	TGATTGCTTGTGGACGGACCAGCTC	SEQ ID NO:358
B1961880.V1.3_at	TTCTCATCGCCGGACAACTATTGGA	SEQ ID NO:359
PREDICTED: Homo sapiens zinc finger, SWIM domain containing 6 (ZSWIM6), mRNA		
B1961900.V1.3_at	GTTAAAAGGCTGACCCACGTGGCTT	SEQ ID NO:360

Probe Set Name	Sequence	Sequence Identifier
B1961900.V1.3_at	AGAACACCTCCATCCTGTGATAAGT	SEQ ID NO:361
B1961900.V1.3_at	ACGTGGCTTTGCAGTGCTGTTCGTC	SEQ ID NO:362
B1961900.V1.3_at	AAAAGTCCACACAGCTCTCCTGTTT	SEQ ID NO:363
B1961900.V1.3_at	GTCTACGTTCACAGCCTCAAAAAAG	SEQ ID NO:364
B1961900.V1.3_at	GCTGTTCGTCCAGAAGCATGGCACA	SEQ ID NO:365
B1961900.V1.3_at	GAACAGAGCCACACCGGTATTATAT	SEQ ID NO:366
B1961900.V1.3_at	GTTCTATTGCGTTTGCTGACTAAAT	SEQ ID NO:367
B1961900.V1.3_at	GGTTTGTTTTTACTTGAGCCTGCCT	SEQ ID NO:368
B1961900.V1.3_at	GGATTCAGCTTTACTCCTTTGTAAC	SEQ ID NO:369
B1961900.V1.3_at	TGAGCCTGCCTTTGTACCCTTTTTA	SEQ ID NO:370
Equus caballus interleukin-4 receptor alpha-chain mRNA.		
B1961932.V1.3_at	AGGATTTGCCTAGAGAGGCCCGTTC	SEQ ID NO:371
B1961932.V1.3_at	TGTTACCCGAGTCTGACCCAGTCCT	SEQ ID NO:372
B1961932.V1.3_at	GAATGACTTAGGAGGCCCCAGGAAA	SEQ ID NO:373
B1961932.V1.3_at	ATCACTGGATTGGATGCTGAGCCTA	SEQ ID NO:374
B1961932.V1.3_at	AGTCCTGGGTTAGCTGCCGCCATAT	SEQ ID NO:375
B1961932.V1.3_at	AGAGCTTCATCTAGCTGGCACCAGA	SEQ ID NO:376
B1961932.V1.3_at	GCTGCCGCCATATCACTGGATTGGA	SEQ ID NO:377
B1961932.V1.3_at	GATGCTGAGCCTAGAAACTGATCAA	SEQ ID NO:378
B1961932.V1.3_at	GTTCCTTCAACAGAGCTTCATCTAG	SEQ ID NO:379
B1961932.V1.3_at	TGGCACCAGAGGCAGGATTGCACCT	SEQ ID NO:380
B1961932.V1.3_at	TTGCACCTGTGGTGGGTGCTTAGCC	SEQ ID NO:381
Equus caballus interleukin-4 receptor alpha-chain mRNA.		
B1961932.V1.3_s_at	AGGGAGTGGGTCACAGCCCATGACC	SEQ ID NO:382
B1961932.V1.3_s_at	ATGGGATCCCCAGAGTGGACCTGCC	SEQ ID NO:383
B1961932.V1.3_s_at	ATGGAGAGCGTTGCTGGCAGCCATA	SEQ ID NO:384
B1961932.V1.3_s_at	AGTGACAGTTTGCTGTCAGGTCCCC	SEQ ID NO:385
B1961932.V1.3_s_at	AGACCTTGGGTCGAGTAACGCTTGT	SEQ ID NO:386
B1961932.V1.3_s_at	ACGTTTTGCCTGCACATGGCTCAGA	SEQ ID NO:387
B1961932.V1.3_s_at	GCCAGTTTGTGCACCCATGGAGAGC	SEQ ID NO:388
B1961932.V1.3_s_at	GAAATTGTGATTAGCCGGTAGTGAC	SEQ ID NO:389
B1961932.V1.3_s_at	GAGTAACGCTTGTTTGTGTGTATCT	SEQ ID NO:390
B1961932.V1.3_s_at	GGCATTCCAGACAGCTGACCCGGCA	SEQ ID NO:391
B1961932.V1.3_s_at	TGGGCCTCCTCTTAGGCATGGGATC	SEQ ID NO:392
Equus caballus adenosine A2A receptor mRNA		
BM734452.V1.3_at	AGACTTTCCCAGGTTCGGGAGCTGC	SEQ ID NO:393
BM734452.V1.3_at	AAGTGGAGGCTCTAGCTGACTGCCT	SEQ ID NO:394
BM734452.V1.3_at	CTCAGAGCTGCCCAAGTGGAGGCTC	SEQ ID NO:395
BM734452.V1.3_at	CCGACTCCAGCAGCACGTAGAAGTG	SEQ ID NO:396
BM734452.V1.3_at	GCCGTGAGCTGCCATGTGCTTCTCA	SEQ ID NO:397
BM734452.V1.3_at	GCTGCTGTGTCCAGAGGTGGCATTT	SEQ ID NO:398
BM734452.V1.3_at	GTAAGCGCGAGGAAATCCTTTTTAT	SEQ ID NO:399

Probe Set Name	Sequence	Sequence Identifier
BM734452.V1.3_at	GGCATTTGACTATTTTTGACCAGGA	SEQ ID NO:400
BM734452.V1.3_at	GGCTGCTGGGTCTGTTGTCAGTCCT	SEQ ID NO:401
BM734452.V1.3_at	TGTCAGTCCTGCTGCTAACCTGGCA	SEQ ID NO:402
BM734452.V1.3_at	TTTTATTGTATTATCTTCCCTCCCT	SEQ ID NO:403
No Homology		
BM734531.V1.3_at	ACCACTTCATGTTCTCTACAGAGCT	SEQ ID NO:404
BM734531.V1.3_at	ACAGAGCTGTCCAGAGCCGAGGCTG	SEQ ID NO:405
BM734531.V1.3_at	AAACGAGTCCGAGGGCACAGCCAGG	SEQ ID NO:406
BM734531.V1.3_at	CGTTGCCCGCTGTTGGTCATGACAA	SEQ ID NO:407
BM734531.V1.3_at	GAGTCTCTGTCAGGATCCTTTTGAA	SEQ ID NO:408
BM734531.V1.3_at	GAGTCACCCAAGGAACTTATGCAGA	SEQ ID NO:409
BM734531.V1.3_at	GTCCTGTGGCTTTTGTGTGTCTCTC	SEQ ID NO:410
BM734531.V1.3_at	GGCCTTGCTTGAGAGAGGTCCATCC	SEQ ID NO:411
BM734531.V1.3_at	GGTCACTTAGCAGCGACTTCTTGGA	SEQ ID NO:412
BM734531.V1.3_at	GGAGCCAGGTGTCTGCATTTGAACA	SEQ ID NO:413
BM734531.V1.3_at	TTATGCAGATGCCATGTCCTCACTC	SEQ ID NO:414
Human UbA52 adrenal mRNA for ubiquitin-52 amino acid fusion protein.		
BM734661.V1.3_at	ATTTGCCGCAAGTGTTATGCTCGCC	SEQ ID NO:415
BM734661.V1.3_at	ATCTTTGTGAAGACCCTGACGGGCA	SEQ ID NO:416
BM734661.V1.3_at	AACCTGCGCCCCAAGAAGAAGGTCA	SEQ ID NO:417
BM734661.V1.3_at	AGCAGCGTTTGATTTTTGCCGGCAA	SEQ ID NO:418
BM734661.V1.3_at	GAAGGTCAAATAAGGCCCCTCCTCT	SEQ ID NO:419
BM734661.V1.3_at	CACTCTCTCAGACTACAATATCCAG	SEQ ID NO:420
BM734661.V1.3_at	GCAAGAAGAAGTGCGGCCACACCAA	SEQ ID NO:421
BM734661.V1.3_at	GACGCAGACATGCAGATCTTTGTGA	SEQ ID NO:422
BM734661.V1.3_at	GGTTGAGCCCAGTGACACCATTGAG	SEQ ID NO:423
BM734661.V1.3_at	TCGTGCTGTCAACTGCCGCAAGAAG	SEQ ID NO:424
BM734661.V1.3_at	TTTTGCCGGCAAACAGCTGGAGGAC	SEQ ID NO:425
Homo sapiens STAT4 mRNA.		
BM734780.V1.3_at	AGTCATCTCTTATTCTTCATCTTTG	SEQ ID NO:426
BM734780.V1.3_at	ACAGGATGACCTCTTGACACTCAAA	SEQ ID NO:427
BM734780.V1.3_at	AATAAAGGCCGCTTGTCTGCTTTGC	SEQ ID NO:428
BM734780.V1.3_at	GAAAACCCTCTGAAGTACCTGTATC	SEQ ID NO:429
BM734780.V1.3_at	GAGAGAAAACCTGAGTCCCACGACC	SEQ ID NO:430
BM734780.V1.3_at	TGGCATGACACTCCCAATTGGGTGT	SEQ ID NO:431
BM734780.V1.3_at	GATGAAGTCTCCATATTCTGCCGAA	SEQ ID NO:432
BM734780.V1.3_at	GGTTGAAGTCTGAAGCTCTGCTCTC	SEQ ID NO:433
BM734780.V1.3_at	TGATCTTTGCCAACAGTCATCTCTT	SEQ ID NO:434
BM734780.V1.3_at	TATGTTCCTTCTGTTTTTATCCCCA	SEQ ID NO:435
BM734780.V1.3_at	TTTGCTGACATCCTTCGAGACTACA	SEQ ID NO:436
Homo sapiens phosphate cytidylyltransferase 1, choline, alpha isoform, mRNA (cDNA clone MGC:49915		

Probe Set Name	Sequence	Sequence Identifier
IMAGE:5744747)		
BM734844.V1.3_at	ATGTTTGCTCCAACACAGAGGACAG	SEQ ID NO:437
BM734844.V1.3_at	ACATCAGACATCATCACCCGAATTG	SEQ ID NO:438
BM734844.V1.3_at	AAGGCTGCAGCCTATGATATCAGTG	SEQ ID NO:439
BM734844.V1.3_at	CATCACCTCCAGAAGCTCTTTGTTG	SEQ ID NO:440
BM734844.V1.3_at	GAAATACCACTTGCAGGAGCGAGTT	SEQ ID NO:441
BM734844.V1.3_at	GACAGAAGGTATCTCCACATCAGAC	SEQ ID NO:442
BM734844.V1.3_at	GATGGCCTTTCTCTGGCAAGACTTC	SEQ ID NO:443
BM734844.V1.3_at	GATGCTGCAGGCCATCAGTCCAAAG	SEQ ID NO:444
BM734844.V1.3_at	GTCCGGGACTATGATGTGTACGCGA	SEQ ID NO:445
BM734844.V1.3_at	GGGCTACACAGCCAAGGAGCTCAAT	SEQ ID NO:446
BM734844.V1.3_at	TCAGTCCAAAGCAGAGTCCCAGCAG	SEQ ID NO:447
No Homology		
BM734891.V1.3_at	ACTGGTATTCTCAGCTTCGTATGCT	SEQ ID NO:448
BM734891.V1.3_at	AAGGATCCTCCTTCTGGACTTGTTT	SEQ ID NO:449
BM734891.V1.3_at	CAGCGAGATCAGCAAGGCCTTTTCT	SEQ ID NO:450
BM734891.V1.3_at	CAATGTGCATGTTTCAGACCTTCTG	SEQ ID NO:451
BM734891.V1.3_at	GCTTGCCACTGCCTTTGGGATATAG	SEQ ID NO:452
BM734891.V1.3_at	TAATGGGTCCCTTCAGTCAGTGGCA	SEQ ID NO:453
BM734891.V1.3_at	GTGACTTTTGGTTACCTGGGCACAC	SEQ ID NO:454
BM734891.V1.3_at	GGTAGTGTTGGATCTCAGCCACCCA	SEQ ID NO:455
BM734891.V1.3_at	TCGTATGCTGCAGTACCTGTGGACA	SEQ ID NO:456
BM734891.V1.3_at	TATAGGGACTGCAGCCTTTGTTTCT	SEQ ID NO:457
BM734891.V1.3_at	TTCTGCTCTCTCTGGAATGGGTAGT	SEQ ID NO:458
Homo sapiens matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase), mRNA (cDNA clone		
BM734900.V1.3_at	ACGACGTCTTCCAGTACCGAGAGAA	SEQ ID NO:459
BM734900.V1.3_at	ACTGGCGCGTGAGTTCCCGGAATGA	SEQ ID NO:460
BM734900.V1.3_at	AAGTGGGCTACGTGAGCTTCGACCT	SEQ ID NO:461
BM734900.V1.3_at	GCTGGATTCCGCCTTTGAGGAGCCA	SEQ ID NO:462
BM734900.V1.3_at	GAAGGAGCCAGTTTGCCGGTTTCAA	SEQ ID NO:463
BM734900.V1.3_at	GAAGATTTTCTTCTTCTCTGGGCGC	SEQ ID NO:464
BM734900.V1.3_at	GAGGAGCCACTCACCAAGAAGATTT	SEQ ID NO:465
BM734900.V1.3_at	GTGTCAGCCCGGTGGACCAGATGTT	SEQ ID NO:466
BM734900.V1.3_at	GTGTACACAGGCAAGTCGGCGCTAG	SEQ ID NO:467
BM734900.V1.3_at	GGTTTCAAACTGGTGGGTCTGTTCT	SEQ ID NO:468
BM734900.V1.3_at	TAGGCCCGAGGCGTCTGGACAAGCT	SEQ ID NO:469
Homo sapiens S100 calcium binding protein P, mRNA.		
BM734933.V1.3_at	AGGGCAGCAAGCAGAGCCTGACCAA	SEQ ID NO:470
BM734933.V1.3_at	AAAGCTCTTGTTGGCAGTCGTTTCC	SEQ ID NO:471
BM734933.V1.3_at	GCCGAGGTGGACTTCAGCGAGTTCA	SEQ ID NO:472

Probe Set Name	Sequence	Sequence Identifier
BM734933.V1.3_at	CCTGGCGTCCAGAAAGCTCTTGTTG	SEQ ID NO:473
BM734933.V1.3_at	GAGCATGATCATCGACGTCTTTGCC	SEQ ID NO:474
BM734933.V1.3_at	GAGTTCATCGTGTTTGTGGCCGCGC	SEQ ID NO:475
BM734933.V1.3_at	GAGGTGGGACATTTCCTCGGCCACG	SEQ ID NO:476
BM734933.V1.3_at	GTGGGTCCAAATCCAGCACCATGAC	SEQ ID NO:477
BM734933.V1.3_at	GGTGCCGTGGACAAACTGCTCAAGG	SEQ ID NO:478
BM734933.V1.3_at	TCATGGAGAAGGAGCTCCCGGGCTT	SEQ ID NO:479
BM734933.V1.3_at	TCAAGGACCTGGACGCCAACGGAGA	SEQ ID NO:480
Human mRNA for coupling protein G(s) alpha-subunit (alpha-S1) (stimulatory regulatory component Gs of adenylyl cyclase).		
BM734975.V1.3_at	ATGATTAACAAAGCCACCTTTCCCT	SEQ ID NO:481
BM734975.V1.3_at	ATTGTTCACGCAGTTAATCACCCAC	SEQ ID NO:482
BM734975.V1.3_at	ATCTCTGTGATTCTGTTCCTCAACA	SEQ ID NO:483
BM734975.V1.3_at	ATGCACCTCCGTCAGTATGAGCTGC	SEQ ID NO:484
BM734975.V1.3_at	CTGCTCGCTGAGAAAGTCCTTGCTG	SEQ ID NO:485
BM734975.V1.3_at	GCTCCCTTCAGCTTGGTTAAATATA	SEQ ID NO:486
BM734975.V1.3_at	GAATTTCTGAGAATCAGCCCCGCTA	SEQ ID NO:487
BM734975.V1.3_at	GACTACTTTCCAGAATTTGCTCGCT	SEQ ID NO:488
BM734975.V1.3_at	GTTCCCTCTCTCTTTCAGTAAGTAA	SEQ ID NO:489
BM734975.V1.3_at	GGCCAAGTACTTCATCCGTGACGAA	SEQ ID NO:490
BM734975.V1.3_at	TCGCTACACTACTCCTGAGGATGCT	SEQ ID NO:491
Human mRNA for macrophage inflammatory protein-2alpha (MIP2alpha)		
BM735057.V1.3_s_at	AAGGGCAGCTCCGACTGACCAGAGG	SEQ ID NO:492
BM735057.V1.3_s_at	GCTGTAGCTGAAGTAGGCCCTGCCC	SEQ ID NO:493
BM735057.V1.3_s_at	GCAGCTCCGACTGACCAGAGGAAGA	SEQ ID NO:494
BM735057.V1.3_s_at	GAAGTAGGCCCTGCCCTTACAGGAA	SEQ ID NO:495
BM735057.V1.3_s_at	GAAGCTGATCAGTGGCTGTAGCTGA	SEQ ID NO:496
BM735057.V1.3_s_at	GACTGACCAGAGGAAGAAGCTGATC	SEQ ID NO:497
BM735057.V1.3_s_at	GATGCTAAACAAGGGCAGCTCCGAC	SEQ ID NO:498
BM735057.V1.3_s_at	GGAAGTTTGTCTCAACCCTGAAGCC	SEQ ID NO:499
BM735057.V1.3_s_at	GGCCCTGCCCTTACAGGAATCAAAG	SEQ ID NO:500
BM735057.V1.3_s_at	TGGACAGGAAGTTTGTCTCAACCCT	SEQ ID NO:501
BM735057.V1.3_s_at	TAAACAAGGGCAGCTCCGACTGACC	SEQ ID NO:502
Horse serpin mRNA.		
BM735091.V1.3_at	ATGCTTGCCATGCTGATGCCAGAGG	SEQ ID NO:503
BM735091.V1.3_at	ATCTAGCCCGCCTAGGTGTACAAGA	SEQ ID NO:504
BM735091.V1.3_at	CATTCATTTTCTTCATTCGGCACAA	SEQ ID NO:505
BM735091.V1.3_at	GCTAACATCCTGTTCTTAGGCAGAT	SEQ ID NO:506
BM735091.V1.3_at	GCAAAGCTGATCTGTCTGGCATGTC	SEQ ID NO:507
BM735091.V1.3_at	GAATCTGTATCTCGCTGAAGTCAAT	SEQ ID NO:508
BM735091.V1.3_at	GAAAATTTCAATGCCGACCATCCAT	SEQ ID NO:509

Probe Set Name	Sequence	Sequence Identifier
BM735091.V1.3_at	GGGCCAGAGATCTTTTCGTATCGAA	SEQ ID NO:510
BM735091.V1.3_at	TGAAGTCAATGTCCACTTGCCCAGG	SEQ ID NO:511
BM735091.V1.3_at	TTTGGCGTGGGTAGCTATTTTCCTT	SEQ ID NO:512
BM735091.V1.3_at	TTAGGCAGATTTTCTTCCCCTTAGA	SEQ ID NO:513
Equus caballus mRNA for ferritin light chain.		
BM735286.V1.3_at	AGGAGCCTCCGGAGTCCAGCGGCCT	SEQ ID NO:514
BM735286.V1.3_at	AGCTTTTTAACTAGCCTGGAGCCTT	SEQ ID NO:515
BM735286.V1.3_at	CGTCAGAGCTTCTGCCTGAGCCTCT	SEQ ID NO:516
BM735286.V1.3_at	CTGCAGCCACTAGAGATAGCTTTTT	SEQ ID NO:517
BM735286.V1.3_at	CTCCGGAGTCCAGCGGCCTTTGAGG	SEQ ID NO:518
BM735286.V1.3_at	CTGGCGTCAGAGCTTCTGCCTGAGC	SEQ ID NO:519
BM735286.V1.3_at	GAGATAGCTTTTTAACTAGCCTGGA	SEQ ID NO:520
BM735286.V1.3_at	TTTGGTATCCCCCTGGCGTCAGAGC	SEQ ID NO:521
BM735286.V1.3_at	TCCCTGCAGCCACTAGAGATAGCTT	SEQ ID NO:522
BM735286.V1.3_at	TTTTAACTAGCCTGGAGCCTTCTGC	SEQ ID NO:523
BM735286.V1.3_at	TAACTAGCCTGGAGCCTTCTGCCCA	SEQ ID NO:524
No Homology		
BM735386.V1.3_at	ATTTGCTGACCTTGTGGTGCTCTCA	SEQ ID NO:525
BM735386.V1.3_at	AAGTTGTCACGTGCAGTGTCTTTCT	SEQ ID NO:526
BM735386.V1.3_at	AAGGGCAATCCTGCTTCACTGGTGT	SEQ ID NO:527
BM735386.V1.3_at	GCTGGTGCCCCTGTAAAGAGGCTTT	SEQ ID NO:528
BM735386.V1.3_at	GAAGTTGTCACCATGAAGTTGTCAC	SEQ ID NO:529
BM735386.V1.3_at	GAGCGTTTCCTTTACCTGGAAGTTG	SEQ ID NO:530
BM735386.V1.3_at	GAGACCTGTTGTGCTGTGTTATTTT	SEQ ID NO:531
BM735386.V1.3_at	GATGGCTGTTTTCCTGTCCCAGAGA	SEQ ID NO:532
BM735386.V1.3_at	GATGTCTGACCTTAGTGTTCCAAAC	SEQ ID NO:533
BM735386.V1.3_at	GTTAAGTATGTGGTTCCTTCTCAGA	SEQ ID NO:534
BM735386.V1.3_at	TAAAGGATGTCCTGGTGCTGGCTCA	SEQ ID NO:535
No Homology		
BM735452.V1.3_at	CGAACCCCGGAAGTCTGCAAAATTG	SEQ ID NO:536
BM735452.V1.3_at	AGGATGACTCGGGTCCAGTGGCCCA	SEQ ID NO:537
BM735452.V1.3_at	AAGTCTGCAAAATTGGGTGCCCCAA	SEQ ID NO:538
BM735452.V1.3_at	CTGCTCTCTGCTCCCTAAATTATTG	SEQ ID NO:539
BM735452.V1.3_at	CCAGAATCTGCCCACGGAGTCGGTG	SEQ ID NO:540
BM735452.V1.3_at	CCCCGGTTTCATATCTGTATTTATA	SEQ ID NO:541
BM735452.V1.3_at	GGGTGCCCCAAGAGCTGGAAACTCA	SEQ ID NO:542
BM735452.V1.3_at	GAGGCCTCAGTGCAGTGCCTTCCCG	SEQ ID NO:543
BM735452.V1.3_at	GTGCGCAGGTCCCACTCAGGATGAC	SEQ ID NO:544
BM735452.V1.3_at	GGAAACTCAGGAAACCCCAGGTGCT	SEQ ID NO:545
BM735452.V1.3_at	TTAATATATGCAATTCCCCATCCCT	SEQ ID NO:546
Homo sapiens male-specific lethal 3-like 1 (Drosophila), transcript variant 1, mRNA		

Probe Set Name	Sequence	Sequence Identifier
BM780999.V1.3_at	TACTTCTTAGGTACCTGAACGGCCT	SEQ ID NO:547
BM780999.V1.3_at	ATTTGAGTTGCTTACCTACTGTAGT	SEQ ID NO:548
BM780999.V1.3_at	AGTGTGTCTAGGTTAGGCTGTTTCA	SEQ ID NO:549
BM780999.V1.3_at	AAAGCATTTCCTGTCTTGTTTGAGA	SEQ ID NO:550
BM780999.V1.3_at	GCTTGTTACAGTTCATTTTCTCTAA	SEQ ID NO:551
BM780999.V1.3_at	GACAGGCAGGCCCATTAATTTGAGT	SEQ ID NO:552
BM780999.V1.3_at	GATGGTGGGCCTTCAGACAGAGTAC	SEQ ID NO:553
BM780999.V1.3_at	GATGAGGCCGAGCAACTCTGTCCAA	SEQ ID NO:554
BM780999.V1.3_at	GGAAACCGCAAGGTAGTCCCAGAAT	SEQ ID NO:555
BM780999.V1.3_at	TAATGTTATGGTTCCCTTTCTGTAA	SEQ ID NO:556
BM780999.V1.3_at	TTGCCACTGTACACGTGATCTGTGA	SEQ ID NO:557
Homo sapiens replication protein A1, 70kDa, mRNA		
BM781033.V1.3_at	AGATAGCCTTCCTTCAGGGTTTAAT	SEQ ID NO:558
BM781033.V1.3_at	AAAGGCGCTCTCTTTCTAGAGGTGC	SEQ ID NO:559
BM781033.V1.3_at	AAAGCCTTGCTTTAGTTTCACTTCA	SEQ ID NO:560
BM781033.V1.3_at	AATTGACCCTAAATCTGCAGACAGT	SEQ ID NO:561
BM781033.V1.3_at	CAGGGACATCCACGCAACTACAAAG	SEQ ID NO:562
BM781033.V1.3_at	GAATGCACACTTTTTCTACCTGTAC	SEQ ID NO:563
BM781033.V1.3_at	GAAGAAGCCCTTTGTTTCTCTTGCT	SEQ ID NO:564
BM781033.V1.3_at	GACATTTCTGCAACTTGGGTTCCTT	SEQ ID NO:565
BM781033.V1.3_at	GTAAGCGCGTCTTCCTAGAATTCAA	SEQ ID NO:566
BM781033.V1.3_at	TAACTAGGTTTCTGCTCCATTGGTG	SEQ ID NO:567
BM781033.V1.3_at	TACCTGTACATATTTCTTGCGTTTG	SEQ ID NO:568
Human mRNA for cathepsin H		
BM781103.V1.3_at	ATCCCTCTGGTGTGAGCCAGGATGG	SEQ ID NO:569
BM781103.V1.3_at	AAGAATATTCTTTCCTTCCTGAAGG	SEQ ID NO:570
BM781103.V1.3_at	CACCCACACCTTCTGATGCAAAGGA	SEQ ID NO:571
BM781103.V1.3_at	CAGCCTTGTGCCTTTTAAGCATGAT	SEQ ID NO:572
BM781103.V1.3_at	CATTGGTGGAAGTCCTGCCCTGGAG	SEQ ID NO:573
BM781103.V1.3_at	CCCCGTGCTGTGTCCAGAAATCTAA	SEQ ID NO:574
BM781103.V1.3_at	GCAGCCTGGCCATTGGTGGAAGTCC	SEQ ID NO:575
BM781103.V1.3_at	GAAGAATTCCACCAAGCAACAAGCC	SEQ ID NO:576
BM781103.V1.3_at	GATGCAAAGGATCACCAGCCTTGTG	SEQ ID NO:577
BM781103.V1.3_at	TTCCTTCCTGAAGGGCTACTTTTCA	SEQ ID NO:578
BM781103.V1.3_at	TTAACTGACTCAAACCCACGTGGAC	SEQ ID NO:579
Homo sapiens transforming acidic coiled-coil containing protein 3 (TACC3) mRNA		
BM781237.V1.3_s_at	GTACTACAGTACAGCCAGAAGGACC	SEQ ID NO:580
BM781237.V1.3_s_at	AGCAGTCCTTATACCTCAAGTTCGA	SEQ ID NO:581
BM781237.V1.3_s_at	AAGTTCGACCCGCTCCTGATGGACA	SEQ ID NO:582
BM781237.V1.3_s_at	AAGAGAACCTGTCGCTCAGGAGCGA	SEQ ID NO:583
BM781237.V1.3_s_at	GGACCCATCGTGGACGTACTACAGT	SEQ ID NO:584

Probe Set Name	Sequence	Sequence Identifier
BM781237.V1.3_s_at	GTGGAACTTGACTTCCTAGGCCCTC	SEQ ID NO:585
BM781237.V1.3_s_at	TGGACCCACCTTTGTGTGTCCTCGG	SEQ ID NO:586
BM781237.V1.3_s_at	TGATGGACAGCCCTCAGAGACCTGC	SEQ ID NO:587
BM781237.V1.3_s_at	TCCGGATGTGCCTGTGCTGGACCCA	SEQ ID NO:588
BM781237.V1.3_s_at	TGCCGCCAATCTCGTGGAACTTGAC	SEQ ID NO:589
BM781237.V1.3_s_at	TCCCCGCGACAGACAGTGTGCAGGA	SEQ ID NO:590
Homo sapiens chromosome 6 open reading frame 166, mRNA		
BM781278.V1.3_at	ACATGCATTCTTCCTCAGTGGACCA	SEQ ID NO:591
BM781278.V1.3_at	AAAGAACAGCCCTTATTCACTCTAC	SEQ ID NO:592
BM781278.V1.3_at	CTGATGTCAATACCACCCGGATGTG	SEQ ID NO:593
BM781278.V1.3_at	CAGCCTGCTAGTTATGTTTCATGAA	SEQ ID NO:594
BM781278.V1.3_at	CACGTTTTCTGCATTTGTGGGCTGC	SEQ ID NO:595
BM781278.V1.3_at	TCTGCAACATCCTCACCATTAAAAA	SEQ ID NO:596
BM781278.V1.3_at	GTGGCCTCATTTGCTGTATCATTAC	SEQ ID NO:597
BM781278.V1.3_at	TGGCAACCACTTTAGGCAGCAACTG	SEQ ID NO:598
BM781278.V1.3_at	TGTGGACCTTTGCTACCTGTATTAA	SEQ ID NO:599
BM781278.V1.3_at	TTCAAGCTTTCGTCAGTGGCAACCA	SEQ ID NO:600
BM781278.V1.3_at	TTATTCACTCTACGGCAGGTTGGGA	SEQ ID NO:601
Homo sapiens KIAK0002 mRNA.		
BM781319.V1.3_at	ATAACCTGTTATTCTGACTAGCTTA	SEQ ID NO:602
BM781319.V1.3_at	ATGTTCATTACCCTTGTACCATGTA	SEQ ID NO:603
BM781319.V1.3_at	AGTGCCTTACTGACTGTAGCCATTA	SEQ ID NO:604
BM781319.V1.3_at	GAGTCAATGTTATTCTCTCACAATG	SEQ ID NO:605
BM781319.V1.3_at	GATCTCTCTCTCTCAGTTACAGTTT	SEQ ID NO:606
BM781319.V1.3_at	GTTCTTACTGGCCAACTCTTAAATC	SEQ ID NO:607
BM781319.V1.3_at	GTTTCTCATCTTGGACTTCTTTTAT	SEQ ID NO:608
BM781319.V1.3_at	GTGTGATGCCATATCGAGTCAATGT	SEQ ID NO:609
BM781319.V1.3_at	TGTACCATGTACCTCAGATCTCTCT	SEQ ID NO:610
BM781319.V1.3_at	TCACTGGGCCATTGGATTTTTTCCA	SEQ ID NO:611
BM781319.V1.3_at	TAAGAGGTCCTATCTGTTCAGTGTT	SEQ ID NO:612
Homo sapiens inhibitor of Bruton agammaglobulinemia tyrosine kinase (IBTK), mRNA		
BM781379.V1.3_at	ATTCGGCAACCCTGATGAGTTTGTC	SEQ ID NO:613
BM781379.V1.3_at	AGGGACCACTGGCAGTACCTATGTG	SEQ ID NO:614
BM781379.V1.3_at	AGCATGGATGCTAGTTCGCCGTGGA	SEQ ID NO:615
BM781379.V1.3_at	AAAACCCTTGGCTTTGATTCAGATT	SEQ ID NO:616
BM781379.V1.3_at	GTTGAAAGGACACCGCAGGGACCAC	SEQ ID NO:617
BM781379.V1.3_at	GAGGAGCACGCGATACAAGATTTAT	SEQ ID NO:618
BM781379.V1.3_at	GATTCAGATTGAGGAGCACGCGATA	SEQ ID NO:619
BM781379.V1.3_at	GTTCGCCGTGGACTTGAGATGTATT	SEQ ID NO:620
BM781379.V1.3_at	GGTGCATTAGCTATTATTTCTGATC	SEQ ID NO:621
BM781379.V1.3_at	GGTTTTCTATGAGGCATTCGGCAAC	SEQ ID NO:622

Probe Set Name	Sequence	Sequence Identifier
BM781379.V1.3_at	GGATCTAATTTCTTTGCTGCAGTTT	SEQ ID NO:623
No Homology		
BM781394.V1.3_at	ACCAGTGCTGAACATTAGTGCCTTT	SEQ ID NO:624
BM781394.V1.3_at	GAACCTGCTGAATTTAACTTAACCG	SEQ ID NO:625
BM781394.V1.3_at	AAAATACAGTCAACCCTTCACCATG	SEQ ID NO:626
BM781394.V1.3_at	AAGAGTTCAGCTTCACGTTTGCCAA	SEQ ID NO:627
BM781394.V1.3_at	CAACAGGCGGAGACAGCTGTCCTTT	SEQ ID NO:628
BM781394.V1.3_at	CCATATCACCTGCTATTTCCAAGAA	SEQ ID NO:629
BM781394.V1.3_at	GCTGCATCTCATACAATGGCTCTCT	SEQ ID NO:630
BM781394.V1.3_at	GAAACAGCCCGATACATAACACTCC	SEQ ID NO:631
BM781394.V1.3_at	TCTGCCCATCAATTACACTTTCTTT	SEQ ID NO:632
BM781394.V1.3_at	TAACCGAGAGGATCACCGTGACAAA	SEQ ID NO:633
BM781394.V1.3_at	TAATGCTGGCATTTTGGATACTACC	SEQ ID NO:634
No Homology		
BM781409.V1.3_at	ATGGATCCCCTTATTATTCTTTCAC	SEQ ID NO:635
BM781409.V1.3_at	AGTTTTTACATCTGCCTCAAGGCCT	SEQ ID NO:636
BM781409.V1.3_at	AGAATGAAACTGAGTCTCCCTGGCC	SEQ ID NO:637
BM781409.V1.3_at	AGATCCTTCGCTTGTCTGCTTAAAA	SEQ ID NO:638
BM781409.V1.3_at	AATTCTGAACAACTCTCTGCAACTG	SEQ ID NO:639
BM781409.V1.3_at	GTTCCTCCTTTTCTTTAGGTCTCAG	SEQ ID NO:640
BM781409.V1.3_at	GCACGAGCTGACCTGGAGTACTACA	SEQ ID NO:641
BM781409.V1.3_at	GACTTCCCAGTGCACTCAGAATGAA	SEQ ID NO:642
BM781409.V1.3_at	GAGTTCTCTATGTCACAGTTTTTAC	SEQ ID NO:643
BM781409.V1.3_at	GTCTCAGCTTACATATGTCACCTTC	SEQ ID NO:644
BM781409.V1.3_at	TTGTTTATCACTGTATCCCTAGCAC	SEQ ID NO:645
No Homology		
BM781416.V1.3_at	ATGCTGCAGCTGTTTGTCAGGAACA	SEQ ID NO:646
BM781416.V1.3_at	AGTATTTGCCATCACATGCTGCAGC	SEQ ID NO:647
BM781416.V1.3_at	ACAATTACTGGCTTTTCTGCTGTAA	SEQ ID NO:648
BM781416.V1.3_at	CAGTAATCACGCTGCAGAAATTGGC	SEQ ID NO:649
BM781416.V1.3_at	GAACGCAGCAGCAGGGTACGTAGCA	SEQ ID NO:650
BM781416.V1.3_at	GAAATTGGCAGCCTGCACCTTATGC	SEQ ID NO:651
BM781416.V1.3_at	TGTCCGTTTTTATTTGGGCATCCAC	SEQ ID NO:652
BM781416.V1.3_at	GGGCATCCACCACAGACAATTTAAA	SEQ ID NO:653
BM781416.V1.3_at	GGTGTCATTCATTCATTCAGTAATC	SEQ ID NO:654
BM781416.V1.3_at	TAAATTTCGTAGATGCGCTCAGAAC	SEQ ID NO:655
BM781416.V1.3_at	TTATGCGTCACCATTACCTTTAGTC	SEQ ID NO:656
Homo sapiens cysteine-rich motor neuron 1 (CRIM1)		
BM781438.V1.3_at	ATATGATTTATCCTGAGTGCTGTAT	SEQ ID NO:657
BM781438.V1.3_at	ATCACTCTTTTACTTTGGTTCCTGT	SEQ ID NO:658
BM781438.V1.3_at	AGATACCCAGTATGCTTAATGTGAA	SEQ ID NO:659
BM781438.V1.3_at	ACTTGGACAGAGGTTGCTGAACTTT	SEQ ID NO:660

Probe Set Name	Sequence	Sequence Identifier
BM781438.V1.3_at	AAAGGTGTTCTAGCTGTTTGCATCA	SEQ ID NO:661
BM781438.V1.3_at	AAAATAGAGTTACATCAGCCTGATT	SEQ ID NO:662
BM781438.V1.3_at	GTTGACAATTAATCCATTCCTGGCA	SEQ ID NO:663
BM781438.V1.3_at	GTGCTGTATCTATCACTCTTTTACT	SEQ ID NO:664
BM781438.V1.3_at	TGGTTCCTGTTGTGCTCTTGTAAAA	SEQ ID NO:665
BM781438.V1.3_at	TAAATGCTTGCTTTTTGTTTTTTCA	SEQ ID NO:666
BM781438.V1.3_at	TTGTTTTTTCAATCATGGCCATATT	SEQ ID NO:667
Homo sapiens RNF4 mRNA.		
Foe1216.V1.3_at	ATTGCCATGAAGTTCCTGCTGGGCT	SEQ ID NO:668
Foe1216.V1.3_at	CTTTCCCTTCCTCAATGTACATAGT	SEQ ID NO:669
Foe1216.V1.3_at	TGACTTTTTGACTGTTGGGCTCACT	SEQ ID NO:670
Foe1216.V1.3_at	GCTGGGCTTCGTGGAAACACTGTTT	SEQ ID NO:671
Foe1216.V1.3_at	GATGATACCCAGACTTCAGGAGCCA	SEQ ID NO:672
Foe1216.V1.3_at	GGGCAGGACATCAGTTTTCATCAGT	SEQ ID NO:673
Foe1216.V1.3_at	GGAGTGTTCCTCCTTTATGTGAAAA	SEQ ID NO:674
Foe1216.V1.3_at	TGGGCTCACTTCCAGTTAGTTTGAA	SEQ ID NO:675
Foe1216.V1.3_at	TTCCGGTTAGACGTCATTGCCATGA	SEQ ID NO:676
Foe1216.V1.3_at	TATCCGTGTATGTCAGTCTGTTTTG	SEQ ID NO:677
Foe1216.V1.3_at	TTTGGACTCCTCTGCTAGTGTTACA	SEQ ID NO:678
No Homology		
Foe1263.V1.3_at	ATCTCTTGGAGTTTCAGTACTGTCA	SEQ ID NO:679
Foe1263.V1.3_at	AGAGGTGGTCTGTAATGGATTCAAA	SEQ ID NO:680
Foe1263.V1.3_at	ACATAGTTCCACTGTCATTTCTGAA	SEQ ID NO:681
Foe1263.V1.3_at	AAAAAGCTCGACAGCACTCAGGTCC	SEQ ID NO:682
Foe1263.V1.3_at	AACTAATAGGTTACTGCTTCCCACA	SEQ ID NO:683
Foe1263.V1.3_at	CCAGTCCATCTCGTTTCTTTATAAA	SEQ ID NO:684
Foe1263.V1.3_at	GCTTCCCACACTACATTGGTTCAAA	SEQ ID NO:685
Foe1263.V1.3_at	GCTCTTTAAGTCATAGCACCGGTAA	SEQ ID NO:686
Foe1263.V1.3_at	GAGTTCCGGTATCTAAGTCACAATT	SEQ ID NO:687
Foe1263.V1.3_at	GGTTGCAGCAAACTTTTTAACTGAT	SEQ ID NO:688
Foe1263.V1.3_at	TAAAGGCATTGTTCCTTCCAGTCCA	SEQ ID NO:689
Human 3-hydroxyacyl-CoA dehydrogenase, isoform 2 mRNA.		
Foe1317.V1.3_at	ATAATTGCCTGAATTCGTTCCCTTG	SEQ ID NO:690
Foe1317.V1.3_at	AGGGAAGCACTTCCTCCGAGGGCAT	SEQ ID NO:691
Foe1317.V1.3_at	CTTCTGAACCTTGTCATTTTCGTGA	SEQ ID NO:692
Foe1317.V1.3_at	AGCAGTGTCGAGAGCCATCGCGTGT	SEQ ID NO:693
Foe1317.V1.3_at	GCAAGCTGCCTGTAAATCGACTCTA	SEQ ID NO:694
Foe1317.V1.3_at	GAATGATGACTGTCTGTCTCTCTTT	SEQ ID NO:695
Foe1317.V1.3_at	GAAATGCAGTCTTTTAACCTATGAA	SEQ ID NO:696
Foe1317.V1.3_at	GTAACGGCAGATTTCTCCATTGAGA	SEQ ID NO:697
Foe1317.V1.3_at	GTCTCTCTTTTTTCCGTGACAAATC	SEQ ID NO:698
Foe1317.V1.3_at	GGAAGAGGTTTCATTCACACCCGAA	SEQ ID NO:699

Probe Set Name	Sequence	Sequence Identifier
Foe1317.V1.3_at	TACACCCTTGGTGCCTTGGAGCAAA	SEQ ID NO:700
Homo sapiens mRNA; cDNA DKFZp434I0612 (from clone DKFZp434I0612).		
Foe1324.V1.3_at	AAACCTTTTGGTGTACATCCTCTGG	SEQ ID NO:701
Foe1324.V1.3_at	AGATATCTGTCTCATTCATTCCACT	SEQ ID NO:702
Foe1324.V1.3_at	ACTTGCACTGTCTCCTGGGATCTTG	SEQ ID NO:703
Foe1324.V1.3_at	AACAAGTGGCTTCCTTTTTGAGATA	SEQ ID NO:704
Foe1324.V1.3_at	CTTTCTTTCCACAGCACTTTTGATA	SEQ ID NO:705
Foe1324.V1.3_at	CTCCCTGTGGCACTTGACATTTTAA	SEQ ID NO:706
Foe1324.V1.3_at	GTAAGGCAATCTTTCCTGTTGTAAA	SEQ ID NO:707
Foe1324.V1.3_at	GTGTGATCCCATCATGAGTTCATTG	SEQ ID NO:708
Foe1324.V1.3_at	TGGGATCTTGTCTGCAGCCCGACGT	SEQ ID NO:709
Foe1324.V1.3_at	GGCCCCTTAAGTGCTGCCAGAAGCA	SEQ ID NO:710
Foe1324.V1.3_at	TTCTGGTTATCATTTATCCTCCCTG	SEQ ID NO:711
No Homology		
Foe146.V1.3_at	ATTGTGGATTTGTCAGTTTCTCTCT	SEQ ID NO:712
Foe146.V1.3_at	ATTCTTCATAAGAGCTGTTGCCAAA	SEQ ID NO:713
Foe146.V1.3_at	ATTCATTTCACTGTACTCTTGCCAG	SEQ ID NO:714
Foe146.V1.3_at	ATCACTCCAGTGATGGTTGTGGTGG	SEQ ID NO:715
Foe146.V1.3_at	AAAGCATAGTTCAGTGCCACTCACA	SEQ ID NO:716
Foe146.V1.3_at	AAGTATGTTGAAGTGTCTCTCTGTC	SEQ ID NO:717
Foe146.V1.3_at	AAGTGTCTCTCTGTCATTGTGGATT	SEQ ID NO:718
Foe146.V1.3_at	AATTGCCCTTGTCTCATAATGCTTT	SEQ ID NO:719
Foe146.V1.3_at	CAGGTGCCTAATGTGCGGTCTTTAA	SEQ ID NO:720
Foe146.V1.3_at	TGTCTACTTGGTTTTACCACCTTCT	SEQ ID NO:721
Foe146.V1.3_at	TCAGTTTCTCTCTGCATTTCTCAGA	SEQ ID NO:722
Homo sapiens fucosyltransferase 8 (alpha (1,6) fucosyltransferase) (FUT8), transcript variant 1		
Foe148.V1.3_at	ATCAGTTCATCCACCTCATTATTAA	SEQ ID NO:723
Foe148.V1.3_at	AGGTTGATTCTTAGCCAGTGGTGGT	SEQ ID NO:724
Foe148.V1.3_at	AGTGTTTCTGGACATTTCTCTTTGA	SEQ ID NO:725
Foe148.V1.3_at	CAGGTTCTTTAGTACTCAGTGTTTC	SEQ ID NO:726
Foe148.V1.3_at	GTGACCTAACGAGAAGACCCGCATA	SEQ ID NO:727
Foe148.V1.3_at	GATGCCTCATTGGTGGAATTCCTCT	SEQ ID NO:728
Foe148.V1.3_at	GTATTGTAACCGCTGAATTCACTCC	SEQ ID NO:729
Foe148.V1.3_at	GTGCCTATATCCGAGAGACCTATGT	SEQ ID NO:730
Foe148.V1.3_at	GTGAGACTTCAAACATGGTGCCTAT	SEQ ID NO:731
Foe148.V1.3_at	TCAAACCCATGCACAGTCCAATAAT	SEQ ID NO:732
Foe148.V1.3_at	TACTTTGCCCCTTCTTTCAAGATTA	SEQ ID NO:733
Homo sapiens tripeptidyl peptidase II mRNA		
Foe443.V1.3_at	AGGACTTTCAGTTGGGTTGCAGCTA	SEQ ID NO:734
Foe443.V1.3_at	CCATAACTTTTAACTGCAAGCCAGT	SEQ ID NO:735
Foe443.V1.3_at	AACATCCTCTTGACGTGCAGAGCAT	SEQ ID NO:736

Probe Set Name	Sequence	Sequence Identifier
Foe443.V1.3_at	AATTGCTGGAGCATAACTGCTTCAA	SEQ ID NO:737
Foe443.V1.3_at	CAGGGTTTTAACATGCTTGACTTTA	SEQ ID NO:738
Foe443.V1.3_at	GTACACCATATCACTCTGATACCTT	SEQ ID NO:739
Foe443.V1.3_at	GTGCCAGACAGCTAAATCTTTATCA	SEQ ID NO:740
Foe443.V1.3_at	GGGTTGCAGCTATTACACGCATGAT	SEQ ID NO:741
Foe443.V1.3_at	GGAGTTATTTCAGGCCAATCATTTT	SEQ ID NO:742
Foe443.V1.3_at	TGTCTGCCAGCACCAAGGACTTTCA	SEQ ID NO:743
Foe443.V1.3_at	GGCCAATCATTTTTAACATCCTCTT	SEQ ID NO:744
Equus caballus Toll-like receptor 4 mRNA, complete cds		
GI9717252-3_at	ATCTTTGACATCTTAGCCATCCTAA	SEQ ID NO:745
GI9717252-3_at	AGAAGGCTCCTGATTCAGATCCTCC	SEQ ID NO:746
GI9717252-3_at	ACATCGTCTCCCAAGTCTTTTGAAT	SEQ ID NO:747
GI9717252-3_at	ACAGGACTGCTAATCCCTTTGAGTT	SEQ ID NO:748
GI9717252-3_at	AAACATCCTGGTCATTCTTTAGCGT	SEQ ID NO:749
GI9717252-3_at	AAGTCAGCTAAGGAGTCCGTGCCAG	SEQ ID NO:750
GI9717252-3_at	GCTGCAACATACCAGGCATTGTGCT	SEQ ID NO:751
GI9717252-3_at	GAATGGAAACCATCTCATCTTTGAC	SEQ ID NO:752
GI9717252-3_at	GACTGGGCCCCAGTGAGTTCAGAAA	SEQ ID NO:753
GI9717252-3_at	GGCAGGTGATTCTGTCGTGCACAAG	SEQ ID NO:754
GI9717252-3_at	TCTCTGTTCAATTTTCCCTTTTCTA	SEQ ID NO:755
Equus caballus Toll-like receptor 4 mRNA, complete cds		
GI9717252-3M_at	ATAAGTTCTATTTCCACCTGATGCT	SEQ ID NO:756
GI9717252-3M_at	AGAGACTTCATTCCTGGTGTGGCCA	SEQ ID NO:757
GI9717252-3M_at	AAAGTTATTGTCGTGGTGTCCCAGC	SEQ ID NO:758
GI9717252-3M_at	CAGCACTTCATTCAGAGCCGATGGT	SEQ ID NO:759
GI9717252-3M_at	GCGGGTCGGTTTTCAGTATACTCAT	SEQ ID NO:760
GI9717252-3M_at	CTGATGCTTCTTGCTGGCTGCAAAA	SEQ ID NO:761
GI9717252-3M_at	GCATGCCCGTGCTGGGTTTTAACAA	SEQ ID NO:762
GI9717252-3M_at	GATGCCTTTGTTATCTACTCAAGCC	SEQ ID NO:763
GI9717252-3M_at	GGTGTGTGCAATACCCTTACAGATG	SEQ ID NO:764
GI9717252-3M_at	TGAGTATGAGATTGCCCAGACCTGG	SEQ ID NO:765
GI9717252-3M_at	TTAACAATGCCACCTGTCAGATTAG	SEQ ID NO:766
Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12).		
WBC001D02_V1.3_at	ATATAGAAGCTCCATGGGCTGCCCA	SEQ ID NO:767
WBC001D02_V1.3_at	GAGGGAAACGACTCCTTGTCTTTCA	SEQ ID NO:768
WBC001D02_V1.3_at	AGGAGACCTGGTTGCCTTATACCTT	SEQ ID NO:769
WBC001D02_V1.3_at	AGATTCATGCGATCCAGTCTGTATA	SEQ ID NO:770
WBC001D02_V1.3_at	CTGTGATGACCGAGAAGCCTTTCTT	SEQ ID NO:771
WBC001D02_V1.3_at	GAACACGGAATAAACTCCCACTGCA	SEQ ID NO:772
WBC001D02_V1.3_at	GGCTGCCCATCTGTAGATAGCTGTA	SEQ ID NO:773
WBC001D02_V1.3_at	GGCTCCTTTGGATATTCTGTGATGA	SEQ ID NO:774

Probe Set Name	Sequence	Sequence Identifier
WBC001D02_V1.3_at	TGCACATCCTGTCTACACCATAAGT	SEQ ID NO:775
WBC001D02_V1.3_at	TTGCCTTATACCTTTACGCGAACAC	SEQ ID NO:776
WBC001D02_V1.3_at	TTGTCTTTCATGCTGTGAGGCTCCT	SEQ ID NO:777
Homo sapiens protein tyrosine phosphatase type IVA, member 2		
WBC001F10_V1.3_at	ATCAGTGCCTGCCTGCGTTAGGAGA	SEQ ID NO:778
WBC001F10_V1.3_at	AGAACTGGATTTTCTTCCTCAAAAT	SEQ ID NO:779
WBC001F10_V1.3_at	AAACTTTTCCCTTTGACATGCTCTG	SEQ ID NO:780
WBC001F10_V1.3_at	CAGCATGTCCTGTAAGCTCAGATAG	SEQ ID NO:781
WBC001F10_V1.3_at	CATGCTCTGATTTTTGTTGTTTGGG	SEQ ID NO:782
WBC001F10_V1.3_at	GACTCCAAGGGTTTTGATCAGTATC	SEQ ID NO:783
WBC001F10_V1.3_at	GATAGACTCTGTTGACTCCAAGGGT	SEQ ID NO:784
WBC001F10_V1.3_at	GTGTGCAGCCTGATTTAAAACCAAC	SEQ ID NO:785
WBC001F10_V1.3_at	GTGTGTGCGGTGTCCACCAGTATCA	SEQ ID NO:786
WBC001F10_V1.3_at	GGAGAATTACATTCCTGGTTCTGTA	SEQ ID NO:787
WBC001F10_V1.3_at	TTGCTAGCTGAAGCCAGTTTGACAT	SEQ ID NO:788
Homo sapiens retinoblastoma-like 2 (p130), mRNA		
WBC001F11_V1.3_at	ATTAAGAGGGATCAGCTGGCTAAGT	SEQ ID NO:789
WBC001F11_V1.3_at	ATATCTTTGAGTGTGTTCCTGGCAG	SEQ ID NO:790
WBC001F11_V1.3_at	ATCTTCTTTGATGCTTTTGTACTTT	SEQ ID NO:791
WBC001F11_V1.3_at	TTGTTAAAGCCCCAGTAGCCACCTT	SEQ ID NO:792
WBC001F11_V1.3_at	AAATTATGACCTCTTCCTTTAGGAG	SEQ ID NO:793
WBC001F11_V1.3_at	AAACCTCTCAGATACTGCTACTGTA	SEQ ID NO:794
WBC001F11_V1.3_at	GCTATTGTTCCAGCAGTTTTAACGT	SEQ ID NO:795
WBC001F11_V1.3_at	GAAATTCTCCAGTTTTTGATTATTA	SEQ ID NO:796
WBC001F11_V1.3_at	GTAGCCACCTTTTGGGCATATTTGA	SEQ ID NO:797
WBC001F11_V1.3_at	TACTAGGTAACTTCACATTGCTCTG	SEQ ID NO:798
WBC001F11_V1.3_at	TATACACCTTTATTAATCGCTATTG	SEQ ID NO:799
Homo sapiens TRAF-interacting protein with a forkhead-associated domain, mRNA (cDNA clone MGC:20791 IMAGE:4763971)		
WBC004E04_V1.3_at	ACGAAGTGGTGTGCCGGTACTGATC	SEQ ID NO:800
WBC004E04_V1.3_at	CAACGGTCATTTGTTTTCAAGGTCA	SEQ ID NO:801
WBC004E04_V1.3_at	ACTAGTGTTGTAGCCTGTTGGTACT	SEQ ID NO:802
WBC004E04_V1.3_at	AAGGAACTCTCTCTTGGTTTGGTCA	SEQ ID NO:803
WBC004E04_V1.3_at	GTTAGTCATCGATTTGGTCTCCTGT	SEQ ID NO:804
WBC004E04_V1.3_at	GTACTTATAGTACCAGTGTCCTGGA	SEQ ID NO:805
WBC004E04_V1.3_at	GGTCATATTATTTCACAACGGTCAT	SEQ ID NO:806
WBC004E04_V1.3_at	TGTTATTGTTATCTGCTGTGCTGGC	SEQ ID NO:807
WBC004E04_V1.3_at	TCTCCTGTTGCATTCCTGGATGTAT	SEQ ID NO:808
WBC004E04_V1.3_at	TCCCCTTCGTTACTGTGGTATGTTA	SEQ ID NO:809
WBC004E04_V1.3_at	TAGACGCTCCGCTTACGAAGTGGTG	SEQ ID NO:810
Homo sapiens neural precursor cell expressed,		

Probe Set Name	Sequence	Sequence Identifier
developmentally down-regulated 1		
WBC004G01_V1.3_at	ATTCTTTGTGTGCTGTGTGTATTAT	SEQ ID NO:811
WBC004G01_V1.3_at	AACTATACCTTGTATACCGCACTCC	SEQ ID NO:812
WBC004G01_V1.3_at	AAGTGTGTTTGCCTACATGCTGTAT	SEQ ID NO:813
WBC004G01_V1.3_at	CTTCTTGTAGTCTCTTCTTCCAAAG	SEQ ID NO:814
WBC004G01_V1.3_at	CTGCCCCATTTTGACTTCTGAGATG	SEQ ID NO:815
WBC004G01_V1.3_at	GCCTTTTTCTATACATGCACTTAAC	SEQ ID NO:816
WBC004G01_V1.3_at	GATCCATTATTATTTTCCTATTGCC	SEQ ID NO:817
WBC004G01_V1.3_at	GTGATCTGCAGCTTCAGTGGTGTAA	SEQ ID NO:818
WBC004G01_V1.3_at	GTGTACATCTGCTTGTGTGATCTGC	SEQ ID NO:819
WBC004G01_V1.3_at	GTGCTAATGTGATCTTTCTCCTGAC	SEQ ID NO:820
WBC004G01_V1.3_at	TACTGGCGTGTTTACCTTCTTGTAG	SEQ ID NO:821
No homology		
WBC004G09_V1.3_at	TCACCAGTCAGTTGCTCACAAAGTC	SEQ ID NO:822
WBC004G09_V1.3_at	ATGCAGATCATACCACCCCAAAGTA	SEQ ID NO:823
WBC004G09_V1.3_at	AGTATTTTAATTGCACCTTAGTGAA	SEQ ID NO:824
WBC004G09_V1.3_at	AAGGTAACTTGTCCAAAGCCAGAAT	SEQ ID NO:825
WBC004G09_V1.3_at	AAAACTAGTATGCTGGCTTGAAATA	SEQ ID NO:826
WBC004G09_V1.3_at	AAGAATCTAGACTTCACCAGTCAGT	SEQ ID NO:827
WBC004G09_V1.3_at	CTTTACACTGTTACCTGCTTAGGAA	SEQ ID NO:828
WBC004G09_V1.3_at	GAGGGAGATAATAGCCCTCCCACCA	SEQ ID NO:829
WBC004G09_V1.3_at	GTTTGAACAGTTGTGTCCAGATTGA	SEQ ID NO:830
WBC004G09_V1.3_at	TACCACCCCAAAGTAGCTCTTTAAT	SEQ ID NO:831
WBC004G09_V1.3_at	TACTGGAATCCTTTACACTGTTACC	SEQ ID NO:832
No homology		
WBC005D09_V1.3_at	AAATCACTTTTCTTTCCCACTGACT	SEQ ID NO:833
WBC005D09_V1.3_at	CACTGACTGTTTTTTCTGCTTGTTG	SEQ ID NO:834
WBC005D09_V1.3_at	CTTGTGGGTATTGCTGTCTTGTTTT	SEQ ID NO:835
WBC005D09_V1.3_at	CTGCCCATTGGCCTGAAAATACTCA	SEQ ID NO:836
WBC005D09_V1.3_at	CTCCTTATCGCTTACAGTGTTCTTA	SEQ ID NO:837
WBC005D09_V1.3_at	GAATGAAATTTCCTACGCACTACTG	SEQ ID NO:838
WBC005D09_V1.3_at	GAGAACCTCGTGTCTGTTCTGATTC	SEQ ID NO:839
WBC005D09_V1.3_at	GATATGTTCTTGTATTGACTGCCCA	SEQ ID NO:840
WBC005D09_V1.3_at	TCCTTCCCTGATGCTAAATTTCCAA	SEQ ID NO:841
WBC005D09_V1.3_at	TAAGGTCCCTTCTAACTTTCATGTC	SEQ ID NO:842
WBC005D09_V1.3_at	TTAGGCAATCTTTCTTCTCCTTATC	SEQ ID NO:843
No homology		
WBC005E06_V1.3_at	ATTAGCTCTGTGGTGTCAGGCTCTA	SEQ ID NO:844
WBC005E06_V1.3_at	AGTGCATCTGTGTATCCTGGTTTAA	SEQ ID NO:845
WBC005E06_V1.3_at	AGCCATTTAAGGGTGGACCTCCACG	SEQ ID NO:846
WBC005E06_V1.3_at	AGCCTTTTCAGCCTCCATTTTGAAG	SEQ ID NO:847
WBC005E06_V1.3_at	AAGAGGACCTCTGACTTGCTTGAGA	SEQ ID NO:848

Probe Set Name	Sequence	Sequence Identifier
WBC005E06_V1.3_at	CAGGCTCTAGAGTTACTTCTTGTCA	SEQ ID NO:849
WBC005E06_V1.3_at	GCATAGTTTGCAGCCGTGTGGTAGT	SEQ ID NO:850
WBC005E06_V1.3_at	GAAAATTAGCTCTCTGCCATGGTTT	SEQ ID NO:851
WBC005E06_V1.3_at	GAGTTCTGTCAGACTTTTCCTTTTT	SEQ ID NO:852
WBC005E06_V1.3_at	GATTGTTCCTTGCATTTCTGAGTAT	SEQ ID NO:853
WBC005E06_V1.3_at	GGACCTCCACGACGATTCTGAAAAT	SEQ ID NO:854
Homo sapiens vaccinia related kinase 2, mRNA (cDNA clone MGC:34431 IMAGE:5221315).		
WBC005F01_V1.3_at	AGTCCAGGACCATACAGCTTCACAG	SEQ ID NO:855
WBC005F01_V1.3_at	CAACCTACCAACACTGAATCATCAT	SEQ ID NO:856
WBC005F01_V1.3_at	GAAACCCATCCAGATTTTACCAGTG	SEQ ID NO:857
WBC005F01_V1.3_at	GTTCTACAGGATTTTGGCTTACTCA	SEQ ID NO:858
WBC005F01_V1.3_at	GTGGCATACAATTCCCAAATTCATT	SEQ ID NO:859
WBC005F01_V1.3_at	GGTATACATATGCTTCTACGCCTGG	SEQ ID NO:860
WBC005F01_V1.3_at	GGCAGATGTGTATTATTATGGCTTC	SEQ ID NO:861
WBC005F01_V1.3_at	GGCTTCATCATTCTTTTTCTTTTGG	SEQ ID NO:862
WBC005F01_V1.3_at	GGCTTACTCAGTTTGCTCTTAGTGA	SEQ ID NO:863
WBC005F01_V1.3_at	TGTCTTGCTTTATATTTTCTCTGAA	SEQ ID NO:864
WBC005F01_V1.3_at	TTCTACGCCTGGTATGGAGGTCACA	SEQ ID NO:865
Polymeric immunoglobulin receptor 3 precursor (PIGR3)		
WBC005F10_V1.3_at	TTTCGACTGGCGCAACGTTTGGTAA	SEQ ID NO:866
WBC005F10_V1.3_at	ATAACTTTTGTACCGTGCCCTCTAT	SEQ ID NO:867
WBC005F10_V1.3_at	AGTGGTTAAGGCTTCCTATCCAGAA	SEQ ID NO:868
WBC005F10_V1.3_at	AGCCCAGCTTCCTGAGTACCAATAA	SEQ ID NO:869
WBC005F10_V1.3_at	CAGTGACTGACCCATATGTAGCAAA	SEQ ID NO:870
WBC005F10_V1.3_at	GCCTGCAGCGTGAGAAGACTTCCCA	SEQ ID NO:871
WBC005F10_V1.3_at	GCTGCTCACTCACTGTGGGATGTTA	SEQ ID NO:872
WBC005F10_V1.3_at	GATAATACCCACTTTCTAGGATTGT	SEQ ID NO:873
WBC005F10_V1.3_at	GATGTTATGAAAGCGACCCTTCCAA	SEQ ID NO:874
WBC005F10_V1.3_at	TAACGTTTGACCCTGAGGCCCAGAG	SEQ ID NO:875
WBC005F10_V1.3_at	TTCCTTCTGGATCGTTTCTCCAAGA	SEQ ID NO:876
No Homology		
WBC007A08_V1.3_at	ATGTATGAGACAGCTTCCTCCATTG	SEQ ID NO:877
WBC007A08_V1.3_at	AGTGCCCTTTCAGTATACCGTGTTG	SEQ ID NO:878
WBC007A08_V1.3_at	AAATGCTTTCTCTGTGCTTTCGTTA	SEQ ID NO:879
WBC007A08_V1.3_at	AAACAAATCTCTTCTACCAGCTTGC	SEQ ID NO:880
WBC007A08_V1.3_at	AATCCAGGTCTTCTGATTCTCATTC	SEQ ID NO:881
WBC007A08_V1.3_at	AATCAGTCGAGGTCAGCAGTTTGTA	SEQ ID NO:882
WBC007A08_V1.3_at	GCTTGCACTCAGACCAACTTGGAAA	SEQ ID NO:883
WBC007A08_V1.3_at	GAATTGTTGTTCTTCCTCTTTCCTA	SEQ ID NO:884
WBC007A08_V1.3_at	GAGCCCTCTGTCTGTGTTTTCATCA	SEQ ID NO:885
WBC007A08_V1.3_at	GATTGCAGCTCCTTATTTACTGGAA	SEQ ID NO:886

Probe Set Name	Sequence	Sequence Identifier
WBC007A08_V1.3_at	GTATACCGTGTTGCCTCTAAAGATT	SEQ ID NO:887
Homo sapiens mRNA for enolase 1 variant, clone: adSE00169		
WBC007F03_V1.3_at	ATTGTCATCTCTGAGGTGTCCACAG	SEQ ID NO:888
WBC007F03_V1.3_at	AGGTCCCCAGAGGTTTTGTGTGCAA	SEQ ID NO:889
WBC007F03_V1.3_at	AAATCATTGTTTTTCTCACCTCGCT	SEQ ID NO:890
WBC007F03_V1.3_at	GAAACCCTGGCTCTGTAATCATGTG	SEQ ID NO:891
WBC007F03_V1.3_at	GATCAAGACTGGTGCACCTTGCCGA	SEQ ID NO:892
WBC007F03_V1.3_at	GTCTGGAGCCGTGTGTTGTATCTAC	SEQ ID NO:893
WBC007F03_V1.3_at	GGTAGTTGTTAACTGGCCTCTCCTA	SEQ ID NO:894
WBC007F03_V1.3_at	GGCCAAGTACAACCAGATCCTCAGA	SEQ ID NO:895
WBC007F03_V1.3_at	TGCAGTCACTGGTCAGCTCATTAGA	SEQ ID NO:896
WBC007F03_V1.3_at	TTTGCCGGCAGGAACTTCAGAAACC	SEQ ID NO:897
WBC007F03_V1.3_at	TACTGTTCTCACTGCTTCCTTAGAA	SEQ ID NO:898
Homo sapiens matrix metalloproteinase 8 (neutrophil collagenase) (MMP8), mRNA.		
WBC008A10_V1.3_at	AAAGCTATGTGCAAGTCCCAACCTC	SEQ ID NO:899
WBC008A10_V1.3_at	AAATCTGGTGCTATTTTCCACTCTT	SEQ ID NO:900
WBC008A10_V1.3_at	AAACACGTTTTAAGGCTATCTGCTA	SEQ ID NO:901
WBC008A10_V1.3_at	AAGAACATGGCTCTTCTGACGCCTT	SEQ ID NO:902
WBC008A10_V1.3_at	AAGGAAGGATCCTCCCTAGAGCCTT	SEQ ID NO:903
WBC008A10_V1.3_at	CCAACCTCGGGTACCTATGAATGTA	SEQ ID NO:904
WBC008A10_V1.3_at	GCTCCTATATTCCAAAGTCTCTTTA	SEQ ID NO:905
WBC008A10_V1.3_at	GATAGTACTCCTTGCGTTTATTGAA	SEQ ID NO:906
WBC008A10_V1.3_at	GTGAGTTGAATTGTGTTCCCCAAAA	SEQ ID NO:907
WBC008A10_V1.3_at	TGACGCCTTGATTTTGCACTCACAG	SEQ ID NO:908
WBC008A10_V1.3_at	TTCGTCACCTCTCTATTCATTATTT	SEQ ID NO:909
Homo sapiens cDNA FLJ33312 fis, clone BNGH42005968, weakly similar to DIPZ PROTEIN.		
WBC008A12_V1.3_at	ATCTGTCAGCGTGTTTCTTTACTAC	SEQ ID NO:910
WBC008A12_V1.3_at	AGTGGCTGCATCTCCAGGACAGACT	SEQ ID NO:911
WBC008A12_V1.3_at	GAAGACATTACCCAGACTACCTAAA	SEQ ID NO:912
WBC008A12_V1.3_at	AAGCTGAGATTAGACCTCCCATCGG	SEQ ID NO:913
WBC008A12_V1.3_at	GTAGCGCAGACAGCAGTGCCTGTAT	SEQ ID NO:914
WBC008A12_V1.3_at	GTAGATGGCCCATTCCCAGAAGAAA	SEQ ID NO:915
WBC008A12_V1.3_at	GGAATTTTGTTCAGTCAGCCTTTAC	SEQ ID NO:916
WBC008A12_V1.3_at	GGAGCACCCAGTTGCTGGTTTCTAA	SEQ ID NO:917
WBC008A12_V1.3_at	TGCTGAGTTCTAGCCACTGATCTTA	SEQ ID NO:918
WBC008A12_V1.3_at	TAGAGAGCATTTCCAATCAACCCAC	SEQ ID NO:919
WBC008A12_V1.3_at	TTTATTTCTGCCTCTGGATACCAAG	SEQ ID NO:920
Homo sapiens cDNA: FLJ21472 fis, clone COL04936.		
WBC008D09_V1.3_at	ATTTCTACAAGTCAACCTCCAATTC	SEQ ID NO:921
WBC008D09_V1.3_at	AGTTTCACTGAGTTTGCTGGCTTTT	SEQ ID NO:922

Probe Set Name	Sequence	Sequence Identifier
WBC008D09_V1.3_at	AGCCTCCTACAGTGCTTTAGTCATA	SEQ ID NO:923
WBC008D09_V1.3_at	AAATGCTCATACATGTTCCCTTTTC	SEQ ID NO:924
WBC008D09_V1.3_at	CACATAATGCTTTCTTTTTGGTCTT	SEQ ID NO:925
WBC008D09_V1.3_at	CATCATCCATGCCTTATCAATTTCT	SEQ ID NO:926
WBC008D09_V1.3_at	GCTATGTGTGAAAGAGCCTCCTACA	SEQ ID NO:927
WBC008D09_V1.3_at	GAGCCTTAATTTCGTCCCTATTGAA	SEQ ID NO:928
WBC008D09_V1.3_at	TGCCTGCATAGACTTACCCAGATGT	SEQ ID NO:929
WBC008D09_V1.3_at	TATAAAACCGGTTAGTGTCCTACAG	SEQ ID NO:930
WBC008D09_V1.3_at	TATTTCCCAGGAGTCAGATGGCCCT	SEQ ID NO:931
Homo sapiens integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12), transcript variant 1A, mRNA (cDNA clone MGC:17220 IMAGE:3924411).		
WBC009F04_V1.3_at	ATCTTGGTAACTTTTATGCCTTCTT	SEQ ID NO:932
WBC009F04_V1.3_at	AGGCCTTAATTTCCATAGTACTTGC	SEQ ID NO:933
WBC009F04_V1.3_at	AGTGCCGTAATAGACCGCTGTATAG	SEQ ID NO:934
WBC009F04_V1.3_at	AGTTACTTCTCACTGTCAGAGCTGC	SEQ ID NO:935
WBC009F04_V1.3_at	ACCTGTGTGCCATTTTGAGAGTTAC	SEQ ID NO:936
WBC009F04_V1.3_at	AATTCGCCTCTTAGTGAACGTGTGA	SEQ ID NO:937
WBC009F04_V1.3_at	GCGACTCTTATTTTCAGGCAGTGCC	SEQ ID NO:938
WBC009F04_V1.3_at	TGAAGCCTGGTGCTTTTTACCACCT	SEQ ID NO:939
WBC009F04_V1.3_at	GGCTTACGCAACAGCTGTCACTTAA	SEQ ID NO:940
WBC009F04_V1.3_at	TTTCATACCAGTCACATCCTTGTTT	SEQ ID NO:941
WBC009F04_V1.3_at	TCAGAGCTGCCCATTTTGTTTCATA	SEQ ID NO:942
No Homology		
WBC009H07_V1.3_at	AGCATTTCATGTGTCTAGTGTGGCA	SEQ ID NO:943
WBC009H07_V1.3_at	AGCCACCCGATGTTGCGTTTGGAAG	SEQ ID NO:944
WBC009H07_V1.3_at	ACAGTATGGCTGTTTGCTTTGTCCT	SEQ ID NO:945
WBC009H07_V1.3_at	AAACTCGTTTTGCTTCTTTGTATAT	SEQ ID NO:946
WBC009H07_V1.3_at	CCAGGTGACATTCTTTCCAGGTACA	SEQ ID NO:947
WBC009H07_V1.3_at	GCCTTGGGTTTATTGTGCACAGTTT	SEQ ID NO:948
WBC009H07_V1.3_at	GCGAGATTTAGTACACCTGCACAGT	SEQ ID NO:949
WBC009H07_V1.3_at	GCACATCCTGTTCACCTGTTGGTGA	SEQ ID NO:950
WBC009H07_V1.3_at	GAAGTGTTTGTTGCTCCCGTTGGAG	SEQ ID NO:951
WBC009H07_V1.3_at	GGCGTTCTTAGAAAGTACCCTGTCT	SEQ ID NO:952
WBC009H07_V1.3_at	GGCATTTCTGGATGCGGCTGTCACA	SEQ ID NO:953
Homo sapiens nuclear autoantigen GS2NA mRNA.		
WBC011D03_V1.3_at	AAGTCAGATTTTTGCCCATAGTGGA	SEQ ID NO:954
WBC011D03_V1.3_at	AAGTGAGTCCATGACAGCTTCTCTG	SEQ ID NO:955
WBC011D03_V1.3_at	CACCTGCCGGGATTTCATACTTAAA	SEQ ID NO:956
WBC011D03_V1.3_at	AATTCACTCTCAGTTTGTAAGCCCC	SEQ ID NO:957
WBC011D03_V1.3_at	GCAGACCCTTCATATCTTGGATACG	SEQ ID NO:958
WBC011D03_V1.3_at	CTGCACACCTTACATTTCACAATTT	SEQ ID NO:959

Probe Set Name	Sequence	Sequence Identifier
WBC011D03_V1.3_at	CCCACGTCAGGATCATGTTTCTTTA	SEQ ID NO:960
WBC011D03_V1.3_at	GAAAAGCTACATGCCAACTACCAGA	SEQ ID NO:961
WBC011D03_V1.3_at	GTATGTATTACCTGTCTGTCGAGGA	SEQ ID NO:962
WBC011D03_V1.3_at	GTGACTGTTTGCTGTGTATGTGCCA	SEQ ID NO:963
WBC011D03_V1.3_at	GGAGATGCTGCATAAGGCCCCACGT	SEQ ID NO:964
No Homology		
WBC011F05_V1.3_at	ATAACCTGTTTCCTCTAAGATCTTG	SEQ ID NO:965
WBC011F05_V1.3_at	ACAGGGTGTTTCCACTTGTGTAGCA	SEQ ID NO:966
WBC011F05_V1.3_at	AAAACTCTACTAGGGCTCTTGCTGA	SEQ ID NO:967
WBC011F05_V1.3_at	AAAAGGCATCTTTGTTCTCAACAGA	SEQ ID NO:968
WBC011F05_V1.3_at	AAGCAGACGTCTCTGAGCGTTTCCA	SEQ ID NO:969
WBC011F05_V1.3_at	GAGCGTTTCCAGTGTTTTATCCAAA	SEQ ID NO:970
WBC011F05_V1.3_at	GCTGACTTCAGTGCCTTTTGTAAAT	SEQ ID NO:971
WBC011F05_V1.3_at	GAGATTCTTTCTCCTCGTTAAGTTT	SEQ ID NO:972
WBC011F05_V1.3_at	GAGGATGCCCAAGACCGAGCAACAG	SEQ ID NO:973
WBC011F05_V1.3_at	GATTTTCCTCAACTTGCTTTTTGGG	SEQ ID NO:974
WBC011F05_V1.3_at	TAAGATCTTGCTATACTGTCCTGTA	SEQ ID NO:975
No Homology		
WBC012A03_V1.3_at	ATCTATTTGGTTAGGCCTAGGCCAT	SEQ ID NO:976
WBC012A03_V1.3_at	ATCGCCCCTTTTTATTCAACATCTG	SEQ ID NO:977
WBC012A03_V1.3_at	AGTGCCCTGAGTGATGTCCAGTTCC	SEQ ID NO:978
WBC012A03_V1.3_at	AGTCCCCATATGTGTTAATGTCTCA	SEQ ID NO:979
WBC012A03_V1.3_at	AGCGTGGACTGTGCCTGAGACCGAC	SEQ ID NO:980
WBC012A03_V1.3_at	CTAGGCCATGCCTTGGCTGAGTATA	SEQ ID NO:981
WBC012A03_V1.3_at	GTCCAGTTCCATTAGACACTCTGTC	SEQ ID NO:982
WBC012A03_V1.3_at	GGTGACTGTGAGAAATCGCCCCTTT	SEQ ID NO:983
WBC012A03_V1.3_at	TGTACAGAGGCATTCAGCGTGGACT	SEQ ID NO:984
WBC012A03_V1.3_at	TAGTCTGTACGTGAACTGCTCCAAG	SEQ ID NO:985
WBC012A03_V1.3_at	TTTACTCTGTTAGGAATCTTCTCGA	SEQ ID NO:986
H.sapiens mRNA for inwardly rectifing potassium channel Kir4.2.		
WBC012C10_V1.3_at	AACGTCTGACGGCAGTGGTGTCACT	SEQ ID NO:987
WBC012C10_V1.3_at	CTTTTCCTTTGATCTGGTGGCTAAA	SEQ ID NO:988
WBC012C10_V1.3_at	GCATTTCCATGTTTGAGAGGCTTCC	SEQ ID NO:989
WBC012C10_V1.3_at	GCACCTTTTATTGCGCAGATGCTGA	SEQ ID NO:990
WBC012C10_V1.3_at	GAGGACCCTTTTGTTACAGCAGAGC	SEQ ID NO:991
WBC012C10_V1.3_at	GAGGCTTCCTTTTAAATGCTTTGTC	SEQ ID NO:992
WBC012C10_V1.3_at	GTGGATGCACTCTCAAAAAACCTCA	SEQ ID NO:993
WBC012C10_V1.3_at	GGAAGAGCCCGGACTGCACCTTTTA	SEQ ID NO:994
WBC012C10_V1.3_at	GGCTACAAACTTGATCTTTTCCTTT	SEQ ID NO:995
WBC012C10_V1.3_at	TGGTGTCACTGCTGTTTAACTCTGC	SEQ ID NO:996
WBC012C10_V1.3_at	TTAACTCTGCGAGCTGTTTCCACAT	SEQ ID NO:997

Probe Set Name	Sequence	Sequence Identifier
No homology.		
WBC012E05_V1.3_at	ATGTACCTGCTGATCATCACTGTGT	SEQ ID NO:998
WBC012E05_V1.3_at	AAATCTTTCAATAACCTGCCAGTGG	SEQ ID NO:999
WBC012E05_V1.3_at	GACCGTCCTGACTGTATATTTTCAA	SEQ ID NO:1000
WBC012E05_V1.3_at	GACGTTGTCTGTGATGGTGTCCACG	SEQ ID NO:1001
WBC012E05_V1.3_at	GAGATCATGCTTGCGTTACTAGGAC	SEQ ID NO:1002
WBC012E05_V1.3_at	GTCTGAGCCTCATGTACCTATTTGA	SEQ ID NO:1003
WBC012E05_V1.3_at	GTATTCTGACTCTAACATGGACTTT	SEQ ID NO:1004
WBC012E05_V1.3_at	GGATATGCTCACTGATCTGTGCTTA	SEQ ID NO:1005
WBC012E05_V1.3_at	TCAGCCTTGCTGGATTTGGAGTCTT	SEQ ID NO:1006
WBC012E05_V1.3_at	TTGTACATCTCACTGCTTAGCTTAG	SEQ ID NO:1007
WBC012E05_V1.3_at	TTCTCTTCAGGTGCAGCCTTACTGG	SEQ ID NO:1008
Homo sapiens sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase), transcript variant 2, mRNA		
WBC013A09_V1.3_at	AGCTCAGGCCCGATCTGCTTGGGAA	SEQ ID NO:1009
WBC013A09_V1.3_at	AGCCCATCTCTCTGAAGGGATTTAT	SEQ ID NO:1010
WBC013A09_V1.3_at	AATTCCTGGCTCTCTTTATGTTCTG	SEQ ID NO:1011
WBC013A09_V1.3_at	GCCGCTTACTGCTGCGTGAACTAAT	SEQ ID NO:1012
WBC013A09_V1.3_at	GAATTGCAGGAAAGCCCATCTCTCT	SEQ ID NO:1013
WBC013A09_V1.3_at	GAAGGTGGCATTCCATCAGCAGAAG	SEQ ID NO:1014
WBC013A09_V1.3_at	GTAGCCATCTATTCAGCCTATATCA	SEQ ID NO:1015
WBC013A09_V1.3_at	GTGAACTAATCTTTTCCACCTCTCT	SEQ ID NO:1016
WBC013A09_V1.3_at	TGGTGTGGGACCCTGAGACTACACT	SEQ ID NO:1017
WBC013A09_V1.3_at	TCATGATATCCTCTAATCCTTCCAA	SEQ ID NO:1018
WBC013A09_V1.3_at	TTAATTCTGTGCTCTCTCTATATGG	SEQ ID NO:1019
Homo sapiens nucleosome assembly protein 1-like 2 mRNA.		
WBC013A11_V1.3_at	ATCCTTGCTGCAGACTTTGAAATTG	SEQ ID NO:1020
WBC013A11_V1.3_at	AACAGTTTCCAATGACTCTTTCTTT	SEQ ID NO:1021
WBC013A11_V1.3_at	TACGTGAGCGTATAATCCCAAGATC	SEQ ID NO:1022
WBC013A11_V1.3_at	GATGCTGAAGCTATCCTTGCTGCAG	SEQ ID NO:1023
WBC013A11_V1.3_at	GATTCTGATCCCTTTTCTTTTGATG	SEQ ID NO:1024
WBC013A11_V1.3_at	GTTGTTGTTTGTTTGTTTGCTTGCT	SEQ ID NO:1025
WBC013A11_V1.3_at	GTGGGACAGTTCGTACTGTGACCAA	SEQ ID NO:1026
WBC013A11_V1.3_at	GGTCTTCTGCTTCCCTGGAAAGGAT	SEQ ID NO:1027
WBC013A11_V1.3_at	TGAGGATAACCTGCACTGGTCTTCT	SEQ ID NO:1028
WBC013A11_V1.3_at	TGCTTGCTTTTGTTTTTGCAGCCTA	SEQ ID NO:1029
WBC013A11_V1.3_at	TTGCCCCTCCTGAAGTTCCTGAGAG	SEQ ID NO:1030
Homo sapiens nucleosome assembly protein 1-like 2 mRNA.		
WBC013E05_V1.3_at	ATCCGAGCCCTACGCTCAGGTGGTG	SEQ ID NO:1031
WBC013E05_V1.3_at	AGGTGGTGCCTTAAGACGCCAAGGA	SEQ ID NO:1032
WBC013E05_V1.3_at	AGCTCTCATACTCTTCAGAATTCTC	SEQ ID NO:1033
WBC013E05_V1.3_at	AAGACTGATGATTCCTTCCTGAAGA	SEQ ID NO:1034

Probe Set Name	Sequence	Sequence Identifier
WBC013E05_V1.3_at	GATGATTCCTTCCTGAAGATCAGTT	SEQ ID NO:1035
WBC013E05_V1.3_at	TGTCTCCATGGAAGCAATAATTCTC	SEQ ID NO:1036
WBC013E05_V1.3_at	TGCTAGATGACCTCGCACTATTTAC	SEQ ID NO:1037
WBC013E05_V1.3_at	TAGGGACCTGATCCATGTCTCCATG	SEQ ID NO:1038
WBC013E05_V1.3_at	TAATCTCTAGGGACCTGATCCATGT	SEQ ID NO:1039
WBC013E05_V1.3_at	TACGCTCAGGTGGTGCCTTAAGACG	SEQ ID NO:1040
WBC013E05_V1.3_at	TTTTCCTCCCCAAGACTGATGATTC	SEQ ID NO:1041
Homo sapiens cDNA FLJ45679 fis, clone ERLTF2001835		
WBC013E10_V1.3_at	AGAGGATCTCTCTTTTGAAAAGCTA	SEQ ID NO:1042
WBC013E10_V1.3_at	AAGAACACTTACAGCTCATATACAG	SEQ ID NO:1043
WBC013E10_V1.3_at	AAGGAGTTTCCTGTGGTTTCTGCCG	SEQ ID NO:1044
WBC013E10_V1.3_at	CGACTATTACTTTCTCTCAAGTGCC	SEQ ID NO:1045
WBC013E10_V1.3_at	GAATATGTTCTCCTTTGTAGCCTCT	SEQ ID NO:1046
WBC013E10_V1.3_at	GAAAAACACAGCTTAGCCCCTTCCT	SEQ ID NO:1047
WBC013E10_V1.3_at	GTAGAATGACACCAAAGCTGCAACT	SEQ ID NO:1048
WBC013E10_V1.3_at	GGAAATCAGTCAGTACCATCGTTAA	SEQ ID NO:1049
WBC013E10_V1.3_at	TTGTAGCCTCTTGACAAAGCAGGAA	SEQ ID NO:1050
WBC013E10_V1.3_at	TTGTCCACTGAAACTTTGCTAACGT	SEQ ID NO:1051
WBC013E10_V1.3_at	TTCCTCTAGCCTTCAGTCAATTTTT	SEQ ID NO:1052
No Homology		
WBC014E06_V1.3_at	ATGTATGCGTGAGAAGGCCCCGTGA	SEQ ID NO:1053
WBC014E06_V1.3_at	ATTTATTTTTGGTTCTCTGCTGTAA	SEQ ID NO:1054
WBC014E06_V1.3_at	AGGCCCCGTGATATAATAGTGCTTA	SEQ ID NO:1055
WBC014E06_V1.3_at	ACCACACTTCTGTTGTCTTTTCAAA	SEQ ID NO:1056
WBC014E06_V1.3_at	GTTACCTGCCTCCAGAGTTCTAAAA	SEQ ID NO:1057
WBC014E06_V1.3_at	GTATGCTCAGCACCTAATGCACATA	SEQ ID NO:1058
WBC014E06_V1.3_at	GTATTTTCAAACAGCTTTTCAGGAT	SEQ ID NO:1059
WBC014E06_V1.3_at	TCTGTTGTAATTGCGTGTCTGTCCT	SEQ ID NO:1060
WBC014E06_V1.3_at	TAAAATCACCTTTACTGACGGTTGT	SEQ ID NO:1061
WBC014E06_V1.3_at	TAGTGCTTAGCATTCTCTGTTGTAA	SEQ ID NO:1062
WBC014E06_V1.3_at	TTTCCTCTTGTCCTTAAACTCCATA	SEQ ID NO:1063
Homo sapiens purinergic receptor P2Y, G-protein coupled, 13, transcript variant 2		
WBC014H06_V1.3_at	CTAACATTTGTATGGACCCCTTCAT	SEQ ID NO:1064
WBC014H06_V1.3_at	CAGCAGGACTGATTGCCGGGTGCAA	SEQ ID NO:1065
WBC014H06_V1.3_at	ACCGTTTTTGTCCTAATGCTTCTGT	SEQ ID NO:1066
WBC014H06_V1.3_at	ACCTCTCTGCCAAACGTGATCTTAA	SEQ ID NO:1067
WBC014H06_V1.3_at	AAATCACACCATCCAGACTGACAAT	SEQ ID NO:1068
WBC014H06_V1.3_at	AACAACTCTCTTTTTGGCAGCAACT	SEQ ID NO:1069
WBC014H06_V1.3_at	AAGCCACACCGTCGTCTGTGAGAAA	SEQ ID NO:1070
WBC014H06_V1.3_at	CTTTGCTCCATTTCATTTTGCCAGA	SEQ ID NO:1071
WBC014H06_V1.3_at	GAGAAAGTGCGCCTCCTTAAAGGGT	SEQ ID NO:1072

Probe Set Name	Sequence	Sequence Identifier
WBC014H06_V1.3_at	GCTTCTGTTTTATGTGGTGATCGCA	SEQ ID NO:1073
WBC014H06_V1.3_at	TAAAGTGTTCGTTGTGGTGGCCGTC	SEQ ID NO:1074
Homo sapiens copine III		
WBC015B08_V1.3_at	ATAGTGTGCAGTTAGCGTGGTCCCC	SEQ ID NO:1075
WBC015B08_V1.3_at	AGGCTCTTCTGTGCTTCTATGATAT	SEQ ID NO:1076
WBC015B08_V1.3_at	AGTGCCTTGTTCTGATTTTTGTTCT	SEQ ID NO:1077
WBC015B08_V1.3_at	AGAGGCAGCCTTTCCAGAGCAAATC	SEQ ID NO:1078
WBC015B08_V1.3_at	AAGTCGTCACGATCGCGAGAGTTGA	SEQ ID NO:1079
WBC015B08_V1.3_at	CTGTCTCTTTATGTGTGCGGTTTAT	SEQ ID NO:1080
WBC015B08_V1.3_at	CCCGCTGCCTGTACTGAATAGTGTG	SEQ ID NO:1081
WBC015B08_V1.3_at	GTATCTTCCGTTTGAATTCCCTTTG	SEQ ID NO:1082
WBC015B08_V1.3_at	GTGCCTGGGCAGATGTAGTTTCTCC	SEQ ID NO:1083
WBC015B08_V1.3_at	TGCTTTGCCTTTTTCGTTCTGTAAA	SEQ ID NO:1084
WBC015B08_V1.3_at	TTTAATAAACTCCTCCTGTCTCTTT	SEQ ID NO:1085
No Homology		
WBC016A12_V1.3_at	ATGCAGATCAGATGGCGTTTCTCCC	SEQ ID NO:1086
WBC016A12_V1.3_at	ACGTGTTCAGACTTGTGTTTTCATA	SEQ ID NO:1087
WBC016A12_V1.3_at	AAGTATGGGCTGTTTCACGTGTTCA	SEQ ID NO:1088
WBC016A12_V1.3_at	GACTATGTACTGTCCACCTGCATTA	SEQ ID NO:1089
WBC016A12_V1.3_at	GATTGATTTCCTACTAGTCTTTGAC	SEQ ID NO:1090
WBC016A12_V1.3_at	GTTTCTCCCAGCTCAGTGGATTTTC	SEQ ID NO:1091
WBC016A12_V1.3_at	GGAGCCTGGCTTATTTGATTGATTT	SEQ ID NO:1092
WBC016A12_V1.3_at	GGAAGTCCCTGTTCTGACTATGTAC	SEQ ID NO:1093
WBC016A12_V1.3_at	TCCCTTCATTCTGGTTTCCATGTGA	SEQ ID NO:1094
WBC016A12_V1.3_at	TCACCAACTCCCTTTTGGATTTCAT	SEQ ID NO:1095
WBC016A12_V1.3_at	TAAACAACCATGTCTGCATCTAGGG	SEQ ID NO:1096
Homo sapiens mRNA for HsMcm6.		
WBC016G11_V1.3_at	ATGATGTGTGTATCTTCCTGGGAAA	SEQ ID NO:1097
WBC016G11_V1.3_at	ACTGTGCTGCTTTTCATGTGTAGGA	SEQ ID NO:1098
WBC016G11_V1.3_at	GAATGCTTCTGGGAGTGATGCTTCA	SEQ ID NO:1099
WBC016G11_V1.3_at	GAAGAAGATCCCTACCTGGTGGTTA	SEQ ID NO:1100
WBC016G11_V1.3_at	GAGTCTGCATGGAGCTCTCCTAGAG	SEQ ID NO:1101
WBC016G11_V1.3_at	GTTAACCCTAACTACCTGCTTGAAG	SEQ ID NO:1102
WBC016G11_V1.3_at	GTTTCTGTCATACGCTTTTATACCA	SEQ ID NO:1103
WBC016G11_V1.3_at	GGATGGTTGTGTCATGTTTCTGTCA	SEQ ID NO:1104
WBC016G11_V1.3_at	GGCTTTAGCCCTTTGTTTACTGTGC	SEQ ID NO:1105
WBC016G11_V1.3_at	TCACCCACTACGATCATGTTCTAAT	SEQ ID NO:1106
WBC016G11_V1.3_at	TAACCCGAGAAACTGCAGCCTGCTG	SEQ ID NO:1107
Homo sapiens G protein-coupled receptor 155		
WBC017B09_V1.3_at	AGGAGACCTTCCGAGTTACAGCAAC	SEQ ID NO:1108
WBC017B09_V1.3_at	ACACACGTCCTGTTATGTGCATGAA	SEQ ID NO:1109
WBC017B09_V1.3_at	AAAGCCTCGTTGCTGTACCAGGAGA	SEQ ID NO:1110

Probe Set Name	Sequence	Sequence Identifier
WBC017B09_V1.3_at	AAACCTGCATGGAAGCCTAGTGTAT	SEQ ID NO:1111
WBC017B09_V1.3_at	GAATCGGAACATCTTTTCCCATGGG	SEQ ID NO:1112
WBC017B09_V1.3_at	GATGCTTTCAGCAGAACTGTCTTGC	SEQ ID NO:1113
WBC017B09_V1.3_at	GTAACTTTTACTCCTCTTGACAAGC	SEQ ID NO:1114
WBC017B09_V1.3_at	TGTCCACACTGTAACTCTCATTATG	SEQ ID NO:1115
WBC017B09_V1.3_at	TGCAGGCACCTCAGACTCAAGTGGA	SEQ ID NO:1116
WBC017B09_V1.3_at	TTGATTCACATGCATGCAGGCACCT	SEQ ID NO:1117
WBC017B09_V1.3_at	TTGCTGCGGCACTTTGTTTTAACAT	SEQ ID NO:1118
No homology		
WBC017C08_V1.3_at	ATGCTACCTTTTTAGGTTGTCCTGA	SEQ ID NO:1119
WBC017C08_V1.3_at	AAGTTGGTACAGTTATTTTCCTCAT	SEQ ID NO:1120
WBC017C08_V1.3_at	AATACCCGTATTTTAGTTGTCATAG	SEQ ID NO:1121
WBC017C08_V1.3_at	CGGTGTGACTTTGCTTAGGTTTCTC	SEQ ID NO:1122
WBC017C08_V1.3_at	GCCATCTTTGGCCAAGTGTTAGGAG	SEQ ID NO:1123
WBC017C08_V1.3_at	GAGTTTTGGCTTTGTAGTCAGGCAA	SEQ ID NO:1124
WBC017C08_V1.3_at	GTCAGGCAAGCCTATGTTGGGTCCT	SEQ ID NO:1125
WBC017C08_V1.3_at	GTGTATTCTCTTACTCTTGAGCTTT	SEQ ID NO:1126
WBC017C08_V1.3_at	GGCTGTTGCCACTTAATAGCGGTGT	SEQ ID NO:1127
WBC017C08_V1.3_at	TGAGCCTCATTATCCACATCTGTAA	SEQ ID NO:1128
WBC017C08_V1.3_at	TTAGGTTTCTCAACTTCGCTGAGCC	SEQ ID NO:1129
Human transcriptional repressor (CTCF) mRNA.		
WBC018B05_V1.3_at	ATTATGAGCGGGTCACAGCAGCCCT	SEQ ID NO:1130
WBC018B05_V1.3_at	ATCATGTAGCAGAACGGCACCCAGA	SEQ ID NO:1131
WBC018B05_V1.3_at	AGAGCCTCAGTCTTGCTGATTTCAA	SEQ ID NO:1132
WBC018B05_V1.3_at	GCCATCAGTTAGCTATCAGACTCTA	SEQ ID NO:1133
WBC018B05_V1.3_at	GCGGAGCCAGCATTTGAACCTTGTA	SEQ ID NO:1134
WBC018B05_V1.3_at	GACATTTTCTTTGCTCTGTTTGTAG	SEQ ID NO:1135
WBC018B05_V1.3_at	GAGATCGTGAATTCCAGCCCGCGGA	SEQ ID NO:1136
WBC018B05_V1.3_at	GATTCTTGCACATGAACTGTCACAC	SEQ ID NO:1137
WBC018B05_V1.3_at	GTTTGTGTTCTGTAAATCCTCTGTT	SEQ ID NO:1138
WBC018B05_V1.3_at	GGAGGATCTACTGCTGTACAGCTAA	SEQ ID NO:1139
WBC018B05_V1.3_at	TGATTTCCCATCGACATTTTCTTTG	SEQ ID NO:1140
No homology		
WBC018D03_V1.3_at	ATGTCTTGGATTGCACTTTCGTGGA	SEQ ID NO:1141
WBC018D03_V1.3_at	AGTTGGTGGCTCCAGTTTGCTTTTC	SEQ ID NO:1142
WBC018D03_V1.3_at	AGCAGCCTTGGTCGTTTTCGTTGGA	SEQ ID NO:1143
WBC018D03_V1.3_at	AGCTCATCTCAATGTCCTGTTGACT	SEQ ID NO:1144
WBC018D03_V1.3_at	GGTTTTGATTCCTCTGCTAGGACGC	SEQ ID NO:1145
WBC018D03_V1.3_at	GAAATCTTTGGTTTTGTCCTGTGAG	SEQ ID NO:1146
WBC018D03_V1.3_at	GTAGATCACCGAAACTAACTTGCTG	SEQ ID NO:1147
WBC018D03_V1.3_at	GTCCTGTGAGACCAGTGCTTGACAT	SEQ ID NO:1148
WBC018D03_V1.3_at	TGCTTGACATCGTCTGTTCGCCTGA	SEQ ID NO:1149

Probe Set Name	Sequence	Sequence Identifier
WBC018D03_V1.3_at	TAGGACGCTGCCTAAACCAGCTCAT	SEQ ID NO:1150
WBC018D03_V1.3_at	TTTCTCTTCGGTCTCGTGGTAGCAG	SEQ ID NO:1151
Human mRNA for integrin alpha-4 subunit		
WBC018F03_V1.3_at	AATTTAACCTCACTGGATTGGCACC	SEQ ID NO:1152
WBC018F03_V1.3_at	ATCAGGGCATTCTTATGTGAACTTG	SEQ ID NO:1153
WBC018F03_V1.3_at	ATTAGGCCAGATTCTGCCCAGTTAG	SEQ ID NO:1154
WBC018F03_V1.3_at	AGATTGCTGGATAACATGACTTTCA	SEQ ID NO:1155
WBC018F03_V1.3_at	AAATGATGGCATTTCAGATTGCTGG	SEQ ID NO:1156
WBC018F03_V1.3_at	GCCCAGTTAGATATTTTGCACAGTT	SEQ ID NO:1157
WBC018F03_V1.3_at	GAACACAGCTCCCAATTAGGCCAGA	SEQ ID NO:1158
WBC018F03_V1.3_at	GTACCTGCAATGTTTACTTTCAGTT	SEQ ID NO:1159
WBC018F03_V1.3_at	GGAACATTAGTTCTTTCTTATTCAG	SEQ ID NO:1160
WBC018F03_V1.3_at	TTGGCACCTCCCCAGGAAAATCAGG	SEQ ID NO:1161
WBC018F03_V1.3_at	TTGTGGTTTGTCTGTACCAGGCCAT	SEQ ID NO:1162
No Homology		
WBC019B05_V1.3_at	ATATATGCTGTCTGTTTTGTGTACA	SEQ ID NO:1163
WBC019B05_V1.3_at	AACTCACTCTTACAGTAGTCTGCTT	SEQ ID NO:1164
WBC019B05_V1.3_at	AATGTTGTCTTTTAAATACTCCGAT	SEQ ID NO:1165
WBC019B05_V1.3_at	CAAGCCATTTGTGGGAATCCTAAAA	SEQ ID NO:1166
WBC019B05_V1.3_at	CCAGCTGTTTATTTTATTGAGTCCT	SEQ ID NO:1167
WBC019B05_V1.3_at	GAGTAACAAACTCAGCCTTCTGTAA	SEQ ID NO:1168
WBC019B05_V1.3_at	GAGGATCATCTGACTTTTCACTTAC	SEQ ID NO:1169
WBC019B05_V1.3_at	GTAGTCTGCTTATTTCCAGCTGTTT	SEQ ID NO:1170
WBC019B05_V1.3_at	GTGCTTTATGTACTGTTATCCTATA	SEQ ID NO:1171
WBC019B05_V1.3_at	TGTAAAAACTCCTTTTCTGCCACAC	SEQ ID NO:1172
WBC019B05_V1.3_at	TTGGGTTTTCTTTTCAACTCACTCT	SEQ ID NO:1173
Human proline-rich protein (PRP) mRNA.		
WBC019C11_V1.3_at	ATGTAAAGCTCTGTGTCCGAAACCA	SEQ ID NO:1174
WBC019C11_V1.3_at	AGTTTATCCACTTTACCATCTCTTT	SEQ ID NO:1175
WBC019C11_V1.3_at	AAAAATCATGCAGTGTCTCCCAAAG	SEQ ID NO:1176
WBC019C11_V1.3_at	GCTGTATAAGCTGTCTCTGGAGATC	SEQ ID NO:1177
WBC019C11_V1.3_at	GAAAAATGTACCTTGCTGCCTTCAA	SEQ ID NO:1178
WBC019C11_V1.3_at	GACGGCTGTCTGTGGTTAAGGATCA	SEQ ID NO:1179
WBC019C11_V1.3_at	GTGACATGTTTTTGCTTTCCTGGAC	SEQ ID NO:1180
WBC019C11_V1.3_at	GGTTGGTCTCCAAAGTATCACTTGC	SEQ ID NO:1181
WBC019C11_V1.3_at	TGAGAACGGCCCTGGAGCTGTATAA	SEQ ID NO:1182
WBC019C11_V1.3_at	TGACCCTCACTATCGTTTGGTTGGT	SEQ ID NO:1183
WBC019C11_V1.3_at	TTTTGTGCCATCACTCCTGGTAATA	SEQ ID NO:1184
Human translation initiation factor 3 large subunit mRNA.		
WBC020F05_V1.3_at	ATGACCGTCGTCGTGAGCGAGATGA	SEQ ID NO:1185
WBC020F05_V1.3_at	ATGGATGGACCACGGTACGACGTTA	SEQ ID NO:1186

Probe Set Name	Sequence	Sequence Identifier
WBC020F05_V1.3_at	AGATTGATCATGCACCGTATCCACA	SEQ ID NO:1187
WBC020F05_V1.3_at	AGTTCTTGGAGACGTGCTGATGACA	SEQ ID NO:1188
WBC020F05_V1.3_at	ACATAGGTTTGATCACATTCGCGGA	SEQ ID NO:1189
WBC020F05_V1.3_at	AAGAGGACCTCCTTTGAGATCAGAA	SEQ ID NO:1190
WBC020F05_V1.3_at	CGCGGATTATTAGACTTGTGCTTCA	SEQ ID NO:1191
WBC020F05_V1.3_at	GAGAGATTCGAGTCGCCGTGACGAT	SEQ ID NO:1192
WBC020F05_V1.3_at	GATAGGGAATCTCTTCGTCGTACTA	SEQ ID NO:1193
WBC020F05_V1.3_at	GGATTCTTTAATGTTGTCTCACCAT	SEQ ID NO:1194
WBC020F05_V1.3_at	TGGGTTCGAACTCATGTGTCACATA	SEQ ID NO:1195
Human CSaids binding protein (CSBP1) mRNA		
WBC020H01_V1.3_at	ATGGCAATCACAGCTCGCCTGGGAT	SEQ ID NO:1196
WBC020H01_V1.3_at	AGGTCAAATCCTCACGATGCACAGC	SEQ ID NO:1197
WBC020H01_V1.3_at	ACAGTGCGGTGATGCATGCGCTCCA	SEQ ID NO:1198
WBC020H01_V1.3_at	AAAGCTACTTCCAGTGTTGGCTATG	SEQ ID NO:1199
WBC020H01_V1.3_at	AAGGCCTCATCTCCTTTATATGCAG	SEQ ID NO:1200
WBC020H01_V1.3_at	AAGGTGTTTCCATTTCTCCATCACA	SEQ ID NO:1201
WBC020H01_V1.3_at	CATCTCCTGATTTCTCTGAACGGAA	SEQ ID NO:1202
WBC020H01_V1.3_at	CTGAACTCAGCTGGAGCCTGTGGAA	SEQ ID NO:1203
WBC020H01_V1.3_at	GAAGAGCTCCTTGGTTTCTGAGCAT	SEQ ID NO:1204
WBC020H01_V1.3_at	GACCCTGGGTCAACTGGAGTGAGAA	SEQ ID NO:1205
WBC020H01_V1.3_at	GAGGGCCCACATATTTAAATCTTCT	SEQ ID NO:1206
No homology		
WBC021E02_V1.3_at	TGATCGTTCACAAGCGTACTCACGC	SEQ ID NO:1207
WBC021E02_V1.3_at	GCAGTTTTTTGTACTTGATCGTTCA	SEQ ID NO:1208
WBC021E02_V1.3_at	GAATGTGGTAAAGCCCTCAGTTGTC	SEQ ID NO:1209
WBC021E02_V1.3_at	GTACTCACGCTGGAGAGAAACCTTA	SEQ ID NO:1210
WBC021E02_V1.3_at	GAACCACACTGGAGAGATGCTCTAG	SEQ ID NO:1211
WBC021E02_V1.3_at	GAAACATGGGAAGCCCTTCACTGTT	SEQ ID NO:1212
WBC021E02_V1.3_at	GAGAATCTCATCACAACCTGGCATG	SEQ ID NO:1213
WBC021E02_V1.3_at	GTACCATGAAAGCACTTACCTGCAG	SEQ ID NO:1214
WBC021E02_V1.3_at	TCAGTTGTCCCAATTCACTTTGAAG	SEQ ID NO:1215
WBC021E02_V1.3_at	TTCCCATTTCCTTTTGGTACCATGA	SEQ ID NO:1216
WBC021E02_V1.3_at	TTACCTGCAGAGAAATCCTGTCAGT	SEQ ID NO:1217
No homology		
WBC021E07_V1.3_at	AGTTCCCCTTCAAGGAGCCAGAGAG	SEQ ID NO:1218
WBC021E07_V1.3_at	ACCAGCAGCTGGAAGCACCAAGTAT	SEQ ID NO:1219
WBC021E07_V1.3_at	AACACACTGATTTCTTCTTGGGTCC	SEQ ID NO:1220
WBC021E07_V1.3_at	CTGAGCTTCAGCACACTGGCAGAGA	SEQ ID NO:1221
WBC021E07_V1.3_at	CGATCAGAGCTGTCCCTCAAGGAGG	SEQ ID NO:1222
WBC021E07_V1.3_at	GAGTTTTATCAGCAGAATTCCCTAA	SEQ ID NO:1223
WBC021E07_V1.3_at	GAGGAGAAACTCCAGGCTCTGAGCC	SEQ ID NO:1224
WBC021E07_V1.3_at	GATTATTCTGAATACTGCTGAGCTT	SEQ ID NO:1225

Probe Set Name	Sequence	Sequence Identifier
WBC021E07_V1.3_at	GATTGTTTCAAGTCGCTGGACACCA	SEQ ID NO:1226
WBC021E07_V1.3_at	GGGTGATGCCTTGTCATGGTTAATT	SEQ ID NO:1227
WBC021E07_V1.3_at	GGAGAGCCATTAGCAAACCAGCAGC	SEQ ID NO:1228
Homo sapiens T-cell receptor interacting molecule, mRNA (cDNA clone MGC:34314 IMAGE:5227396).		
WBC022B03_V1.3_at	AGAGTGTCCGTTTGTACACGCCAAA	SEQ ID NO:1229
WBC022B03_V1.3_at	AGATGAGCAGTTACACGCGACGGAT	SEQ ID NO:1230
WBC022B03_V1.3_at	CTGGACTCTGATCTAGCTCAATGAT	SEQ ID NO:1231
WBC022B03_V1.3_at	GCCTTTCTATGACTGCTTTGGTTGA	SEQ ID NO:1232
WBC022B03_V1.3_at	GAACCTATGAACTAGCTGGACTCTG	SEQ ID NO:1233
WBC022B03_V1.3_at	GAAACACGATCCTTATTTGCCAGAC	SEQ ID NO:1234
WBC022B03_V1.3_at	GAAATTCCCATATGACACACTGTGA	SEQ ID NO:1235
WBC022B03_V1.3_at	GACAGCCTGATCGTTTGTTGGTGAG	SEQ ID NO:1236
WBC022B03_V1.3_at	GTTGATAGTTTTGCACCTGAGGACC	SEQ ID NO:1237
WBC022B03_V1.3_at	TGAGATGGTGACTTTCCTCTTATCC	SEQ ID NO:1238
WBC022B03_V1.3_at	TGATGATCCCATCAGGCTGTTCGGA	SEQ ID NO:1239
PREDICTED: Bos taurus similar to Caspase recruitment domain protein 8 (Apoptotic protein NDPP1) (DACAR) (CARD-inhibitor of NF-kappaB activating ligand) (CARDINAL) (Tumor-upregulated CARD-containing antagonist of CASP9) (TUCAN) (LOC511229), partial mRNA		
WBC022C04_V1.3_at	AGCCCATTGGCTCTTATTAATCAGT	SEQ ID NO:1240
WBC022C04_V1.3_at	AGAACGGTGATCTCTTCTTGAGGAA	SEQ ID NO:1241
WBC022C04_V1.3_at	AACTATAGCTTTGCCTGTGAAGAAC	SEQ ID NO:1242
WBC022C04_V1.3_at	TAGCCTTAGCCGCACCAAGGGAGAA	SEQ ID NO:1243
WBC022C04_V1.3_at	CCATTAGTCTTCTGTAGGTGTTAGC	SEQ ID NO:1244
WBC022C04_V1.3_at	CCAGGGAATATCGAGCCCATTGGCT	SEQ ID NO:1245
WBC022C04_V1.3_at	TAAGCTGGTTTCCTAACATTTTCAA	SEQ ID NO:1246
WBC022C04_V1.3_at	GTCAGGGATCCTGTGGAGTTCAAAT	SEQ ID NO:1247
WBC022C04_V1.3_at	GATCATTTGCTCCACTCAGAGGTAG	SEQ ID NO:1248
WBC022C04_V1.3_at	GTAGATGTTATCATTCTCCCAGAAT	SEQ ID NO:1249
WBC022C04_V1.3_at	TTTTCAACCTTGCTCATACTCTGGA	SEQ ID NO:1250
No homology		
WBC022D03_V1.3_at	AGGGACGATACTTCTTACTGTTGTT	SEQ ID NO:1251
WBC022D03_V1.3_at	AGCAGTTTATGTGGTTGATTCTCAA	SEQ ID NO:1252
WBC022D03_V1.3_at	ACGCTGGATTGTAGTCTGTTTACTT	SEQ ID NO:1253
WBC022D03_V1.3_at	AACAGTGGTCTCTTTGACAAGGCAT	SEQ ID NO:1254
WBC022D03_V1.3_at	CTTCTTACTGTTGTTGACGCTGGAT	SEQ ID NO:1255
WBC022D03_V1.3_at	GCAGGGTGATGCTGTCTGGTCTTCA	SEQ ID NO:1256
WBC022D03_V1.3_at	GACTGTATCTTATCCACCATTGTAT	SEQ ID NO:1257
WBC022D03_V1.3_at	TTTATCCTAACAGTGGCCCTTTGCA	SEQ ID NO:1258
WBC022D03_V1.3_at	TGTTTACTTGTCTTTCTCTTTCGTA	SEQ ID NO:1259
WBC022D03_V1.3_at	TCTTCAGCTCTTCACACTTACTTAA	SEQ ID NO:1260
WBC022D03_V1.3_at	TTAAGACCTGGCCTTGACTGAATTT	SEQ ID NO:1261

Probe Set Name	Sequence	Sequence Identifier
No homology		
WBC023F12_V1.3_at	GACCGTAAAACTATGTTCAGGCACT	SEQ ID NO:1262
WBC023F12_V1.3_at	AATACCAGCAAGTCATGTCTTGTGT	SEQ ID NO:1263
WBC023F12_V1.3_at	AATTGATTGCTGACTTGACCTGCCT	SEQ ID NO:1264
WBC023F12_V1.3_at	GACCTGCCTGGTCAAATATCTGAAT	SEQ ID NO:1265
WBC023F12_V1.3_at	GATGGCATTACTGGGTAGATTCTAA	SEQ ID NO:1266
WBC023F12_V1.3_at	GATTCTAACCCATGATTCTAACTGT	SEQ ID NO:1267
WBC023F12_V1.3_at	GTTACAGTTCAAATTGTCCCACTTC	SEQ ID NO:1268
WBC023F12_V1.3_at	GTATTACCCTCTATCATAACACACT	SEQ ID NO:1269
WBC023F12_V1.3_at	GTAACTATTGTTGCTATTCATGTAA	SEQ ID NO:1270
WBC023F12_V1.3_at	TACTGTATCAGCTGTAGTTGGGTGA	SEQ ID NO:1271
WBC023F12_V1.3_at	TTCAGGCACTTACTCTTCGTTTATA	SEQ ID NO:1272
Adducin 3 (gamma) (ADD3), transcript variant 2		
WBC024B05_V1.3_at	ATGAACCTCTGTGTCCTGTGGAAAA	SEQ ID NO:1273
WBC024B05_V1.3_at	ATGAGCCAATGAACCTCTGTGTCCT	SEQ ID NO:1274
WBC024B05_V1.3_at	AGTGAACTATTTGCACCTTTTGCTA	SEQ ID NO:1275
WBC024B05_V1.3_at	CACCTTTTGCTAATGCCTCTATTTA	SEQ ID NO:1276
WBC024B05_V1.3_at	CAGTGTTTTAATCTCTTAGTGGAAA	SEQ ID NO:1277
WBC024B05_V1.3_at	CTGGTTCTGTTTGGCGTATGTGTAT	SEQ ID NO:1278
WBC024B05_V1.3_at	GCCTCTATTTACTTGCTTTGGCATA	SEQ ID NO:1279
WBC024B05_V1.3_at	GATCTCACTAACTACTGGAATCAGT	SEQ ID NO:1280
WBC024B05_V1.3_at	GTAACCTGTGAACTATGCTTTTCCA	SEQ ID NO:1281
WBC024B05_V1.3_at	GGAAACTCTCAGTTGCTTAATTCTG	SEQ ID NO:1282
WBC024B05_V1.3_at	GGAAATTTCATTTTAGATCTCACTA	SEQ ID NO:1283
No homology		
WBC024F08_V1.3_at	ATGTGTGTCTCTATGTACCCAAGCC	SEQ ID NO:1284
WBC024F08_V1.3_at	AGCTCTGCAAGTCACTTACCTGAAG	SEQ ID NO:1285
WBC024F08_V1.3_at	AGACTCAGGGATGCTGTTTCCAGCT	SEQ ID NO:1286
WBC024F08_V1.3_at	AGCGTGTGTCTACATGTGTGTCTCT	SEQ ID NO:1287
WBC024F08_V1.3_at	AAGCACAGTGTCTCTCGAATTTCGG	SEQ ID NO:1288
WBC024F08_V1.3_at	GAGAGGCGAGCATCTGGCTGTACTT	SEQ ID NO:1289
WBC024F08_V1.3_at	GTACCCTCCTCACATTTTTGCATAT	SEQ ID NO:1290
WBC024F08_V1.3_at	GGTGGCCACCTGCATGAGTGTATTA	SEQ ID NO:1291
WBC024F08_V1.3_at	GGATGCATTCTCTTGTTTTGCTTGA	SEQ ID NO:1292
WBC024F08_V1.3_at	TGAGTCCTGTGAGATGCCCTTGTTA	SEQ ID NO:1293
WBC024F08_V1.3_at	TCTGGTTCTCTCTCTCAGGAATAAG	SEQ ID NO:1294
Horse serpin mRNA.		
WBC024G03_V1.3_at	AGTAAAGCACCCCAATTAAGGCCTG	SEQ ID NO:1295
WBC024G03_V1.3_at	AAAATGCTGCATTTTCTTGCTCCCA	SEQ ID NO:1296
WBC024G03_V1.3_at	CCAGCTTCTTGCGTTTTCTGATGAA	SEQ ID NO:1297
WBC024G03_V1.3_at	GACAAACTCGTCTTGACCGTTGTTT	SEQ ID NO:1298
WBC024G03_V1.3_at	GTTGTTACACCAGTGCGATGGCTTT	SEQ ID NO:1299

Probe Set Name	Sequence	Sequence Identifier
WBC024G03_V1.3_at	GGCACAAAGATCTCACTGTTACCCA	SEQ ID NO:1300
WBC024G03_V1.3_at	TAGGGCAGCACTCCAATTTCAAACT	SEQ ID NO:1301
WBC024G03_V1.3_at	TTTTGTTCTCCTTTATCCTACCTGA	SEQ ID NO:1302
WBC024G03_V1.3_at	TTCAAACTGTTAGCCACCTGGTGAT	SEQ ID NO:1303
WBC024G03_V1.3_at	TTGTTTCTAACCCTTTGTTCCACAG	SEQ ID NO:1304
WBC024G03_V1.3_at	TTGCTCCCACAAAGCTGGTATGCTG	SEQ ID NO:1305
No homology		
WBC024G08_V1.3_at	AGTGAACTTGTCCTTGCCAGATGGG	SEQ ID NO:1306
WBC024G08_V1.3_at	ACTCAGCAGTGAGTTGCCTGTGGCT	SEQ ID NO:1307
WBC024G08_V1.3_at	AAATAAGTGCATTCTCCTCAGAGGA	SEQ ID NO:1308
WBC024G08_V1.3_at	CTCCATGCCTTCAACTCAACAAATG	SEQ ID NO:1309
WBC024G08_V1.3_at	GCTGGAAACAAGCTGTGCCTTCAAA	SEQ ID NO:1310
WBC024G08_V1.3_at	GCCTATGTAGGCCTTTTCTGCAGAA	SEQ ID NO:1311
WBC024G08_V1.3_at	GTCTTTAAGCATCTTCAGCTCTGAT	SEQ ID NO:1312
WBC024G08_V1.3_at	GGGCTTTTTGTTCAGTCTGTATCAG	SEQ ID NO:1313
WBC024G08_V1.3_at	GGAAACTATTTCTAACATCTGGTGA	SEQ ID NO:1314
WBC024G08_V1.3_at	TGGCTGTCTTTTCTTGTATTCTGTA	SEQ ID NO:1315
WBC024G08_V1.3_at	TCAGAACAGCGTTTGTGCTCCATGC	SEQ ID NO:1316
Homo sapiens interferon gamma receptor 2 (interferon gamma transducer 1), mRNA		
WBC024H07_V1.3_at	ATTTTGTTCATTGTCGGTTGGGCCA	SEQ ID NO:1317
WBC024H07_V1.3_at	ATTTTCTCAATCATACACGTCGTTA	SEQ ID NO:1318
WBC024H07_V1.3_at	AGGCAGGTCACCTAATCTGTCTCAG	SEQ ID NO:1319
WBC024H07_V1.3_at	AGGACTGAGCTCCTGAAGCTGCTGA	SEQ ID NO:1320
WBC024H07_V1.3_at	CCAGTCTCCCAGCTTAAAACGTGAT	SEQ ID NO:1321
WBC024H07_V1.3_at	AAATGGCTCTGGCACACCTGTGATA	SEQ ID NO:1322
WBC024H07_V1.3_at	GAAGCTGCTGATGTCCCTGTCAGGA	SEQ ID NO:1323
WBC024H07_V1.3_at	GAAGATGTTCTCCAAAGCACTTTGA	SEQ ID NO:1324
WBC024H07_V1.3_at	GAAGCAAAGCATTGGCCTGCTCCAC	SEQ ID NO:1325
WBC024H07_V1.3_at	GTGTCTGTCGTTGTGTTTCCAGAGA	SEQ ID NO:1326
WBC024H07_V1.3_at	TGTCAGGACTTTACGGAGCCCACTA	SEQ ID NO:1327
No homology		
WBC025A06_V1.3_at	ATCGTGTCAGCACAGAAACCTTCTC	SEQ ID NO:1328
WBC025A06_V1.3_at	AGAGAATTAGTCACTGGGCCAGGCG	SEQ ID NO:1329
WBC025A06_V1.3_at	ACAATTCAGAAGTGTCCAGCCCAGC	SEQ ID NO:1330
WBC025A06_V1.3_at	AACCTTCTCAGGTACAGGCTTTGTT	SEQ ID NO:1331
WBC025A06_V1.3_at	GCTTCCCACGGAACTGAGCAGAGAA	SEQ ID NO:1332
WBC025A06_V1.3_at	GAAGGGCAGCCCACTGGCATCGTGT	SEQ ID NO:1333
WBC025A06_V1.3_at	GGTGTGAAAGACTCCTGCTATTATA	SEQ ID NO:1334
WBC025A06_V1.3_at	TGTGTCGGTTACCACTCAAGACGCA	SEQ ID NO:1335
WBC025A06_V1.3_at	TCCAGTGTGGTGGTTAGTCTGCCTT	SEQ ID NO:1336
WBC025A06_V1.3_at	TATTATAAGCACTCAGTCCGCTTCC	SEQ ID NO:1337

Probe Set Name	Sequence	Sequence Identifier
WBC025A06_V1.3_at	TTGCGGTTCTGGACTTTGTTTTTAT	SEQ ID NO:1338
Homo sapiens TBP-interacting protein, mRNA		
WBC025C03_V1.3_at	AGTTCCAGTCGCAGATCAGCTCCAA	SEQ ID NO:1339
WBC025C03_V1.3_at	AGATGTTTGCTCCATACGGGACCAT	SEQ ID NO:1340
WBC025C03_V1.3_at	AGAGCCCGCTGATGAGCGAGTTCCA	SEQ ID NO:1341
WBC025C03_V1.3_at	AGACAGTTTGGCTTTCTTCCATTGT	SEQ ID NO:1342
WBC025C03_V1.3_at	AACTGAAGCGATCGGCCATGAGAGC	SEQ ID NO:1343
WBC025C03_V1.3_at	GAAAGACTCATCGTCCACTAACTTG	SEQ ID NO:1344
WBC025C03_V1.3_at	GGGACCATTACGTTGACCATACGAT	SEQ ID NO:1345
WBC025C03_V1.3_at	GTGTATTTCCATAATCCAGAGGTTG	SEQ ID NO:1346
WBC025C03_V1.3_at	GGTCCAGTATCTATTTGCCCTGTAA	SEQ ID NO:1347
WBC025C03_V1.3_at	GGCAGCCATCTTTGAGAGCATCCAG	SEQ ID NO:1348
WBC025C03_V1.3_at	TGACCATTCCCGAGGCCGAGAAGAG	SEQ ID NO:1349
No Homology.		
WBC027B01_V1.3_at	ATCTTGGCACCTTGCTCTTTTAGAA	SEQ ID NO:1350
WBC027B01_V1.3_at	AAAATACATTGCTCACCTTTCCTGT	SEQ ID NO:1351
WBC027B01_V1.3_at	AACTCTAGAACTCTCAGACGCTGCG	SEQ ID NO:1352
WBC027B01_V1.3_at	GATTCTCAGGGAAACTCCGACTGGA	SEQ ID NO:1353
WBC027B01_V1.3_at	GCTAGATTTCAAAGGCTCGCTTCGC	SEQ ID NO:1354
WBC027B01_V1.3_at	CTGGATTTATTTTTCTACCTGTGTA	SEQ ID NO:1355
WBC027B01_V1.3_at	GCTGGTGCTCTATAGTTTTGTTCTC	SEQ ID NO:1356
WBC027B01_V1.3_at	GTAAAATCCTGTCAGACCACCGATA	SEQ ID NO:1357
WBC027B01_V1.3_at	GTACATCTAGTTCCTCACCATAGAA	SEQ ID NO:1358
WBC027B01_V1.3_at	TCGCTTCGCAAAAATACTCCATCTT	SEQ ID NO:1359
WBC027B01_V1.3_at	TTCAGCCCCTGAAGCTTGCTAATAT	SEQ ID NO:1360
No homology		
WBC027D09_V1.3_at	ATTTTTGCTGCCATACACTAACTCA	SEQ ID NO:1361
WBC027D09_V1.3_at	ATTTTGCCTGCACTCTTCATTCTTA	SEQ ID NO:1362
WBC027D09_V1.3_at	GAAACTTATGGAATGTGACCCTGAT	SEQ ID NO:1363
WBC027D09_V1.3_at	GAGGATGCCACAGAGGTTTGCAAGA	SEQ ID NO:1364
WBC027D09_V1.3_at	GATGTGTGGCAAATACTCAATGTTA	SEQ ID NO:1365
WBC027D09_V1.3_at	GTGTTATTGCATTAGCTCCCTTCGA	SEQ ID NO:1366
WBC027D09_V1.3_at	GGAGCTACTTCACAATTTTGCCTGC	SEQ ID NO:1367
WBC027D09_V1.3_at	TGGAAGCACCAAATACTGTCTTATT	SEQ ID NO:1368
WBC027D09_V1.3_at	TTCGATGGGCATCTCTATGAATTAG	SEQ ID NO:1369
WBC027D09_V1.3_at	TAACCCCTTGCACCATGACTGATGT	SEQ ID NO:1370
WBC027D09_V1.3_at	TTGTGATCACTCTTTCTGACGCATA	SEQ ID NO:1371
Homo sapiens collagenase mRNA.		
WBC027F05_V1.3_at	ATACTGGGCTCTGAATGGCTATGAC	SEQ ID NO:1372
WBC027F05_V1.3_at	ATGACATTCAGCAAGGTTATCCCAA	SEQ ID NO:1373
WBC027F05_V1.3_at	AGATGACTTCTTTCTTTTCTTCAGC	SEQ ID NO:1374
WBC027F05_V1.3_at	AGCATAGCAAGTACCTTTCCAGGAA	SEQ ID NO:1375

Probe Set Name	Sequence	Sequence Identifier
WBC027F05_V1.3_at	AATTTCATTTCTCTGTTCTGGCCAT	SEQ ID NO:1376
WBC027F05_V1.3_at	CTTCCCAAGCAGTGTCCAAGCAATT	SEQ ID NO:1377
WBC027F05_V1.3_at	TCAGCGGACCAGTTTATTATGCATT	SEQ ID NO:1378
WBC027F05_V1.3_at	GAAGCAGGTTATCCCCAAAGCATAG	SEQ ID NO:1379
WBC027F05_V1.3_at	GACATATCAAACTACGGCTTCCCAA	SEQ ID NO:1380
WBC027F05_V1.3_at	TGATGCAGCTGTTTCCTATAGGAGT	SEQ ID NO:1381
WBC027F05_V1.3_at	TTTCTCTCCTGTGTTCCATTAGGTA	SEQ ID NO:1382
Homo sapiens ribosomal protein S8, mRNA (cDNA clone MGC:90249 IMAGE:6527505).		
WBC027H11_V1.3_at	ATGTATCGCTTCCAGACCAGGCCAG	SEQ ID NO:1383
WBC027H11_V1.3_at	AGGCAAATAAGTCCCTCTGGTCCTA	SEQ ID NO:1384
WBC027H11_V1.3_at	AGGGCAAGCTTCTCGCATGTATCGC	SEQ ID NO:1385
WBC027H11_V1.3_at	AAAATCAGCAGTCTCCTGGAGGAGC	SEQ ID NO:1386
WBC027H11_V1.3_at	AAGACCCTGGTGAAGAACTGCATCG	SEQ ID NO:1387
WBC027H11_V1.3_at	CAGACGGCTATGTGCTCGAGGGCAA	SEQ ID NO:1388
WBC027H11_V1.3_at	GAAAGCCCTACCACAAGAAGCGGAA	SEQ ID NO:1389
WBC027H11_V1.3_at	GAACTGCATCGTGCTGGTTGACAGC	SEQ ID NO:1390
WBC027H11_V1.3_at	GGCAAGGAGCTGGAGTTCTATCTGA	SEQ ID NO:1391
WBC027H11_V1.3_at	GGAGCAGTTCCAGCAGGGCAAGCTT	SEQ ID NO:1392
WBC027H11_V1.3_at	GGCTCCGAGTGCTGTACGCGCAAAA	SEQ ID NO:1393
Homo sapiens hypothetical protein FLJ25421, mRNA (cDNA clone MGC:33348 IMAGE:4831324).		
WBC028D04_V1.3_at	GTGGTAAGACCTCAAACTGCAAGTG	SEQ ID NO:1394
WBC028D04_V1.3_at	ACAAGCCTTTGCCTTGACTGAGGAG	SEQ ID NO:1395
WBC028D04_V1.3_at	AAATCTTTCTTTTCTTGTGGATGAC	SEQ ID NO:1396
WBC028D04_V1.3_at	AAGCCCTTTATTTTACAACTCTGTG	SEQ ID NO:1397
WBC028D04_V1.3_at	AACTCTGTGGAGCTTCATTATTAAC	SEQ ID NO:1398
WBC028D04_V1.3_at	GATGGTTTGATTTCTCTTTGTCAGG	SEQ ID NO:1399
WBC028D04_V1.3_at	GTACGTGTCACATGTTCTCGTGTCG	SEQ ID NO:1400
WBC028D04_V1.3_at	GTGACTATTGCAGAGCCTTTGGATA	SEQ ID NO:1401
WBC028D04_V1.3_at	TCGTGTCGGGTTTCAGGCTCTGCAA	SEQ ID NO:1402
WBC028D04_V1.3_at	TCATGCTCTGTACTTGACCTCAAAA	SEQ ID NO:1403
WBC028D04_V1.3_at	TATAGATTCTCATCACTGTGGCGAA	SEQ ID NO:1404
Homo sapiens regulator of G-protein signaling 13 mRNA.		
WBC028E11_V1.3_at	ATTCAGGAAGTATTCCGCCAGCCAT	SEQ ID NO:1405
WBC028E11_V1.3_at	ATCACAGTCTTCTTCCGAATCTGAT	SEQ ID NO:1406
WBC028E11_V1.3_at	AAAGATGCCATACATTTGCCTTTGG	SEQ ID NO:1407
WBC028E11_V1.3_at	GAGGCATAGCTCCACGTTAGGACTG	SEQ ID NO:1408
WBC028E11_V1.3_at	GAGTAATTAGCCCTCGTCTTTGGAC	SEQ ID NO:1409
WBC028E11_V1.3_at	GAGATAGCGGCAGTCAGTCATTTGA	SEQ ID NO:1410
WBC028E11_V1.3_at	GTCCACATTTGGGTTCATTCCTAAG	SEQ ID NO:1411
WBC028E11_V1.3_at	GGACTTACCCAGTTATACGGAGCAC	SEQ ID NO:1412
WBC028E11_V1.3_at	TGGTCACGGAAACATGCCCAGATGA	SEQ ID NO:1413

Probe Set Name	Sequence	Sequence Identifier
WBC028E11_V1.3_at	TGCCGCATTGGCTCATATTCAGGAA	SEQ ID NO:1414
WBC028E11_V1.3_at	TTTGAGGTCCTAGCGATCAGGCATC	SEQ ID NO:1415
Homo sapiens mRNA for KIAA1689 protein, partial cds		
WBC028G09_V1.3_at	CTCCTGAACACTTACGTCTTAGCAA	SEQ ID NO:1416
WBC028G09_V1.3_at	ACACCTGTGTTTAATCTGATTCATG	SEQ ID NO:1417
WBC028G09_V1.3_at	AACTTTGTTAACATCCGTCTCTTGC	SEQ ID NO:1418
WBC028G09_V1.3_at	AATCATGTTATCTTTGGGCAGTCGT	SEQ ID NO:1419
WBC028G09_V1.3_at	CGTCTCTTGCACATCTACAACAAAT	SEQ ID NO:1420
WBC028G09_V1.3_at	GCATTCGAGAATCAAGTCAGCCAGA	SEQ ID NO:1421
WBC028G09_V1.3_at	GACCATGTATACTCTCTTGCTTGAA	SEQ ID NO:1422
WBC028G09_V1.3_at	TGGAGAGACCTGTTCACACCTGTGT	SEQ ID NO:1423
WBC028G09_V1.3_at	TGGGCAGTCGTTGCATTCGAGAATC	SEQ ID NO:1424
WBC028G09_V1.3_at	TGAATATCCACTGTTTACCACCATG	SEQ ID NO:1425
WBC028G09_V1.3_at	TTTTCTTGGCTTTTCCTCCTGAACA	SEQ ID NO:1426
Homo sapiens protein associated with Myc mRNA.		
WBC030C11_V1.3_at	ATTACCGTCATTGGCCTGTGAAGCA	SEQ ID NO:1427
WBC030C11_V1.3_at	AGTGCAATACTGAGTGTGCCTCATT	SEQ ID NO:1428
WBC030C11_V1.3_at	AATCCTGTACAATTGCATCACGGGT	SEQ ID NO:1429
WBC030C11_V1.3_at	CGGGACCATTTTGACATCCATGAAA	SEQ ID NO:1430
WBC030C11_V1.3_at	GAATATTCTGGTTTATTTCCTAGAC	SEQ ID NO:1431
WBC030C11_V1.3_at	GAAGGATGCCAAATACCATGTACAT	SEQ ID NO:1432
WBC030C11_V1.3_at	GAATGATGCTGGCTTTCAAGCAAAA	SEQ ID NO:1433
WBC030C11_V1.3_at	GTATACTACCTTTTTGTAATCCTGT	SEQ ID NO:1434
WBC030C11_V1.3_at	GTGCCTCATTATCTTGCAGCTGTAA	SEQ ID NO:1435
WBC030C11_V1.3_at	GTGTTTGCATGTGGCCATTACCGTC	SEQ ID NO:1436
WBC030C11_V1.3_at	TCCCCATTATTTCGGTTTATCTTCT	SEQ ID NO:1437
Homo sapiens progestin and adipoQ receptor family member XI (PAQR11)		
WBC031B06_V1.3_at	ATAAATGAGCAGACCCTGCCTTTGG	SEQ ID NO:1438
WBC031B06_V1.3_at	AGATGCCTGTTGTTTTATTGTGTAT	SEQ ID NO:1439
WBC031B06_V1.3_at	AGAAACTCATGCATCTGTGGTCCAT	SEQ ID NO:1440
WBC031B06_V1.3_at	CACCGCTATCTGCATGATTCTGAAC	SEQ ID NO:1441
WBC031B06_V1.3_at	CTGCCTTTGGATTGGGTGCTGATAA	SEQ ID NO:1442
WBC031B06_V1.3_at	GAAGTCTGCTCAAAGTAACCTGTCA	SEQ ID NO:1443
WBC031B06_V1.3_at	GATTAATCTCCTCTTGGTGTTTTGA	SEQ ID NO:1444
WBC031B06_V1.3_at	GTTTCCCCTCAGTGTCTTATATTAA	SEQ ID NO:1445
WBC031B06_V1.3_at	GGGTGCTGATAACGACTATTTTCTA	SEQ ID NO:1446
WBC031B06_V1.3_at	GGTCCATGGGTTATATCCTGGCTCA	SEQ ID NO:1447
WBC031B06_V1.3_at	TATTATTTTTGGTTTCCCCTCAGTG	SEQ ID NO:1448
Homo sapiens ribosomal protein L4, mRNA (cDNA clone MGC:87190 IMAGE:5259747).		
WBC031C11_V1.3_at	CGTGGGACGTTTTTGCATTTGGACT	SEQ ID NO:1449
WBC031C11_V1.3_at	GCTAAACCCGTATGCGAAGACCATG	SEQ ID NO:1450

Probe Set Name	Sequence	Sequence Identifier
WBC031C11_V1.3_at	AGGCCAAGAATCACAAACTCCGGGT	SEQ ID NO:1451
WBC031C11_V1.3_at	AGATGATCTTTATGGCACTTGGCGT	SEQ ID NO:1452
WBC031C11_V1.3_at	AGCCTGCTGCGTAAACTTGTTTGTT	SEQ ID NO:1453
WBC031C11_V1.3_at	AAGAGTAACTACAACCTTCCCATGC	SEQ ID NO:1454
WBC031C11_V1.3_at	AAGCGCTTTCCGCAAGTTAGATGAT	SEQ ID NO:1455
WBC031C11_V1.3_at	GAAGACCATGCGCAGGAACACCATT	SEQ ID NO:1456
WBC031C11_V1.3_at	GAAGATTCATCGCAGGGTCCTGAAG	SEQ ID NO:1457
WBC031C11_V1.3_at	GTAAAGCTGCTTCCCTCAAGAGTAA	SEQ ID NO:1458
WBC031C11_V1.3_at	GGTCACATCATTTTGGACAGCTCCT	SEQ ID NO:1459
Homo sapiens syntenin (sycl) mRNA.		
WBC031D02_V1.3_at	ATAGGACAAACTTCTGACTCCCTTC	SEQ ID NO:1460
WBC031D02_V1.3_at	AACCGTGCTACTTTGGCATGGTCAT	SEQ ID NO:1461
WBC031D02_V1.3_at	AAATGTAACTACTGCTGCCTTTCTG	SEQ ID NO:1462
WBC031D02_V1.3_at	AAATGTTCAGCAGCCCAGAGCAGTT	SEQ ID NO:1463
WBC031D02_V1.3_at	GAAACCCACCATGCAGTTCTGTATT	SEQ ID NO:1464
WBC031D02_V1.3_at	GACTCCCTTCTTTCATTTTTAGATT	SEQ ID NO:1465
WBC031D02_V1.3_at	GTTACTGGTATCACTTTCTGAGAAA	SEQ ID NO:1466
WBC031D02_V1.3_at	GGTAATTTGTTCCATGTCCTGACTC	SEQ ID NO:1467
WBC031D02_V1.3_at	GGCAGTGACACTTAACCTGATTTTT	SEQ ID NO:1468
WBC031D02_V1.3_at	TAATTTGGGCATTCTACTCTTAGCA	SEQ ID NO:1469
WBC031D02_V1.3_at	TAAACTGTCGCCTTAACTATGCTAA	SEQ ID NO:1470
Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 14, mRNA		
WBC031G11_V1.3_at	AAATGGAGATTGGACCCCGATCTTC	SEQ ID NO:1471
WBC031G11_V1.3_at	CCTCTGGTCATTGAGCCTTTGGATA	SEQ ID NO:1472
WBC031G11_V1.3_at	GTATTTTAGTTCTCAGTTCTCACCA	SEQ ID NO:1473
WBC031G11_V1.3_at	GAACAGGTGACTTTCCTCTAACTGT	SEQ ID NO:1474
WBC031G11_V1.3_at	GATCTTCCCTTTCTTGTATGTTGCT	SEQ ID NO:1475
WBC031G11_V1.3_at	GTGTGAGCTCAGGACATGTGGCCTC	SEQ ID NO:1476
WBC031G11_V1.3_at	GGTCATCTACTTTCCCAGTATTTTT	SEQ ID NO:1477
WBC031G11_V1.3_at	TTTTCCCGTTTCTCAGTGACCAGAT	SEQ ID NO:1478
WBC031G11_V1.3_at	TGCTTACACATTTCAGGCCCTTTAG	SEQ ID NO:1479
WBC031G11_V1.3_at	TTTACACTTGCTACAGGTCACGGAC	SEQ ID NO:1480
WBC031G11_V1.3_at	TTCTGGCTCCTCAAAAGCAGTGGGT	SEQ ID NO:1481
Homo sapiens hypothetical protein MGC12966, mRNA		
WBC032D03_V1.3_at	AGATACCGTGTCTTCAGACTGTCTC	SEQ ID NO:1482
WBC032D03_V1.3_at	AACCCTAGCAGCGTTGCCTGAGATA	SEQ ID NO:1483
WBC032D03_V1.3_at	GAGGCCCTACGGTGAAAGTTGCAAT	SEQ ID NO:1484
WBC032D03_V1.3_at	GCTGAATATTACTACACCGTGTGCT	SEQ ID NO:1485
WBC032D03_V1.3_at	GTATTCGTAAAAGTCAGCCCCTCGG	SEQ ID NO:1486
WBC032D03_V1.3_at	GTAGGCTGTTACCATTTCTGCGTTT	SEQ ID NO:1487
WBC032D03_V1.3_at	TGAGATTTTTCTGAGGTGTCCCCTT	SEQ ID NO:1488

Probe Set Name	Sequence	Sequence Identifier
WBC032D03_V1.3_at	TCCCCTTTTGTTGATACCTTCGATA	SEQ ID NO:1489
WBC032D03_V1.3_at	TCTGACCATCTACCGGAAGTGCGTA	SEQ ID NO:1490
WBC032D03_V1.3_at	TAAAAACGAGCTTGCGACTCTGCCG	SEQ ID NO:1491
WBC032D03_V1.3_at	TACTTGCTCTGAACCTTGCTGAGTT	SEQ ID NO:1492
Homo sapiens mRNA; cDNA DKFZp686H1588		
WBC032H02_V1.3_at	ATACGAGTCAGCTTCTGTAGCATAA	SEQ ID NO:1493
WBC032H02_V1.3_at	AGTGTACAAGCGTCATTTATAGTTT	SEQ ID NO:1494
WBC032H02_V1.3_at	AGTGGCCTCACTTCAAGCAGTTTGC	SEQ ID NO:1495
WBC032H02_V1.3_at	AGCAGTTTGCCTTTGTTCTTTAAAT	SEQ ID NO:1496
WBC032H02_V1.3_at	AACTTTTGCTTACTGTGCTCACATC	SEQ ID NO:1497
WBC032H02_V1.3_at	AATTCTTCCACTTGTTTTACATCAC	SEQ ID NO:1498
WBC032H02_V1.3_at	GTATTATGCTTTTCTGTTGAGGGAG	SEQ ID NO:1499
WBC032H02_V1.3_at	GTGGTTTGTCACTGTAATACGAGTC	SEQ ID NO:1500
WBC032H02_V1.3_at	TTATTTGGGTTAAAGTGGCCTCACT	SEQ ID NO:1501
WBC032H02_V1.3_at	GGTTTGATTTCCTATAATTCTTCCA	SEQ ID NO:1502
WBC032H02_V1.3_at	GGCTTTGAGGATTTTTCTGGCATTA	SEQ ID NO:1503
No Homology		
WBC033D12_V1.3_at	TTTTCCCATAACTGAGCCTACGTGA	SEQ ID NO:1504
WBC033D12_V1.3_at	AAAATGTGTCACTCGCTTTCTTCTG	SEQ ID NO:1505
WBC033D12_V1.3_at	CAGCGTGAACGTACCATAATTTTAA	SEQ ID NO:1506
WBC033D12_V1.3_at	GCTCATGTCTTCATTTGCTTATCCA	SEQ ID NO:1507
WBC033D12_V1.3_at	TTTTCTTTCAGGGAGTTTGCCCCAG	SEQ ID NO:1508
WBC033D12_V1.3_at	GCAACTCTCTAGTGTCAGCGTGTAG	SEQ ID NO:1509
WBC033D12_V1.3_at	GTTGTCCCTTCGGTGGTGTATGAAA	SEQ ID NO:1510
WBC033D12_V1.3_at	TGTAGAGCCCAATACTTCCCAGTAT	SEQ ID NO:1511
WBC033D12_V1.3_at	TATGCATTCCTTTGGTTACTTGTGA	SEQ ID NO:1512
WBC033D12_V1.3_at	TAGTCTCTTGTTTCATTATGCATTC	SEQ ID NO:1513
WBC033D12_V1.3_at	TTGGCAGATTGCTTCAGAGACATGT	SEQ ID NO:1514
Homo sapiens splicing factor, arginine/serine-rich 2, mRNA (cDNA clone MGC:5480 IMAGE:3452024)		
WBC035E01_V1.3_at	ATAACCTAACTTATGCCCCATTTTG	SEQ ID NO:1515
WBC035E01_V1.3_at	ATGGCTATGTAACCCACGAGTGCTA	SEQ ID NO:1516
WBC035E01_V1.3_at	ACGAGTGCTATCTAGGTGACCTTCC	SEQ ID NO:1517
WBC035E01_V1.3_at	ACAATCTCAGTCCTTTTTCTTACAG	SEQ ID NO:1518
WBC035E01_V1.3_at	AACAGTATGTCTTCCTGGGAGGGCA	SEQ ID NO:1519
WBC035E01_V1.3_at	AAGTGAAGTGTCTAGTTGCTGCCCT	SEQ ID NO:1520
WBC035E01_V1.3_at	CAGATGGTACTGCTTGTGCTCTCAA	SEQ ID NO:1521
WBC035E01_V1.3_at	GCAGACTCTGCTATGTTTTCTTTGT	SEQ ID NO:1522
WBC035E01_V1.3_at	GACACATTTCATATCCCACTTGTAG	SEQ ID NO:1523
WBC035E01_V1.3_at	GTTGCTGCCCTTTTTACTGAGTTAA	SEQ ID NO:1524
WBC035E01_V1.3_at	TGAGTCCTAGTTGCCATACCAGGTT	SEQ ID NO:1525
Homo sapiens annexin A2, mRNA		

Probe Set Name	Sequence	Sequence Identifier
WBC036E08_V1.3_at	GAAAATGCTTTCCTGAACCTGGTCC	SEQ ID NO:1526
WBC036E08_V1.3_at	GAACAAGCCCCTGTATTTTGCTGAC	SEQ ID NO:1527
WBC036E08_V1.3_at	GAGCTACAGCCCTTATGACATGTTG	SEQ ID NO:1528
WBC036E08_V1.3_at	GAGGATGATGTTAGCCTTGTGCCCC	SEQ ID NO:1529
WBC036E08_V1.3_at	GGCACGCGCGATAAGGTCCTGATCA	SEQ ID NO:1530
WBC036E08_V1.3_at	TGTGCTTCCTGCTAACAGTTCTAGA	SEQ ID NO:1531
WBC036E08_V1.3_at	TGATCAGAATCATGGTCTCCCGCAG	SEQ ID NO:1532
WBC036E08_V1.3_at	TGACCGACTGTACGACTCCATGAAG	SEQ ID NO:1533
WBC036E08_V1.3_at	TGCCTCTTGTGTACTGTGTCGTAAA	SEQ ID NO:1534
WBC036E08_V1.3_at	TCTAGTCTCTCCTTTTAGCCAAAGA	SEQ ID NO:1535
WBC036E08_V1.3_at	TATTTTAGATGCCTACGCGTTACCC	SEQ ID NO:1536
Homo sapiens programmed cell death 4 (neoplastic transformation inhibitor), transcript variant 1, mRNA		
WBC037C09_V1.3_at	AGGGAGCATACTGATTGGTCTTAAA	SEQ ID NO:1537
WBC037C09_V1.3_at	AAGCTACCTTTTGTAAGTGCCATGT	SEQ ID NO:1538
WBC037C09_V1.3_at	AAGTGCCATGTTTATGACCTAATCA	SEQ ID NO:1539
WBC037C09_V1.3_at	CCATGTTGGCTGCTGCTGTTGAAAT	SEQ ID NO:1540
WBC037C09_V1.3_at	GACCTAATCATTCCAAGTTTTGCAT	SEQ ID NO:1541
WBC037C09_V1.3_at	GACTTATTCATCTTTCCAGGGAGCA	SEQ ID NO:1542
WBC037C09_V1.3_at	GTGGAATATTCTCATAAGCTACCTT	SEQ ID NO:1543
WBC037C09_V1.3_at	GGTGGCCGGAACATCTATTTTTCTA	SEQ ID NO:1544
WBC037C09_V1.3_at	TAAGCTGCTAAAACCCCATGTTGGC	SEQ ID NO:1545
WBC037C09_V1.3_at	TGCCACTCCTTTCTTTCAAGGACAG	SEQ ID NO:1546
WBC037C09_V1.3_at	TTGCATTGATGTCTGACTGCCACTC	SEQ ID NO:1547
Homo sapiens ribosomal protein L3, mRNA (cDNA clone MGC:70878 IMAGE:3852576).		
WBC038A02_V1.3_at	ATCTACAAGATTGGCCAGGGCTACC	SEQ ID NO:1548
WBC038A02_V1.3_at	ATGGCCGCTTCCAGACTGTGGAGGA	SEQ ID NO:1549
WBC038A02_V1.3_at	AGGGCTACCTCATCAAGGACGGCAA	SEQ ID NO:1550
WBC038A02_V1.3_at	AGGTTGACCTCAAGTTCATCGACAC	SEQ ID NO:1551
WBC038A02_V1.3_at	AGAAGCGAGTGCTGACCCTTCGCAA	SEQ ID NO:1552
WBC038A02_V1.3_at	AGAACAATGCCTCCACTGATTACGA	SEQ ID NO:1553
WBC038A02_V1.3_at	AAGTCCCTGCTGGTGCAGACGAAGC	SEQ ID NO:1554
WBC038A02_V1.3_at	GACAAGAGCATCAACCCTCTGGGTG	SEQ ID NO:1555
WBC038A02_V1.3_at	GACCAACGACTTTGTCATGCTGAAA	SEQ ID NO:1556
WBC038A02_V1.3_at	GATGCCAGCATCAGATCGTGCAGCT	SEQ ID NO:1557
WBC038A02_V1.3_at	GTGGCTTTGTCCACTACGGTGAAGT	SEQ ID NO:1558
Homo sapiens ribosomal protein L15, mRNA.		
WBC038B01_V1.3_at	ATATATCGCATTCGTGTGCGCCGTG	SEQ ID NO:1559
WBC038B01_V1.3_at	ATAAGGCGCGCAGACTGGGCTACAA	SEQ ID NO:1560
WBC038B01_V1.3_at	AGAGGGCTGACATCTGCAGGCCGCA	SEQ ID NO:1561
WBC038B01_V1.3_at	AGCTCAAGTTTGCTCGAAGCCTTCA	SEQ ID NO:1562
WBC038B01_V1.3_at	ACTATTGGTGGTTCTCGCCGTGCAG	SEQ ID NO:1563

Probe Set Name	Sequence	Sequence Identifier
WBC038B01_V1.3_at	AAGCCTTCAGTCTGTTGCCGAGGAA	SEQ ID NO:1564
WBC038B01_V1.3_at	GCTTCACCGTTACCGCTAATATAAG	SEQ ID NO:1565
WBC038B01_V1.3_at	GCAAGCCTGTGCATCATGGTGTTAA	SEQ ID NO:1566
WBC038B01_V1.3_at	GACGTGATGCGATTTCTTCTCAGGG	SEQ ID NO:1567
WBC038B01_V1.3_at	GAGAAGGCGCAATACTCTGCAGCTT	SEQ ID NO:1568
WBC038B01_V1.3_at	GAGGTGATCCTCATTGATCCATTCC	SEQ ID NO:1569
Homo sapiens NPF/calponin-like protein, mRNA		
WBC039D09_V1.3_at	ATTACTTCTAGCTTGGTTCCTACAA	SEQ ID NO:1570
WBC039D09_V1.3_at	AGGATAATAGAGCTCCTCTCCTCTG	SEQ ID NO:1571
WBC039D09_V1.3_at	AAAGTCTGTCTTGCCACTATGAGTA	SEQ ID NO:1572
WBC039D09_V1.3_at	AATATTTTCTTCTCTAGCATCGCAC	SEQ ID NO:1573
WBC039D09_V1.3_at	CTAGCATCGCACTGTCATTTTTTGT	SEQ ID NO:1574
WBC039D09_V1.3_at	GTTGGGTCTCAACATTGGCTCAAGA	SEQ ID NO:1575
WBC039D09_V1.3_at	GTAACCTAGCCTGAGACAAGTCCTG	SEQ ID NO:1576
WBC039D09_V1.3_at	GGCTTATCATCTGAGAATGCGCCAT	SEQ ID NO:1577
WBC039D09_V1.3_at	TGCGCCATCTTTTTCTCTGGATAAT	SEQ ID NO:1578
WBC039D09_V1.3_at	TTTTTTCCAGTCCTGCCATATCTAA	SEQ ID NO:1579
WBC039D09_V1.3_at	TTCTGCAGTTGTTTTGCGTTTCACT	SEQ ID NO:1580
Leu-8 pan leukocyte antigen		
WBC039F12_V1.3_at	ACATGCACCTTCAACTGCTCAGAAG	SEQ ID NO:1581
WBC039F12_V1.3_at	AAACATTTGGCTGATTTTTGCTTTT	SEQ ID NO:1582
WBC039F12_V1.3_at	GCAGGATACCAAGCTCTATGTTTTA	SEQ ID NO:1583
WBC039F12_V1.3_at	GATCATCAGGAATCTGGTCCAGCAC	SEQ ID NO:1584
WBC039F12_V1.3_at	GTTGGCATTTATCATTTGGCTGGCA	SEQ ID NO:1585
WBC039F12_V1.3_at	GTTTTATAGACATCAGTCCCTGGAG	SEQ ID NO:1586
WBC039F12_V1.3_at	GTGAAGCAGCCCAGTACATACTTTC	SEQ ID NO:1587
WBC039F12_V1.3_at	GTCATGGTTACTGCATTATCTGGGT	SEQ ID NO:1588
WBC039F12_V1.3_at	GGTCCAGCACTAGTCCAATGTGTCA	SEQ ID NO:1589
WBC039F12_V1.3_at	TGGACAGGAGTTTCACGGCGATCAA	SEQ ID NO:1590
WBC039F12_V1.3_at	TCATCCCTGTGGCAGTCATGGTTAC	SEQ ID NO:1591
Human lymphocyte dihydropyrimidine dehydrogenase		
WBC044E01_V1.3_at	ATATATTTTCTATTACTGCCAAACA	SEQ ID NO:1592
WBC044E01_V1.3_at	ATCTCTTTTTTGTGGCATATTTTAA	SEQ ID NO:1593
WBC044E01_V1.3_at	ATGCAACACCAGTTTGACTATTCTT	SEQ ID NO:1594
WBC044E01_V1.3_at	AATGTGCACTTACCAAAAAATCTGT	SEQ ID NO:1595
WBC044E01_V1.3_at	CCAGTTTGACTATTCTTTCTTTTAG	SEQ ID NO:1596
WBC044E01_V1.3_at	GTTTGCATGCTCTGCTTCGGCGGCC	SEQ ID NO:1597
WBC044E01_V1.3_at	GTAACAATCGGAAGCATATTTCTAT	SEQ ID NO:1598
WBC044E01_V1.3_at	GTATGTCTCTATTTTCATAATCAGC	SEQ ID NO:1599
WBC044E01_V1.3_at	GTACTTTTAGAAATGTGCACTTACC	SEQ ID NO:1600
WBC044E01_V1.3_at	TGGGCACAGACCAGGCCACGCTGTG	SEQ ID NO:1601

Probe Set Name	Sequence	Sequence Identifier
WBC044E01_V1.3_at	TTCATTTATCTCTTTTTTGTGGCAT	SEQ ID NO:1602
H.sapiens mRNA for BS69 protein.		
WBC047A01_V1.3_at	CTCCTCGTTGCTGTGTGCTTAATTA	SEQ ID NO:1603
WBC047A01_V1.3_at	GAACACTTACCTTCTCTGATTGTTT	SEQ ID NO:1604
WBC047A01_V1.3_at	GTTGAGCTTAGCCACTATGCACATT	SEQ ID NO:1605
WBC047A01_V1.3_at	GTTGACACGGTTGCACATTTCCAAT	SEQ ID NO:1606
WBC047A01_V1.3_at	GTAATTATTCATTGTGGCTGTCCAG	SEQ ID NO:1607
WBC047A01_V1.3_at	GGCTGTCCAGTTCTATGATGCATTC	SEQ ID NO:1608
WBC047A01_V1.3_at	TGTTACTTTGGCTTTTTTGTCTCCG	SEQ ID NO:1609
WBC047A01_V1.3_at	TGAGGCGTCGTAACCAAGAACACTT	SEQ ID NO:1610
WBC047A01_V1.3_at	TCGATCCACCCCTATGAGAGCAAGT	SEQ ID NO:1611
WBC047A01_V1.3_at	TGAACCGGGCAGTGACTTGGCGTCT	SEQ ID NO:1612
WBC047A01_V1.3_at	TTAATTAGTGTTGCCACGGTGCTGT	SEQ ID NO:1613
No Homology		
WBC107.V1.3_s_at	ATTCTTTTTCTTTTCCAGTATGAAG	SEQ ID NO:1614
WBC107.V1.3_s_at	ATAGCTTTCATACCTACATTTCAAG	SEQ ID NO:1615
WBC107.V1.3_s_at	ATACCTATCTCAGTTATTCTTTTTC	SEQ ID NO:1616
WBC107.V1.3_s_at	CCAGTATGAAGTTTGCTGAATGTAC	SEQ ID NO:1617
WBC107.V1.3_s_at	GCTAGACTTATTACTGTGCACGAGA	SEQ ID NO:1618
WBC107.V1.3_s_at	GAAGCTGTTCTTGAACTAACACGGA	SEQ ID NO:1619
WBC107.V1.3_s_at	GATTGTCTTGATTTGATCCGAAACA	SEQ ID NO:1620
WBC107.V1.3_s_at	GGGCCGTGTCAGGAAATTACCTATA	SEQ ID NO:1621
WBC107.V1.3_s_at	GGTGTAGAAGCTCAGCTAGACTTAT	SEQ ID NO:1622
WBC107.V1.3_s_at	GGATAATATCTTCATGTTTCTGAAA	SEQ ID NO:1623
WBC107.V1.3_s_at	TGTGCACGAGAGTAAATACCTATCT	SEQ ID NO:1624
No Homology		
WBC117.gRSP.V1.3_at	AAATAATCTTGCAGTACCGGAGTAT	SEQ ID NO:1625
WBC117.gRSP.V1.3_at	GAAACTTTTCCTGTAGAGGGCCGCT	SEQ ID NO:1626
WBC117.gRSP.V1.3_at	GCAAAAGCATTCATCAGCAGCGTGT	SEQ ID NO:1627
WBC117.gRSP.V1.3_at	GAAAGTTTCCCACCTGCTAGGAAAG	SEQ ID NO:1628
WBC117.gRSP.V1.3_at	GAAATGGCCTCAGGAAAGTTTCCCA	SEQ ID NO:1629
WBC117.gRSP.V1.3_at	GACCCTGCCGTCATCATGCAAAAGC	SEQ ID NO:1630
WBC117.gRSP.V1.3_at	GAGGGCCGCTTTGTAAATATTTTAG	SEQ ID NO:1631
WBC117.gRSP.V1.3_at	GAGGGCAACACAATTTCTGTCGCAA	SEQ ID NO:1632
WBC117.gRSP.V1.3_at	TGGCCACTTTTGTCATTCAGCACTT	SEQ ID NO:1633
WBC117.gRSP.V1.3_at	TGAATTTTACCTGTTTTCTACTCTA	SEQ ID NO:1634
WBC117.gRSP.V1.3_at	TACCTATCTAATACAGCAGCCACTG	SEQ ID NO:1635
Homo sapiens CDC14 cell division cycle 14 homolog A (S. cerevisiae) (CDC14A), transcript variant 1, mRNA		
WBC215.gRSP.V1.3_at	AACACTAATTTGTGTGCAGCTATTA	SEQ ID NO:1636
WBC215.gRSP.V1.3_at	AATTGACTACTGTAAATTTTCCACA	SEQ ID NO:1637
WBC215.gRSP.V1.3_at	AATTGTGACCTTTTCTAAAGCTGAA	SEQ ID NO:1638

Probe Set Name	Sequence	Sequence Identifier
WBC215.gRSP.V1.3_at	GAAAGGGAACCATATTGACAGTTTT	SEQ ID NO:1639
WBC215.gRSP.V1.3_at	GACAGTTTTAGTTCTGTGAACACTA	SEQ ID NO:1640
WBC215.gRSP.V1.3_at	GAGACTATTGTACGTGCTTTCAGCA	SEQ ID NO:1641
WBC215.gRSP.V1.3_at	GTTGACTTCAATAACTACAGACCAA	SEQ ID NO:1642
WBC215.gRSP.V1.3_at	GTTTGACTCAGGTTTGTTGACTTCA	SEQ ID NO:1643
WBC215.gRSP.V1.3_at	GTATAGCATAGTAATTCTACTCCAA	SEQ ID NO:1644
WBC215.gRSP.V1.3_at	GTGCTTTCAGCAAAACATCTTATTC	SEQ ID NO:1645
WBC215.gRSP.V1.3_at	GGAGGGCTACCTTGAGACTATTGTA	SEQ ID NO:1646
Homo sapiens hypothetical protein MGC5576, mRNA		
WBC309.V1.3_at	ATTCAGATCTTTTCAGCTGTTCTTG	SEQ ID NO:1647
WBC309.V1.3_at	ATCATACTGTGGTTCTAGGTTATCA	SEQ ID NO:1648
WBC309.V1.3_at	AGGAAAACTCCTCTCTGTAGCACCA	SEQ ID NO:1649
WBC309.V1.3_at	AGTGCCTGGCCATATGCCCAGCAAA	SEQ ID NO:1650
WBC309.V1.3_at	AAAGCAAACTTTTTCCTGTAGAGAG	SEQ ID NO:1651
WBC309.V1.3_at	AAGCAAGCACAGACCGTTCAGCGTA	SEQ ID NO:1652
WBC309.V1.3_at	CTGTAGCACCATTTCTGTTTCTGAG	SEQ ID NO:1653
WBC309.V1.3_at	GAAGTTTTTTCATGTGTTCCCAAAT	SEQ ID NO:1654
WBC309.V1.3_at	GTTAGTGCAGCTCCAGAACTGTCAT	SEQ ID NO:1655
WBC309.V1.3_at	TCAGCTGTTCTTGGGCCGTTATAAA	SEQ ID NO:1656
WBC309.V1.3_at	TTTGATTTACCCTTCATCCATTGGC	SEQ ID NO:1657
Homo sapiens lymphoid enhancer-binding factor 1 (LEF1), mRNA (cDNA clone MGC:60112 IMAGE:6054813)		
WBC310.V1.3_at	AGCCGACCCGTTTGCAGTGAATTTT	SEQ ID NO:1658
WBC310.V1.3_at	ATTTTCTGCCGATCTCTTCTTTTTT	SEQ ID NO:1659
WBC310.V1.3_at	AAAGCCCAGCACTTGAATTGTTCTT	SEQ ID NO:1660
WBC310.V1.3_at	AAACTTTCCCAGATATTCTCAGCCG	SEQ ID NO:1661
WBC310.V1.3_at	GAGTCCTGTTTCGTTTTATTTTCTG	SEQ ID NO:1662
WBC310.V1.3_at	GATGAGTGGCTTCTCTGTGATCACC	SEQ ID NO:1663
WBC310.V1.3_at	GTCATCTAACGTTTGTCATTCCAGT	SEQ ID NO:1664
WBC310.V1.3_at	TGTGATCACCTGTCACGATTCGTGG	SEQ ID NO:1665
WBC310.V1.3_at	TGAATTTTCATTTCCTTCCTTCTTG	SEQ ID NO:1666
WBC310.V1.3_at	TTGCCCCTTGTTGTAAAAAGCCCAG	SEQ ID NO:1667
WBC310.V1.3_at	TTGGTCGAGTGTTCGGCAGAGCCAC	SEQ ID NO:1668
Homo sapiens lymphoid enhancer-binding factor 1, mRNA (cDNA clone MGC:60112 IMAGE:6054813).		
WBC311.V1.3_at	GGTCTTGGAACATAGGAGGTGCTCA	SEQ ID NO:1669
WBC311.V1.3_at	ATTTTTGGCCATATTTCACTTAGTT	SEQ ID NO:1670
WBC311.V1.3_at	AGTATTCCCGTATTGCATTTTGCTA	SEQ ID NO:1671
WBC311.V1.3_at	ACTCACTTTTTAACTGTACACCTTG	SEQ ID NO:1672
WBC311.V1.3_at	AAATGTATTGTTTCAACTCACTTTT	SEQ ID NO:1673
WBC311.V1.3_at	AAATACTAGTTGACTGCACAGCGAG	SEQ ID NO:1674
WBC311.V1.3_at	AATGCATGATGATTATTTTTGGCCA	SEQ ID NO:1675
WBC311.V1.3_at	GACTGCACAGCGAGTAGTGTACTAA	SEQ ID NO:1676

Probe Set Name	Sequence	Sequence Identifier
WBC311.V1.3_at	GAGATGTCCTTATTGGGTAACCATG	SEQ ID NO:1677
WBC311.V1.3_at	GTACACCTTGTAGTTATTTTCTATT	SEQ ID NO:1678
WBC311.V1.3_at	TATTTCACTTAGTTTTTTCAGGCTA	SEQ ID NO:1679
Homo sapiens maltase-glucoamylase mRNA.		
WBC327.V1.3_at	ATTGCCAGGACAGTTCCAGGCTCTG	SEQ ID NO:1680
WBC327.V1.3_at	ATAACTTCTTTTTGCAGTGGTGTGC	SEQ ID NO:1681
WBC327.V1.3_at	AGCGTAATCAGGGATTGGGCCCCAC	SEQ ID NO:1682
WBC327.V1.3_at	CAGTGGTGTGCTTTGAAATTTGTCA	SEQ ID NO:1683
WBC327.V1.3_at	GCTCTGGAGCTAACTAAGCCATCAA	SEQ ID NO:1684
WBC327.V1.3_at	GAAATGCTTAGCTATAGGACTGGGA	SEQ ID NO:1685
WBC327.V1.3_at	GATGTATATAACCACAGTTCCCATA	SEQ ID NO:1686
WBC327.V1.3_at	GTCTTATTTCTATACTCTGCCTGAT	SEQ ID NO:1687
WBC327.V1.3_at	GTGTGCATGTCTATGTGAGCGTAAT	SEQ ID NO:1688
WBC327.V1.3_at	GGAAGAGCCAACTCACCTGAAAGAA	SEQ ID NO:1689
WBC327.V1.3_at	TTGGGCCCCACTCTTGGTAAATACA	SEQ ID NO:1690
Homo sapiens radixin, mRNA (cDNA clone MGC:48283 IMAGE:5284438), complete cds.		
WBC335.V1.3_at	AATTCCAACAGGCTTTTACCATTAG	SEQ ID NO:1691
WBC335.V1.3_at	ATGCTTTCAAGCCTGTGTTCACTTT	SEQ ID NO:1692
WBC335.V1.3_at	ACTAGAGGGTGAACGCTGCTGTTGA	SEQ ID NO:1693
WBC335.V1.3_at	AACGCTGCTGTTGATGCTTTCAAGC	SEQ ID NO:1694
WBC335.V1.3_at	AATCCATTTTTAAAGCTGTGTGAAT	SEQ ID NO:1695
WBC335.V1.3_at	GAGCGTTAAAACAATTGCCATAAAG	SEQ ID NO:1696
WBC335.V1.3_at	GAGAGCACATGTTCATATAGCAATG	SEQ ID NO:1697
WBC335.V1.3_at	GTCACATCAGTTTGATATCAGTGTT	SEQ ID NO:1698
WBC335.V1.3_at	GTGCACTACCATTGTCACATCAGTT	SEQ ID NO:1699
WBC335.V1.3_at	GTGTTCACTTTTCCAGAGCGTTAAA	SEQ ID NO:1700
WBC335.V1.3_at	TTCATTTTGAATTGTGTGCACTACC	SEQ ID NO:1701
No Homology		
WBC374.V1.3_at	ATTTGGGCTTCTAACTGCAGCGTTT	SEQ ID NO:1702
WBC374.V1.3_at	ATTTTGATTATGTTGCTTACCTTGA	SEQ ID NO:1703
WBC374.V1.3_at	ATAATTTAGTGTCTCTGGCACACAC	SEQ ID NO:1704
WBC374.V1.3_at	ATGTTTTCACATTCCTTTGTCCGGA	SEQ ID NO:1705
WBC374.V1.3_at	ACTTCAGTTGTGATCTTGGTGACAT	SEQ ID NO:1706
WBC374.V1.3_at	AACTCAGCATCCTTGTTTTCTGCAA	SEQ ID NO:1707
WBC374.V1.3_at	CCATGTCTTTGTTGTACTTGTGCAG	SEQ ID NO:1708
WBC374.V1.3_at	GACATATCTGTTGGCTTAGGTTTTA	SEQ ID NO:1709
WBC374.V1.3_at	GATGCTTTTGTTTTGGGTTATGGTC	SEQ ID NO:1710
WBC374.V1.3_at	TTATCGCAGATGTTCGGTTGACCAA	SEQ ID NO:1711
WBC374.V1.3_at	TTGTAATTACCTTCCCATGTCTTTG	SEQ ID NO:1712
No Homology		
WBC964.gRSP.V1.3_at	AGTGATTCAGTTTTCTATAGCTTAC	SEQ ID NO:1713

Probe Set Name	Sequence	Sequence Identifier
WBC964.gRSP.V1.3_at	ACCACTGCAAGAGGACGCTGAGATT	SEQ ID NO:1714
WBC964.gRSP.V1.3_at	ACCCTATTTCTCACTGTCTTCATTA	SEQ ID NO:1715
WBC964.gRSP.V1.3_at	ACTGTCTTCATTATTTCACGTAGGA	SEQ ID NO:1716
WBC964.gRSP.V1.3_at	AAAGCCTTGTTATTATTTGATCCTA	SEQ ID NO:1717
WBC964.gRSP.V1.3_at	CACTTCTAACCTGAAAGCTGCTTGG	SEQ ID NO:1718
WBC964.gRSP.V1.3_at	CAAAATGGATCTGTGCGCTGTGGCA	SEQ ID NO:1719
WBC964.gRSP.V1.3_at	GATTTTCTATGTCTTCCACTTCTAA	SEQ ID NO:1720
WBC964.gRSP.V1.3_at	GTGCGCTGTGGCAGAACTGTTATTT	SEQ ID NO:1721
WBC964.gRSP.V1.3_at	GGATTTTACAGCTCAACTAACAGTG	SEQ ID NO:1722
WBC964.gRSP.V1.3_at	TACAGTTTATTTTTTGCACACCCTA	SEQ ID NO:1723
Homo sapiens AT rich interactive domain 5A (MRF1-like), mRNA (cDNA clone MGC:75508 IMAGE:30409017)		
BM734632.V1.3_at	ACCGACTGACGCCTCAGGAGGAAAT	SEQ ID NO:1724
BM734632.V1.3_at	GCTGAGAACTCCAGGCACCGACTGA	SEQ ID NO:1725
BM734632.V1.3_at	AGGGCAGGCTGAGAACTCCAGGCAC	SEQ ID NO:1726
BM734632.V1.3_at	AGTCTTAAAGATGGGCTGCTATTGG	SEQ ID NO:1727
BM734632.V1.3_at	AGAAAGGGCAGCCTCTACCCTAAGC	SEQ ID NO:1728
BM734632.V1.3_at	ACGCCTACCCCACTGAGGTACTGAA	SEQ ID NO:1729
BM734632.V1.3_at	CTGGTCAAAGAACCCCAGCTGGTGT	SEQ ID NO:1730
BM734632.V1.3_at	GGACTTCTTCCCCAGTCTTAAAGAT	SEQ ID NO:1731
BM734632.V1.3_at	TGCATTCCACAAAGGCGGCTCCAGA	SEQ ID NO:1732
BM734632.V1.3_at	TGAGGTACTGAAGCCCATCAGCCAG	SEQ ID NO:1733
BM734632.V1.3_at	TAAGCCTAAAGCCTGCTGGGTGTCC	SEQ ID NO:1734
Homo sapiens sorting nexin 3 (SNX3), transcript variant 1, mRNA.		
WBC028C09_V1.3_at	AATGTGGTGCACACTATAGCCTCAC	SEQ ID NO:1735
WBC028C09_V1.3_at	GAAATAGCTCTCTGTGCTGTTTGAA	SEQ ID NO:1736
WBC028C09_V1.3_at	GAGTAGCTCCCTTCATCTGGAAGAT	SEQ ID NO:1737
WBC028C09_V1.3_at	GTATAACCTGCAGTGTCCTAACTAA	SEQ ID NO:1738
WBC028C09_V1.3_at	GTAGGAGCACTACACCATTGGTTCC	SEQ ID NO:1739
WBC028C09_V1.3_at	GGTTCCCTACCCTACATGTAAGAGA	SEQ ID NO:1740
WBC028C09_V1.3_at	GTGTCATGTTTGCTTCTTGAATCTG	SEQ ID NO:1741
WBC028C09_V1.3_at	TAGAATATTTCTCTTATCCCCTTTT	SEQ ID NO:1742
WBC028C09_V1.3_at	TAGCCTCACAAACCTGTTATTCCAG	SEQ ID NO:1743
WBC028C09_V1.3_at	TTTAGTGAAAATCCCTCATTCTGGC	SEQ ID NO:1744
WBC028C09_V1.3_at	TTACTGGCTTGGTCTTATCTGCACA	SEQ ID NO:1745
Human Lyn B protein mRNA.		
WBC039G08_V1.3_at	ATGCCTATCATGACACTTCTTTCTA	SEQ ID NO:1746
WBC039G08_V1.3_at	AAACTGCTCTCTCTTCCAAAGGGAT	SEQ ID NO:1747
WBC039G08_V1.3_at	AAACATTTTCCTTCCTTGGAGGCTG	SEQ ID NO:1748
WBC039G08_V1.3_at	AACGCGTCACTTGTGAGCCTGCAGA	SEQ ID NO:1749
WBC039G08_V1.3_at	AATGGTCCAGCTTTTCAATTCCACC	SEQ ID NO:1750
WBC039G08_V1.3_at	CTGCAGAACCTTCTAGGGCCTTATA	SEQ ID NO:1751

Probe Set Name	Sequence	Sequence Identifier
WBC039G08_V1.3_at	GAATTTTCTTTGTTGCTTCAGATGA	SEQ ID NO:1752
WBC039G08_V1.3_at	GGAAGCAGCAGCACTTTCCTGGTCT	SEQ ID NO:1753
WBC039G08_V1.3_at	TCCTACCTACAGACTTTTTTGACAG	SEQ ID NO:1754
WBC039G08_V1.3_at	TCCAAGATTTCAGTGATTTCCCCTC	SEQ ID NO:1755
WBC039G08_V1.3_at	TTTCTATTTTCTCTGTGCTTTGGCT	SEQ ID NO:1756
No Homology		
WBC21.V1.3_at	ATTCCTCTGTGTTTTATGTTACTGT	SEQ ID NO:1757
WBC21.V1.3_at	ATCTGATTCCCCTAAATGCGTAGAA	SEQ ID NO:1758
WBC21.V1.3_at	ATCACTATTTTCACTTTGACTGACA	SEQ ID NO:1759
WBC21.V1.3_at	AGAGGCATTAGTGGCTTTGGCTAAA	SEQ ID NO:1760
WBC21.V1.3_at	CAAACTACTTACCTGATTGTCAAGA	SEQ ID NO:1761
WBC21.V1.3_at	AAGCATTGCTGTATCTATTTTTGAA	SEQ ID NO:1762
WBC21.V1.3_at	CAAGTTATGCTGTTTCCTCTATTCT	SEQ ID NO:1763
WBC21.V1.3_at	GACCTGTTAGGCAAAATCACTATTT	SEQ ID NO:1764
WBC21.V1.3_at	TAAGACACTTGATGTATTCCTCTGT	SEQ ID NO:1765
WBC21.V1.3_at	TAGAGACTCTTTCATCCATAAGCCC	SEQ ID NO:1766
WBC21.V1.3_at	TTTAACAAAGCTAACCACATCCCCT	SEQ ID NO:1767
Homo sapiens arachidonate 5-lipoxygenase-activating protein (ALOX5AP)		
WBC040E12_V1.3_at	AAATCATCATAACTCAACTCCTACG	SEQ ID NO:1768
WBC040E12_V1.3_at	AACTTTGTGTCAGCGATACCCTTTA	SEQ ID NO:1769
WBC040E12_V1.3_at	AACTATTATCTCATCCTCTTTTTCG	SEQ ID NO:1770
WBC040E12_V1.3_at	AATACAGGGTTGGTGCTCTCATCTA	SEQ ID NO:1771
WBC040E12_V1.3_at	GAAGTACTTCGTGGGCTATCTGGGA	SEQ ID NO:1772
WBC040E12_V1.3_at	GAAACGCATCATACTGTTCCTGTTC	SEQ ID NO:1773
WBC040E12_V1.3_at	GAGTTAACCTTGCTTTTCCTGGAAG	SEQ ID NO:1774
WBC040E12_V1.3_at	GATCCATTCTGTGTGTTTCTTGACT	SEQ ID NO:1775
WBC040E12_V1.3_at	TGGGCTTCGCGTCTTGAGTTAACCT	SEQ ID NO:1776
WBC040E12_V1.3_at	TACGGTCCTCTTTAGATTGCTGTAA	SEQ ID NO:1777
WBC040E12_V1.3_at	TTGACTTACCCTGCTTTCTGAAGAT	SEQ ID NO:1778
No homology		
BM780906.V1.3_at	AGCTGAAACACATCTCTTGGGTCCT	SEQ ID NO:1779
BM780906.V1.3_at	GCTTCCCATCATAGTTTTGCCGTTA	SEQ ID NO:1780
BM780906.V1.3_at	GATTCCCAGAATGCCATCGATGACC	SEQ ID NO:1781
BM780906.V1.3_at	GTTCCGTTTTCAAGGACCAGTCAGC	SEQ ID NO:1782
BM780906.V1.3_at	GTAACAGTGACTCCTGATTCCCAGA	SEQ ID NO:1783
BM780906.V1.3_at	GTGTGAGCAGCTCCTCCTGTATAGT	SEQ ID NO:1784
BM780906.V1.3_at	TGGAGCTTTTGCCTGTAGCTTGAGA	SEQ ID NO:1785
BM780906.V1.3_at	TGTATAGTCCTCTTCTTCACTGAAT	SEQ ID NO:1786
BM780906.V1.3_at	TCAGTACGTCAGTGGTGGAGCTTTT	SEQ ID NO:1787
BM780906.V1.3_at	TTCACTGAATGCTGGAACCTCCAAC	SEQ ID NO:1788
BM780906.V1.3_at	TTTACCCGCAGTATCAAGCACAAGA	SEQ ID NO:1789

Probe Set Name	Sequence	Sequence Identifier
No homology		
B1961872.V1.3_at	AGATTTGACCTGTTCATGCGTCTGT	SEQ ID NO:1790
B1961872.V1.3_at	TCCGTCTCCCGGCTATATAGTAATC	SEQ ID NO:1791
B1961872.V1.3_at	GAGTTGTCATTTTCTCTTCACTGGA	SEQ ID NO:1792
B1961872.V1.3_at	GTTCATGCGTCTGTGGAGCAGCCCT	SEQ ID NO:1793
B1961872.V1.3_at	GTAATCTTAGGTAGAGTGTTGCCTT	SEQ ID NO:1794
B1961872.V1.3_at	GTCATTTTCTCTTCACTGGATGTTT	SEQ ID NO:1795
B1961872.V1.3_at	TAGAGTGTTGCCTTGTGGGTTACCG	SEQ ID NO:1796
B1961872.V1.3_at	TGGGTTACCGTTTGCTCTGAGACTT	SEQ ID NO:1797
B1961872.V1.3_at	TCTGAGACTTCTCGGATGGACCCAC	SEQ ID NO:1798
B1961872.V1.3_at	TCTCTTCACTGGATGTTTATTTATA	SEQ ID NO:1799
B1961872.V1.3_at	TATGCTCTGTGTATAAGGATGAATT	SEQ ID NO:1800
Equus caballus IL-1RII mRNA for interleukin-1 receptor type II.		
BM781269.V1.3_at	ATGGCACACGAGTCAACATCACTAG	SEQ ID NO:1801
BM781269.V1.3_at	ACCGATCTGTGGTGGATGGCCAACA	SEQ ID NO:1802
BM781269.V1.3_at	ACTAGTTTGCCCTGAGCTGAGTGAA	SEQ ID NO:1803
BM781269.V1.3_at	AAGACAGAAGCTGCCCTGACTTACA	SEQ ID NO:1804
BM781269.V1.3_at	GAAACGCCTCGTACTGCTATGAAAT	SEQ ID NO:1805
BM781269.V1.3_at	GAAATATCGAACTCCGTGTCCAGAA	SEQ ID NO:1806
BM781269.V1.3_at	GATGCGGGCTATTACAGCTGTGTCA	SEQ ID NO:1807
BM781269.V1.3_at	GTGTCATGACCTTGATCCACAATGG	SEQ ID NO:1808
BM781269.V1.3_at	GGACAATGCTCTCTGGATTTTGCCG	SEQ ID NO:1809
BM781269.V1.3_at	TAAGGTGTTTCTGGGAGCCGGCACA	SEQ ID NO:1810
BM781269.V1.3_at	TTGTCAACCTCTGGCTTACTAGTTT	SEQ ID NO:1811
No Homology		
Foe1092.V1.3_at	ACTGTTTCTGGCACCCACTGAAAAA	SEQ ID NO:1812
Foe1092.V1.3_at	ACATGGTCTGACCTGCACTGTTTCT	SEQ ID NO:1813
Foe1092.V1.3_at	ACAACTGCCTTCTCCATGTTTATAC	SEQ ID NO:1814
Foe1092.V1.3_at	GCTTTTCCAGATTTTAGTCTCCTTT	SEQ ID NO:1815
Foe1092.V1.3_at	GAAAACTACTGTGGCCTTTCTGCTT	SEQ ID NO:1816
Foe1092.V1.3_at	GAGTTGGTTCATCCCATTTGAGGAC	SEQ ID NO:1817
Foe1092.V1.3_at	GAGGGAGTCTATTTTCACTCATTCT	SEQ ID NO:1818
Foe1092.V1.3_at	GTGGCTTTTGCCTAACACTTTTGCA	SEQ ID NO:1819
Foe1092.V1.3_at	TGTCTTCCCATATTCATACCTGCAT	SEQ ID NO:1820
Foe1092.V1.3_at	TGCCTTTCTCACCATTTTGGTTTGA	SEQ ID NO:1821
Foe1092.V1.3_at	TAAACTTCTCTGCACTCCATGATGG	SEQ ID NO:1822
No Homology		
WBC001E10_V1.3_at	AACATTAAGCACTGTTGGCCTCCTG	SEQ ID NO:1823
WBC001E10_V1.3_at	AAGATGCTCATCCAGGTCATCCTGA	SEQ ID NO:1824
WBC001E10_V1.3_at	CTGGTGCCCAGTGATCGGAGGTCCA	SEQ ID NO:1825
WBC001E10_V1.3_at	GCCGTGATCATCTCTTGCCTAAGAT	SEQ ID NO:1826

Probe Set Name	Sequence	Sequence Identifier
WBC001E10_V1.3_at	GACAAATTCACAGCTCTCACAGGAA	SEQ ID NO:1827
WBC001E10_V1.3_at	GAAACAGTGTTCTCAACCTTGACAA	SEQ ID NO:1828
WBC001E10_V1.3_at	GAGGGCCCCATTTGAGAAAGTCCGC	SEQ ID NO:1829
WBC001E10_V1.3_at	GTCCAGGTGGAGATGCCGTGATCAT	SEQ ID NO:1830
WBC001E10_V1.3_at	GGTCCTAAATTATTTTCTCTCTCCT	SEQ ID NO:1831
WBC001E10_V1.3_at	GGATCCCTTACTGTGATGTTTGTTC	SEQ ID NO:1832
WBC001E10_V1.3_at	TTCCTTCTGCAGTCTTTAGGGTGAA	SEQ ID NO:1833
No Homology		
WBC038D08_V1.3_at	ATCCGTACCTACCAAGAGCACAGAG	SEQ ID NO:1834
WBC038D08_V1.3_at	ATGAGCAGGTAAAGCCAACGTTTTT	SEQ ID NO:1835
WBC038D08_V1.3_at	AGGGACCTTGCTGCCTTTGATAAAT	SEQ ID NO:1836
WBC038D08_V1.3_at	CTGTGACTGCCATGCTGGTGGGAAA	SEQ ID NO:1837
WBC038D08_V1.3_at	CTGATTCCACACATTTCTCTTTTTT	SEQ ID NO:1838
WBC038D08_V1.3_at	GACTATGGGTTTGGCAGGACTTCTG	SEQ ID NO:1839
WBC038D08_V1.3_at	GAGCAAGTATGCACCCTGTGACTGC	SEQ ID NO:1840
WBC038D08_V1.3_at	GTCGTTATCCATCTTTCTTTTTCTT	SEQ ID NO:1841
WBC038D08_V1.3_at	GGTTAATCTGTTTGCTTTTCACTTA	SEQ ID NO:1842
WBC038D08_V1.3_at	TAAATCCCATGATCAAGCCATCCGT	SEQ ID NO:1843
WBC038D08_V1.3_at	TAAGGACCTGCCTATTGCTGATTCC	SEQ ID NO:1844
Homo sapiens nuclear factor (erythroid-derived 2)-like 2, mRNA		
WBC020H11_V1.3_at	AGCGAATACTCCCTGCAGCAGACGA	SEQ ID NO:1845
WBC020H11_V1.3_at	AATTTCTTAGAACACCATTTGGGCT	SEQ ID NO:1846
WBC020H11_V1.3_at	ACGAGAGACGGCAGCGTGTTCCTTG	SEQ ID NO:1847
WBC020H11_V1.3_at	ACCATTTGGGCTAGTTTCTGTGTAA	SEQ ID NO:1848
WBC020H11_V1.3_at	AAATTGTCTAGCTCTGGCAAAACAT	SEQ ID NO:1849
WBC020H11_V1.3_at	CTAAAAGCTCCTACTGTGATGTGAA	SEQ ID NO:1850
WBC020H11_V1.3_at	GAAGTCTTCAGCATGCTACGTGACG	SEQ ID NO:1851
WBC020H11_V1.3_at	GACGAAGATGGAAGACCTTACTCCC	SEQ ID NO:1852
WBC020H11_V1.3_at	GTTCTTATCTCATTTGTTACGTTCC	SEQ ID NO:1853
WBC020H11_V1.3_at	GTGTTCCTTGTTCCCAAGAGCAGGA	SEQ ID NO:1854
WBC020H11_V1.3_at	GGAAGATGACCTTTTGAGCTAGTGT	SEQ ID NO:1855
Homo sapiens mRNA; cDNA DKFZp686D0662 (from clone DKFZp686D0662).		
WBC033A01_V1.3_at	ATCTCTATCAGGAATACTGCCTCAG	SEQ ID NO:1856
WBC033A01_V1.3_at	ATGCTGGCACATCATTTTGCTGGAG	SEQ ID NO:1857
WBC033A01_V1.3_at	AGAGCATTAACCTGCCTAATCTTCA	SEQ ID NO:1858
WBC033A01_V1.3_at	AACCTGCCTAATCTTCATGGTGAAA	SEQ ID NO:1859
WBC033A01_V1.3_at	AATTACACCTTCTCTATTCTAGTCA	SEQ ID NO:1860
WBC033A01_V1.3_at	GAGTTTTTTATATACTGTAGCCTGA	SEQ ID NO:1861
WBC033A01_V1.3_at	GTGTTTGACTATTTTCCAACTTGTA	SEQ ID NO:1862
WBC033A01_V1.3_at	TGTGCATGCTGCTGTCTCTGTTGGG	SEQ ID NO:1863
WBC033A01_V1.3_at	TATTTTAGTAGCTGATGCTGGCACA	SEQ ID NO:1864

Probe Set Name	Sequence	Sequence Identifier
WBC033A01_V1.3_at	TCTCTATTCTAGTCATGCTGTGCAT	SEQ ID NO:1865
WBC033A01_V1.3_at	TACTGCCTCAGTTATTGAACTTTTT	SEQ ID NO:1866
Homo sapiens membrane-spanning 4-domains, subfamily A, member 6A, transcript variant 1, mRNA (cDNA clone MGC:22650 IMAGE:3934920).		
BM781186.V1.3_at	ATAGGAGCCTTGTGTTTTGTCATCT	SEQ ID NO:1867
BM781186.V1.3_at	AAGCCTTTGGTTCAGAGCAGCCTAG	SEQ ID NO:1868
BM781186.V1.3_at	AAGTTCTCGGGACTATCCAGATCCT	SEQ ID NO:1869
BM781186.V1.3_at	CAGCATTTTACCCAAGCGTTTTCTA	SEQ ID NO:1870
BM781186.V1.3_at	CTGCAAACATTCTGAGCTCTCTATC	SEQ ID NO:1871
BM781186.V1.3_at	GAAGGCTGCTTACCCATTCATAGGA	SEQ ID NO:1872
BM781186.V1.3_at	GAATTATTTTGGCATCGGCTTCCTT	SEQ ID NO:1873
BM781186.V1.3_at	GTCATACTGGCTTCTTTGGGTCCTG	SEQ ID NO:1874
BM781186.V1.3_at	GTCATCTCTGGATCTCTATCAATCA	SEQ ID NO:1875
BM781186.V1.3_at	TAGCTGGAACCAACGGGCTGATCCT	SEQ ID NO:1876
BM781186.V1.3_at	TATCAGCTCTGGTGGGTTTCATCCT	SEQ ID NO:1877
No Homology		
BM734511.V1.3_at	ATCTTCTCAATCTTTCTTTACCGGG	SEQ ID NO:1878
BM734511.V1.3_at	ATGCCTCATCTTAGCAGTGATTTTG	SEQ ID NO:1879
BM734511.V1.3_at	ATCTCTTTCCTCATTTTCCTGATAG	SEQ ID NO:1880
BM734511.V1.3_at	AGGCTTATCTTTTTGTCTAGTGCAA	SEQ ID NO:1881
BM734511.V1.3_at	AAACCTGACTGAGTTTTCCTGTCTA	SEQ ID NO:1882
BM734511.V1.3_at	AAGCTCAGTACACTAATGCCTCATC	SEQ ID NO:1883
BM734511.V1.3_at	AATACGCTTGGCACTGATGGGCACT	SEQ ID NO:1884
BM734511.V1.3_at	CAGACCCCGGATGCTATTTATTCAA	SEQ ID NO:1885
BM734511.V1.3_at	GATGAGGATGGCCTTCCTGTTTCAC	SEQ ID NO:1886
BM734511.V1.3_at	GTTTGAATGAGTCCTTCGTGGGCCA	SEQ ID NO:1887
BM734511.V1.3_at	TTTACCTAAATACTTCCAGCTCCTT	SEQ ID NO:1888
No Homology		
BM734719.V1.3_at	ACGCCAATGGGTCAAACTAACTCTG	SEQ ID NO:1889
BM734719.V1.3_at	AGAAGTCCTCTCTGAGACTCAAGGG	SEQ ID NO:1890
BM734719.V1.3_at	AAAGCCCATGAGCTGCTTCTTTGTT	SEQ ID NO:1891
BM734719.V1.3_at	AAAAATCTCTCATCCTATTCTGCTT	SEQ ID NO:1892
BM734719.V1.3_at	AAGCCTTCCTAAAAGCACACTTGCC	SEQ ID NO:1893
BM734719.V1.3_at	AAGGGCTAAGGCAAGGTCTTCCAGA	SEQ ID NO:1894
BM734719.V1.3_at	CAAGAAATGACAGCCTCCAAGCCTT	SEQ ID NO:1895
BM734719.V1.3_at	GAAGCTTCTTCCCACCTAGAAAGAA	SEQ ID NO:1896
BM734719.V1.3_at	GGTGACAACGCTGGCTGCTGAAAGC	SEQ ID NO:1897
BM734719.V1.3_at	TTTCCACTGTCGTCAGAGCCAACAA	SEQ ID NO:1898
BM734719.V1.3_at	TTCTTTGTTCTCTGTCACGGGACAA	SEQ ID NO:1899
Human mRNA for T3 epsilon chain (20K) of T-cell receptor (from peripheral blood lymphocytes).		
BM781067.V1.3_at	ATCCAGATTATGAGCCCATCCGGAA	SEQ ID NO:1900

Probe Set Name	Sequence	Sequence Identifier
BM781067.V1.3_at	AGGTAAATGAGACAGCCCTTCGCTC	SEQ ID NO:1901
BM781067.V1.3_at	AGAGCCGTCTGACAGTTCCTGAGGA	SEQ ID NO:1902
BM781067.V1.3_at	CAGTGGCCACAATCATCGTAGTCGA	SEQ ID NO:1903
BM781067.V1.3_at	CCTTTGGCAACCGTCTGTGGGAATG	SEQ ID NO:1904
BM781067.V1.3_at	GCTAGGCTCCTTGTCAGCTGAGAGA	SEQ ID NO:1905
BM781067.V1.3_at	GAAGACCCATTATCTCTACCTGAAA	SEQ ID NO:1906
BM781067.V1.3_at	GACCTGTACGCTGGCCTGAATCAGA	SEQ ID NO:1907
BM781067.V1.3_at	GTAGGCCCCTGGATGTTCGTTTGCA	SEQ ID NO:1908
BM781067.V1.3_at	GTTCGTTTGCATCTCCATGAATGTG	SEQ ID NO:1909
BM781067.V1.3_at	GGGCTTACTGCTGCTGGTGTATTAC	SEQ ID NO:1910
H.sapiens mRNA for elongation factor 1-beta.		
BM781233.V1.3_at	ATAGATCTCTTTGGGTCTGATGACG	SEQ ID NO:1911
BM781233.V1.3_at	ATGTGCAGTCCATGGATGTGGCCGC	SEQ ID NO:1912
BM781233.V1.3_at	AGAAGGCCAGTCTGCCAGGAGTGAA	SEQ ID NO:1913
BM781233.V1.3_at	AGAACGCCTTGCACAGTATGAGTCA	SEQ ID NO:1914
BM781233.V1.3_at	AAAGCTTTGGGCAAGTATGGTCCTG	SEQ ID NO:1915
BM781233.V1.3_at	AAGAAACCTGCACTTGTTGCCAAGT	SEQ ID NO:1916
BM781233.V1.3_at	GCGGATCACTGCTTTTGAGGACTAT	SEQ ID NO:1917
BM781233.V1.3_at	GGCTCCTCTAAACTAGTTCCAGTGG	SEQ ID NO:1918
BM781233.V1.3_at	GGTCCTGCGGATGTGGAAGACACCA	SEQ ID NO:1919
BM781233.V1.3_at	TGGATGTGGCCGCTTTCAACAAGAT	SEQ ID NO:1920
BM781233.V1.3_at	TGCCAAGTCTTCCATCTTACTAGAT	SEQ ID NO:1921
Homo sapiens EPK2 mRNA for serine/threonine kinase.		
BM781375.V1.3_at	ATCACTGCTCCAAATATCTCCAAAG	SEQ ID NO:1922
BM781375.V1.3_at	AGTCTGTTTATATCAACGCGCAAAA	SEQ ID NO:1923
BM781375.V1.3_at	AGAAGACGTTTCCACAACATCTCTC	SEQ ID NO:1924
BM781375.V1.3_at	AATGATGTTTCTTTGCTATACTTAA	SEQ ID NO:1925
BM781375.V1.3_at	CCAGTGATTCTGCTGTACTGCCCAG	SEQ ID NO:1926
BM781375.V1.3_at	GAAATGTATTTTCCCTGTGATTGAT	SEQ ID NO:1927
BM781375.V1.3_at	GATACTGTATAACTCGCATAACCTT	SEQ ID NO:1928
BM781375.V1.3_at	GTAATTCTGAGTCACTAGGCACCCT	SEQ ID NO:1929
BM781375.V1.3_at	GGCACCCTATTATGGTTTTACTGCA	SEQ ID NO:1930
BM781375.V1.3_at	TGCCCAGCCATAAAGATCTCCAGAA	SEQ ID NO:1931
BM781375.V1.3_at	TCTCTCTCTACTTCATTCTCATATA	SEQ ID NO:1932
No Homology		
WBC003D11_V1.3_at	ATCTTCATTTCCTCTTAGCTGTCAG	SEQ ID NO:1933
WBC003D11_V1.3_at	AGACAGAGTGTGCATTCCTTCTTGC	SEQ ID NO:1934
WBC003D11_V1.3_at	CATCGGACCAACTTGTAGCTGACTA	SEQ ID NO:1935
WBC003D11_V1.3_at	AATGTGCCCAGGCTGAACTGCTGGA	SEQ ID NO:1936
WBC003D11_V1.3_at	CGATAAGTCTCGCTTGTTCTTGCAC	SEQ ID NO:1937
WBC003D11_V1.3_at	GAGGTTGTCCTTAATCAGCCATCGG	SEQ ID NO:1938
WBC003D11_V1.3_at	GAGGGTGATTCGCATCTTCATTTCC	SEQ ID NO:1939

Probe Set Name	Sequence	Sequence Identifier
WBC003D11_V1.3_at	GTCACATCCATGAGCCCAGTCAAGA	SEQ ID NO:1940
WBC003D11_V1.3_at	GTCATTCCATTATACCAGCTGAGGT	SEQ ID NO:1941
WBC003D11_V1.3_at	TATGGCTTGGCCTTGAGACTTGCTT	SEQ ID NO:1942
WBC003D11_V1.3_at	TTCTTGCCCGTTACACGATAAGTCT	SEQ ID NO:1943
Human lymphoid-restricted membrane protein (Jaw1) mRNA		
WBC013C09_V1.3_at	AGACTTAGACACAATGGGCCACCAC	SEQ ID NO:1944
WBC013C09_V1.3_at	ACAAGGCACTCTGTTTGTCTGTTGC	SEQ ID NO:1945
WBC013C09_V1.3_at	AATGGGATGTCTCTTCAGCTTATGA	SEQ ID NO:1946
WBC013C09_V1.3_at	CTCACAGGCCTGTTTTTCCAAAAGT	SEQ ID NO:1947
WBC013C09_V1.3_at	GCAGCTTTGATGAGCTTCCTCACAG	SEQ ID NO:1948
WBC013C09_V1.3_at	GAGGAAGCCTGCCTATGATCTTTTA	SEQ ID NO:1949
WBC013C09_V1.3_at	TGACACAATAGCTTCCTGGACAACA	SEQ ID NO:1950
WBC013C09_V1.3_at	GGGACTCCTGGATGTCTCTAGAACA	SEQ ID NO:1951
WBC013C09_V1.3_at	TCTGTTGCCTTCATTGTACTGTTTG	SEQ ID NO:1952
WBC013C09_V1.3_at	TATCTTGTGGCCATTTACCAGACTT	SEQ ID NO:1953
WBC013C09_V1.3_at	TTGTGATTATCTCCCCAACTGAAAT	SEQ ID NO:1954
Homo sapiens pro-oncosis receptor inducing membrane injury gene, mRNA		
WBC025B03_V1.3_at	AGTCAGTTTCTTTGGTTCTCTGCAA	SEQ ID NO:1955
WBC025B03_V1.3_at	ACTTTCTTCTATACTTGCTTCTTTA	SEQ ID NO:1956
WBC025B03_V1.3_at	AATTTGCCTTTCAAGTTTCCTGTGC	SEQ ID NO:1957
WBC025B03_V1.3_at	AATTTTGTTTGCAGTCCTTGAGAAT	SEQ ID NO:1958
WBC025B03_V1.3_at	CAAGTTTCCTGTGCTTTGGGTTTGA	SEQ ID NO:1959
WBC025B03_V1.3_at	GACAGGCCTGAAACTTTCTTCTATA	SEQ ID NO:1960
WBC025B03_V1.3_at	GGTGATGCAAACCAATATTCTGCTT	SEQ ID NO:1961
WBC025B03_V1.3_at	GGATCAGCTTTTGGTATTTCATTGT	SEQ ID NO:1962
WBC025B03_V1.3_at	TACCAGTGCTTCAATGCAGTCAGTT	SEQ ID NO:1963
WBC025B03_V1.3_at	TAGTTATGTCTTTTCTCTGTATGTA	SEQ ID NO:1964
WBC025B03_V1.3_at	TTCTGCTTTGGAGCACATTTCCTAA	SEQ ID NO:1965
No Homology		
WBC33.gRSP.V1.3_at	ATGGATATACCACAAGCTGCTTTAT	SEQ ID NO:1966
WBC33.gRSP.V1.3_at	AGCAGTTTGGCTATTCTCAGTCCTT	SEQ ID NO:1967
WBC33.gRSP.V1.3_at	AAAGGTCTCCTGGAATCATGATCAG	SEQ ID NO:1968
WBC33.gRSP.V1.3_at	AATCCATGAACACATCTTCTGTCAG	SEQ ID NO:1969
WBC33.gRSP.V1.3_at	GAGCGTATGCTTTCATTTCTATTGG	SEQ ID NO:1970
WBC33.gRSP.V1.3_at	GATCTTGTACCCTGAAAACTTCCTA	SEQ ID NO:1971
WBC33.gRSP.V1.3_at	GTTGTCTCCTGTTTTGGTTATTACA	SEQ ID NO:1972
WBC33.gRSP.V1.3_at	GTACATCCTGTTAGACATCCTACGT	SEQ ID NO:1973
WBC33.gRSP.V1.3_at	TTTGCCCTCCCAAACGAATTGACTT	SEQ ID NO:1974
WBC33.gRSP.V1.3_at	TGCTTTATCCATTCACCTGTTGACA	SEQ ID NO:1975
WBC33.gRSP.V1.3_at	TTGACAGTCTTTTGGGTTGTCTCCT	SEQ ID NO:1976
Homo sapiens neuronal apoptosis inhibitory protein mRNA		

Probe Set Name	Sequence	Sequence Identifier
WBC014B05_V1.3_at	CAGCTAAATTTGTGTTTTCCGGAAT	SEQ ID NO:1977
WBC014B05_V1.3_at	AACATGTGTTGTCTGCTGGTGACTC	SEQ ID NO:1978
WBC014B05_V1.3_at	AACGGCCTTGGAATTCTCCTGTGAA	SEQ ID NO:1979
WBC014B05_V1.3_at	AACCGCTCTGTACCCTAAATGTTAT	SEQ ID NO:1980
WBC014B05_V1.3_at	AAGGCATACTCGCATGTTGCTAGAT	SEQ ID NO:1981
WBC014B05_V1.3_at	GTTAGATAACCACGCGTCTGAGACT	SEQ ID NO:1982
WBC014B05_V1.3_at	GGTGACTCCATGTTGCTGGATTCTA	SEQ ID NO:1983
WBC014B05_V1.3_at	GGATTCTACATCTGCTCGTCCAGAA	SEQ ID NO:1984
WBC014B05_V1.3_at	GGCTAACTCTAGGAAGGCATTCTTT	SEQ ID NO:1985
WBC014B05_V1.3_at	TACTTTCTCCCTTTTTATACTGCTT	SEQ ID NO:1986
WBC014B05_V1.3_at	TTCCAGAGCCTTTTGAGTCAACACT	SEQ ID NO:1987
No Homology		
BM734943.V1.3_at	ATTTCCTGGTAATCTCAATTCCTGC	SEQ ID NO:1988
BM734943.V1.3_at	ATACGATGCCGTATGATCTGGGCCA	SEQ ID NO:1989
BM734943.V1.3_at	AGACCTTTGCTGTGCGTCCTGGAGC	SEQ ID NO:1990
BM734943.V1.3_at	AGCCATGGTCATTTGTGTTACGTAT	SEQ ID NO:1991
BM734943.V1.3_at	AAACTTTCCTGAGCTTGTCTGAGTC	SEQ ID NO:1992
BM734943.V1.3_at	CAAGGAACCCTTTCTGCAAGTCAGT	SEQ ID NO:1993
BM734943.V1.3_at	CTGTGTGTACTATCTTTGCTGTTGT	SEQ ID NO:1994
BM734943.V1.3_at	GAGGTCCCTGGGAGCAGTTGCACAT	SEQ ID NO:1995
BM734943.V1.3_at	GTCTGAGTCTTGAATCGTTACCACG	SEQ ID NO:1996
BM734943.V1.3_at	GGAGGGTGACATTGCTCAAGCCATG	SEQ ID NO:1997
BM734943.V1.3_at	TCAGCATTCCTGTTTCCCTTATATC	SEQ ID NO:1998
H.sapiens initiation factor 4B cDNA.		
Foe1075.V1.3_at	GTAAAATCCCATCCTTTCGGTTGTG	SEQ ID NO:1999
Foe1075.V1.3_at	AAAGGTAGGGTTTGCCCTCTTCATG	SEQ ID NO:2000
Foe1075.V1.3_at	ATGGCTTGGATTGGCCTAGTAGCTA	SEQ ID NO:2001
Foe1075.V1.3_at	AATACAGTAGCTTGCCTGCTGGGAT	SEQ ID NO:2002
Foe1075.V1.3_at	GAATGAATCATTTACCCAGTGGACA	SEQ ID NO:2003
Foe1075.V1.3_at	GTCCCACTCCTCAATACGTGTAAAA	SEQ ID NO:2004
Foe1075.V1.3_at	GGAAGTGACTTTTAGAGATGCCCAA	SEQ ID NO:2005
Foe1075.V1.3_at	TCAGTCCTAGGTTAGACCCTGTCCA	SEQ ID NO:2006
Foe1075.V1.3_at	TGACACCTTGGTCTTTTGTTTGCAA	SEQ ID NO:2007
Foe1075.V1.3_at	TCTGGATGTATCCTTGTGGGCACAT	SEQ ID NO:2008
Foe1075.V1.3_at	TTCATGTCTACTCCTTCCAAATAGT	SEQ ID NO:2009
No Homology		
WBC038G11_V1.3_at	ATCTGTGGCGGATGTTTCTTCTCTG	SEQ ID NO:2010
WBC038G11_V1.3_at	AGGAGTTCTCCTGAGCTCAGCCGAG	SEQ ID NO:2011
WBC038G11_V1.3_at	AGCAGTTCTTCCTGAACGGCTTTGA	SEQ ID NO:2012
WBC038G11_V1.3_at	AGACTGACAGCTGACTCCCAGGAGT	SEQ ID NO:2013
WBC038G11_V1.3_at	ACGTGCATGTGTCTTCCAGGAGCAT	SEQ ID NO:2014
WBC038G11_V1.3_at	AAACAAGCGACATCAGCACCTGGGA	SEQ ID NO:2015

Probe Set Name	Sequence	Sequence Identifier
WBC038G11_V1.3_at	AAGGAAGGGCTCTGCCTGAGCAGTT	SEQ ID NO:2016
WBC038G11_V1.3_at	GAACTTGGTCGCATTTGGTCTGAAA	SEQ ID NO:2017
WBC038G11_V1.3_at	GAAGGAGTTCCCTGATCGGCTACAG	SEQ ID NO:2018
WBC038G11_V1.3_at	GTGAACTGCCTGTTGAACTTGGTCG	SEQ ID NO:2019
WBC038G11_V1.3_at	GGAGCATTGCACGTTGCCTGTAGAA	SEQ ID NO:2020
Homo sapiens mRNA; cDNA DKFZp686K06110 (from clone DKFZp686K06110).		
WBC031F04_V1.3_at	ATGTGAAACACCTCTTTGCTGCATT	SEQ ID NO:2021
WBC031F04_V1.3_at	ATGTGATTCTGAAGCCTGGCCAATG	SEQ ID NO:2022
WBC031F04_V1.3_at	ACTGAGGACGGCTTTTCCTGGACAA	SEQ ID NO:2023
WBC031F04_V1.3_at	AAAAGTCTTGTAGGTCACTGCGCCA	SEQ ID NO:2024
WBC031F04_V1.3_at	CTGCATTCTTTTTCTTCGCTTACAA	SEQ ID NO:2025
WBC031F04_V1.3_at	GTCTTTAATCATTGGTTCGGCTGCT	SEQ ID NO:2026
WBC031F04_V1.3_at	GGTCTACTTTTTAATGGCTTTCATA	SEQ ID NO:2027
WBC031F04_V1.3_at	TGGAAACGGTTTCACTTGCCCTTTG	SEQ ID NO:2028
WBC031F04_V1.3_at	TGCGCCATCTCAGCCATAGTAGTTG	SEQ ID NO:2029
WBC031F04_V1.3_at	TTCGGCTGCTTTTTGTACTTTGTTT	SEQ ID NO:2030
WBC031F04_V1.3_at	TTGCAGTTTGCTTCCATGTGATTCT	SEQ ID NO:2031
Homo sapiens triggering receptor expressed on myeloid cells 1, mRNA.		
BM734862.V1.3_at	ATCTACATCCATCTGGCAGTTGTGC	SEQ ID NO:2032
BM734862.V1.3_at	ATGAGGATGACCTCTGATCTCCATC	SEQ ID NO:2033
BM734862.V1.3_at	AGCATTGTCATTCCTGTGGCGTGCG	SEQ ID NO:2034
BM734862.V1.3_at	ACAAAGGTTATTTCTGAGGCTCAGG	SEQ ID NO:2035
BM734862.V1.3_at	CTCGTGACTAAGAGCCTGGTCCTTA	SEQ ID NO:2036
BM734862.V1.3_at	CCCTCATTTCACTGATGACCGTGGG	SEQ ID NO:2037
BM734862.V1.3_at	GAAGTCATTTGGATCCTAGGCCCAT	SEQ ID NO:2038
BM734862.V1.3_at	TGGCGTGCGCACTCGTGACTAAGAG	SEQ ID NO:2039
BM734862.V1.3_at	GGCAGCGACATGAGTTGGATCCGTT	SEQ ID NO:2040
BM734862.V1.3_at	TAAAAGAGCAGACACGGCCCCAAAC	SEQ ID NO:2041
BM734862.V1.3_at	TTACTGTCCTGTTTGCTGTCACACA	SEQ ID NO:2042
No Homology		
BM735402.V1.3_at	ATAACCCCACAGCTTGAGTACTTAC	SEQ ID NO:2043
BM735402.V1.3_at	ATTTGCTGAATAACCAGTCCTCTCC	SEQ ID NO:2044
BM735402.V1.3_at	AATTCCGTTTTCACAGAAGGGCTCA	SEQ ID NO:2045
BM735402.V1.3_at	AGAATCTTTTCTCCATGCATGTAAA	SEQ ID NO:2046
BM735402.V1.3_at	GAGTACTTACTGCTTGGCGGGTCAC	SEQ ID NO:2047
BM735402.V1.3_at	GTCCTCTCCTTTTCTGTGAAACTAA	SEQ ID NO:2048
BM735402.V1.3_at	GGGCTCAATTTGTTCCTTATCGTCT	SEQ ID NO:2049
BM735402.V1.3_at	TGGTACTCACCCATGGAGATGCTTA	SEQ ID NO:2050
BM735402.V1.3_at	TCCCACCCAGTTGAGTTATTTGCTT	SEQ ID NO:2051
BM735402.V1.3_at	TTCTCACTTACTTTCCCTTTAGGAG	SEQ ID NO:2052
BM735402.V1.3_at	TTATCGTCTCCCCATTGAAGTGTCG	SEQ ID NO:2053

Probe Set Name	Sequence	Sequence Identifier
Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog 2 (avian) (ETS2), mRNA.		
WBC025E03_V1.3_at	AGACGATTTCCAGTATCTCAGCACA	SEQ ID NO:2054
WBC025E03_V1.3_at	CAGTGTATTCCTGGCCTTTATACGC	SEQ ID NO:2055
WBC025E03_V1.3_at	AAGTCAGACACGCTTCACTAGCAGT	SEQ ID NO:2056
WBC025E03_V1.3_at	CATGCGACTGGGAACATCTTGTTGC	SEQ ID NO:2057
WBC025E03_V1.3_at	CGGTGGCTGCCATCTGTACAGAAGA	SEQ ID NO:2058
WBC025E03_V1.3_at	GCTCGAGCCACATGAAATTGCCAAT	SEQ ID NO:2059
WBC025E03_V1.3_at	GACAATTTGTCTCAATACCCACACG	SEQ ID NO:2060
WBC025E03_V1.3_at	GTTTATCTCTCGGACATCTGTTTAT	SEQ ID NO:2061
WBC025E03_V1.3_at	GGATGTTTTTCTCAAGCAGGCCCTG	SEQ ID NO:2062
WBC025E03_V1.3_at	TGGCAGTTTTGTGTGGTCCAACCTA	SEQ ID NO:2063
WBC025E03_V1.3_at	TTGGGCCTCTTCTTTCTCAAATAAT	SEQ ID NO:2064
No homology		
B1961438.V1.3_at	ATCCAGGGTGGAGTCTATGCAGAAA	SEQ ID NO:2065
B1961438.V1.3_at	CAGAAAAGGGCCTCACCTGCCAGGG	SEQ ID NO:2066
B1961438.V1.3_at	AAGGAGCCTTCTTGAGGTCACTGCA	SEQ ID NO:2067
B1961438.V1.3_at	GAAATGACCCATAATCCAGCAACGC	SEQ ID NO:2068
B1961438.V1.3_at	GACATGAGCGTTTGTGTTTGCTTTA	SEQ ID NO:2069
B1961438.V1.3_at	GAGGTCACTGCATTTGATCTTCATG	SEQ ID NO:2070
B1961438.V1.3_at	GTGGGCAGAGACTTGGCATCATTGT	SEQ ID NO:2071
B1961438.V1.3_at	GGCATCATTGTCATCCAGCAAATAA	SEQ ID NO:2072
B1961438.V1.3_at	TCAGTCTCCCCTAGTCCAGAAAAGG	SEQ ID NO:2073
B1961438.V1.3_at	TGCGCATTGCTTTCCAAGGAGCCTT	SEQ ID NO:2074
B1961438.V1.3_at	TTTGATCTTCATGGCGGCACCTGGA	SEQ ID NO:2075
No homology		
BM780914.V1.3_at	GGGATGCCCAATCCCGGGACCTACA	SEQ ID NO:2076
BM780914.V1.3_at	AAGAACTTTGTGTGCGACCCCGAGG	SEQ ID NO:2077
BM780914.V1.3_at	GAGGTACAGGACTTTGAAACGTTCT	SEQ ID NO:2078
BM780914.V1.3_at	ATAAGAGCCCGTGGGTACTTCACCG	SEQ ID NO:2079
BM780914.V1.3_at	CTACACCGTAAGGATAAGAGCCCGT	SEQ ID NO:2080
BM780914.V1.3_at	TTGAAACGTTCTACGGGATGCCCAA	SEQ ID NO:2081
BM780914.V1.3_at	GGTACTTCACCGGAATCGTGAGCGA	SEQ ID NO:2082
BM780914.V1.3_at	TGATGCGGAAGATCTTCCCGCCCAT	SEQ ID NO:2083
BM780914.V1.3_at	TGCAGAAAGTACTCGCTGATGCGGA	SEQ ID NO:2084
BM780914.V1.3_at	TGAGTGACAGCCTGCAGAACAAGCT	SEQ ID NO:2085
BM780914.V1.3_at	TCCTCGTCCTGATCTGCAGAAAGTA	SEQ ID NO:2086
Equus caballus matrix metalloproteinase 1 precursor (MMP1)		
WBC030E04_V1.3_at	ATAATTTACTTCCACCAATGAGGGT	SEQ ID NO:2087
WBC030E04_V1.3_at	ATTGATACTGGAGAGCAGCCTCAGA	SEQ ID NO:2088
WBC030E04_V1.3_at	ATGACTTTCCTGGAATTGGCGACAA	SEQ ID NO:2089
WBC030E04_V1.3_at	AAGCCAATAGCTGGTTCAACTGCAG	SEQ ID NO:2090

Probe Set Name	Sequence	Sequence Identifier
WBC030E04_V1.3_at	GAATTTTGACTCTCCAGAAAGCCAA	SEQ ID NO:2091
WBC030E04_V1.3_at	GAATGCAATGTTTCGTGTACTGCTA	SEQ ID NO:2092
WBC030E04_V1.3_at	GAAGATGTTTTCCTGAAGAGCCATA	SEQ ID NO:2093
WBC030E04_V1.3_at	GAGATACGAGTCTTCACCAGAGGAA	SEQ ID NO:2094
WBC030E04_V1.3_at	GAGCTGCTACTAGTATTATCCTAAT	SEQ ID NO:2095
WBC030E04_V1.3_at	GATTTACGGATTCATATGGGCCAAT	SEQ ID NO:2096
WBC030E04_V1.3_at	TGGATTTTTCTATTTCTTTCACGGA	SEQ ID NO:2097
No Homology		
BM734654.V1.3_at	ACCTAGACGACCTCTCGGGATTGAC	SEQ ID NO:2098
BM734654.V1.3_at	CGATTCCGTTATGCGGTCCAAGCAA	SEQ ID NO:2099
BM734654.V1.3_at	TGAACGGGACCAGCCAAACGACGGG	SEQ ID NO:2100
BM734654.V1.3_at	AGAACTTCTCATGCTTCATCTACAT	SEQ ID NO:2101
BM734654.V1.3_at	GACCGTGATGGTCAACACCAGCCAA	SEQ ID NO:2102
BM734654.V1.3_at	GACGACGTCCAGTATTTCCTGTATA	SEQ ID NO:2103
BM734654.V1.3_at	GGGATCCAGTTCTTCGATTCCGTTA	SEQ ID NO:2104
BM734654.V1.3_at	GGAATGTCCCCGTTACATGAGCGAC	SEQ ID NO:2105
BM734654.V1.3_at	TCTACATCGTGCACTTCATGATCTG	SEQ ID NO:2106
BM734654.V1.3_at	TTTCGGAGAAGCTCGTCTACACCAA	SEQ ID NO:2107
BM734654.V1.3_at	TTGACCTCTTACAATTACTTCGTGG	SEQ ID NO:2108
No Homology		
BM734722.V1.3_at	CGGGCGACTCGCAGAATCAATACAT	SEQ ID NO:2109
BM734722.V1.3_at	ACAGAGCCCCGGTCAGCGGGTGAAA	SEQ ID NO:2110
BM734722.V1.3_at	AACTGAACGATAACCATCCGACCGA	SEQ ID NO:2111
BM734722.V1.3_at	AATCAATACATTTTCCCGAGTCTGG	SEQ ID NO:2112
BM734722.V1.3_at	TCGGCTGCCTGGTGAAGAGGTTCCT	SEQ ID NO:2113
BM734722.V1.3_at	GCGTTTCTGCAGCTATTTTTCTACT	SEQ ID NO:2114
BM734722.V1.3_at	GGTCCCGCGCATCAAAGACAAACTG	SEQ ID NO:2115
BM734722.V1.3_at	GCGACTTCCAGTACGAGCTGGTCAT	SEQ ID NO:2116
BM734722.V1.3_at	GAAGAGGTTCCTCCGGAGACACAGT	SEQ ID NO:2117
BM734722.V1.3_at	GGAGACACAGTCTGTTCCAGCCGGT	SEQ ID NO:2118
BM734722.V1.3_at	TGAAGTTTGGCCAAGAGGCTTCCCG	SEQ ID NO:2119
Homo sapiens SUI1 isolog		
B1961499.V1.3_at	AGGCCACCCTTCTAGCAGAGTTAAA	SEQ ID NO:2120
B1961499.V1.3_at	AGAACTTGCGGCTTGACTAGCAGCA	SEQ ID NO:2121
B1961499.V1.3_at	AAGAGTGATGCCCTGGTGTCTCCAG	SEQ ID NO:2122
B1961499.V1.3_at	CAGCTGCCCAATGCCATGTGAAGTA	SEQ ID NO:2123
B1961499.V1.3_at	GAGAGAATGTCACCACCTGAGCAGC	SEQ ID NO:2124
B1961499.V1.3_at	GAGTTCCCTGCCCTGAGAGAATGTC	SEQ ID NO:2125
B1961499.V1.3_at	GTCTAGTCTTGAAGTCCCTCATTTA	SEQ ID NO:2126
B1961499.V1.3_at	GGTGATAGGACATCTGGCTTGCCAG	SEQ ID NO:2127
B1961499.V1.3_at	GGCTTGCCAGCGAGGTCTTTTTGAC	SEQ ID NO:2128
B1961499.V1.3_at	TAATGTGATGTTTCGGCCAAGCCCA	SEQ ID NO:2129

Probe Set Name	Sequence	Sequence Identifier
B1961499.V1.3_at	TATGTGTCAGTCACGTAGCCAGCTG	SEQ ID NO:2130
Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1 (GNB2L1), mRNA.		
WBC048H02_V1.3_at	ATCGGCACCCGCTAGAAATACATGG	SEQ ID NO:2131
WBC048H02_V1.3_at	ATCATTGTCTCCTGTGGCTGGGACA	SEQ ID NO:2132
WBC048H02_V1.3_at	AGGCTACCTGAACACTGTCACTGTC	SEQ ID NO:2133
WBC048H02_V1.3_at	AGACTCTGTTTGCTGGCTACACGGA	SEQ ID NO:2134
WBC048H02_V1.3_at	AGAAGTTATCAGTACCAGCAGCAAG	SEQ ID NO:2135
WBC048H02_V1.3_at	AGCTGAAGACCAATCACATCGGCCA	SEQ ID NO:2136
WBC048H02_V1.3_at	GATCCCTCTGTGCTTCTGGAGGCAA	SEQ ID NO:2137
WBC048H02_V1.3_at	GGCCAGGCCATGCTTTGGGATTTAA	SEQ ID NO:2138
WBC048H02_V1.3_at	GGGACATCATCAACGCCTTGTGCTT	SEQ ID NO:2139
WBC048H02_V1.3_at	GGCAAGCACCTTTACACACTAGATG	SEQ ID NO:2140
WBC048H02_V1.3_at	TACACTGTCCAGGATGAGAGCCACT	SEQ ID NO:2141
Pinin, desmosome associated protein (PNN)		
WBC012E07_V1.3_at	AATCAGATCTTTGCAGCTTTGAGGG	SEQ ID NO:2142
WBC012E07_V1.3_at	AATTTGGTTGGCATTTTCTTCATGA	SEQ ID NO:2143
WBC012E07_V1.3_at	CTTTTGTGTTGGCTCTAACTCTGAA	SEQ ID NO:2144
WBC012E07_V1.3_at	CCTCCTCATCTTTAAACCACGTATT	SEQ ID NO:2145
WBC012E07_V1.3_at	GAGCATCATTCTTTTGTCTCCATGG	SEQ ID NO:2146
WBC012E07_V1.3_at	GTTTCCTCACTTTTATTTGCCTTAG	SEQ ID NO:2147
WBC012E07_V1.3_at	GTCTCCATGGTTACTTGTGTGATAC	SEQ ID NO:2148
WBC012E07_V1.3_at	GTGGTCTTGTCTTAACTTTTGTGTT	SEQ ID NO:2149
WBC012E07_V1.3_at	GGAGTATCTGTTGCCCATTACTATA	SEQ ID NO:2150
WBC012E07_V1.3_at	TACTGTTTTTTCTAATCTCCCTTGT	SEQ ID NO:2151
WBC012E07_V1.3_at	TTTAATCTAAGCATTTTCCCCTCCT	SEQ ID NO:2152
Homo sapiens T-cell receptor beta (TCRB) mRNA.		
BM735494.V1.3_at	GGGACACCCGATATAATTCGCCGCT	SEQ ID NO:2153
BM735494.V1.3_at	AGATGATGAAAACCCCAGCTACTGT	SEQ ID NO:2154
BM735494.V1.3_at	AGCTACTGTCTGAGCAGCCGGCTGA	SEQ ID NO:2155
BM735494.V1.3_at	AACAGCTTCAAATCGTTTCTCACCT	SEQ ID NO:2156
BM735494.V1.3_at	AGCCCTACAGGGAGCAGTCAGATGA	SEQ ID NO:2157
BM735494.V1.3_at	ACAACGCTCATTTAAACCTTCACAT	SEQ ID NO:2158
BM735494.V1.3_at	GCACCAGGCTCACTGTCACAGAGAA	SEQ ID NO:2159
BM735494.V1.3_at	GACTCTGCTGTGTATTTCTGTGCCA	SEQ ID NO:2160
BM735494.V1.3_at	GAGACCTCATCTCACGGGTGGGAAA	SEQ ID NO:2161
BM735494.V1.3_at	GTGACCCTACCCAAGGTGGCTGTGT	SEQ ID NO:2162
BM735494.V1.3_at	GTGGCTGTGTTTGAACCTTCGGAAG	SEQ ID NO:2163
No Homology		
Foe1288.V1.3_at	ATCAAGTCCCTTTCAGTGTTCTGAA	SEQ ID NO:2164
Foe1288.V1.3_at	ATCACCTTTGGAAGCCAGCGGCAAT	SEQ ID NO:2165
Foe1288.V1.3_at	AGAGGATGTAACACCACCTTGCCAT	SEQ ID NO:2166

Probe Set Name	Sequence	Sequence Identifier
Foe1288.V1.3_at	AGTCTCTGTCATTCATTTCTGTCGA	SEQ ID NO:2167
Foe1288.V1.3_at	AGCGGCAATGCCATTCTGCTACTAT	SEQ ID NO:2168
Foe1288.V1.3_at	ACTTCCCACAGATTTGTTATCCTCA	SEQ ID NO:2169
Foe1288.V1.3_at	AAGTTTGCCTTGTATCTCCTAGTGC	SEQ ID NO:2170
Foe1288.V1.3_at	AAGACTGCCGTGTGCCCGAGGTATG	SEQ ID NO:2171
Foe1288.V1.3_at	GAGACTGTGATTTGGTTCTTCCTTC	SEQ ID NO:2172
Foe1288.V1.3_at	GAGTAACCATTTCCTTTGTGGCCAA	SEQ ID NO:2173
Foe1288.V1.3_at	TGTGGCCAATCTGTGTATGCTTTTA	SEQ ID NO:2174
Homo sapiens non-POU domain containing, octamer-binding, mRNA		
WBC014G03_V1.3_at	ATATATTACCCCTTCATGTCCTAAG	SEQ ID NO:2175
WBC014G03_V1.3_at	GATTTGTCCCTGATACCTTTGGAGT	SEQ ID NO:2176
WBC014G03_V1.3_at	AATCTTGTGTTAACTTGCCTCCATC	SEQ ID NO:2177
WBC014G03_V1.3_at	CATCCTGTTTTGTTTGCTTTCTCAT	SEQ ID NO:2178
WBC014G03_V1.3_at	GCCTCCATCTTTTTCTTGGGTGAAG	SEQ ID NO:2179
WBC014G03_V1.3_at	GCTGTTCACAGCTTTTCTTGGTAGG	SEQ ID NO:2180
WBC014G03_V1.3_at	GAATGGCCCTTTTGTGTCTATGATG	SEQ ID NO:2181
WBC014G03_V1.3_at	GTGCATACGGTTCTGTTATATCCCA	SEQ ID NO:2182
WBC014G03_V1.3_at	GGTGTACCATGTTTGATTTGTCCCT	SEQ ID NO:2183
WBC014G03_V1.3_at	GGACAGTAACTCTTAGCCTTGCCTA	SEQ ID NO:2184
WBC014G03_V1.3_at	TAATCATTCCATTCTTTGTCCATCC	SEQ ID NO:2185
H.sapiens mRNA for P1 protein (P1.h).		
WBC043B10_V1.3_at	GAGCCAAGAAGGTTTCTCCCGTGTT	SEQ ID NO:2186
WBC043B10_V1.3_at	AAGAGACTGGATCACACTGCCTGCT	SEQ ID NO:2187
WBC043B10_V1.3_at	AAGTCTTTGCCTTTATTCCCTGAAT	SEQ ID NO:2188
WBC043B10_V1.3_at	CTTTGGATTGTTTTATGCTGCTGGA	SEQ ID NO:2189
WBC043B10_V1.3_at	CTCCCGAGCACTTTGGTCCAGAATA	SEQ ID NO:2190
WBC043B10_V1.3_at	GACTAATGCATACTTTTGACCTGAA	SEQ ID NO:2191
WBC043B10_V1.3_at	GTGTTCGTTGGCTGTTTTCTTCCTC	SEQ ID NO:2192
WBC043B10_V1.3_at	GGGCACCTTGGTTTCTGTTTATCCT	SEQ ID NO:2193
WBC043B10_V1.3_at	GGACCAAGACTATTGCTTCTTCATT	SEQ ID NO:2194
WBC043B10_V1.3_at	TGGGAGACATGTGATGACGCCGATC	SEQ ID NO:2195
WBC043B10_V1.3_at	TTCTGTTTATCCTTTCTGTGTTCGT	SEQ ID NO:2196
Human mRNA for calcium-binding protein in macrophages (MRP-14) macrophage migration inhibitory factor (MIF)-related protein.		
B1961539.V1.3_at	ATATCATGGAGGACCTGGATACCAA	SEQ ID NO:2197
B1961539.V1.3_at	ATCATCAATGTCTTCCACCAGTACT	SEQ ID NO:2198
B1961539.V1.3_at	ACGGCCACAGCCACTAATCTGGAGG	SEQ ID NO:2199
B1961539.V1.3_at	CAAGCAGCTGAGTTTCGAGGAGTTC	SEQ ID NO:2200
B1961539.V1.3_at	GAGCTGGCGAACTTCCTCAAGAGTA	SEQ ID NO:2201
B1961539.V1.3_at	GATGCACGAGCATGACCAAGGCCAC	SEQ ID NO:2202
B1961539.V1.3_at	GAGGAGTTCATCATCCTGGTGGCCA	SEQ ID NO:2203

Probe Set Name	Sequence	Sequence Identifier
B1961539.V1.3_at	GGAACTGTCCCAGATGGAGCGCGAC	SEQ ID NO:2204
B1961539.V1.3_at	GGAGAGTGGCCATGGTCACAGCCAT	SEQ ID NO:2205
B1961539.V1.3_at	GGAGCGCGACATAGAGACCATCATC	SEQ ID NO:2206
B1961539.V1.3_at	TGACGCATGCCTCCCATGAGAAGAT	SEQ ID NO:2207
Homo sapiens actin related protein 2/3 complex subunit 1B (41 kD)(ARPC1B) mRNA.		
B1961827.V1.3_at	AGAACAGCGTCAGCCAGATCTCGGT	SEQ ID NO:2208
B1961827.V1.3_at	ACGGTCGCTTTGCTGAATGTTTCTA	SEQ ID NO:2209
B1961827.V1.3_at	GCAGTTCTGCACTACGGGCATGGAC	SEQ ID NO:2210
B1961827.V1.3_at	GAGCTTGGAATCAGCCTTGAAGGAC	SEQ ID NO:2211
B1961827.V1.3_at	GAGCGCTTCCAGAACCTCGACAGGA	SEQ ID NO:2212
B1961827.V1.3_at	GGGAAAGGCCAAGTGCTCGCAGTTC	SEQ ID NO:2213
B1961827.V1.3_at	GTGGGAAGCTTTTCTTACCTGTTGA	SEQ ID NO:2214
B1961827.V1.3_at	GGTCTGGACTCGCTGCACAAGAACA	SEQ ID NO:2215
B1961827.V1.3_at	GGACGTGCCCAAGCAGAACTCGCAG	SEQ ID NO:2216
B1961827.V1.3_at	TGAAGGAACACGTGCCTTTTTCTTA	SEQ ID NO:2217
B1961827.V1.3_at	TGACCTGCCAGGATTATGTTGCCCT	SEQ ID NO:2218
Fibroblast mRNA for aldolase A		
B1961941.V1.3_at	AGGGCTTTAGGCTGTTCTTTCCCAT	SEQ ID NO:2219
B1961941.V1.3_at	AGGAGGAGGCATCCATCAACCTCAA	SEQ ID NO:2220
B1961941.V1.3_at	AGTGGAGGTATTCTAAGGCTGCCCC	SEQ ID NO:2221
B1961941.V1.3_at	AAATACACCCCAAGTGGTCACGCTG	SEQ ID NO:2222
B1961941.V1.3_at	TGAAGCCCAATATGGTAACCCCAGG	SEQ ID NO:2223
B1961941.V1.3_at	GATTGCCATGGCAACTGTCACGGCA	SEQ ID NO:2224
B1961941.V1.3_at	GTCTGTGGTATTGTCTGTGTATGCT	SEQ ID NO:2225
B1961941.V1.3_at	GGAATATGTCAAGCGAGCCCTGGCC	SEQ ID NO:2226
B1961941.V1.3_at	TGGGATCACCTTCCTATCTGGAGGC	SEQ ID NO:2227
B1961941.V1.3_at	TTGCCTCCCTGGTGACATTGGTCTG	SEQ ID NO:2228
B1961941.V1.3_at	TTCATCTCTAACCATGCCTACTAAG	SEQ ID NO:2229
Human hemopoietic cell protein-tyrosine kinase (HCK) gene.		
BM734694.V1.3_at	ATCATGACCCGCTGCTGGAAGAACA	SEQ ID NO:2230
BM734694.V1.3_at	ATCAAGTCGGATGTCTGGTCCTTTG	SEQ ID NO:2231
BM734694.V1.3_at	AGAGTTGGATTCCACTCACAGCTGT	SEQ ID NO:2232
BM734694.V1.3_at	AAGTTGACATTTCTATGGCCTGGGA	SEQ ID NO:2233
BM734694.V1.3_at	CAGAGTGTGCTGGAGGACTTCTACA	SEQ ID NO:2234
BM734694.V1.3_at	GATACAGGATGCCTCGACCAGAGCA	SEQ ID NO:2235
BM734694.V1.3_at	GAGCCAGTACCAACAGCAGCCGTGA	SEQ ID NO:2236
BM734694.V1.3_at	GATTGTCACCTATGGCAGGATCCCT	SEQ ID NO:2237
BM734694.V1.3_at	GGACAATCTCTTTTTGACTCTAGCA	SEQ ID NO:2238
BM734694.V1.3_at	TGCCCCGAGGAGCTTTACAACATCA	SEQ ID NO:2239
BM734694.V1.3_at	TCCTTTGGTGTCCTGCTGATGGAGA	SEQ ID NO:2240
No Homology		

Probe Set Name	Sequence	Sequence Identifier
BM735487.V1.3_at	GAGTTCGAAGTCACCCTAATCACGT	SEQ ID NO:2241
BM735487.V1.3_at	CACCAGGACTCTAGCCCCAGAGTGG	SEQ ID NO:2242
BM735487.V1.3_at	AAATGGAACTCTCCTTTTCGAGCAT	SEQ ID NO:2243
BM735487.V1.3_at	CGGCCCGGACACAAGGAGGAAGCTC	SEQ ID NO:2244
BM735487.V1.3_at	GCGTCTGACCCCAGCGAAGGGCCAG	SEQ ID NO:2245
BM735487.V1.3_at	GAAGGGCCAGCCTTGCTTGGTTCAG	SEQ ID NO:2246
BM735487.V1.3_at	GACTGTGGAGGGACAGGCTTCCCCT	SEQ ID NO:2247
BM735487.V1.3_at	GTTAGCTTCCCCAAAAGAATTGTGT	SEQ ID NO:2248
BM735487.V1.3_at	GTCACCCTAATCACGTAAATGGAAC	SEQ ID NO:2249
BM735487.V1.3_at	GTGCTTGCTTGGGAGTTCGAAGTCA	SEQ ID NO:2250
BM735487.V1.3_at	TAGCCCCAGAGTGGCTCCAGAAGGT	SEQ ID NO:2251
Homo sapiens ring finger protein 10, mRNA (cDNA clone MGC:35311 IMAGE:5177665)		
BM735519.V1.3_at	CAGGCTACCTTCTCCATTTGGTTTT	SEQ ID NO:2252
BM735519.V1.3_at	AGATGTGTGGCCCAAAACTGCTCCA	SEQ ID NO:2253
BM735519.V1.3_at	AGCCTTCATGAAGCTGGACACGCCA	SEQ ID NO:2254
BM735519.V1.3_at	AGAAGCTCCTGTTCAGCACCTCAGT	SEQ ID NO:2255
BM735519.V1.3_at	AATACAGTGTATTTTCCAGCTTCCT	SEQ ID NO:2256
BM735519.V1.3_at	CAAGTGACACTACTGGCCCAGGCTA	SEQ ID NO:2257
BM735519.V1.3_at	CCGTGCTTTTGTTTTGCTGCTGTAA	SEQ ID NO:2258
BM735519.V1.3_at	TGAAAACAGCTTAATTCCTCCTGCC	SEQ ID NO:2259
BM735519.V1.3_at	TGATAACTCGGACCGTGTTCCTGTG	SEQ ID NO:2260
BM735519.V1.3_at	TTCCAGAATTCCTTCAGCCAAGCTA	SEQ ID NO:2261
BM735519.V1.3_at	TTCGGATCCCCTCTCTGAAGAGAAA	SEQ ID NO:2262
Human Fc-epsilon-receptor gamma-chain mRNA.		
BM735585.V1.3_at	ATGATTCCAGCAGTGGTCTTGCTCT	SEQ ID NO:2263
BM735585.V1.3_at	ACCCTACCCCTGTAATGATGCTATG	SEQ ID NO:2264
BM735585.V1.3_at	CTGCCATTAATGCTAGCTGACCCTA	SEQ ID NO:2265
BM735585.V1.3_at	GTACCCGGACCCAGGAGACTTATGA	SEQ ID NO:2266
BM735585.V1.3_at	GAGAGCCTCAGCTTTGCTATATTCT	SEQ ID NO:2267
BM735585.V1.3_at	GATGCCATCCTGTTCTTGTATGGTA	SEQ ID NO:2268
BM735585.V1.3_at	TGTTTATATTCTAGTCTCACCCCTA	SEQ ID NO:2269
BM735585.V1.3_at	TTTCAAACAGATGCCCTTGGTCACA	SEQ ID NO:2270
BM735585.V1.3_at	TAACGGACATCAGTGGTTCCTCTTC	SEQ ID NO:2271
BM735585.V1.3_at	TTGGTTGAACAAGCAGCGGCCCTGG	SEQ ID NO:2272
BM735585.V1.3_at	TTGCTCTTACTCCTTTTGGTTGAAC	SEQ ID NO:2273
Homo sapiens lysosomal-associated membrane protein 1 (LAMP1), mRNA.		
WBC038E02_V1.3_at	AGATTCTGGTGTTTGGTCTCTTCAC	SEQ ID NO:2274
WBC038E02_V1.3_at	ACTGGCTCCATATCATTTGGCTTTC	SEQ ID NO:2275
WBC038E02_V1.3_at	CTGCGTCTGCACTTGTTTGTGTACA	SEQ ID NO:2276
WBC038E02_V1.3_at	CCATGCAAGAGCTGGCACTTTTTTA	SEQ ID NO:2277
WBC038E02_V1.3_at	GACCCTCCTGTGTGCAATGCCGTAA	SEQ ID NO:2278

Probe Set Name	Sequence	Sequence Identifier
WBC038E02_V1.3_at	GTCTCTTCACTCTTGATTCAGATCT	SEQ ID NO:2279
WBC038E02_V1.3_at	GGGAGAGTCTCTGATCTTAACACTT	SEQ ID NO:2280
WBC038E02_V1.3_at	TGTTTGTGTACAGTGATCGCTCTCA	SEQ ID NO:2281
WBC038E02_V1.3_at	TGATTTACTGCTTGCAGCTCAGCGG	SEQ ID NO:2282
WBC038E02_V1.3_at	TGATCGCTCTCACTCTGATTTACTG	SEQ ID NO:2283
WBC038E02_V1.3_at	TTTTCGGTCTTCTGTTTGAGGTTCA	SEQ ID NO:2284
Homo sapiens EGF-like-domain, multiple 5 (EGFL5), mRNA.		
WBC012B04_V1.3_at	ATACGTTAAATTTCAGCCCAAGCAA	SEQ ID NO:2285
WBC012B04_V1.3_at	ATCTTTCTTACTTGTTCCTTATGCG	SEQ ID NO:2286
WBC012B04_V1.3_at	ATGCAAGTTTTCTCTTTAACCCTGA	SEQ ID NO:2287
WBC012B04_V1.3_at	AGGCTTCCTGATGCATTTCTAAATT	SEQ ID NO:2288
WBC012B04_V1.3_at	ACATATGCTGTACTAGGCTTCCTGA	SEQ ID NO:2289
WBC012B04_V1.3_at	AAAACCGTGTCTCATACATATGCTG	SEQ ID NO:2290
WBC012B04_V1.3_at	GAACCTTTTGGTCTGTTATGATCTT	SEQ ID NO:2291
WBC012B04_V1.3_at	GTAACTGTGACAGCAGCCCTGGAAT	SEQ ID NO:2292
WBC012B04_V1.3_at	GTCAGCCAGGGCTTCAGATCTCAGG	SEQ ID NO:2293
WBC012B04_V1.3_at	GGCACAAGCACTCTGTAATACGTTA	SEQ ID NO:2294
WBC012B04_V1.3_at	TTAACCCTGAGCCAGTGACTATGCC	SEQ ID NO:2295
Human mRNA for T200 leukocyte common antigen (CD45, LC-A)		
WBC027E07_V1.3_at	ATAGGGTGGTGGACCTTATGGCCCA	SEQ ID NO:2296
WBC027E07_V1.3_at	ATATTGAGAGTCTCCTGACCTCCAC	SEQ ID NO:2297
WBC027E07_V1.3_at	AGAAAGGCCCTCAGCTGCTGGGAAT	SEQ ID NO:2298
WBC027E07_V1.3_at	ACTTTGTCAAGCTCATTTCCTGGTA	SEQ ID NO:2299
WBC027E07_V1.3_at	GCTGGGAATGCTTGTCCCAACTTGA	SEQ ID NO:2300
WBC027E07_V1.3_at	GAGACTAGTTCTCTCGTGACACCCA	SEQ ID NO:2301
WBC027E07_V1.3_at	GGCCCACATGGCCTCCAAGGAGTAA	SEQ ID NO:2302
WBC027E07_V1.3_at	GGAGCCCTACCTTGTCATGTACCAT	SEQ ID NO:2303
WBC027E07_V1.3_at	GGACCACCAATCACCCAGCAAGAGA	SEQ ID NO:2304
WBC027E07_V1.3_at	TGACCTCCACAGTTTCCATCTCAGA	SEQ ID NO:2305
WBC027E07_V1.3_at	TTGCCCTCAACGACCACTTTGTCAA	SEQ ID NO:2306
No Homology		
WBC030C04_V1.3_at	ATGCGCACATTTACTAGCACCTACT	SEQ ID NO:2307
WBC030C04_V1.3_at	ATGGACTTCCCTGCATTGTATGAGA	SEQ ID NO:2308
WBC030C04_V1.3_at	ATGTGCTGTGTGCTCTGTGTACCCT	SEQ ID NO:2309
WBC030C04_V1.3_at	AGTTGTCTGGCCCAAAGCATCAGCA	SEQ ID NO:2310
WBC030C04_V1.3_at	GAGTTCGATTCCCATCTGAAACGAC	SEQ ID NO:2311
WBC030C04_V1.3_at	GAGACATTTTCCGTTGTCACAACTT	SEQ ID NO:2312
WBC030C04_V1.3_at	GAGAGGTCACCGATGCTGCTAAACA	SEQ ID NO:2313
WBC030C04_V1.3_at	GTGTGGCCTTAGTGACCAATCAGTC	SEQ ID NO:2314
WBC030C04_V1.3_at	TGTGTACCCTCAGATCACGTGAACT	SEQ ID NO:2315
WBC030C04_V1.3_at	TACTGAGGGCTTACCATGTGCTGTG	SEQ ID NO:2316

Probe Set Name	Sequence	Sequence Identifier
WBC030C04_V1.3_at	TTCACCCCTCGGAACATCGATGATG	SEQ ID NO:2317

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

GENE PRIORITY ORDER BASED ON T VALUE

Gene Name	M (24 hours)	T (24 hours)	Holm P (24 hours)	M (72 hours)	T (72 hours)	FDR P (72 hours)
WBC033A01_V1.3_at	-2.662894	-9.962659	0.000017	-1.276358	-4.955679	0.029004
WBC009F04_V1.3_at	-2.022275	-9.836701	0.000021	-0.815793	-4.117344	0.035681
WBC024B05_V1.3_at	-1.664652	-8.335464	0.000280	-0.880469	-4.570119	0.029004
WBC039D09_V1.3_at	-1.872731	-8.327496	0.000284	-1.004384	-4.632601	0.029004
WBC018F03_V1.3_at	-2.361400	-8.148680	0.000394			
WBC004E04_V1.3_at	-2.162850	-8.144995	0.000396	-1.175666	-4.591078	0.029004
WBC012A03_V1.3_at	-1.338388	-7.701847	0.000904	-0.758502	-4.523937	0.029004
WBC001F11_V1.3_at	-1.823749	-7.635242	0.001024	-1.166865	-5.061581	0.026896
WBC33.gRSP.V1.3_at	-2.213668	-7.568092	0.001163	-1.291169	-4.576337	0.029004
BM734943.V1.3_at	-2.502148	-7.546875	0.001211	-1.453158	-4.544783	0.029004
WBC025B03_V1.3_at	-2.621996	-7.517703	0.001281	-1.320582	-3.922683	0.047310
WBC005D09_V1.3_at	-1.776450	-7.461019	0.001428	-0.961345	-4.187062	0.033199
WBC018D03_V1.3_at	-1.288566	-7.385061	0.001652	-0.811415	-4.818958	0.029004
WBC047A01_V1.3_at	-1.489422	-7.333705	0.001822	-0.869908	-4.438289	0.029708
BM781416.V1.3_at	-0.890777	-7.202082	0.002353	-0.636407	-5.333266	0.024866
WBC310.V1.3_at	-2.057025	-7.191047	0.002403	-1.148505	-4.165566	0.033380
WBC038A02_V1.3_at	-1.237604	-7.149217	0.002608			
Foe1324.V1.3_at	-0.967173	-7.065375	0.003076	-0.591431	-4.481723	0.029391
WBC014G03_V1.3_at	-0.822802	-7.018150	0.003375			
WBC031C11_V1.3_at	-1.229890	-7.004847	0.003464			
Foe1317.V1.3_at	-1.393445	-7.004002	0.003469			
WBC025C03_V1.3_at	-1.123663	-7.000843	0.003490			
WBC005F01_V1.3_at	-1.793647	-6.973124	0.003685			
BM781033.V1.3_at	-1.600021	-6.959662	0.003784			
WBC037C09_V1.3_at	-2.315585	-6.944690	0.003897			
WBC013A11_V1.3_at	-1.518652	-6.906258	0.004204			
BM781067.V1.3_at	-2.131608	-6.868123	0.004537			
BM734719.V1.3_at	-1.725505	-6.864147	0.004572			
WBC007A08_V1.3_at	-0.791783	-6.841457	0.004782			
WBC030C11_V1.3_at	-1.786902	-6.811774	0.005075			
BM781233.V1.3_at	-1.079172	-6.802419	0.005170			
BM780999.V1.3_at	-1.147959	-6.682644	0.006574			
WBC011F05_V1.3_at	-1.014702	-6.644981	0.007086			
Foe1263.V1.3_at	-1.368441	-6.628304	0.007327	-0.841507	-4.224840	0.033199
WBC001F10_V1.3_at	-1.108760	-6.592549	0.007874			
B1961856.V1.3_at	-2.437119	-6.490502	0.009699			
WBC014E06_V1.3_at	-1.576883	-6.480146	0.009902			
WBC022D03_V1.3_at	-2.226427	-6.447584	0.010583	-1.403789	-4.212853	0.033199
WBC022B03_V1.3_at	-2.495001	-6.389631	0.011919			
Foe148.V1.3_at	-1.210133	-6.383976	0.012056			
BM734975.V1.3_at	-0.956313	-6.374726	0.012281			
WBC309.V1.3_at	-1.320389	-6.357556	0.012718			
WBC964.gRSP.V1.3_at	-2.148632	-6.308260	0.014086	-1.418636	-4.318625	0.033199
Foe1216.V1.3_at	-0.610111	-6.295728	0.014454			
B1961438.V1.3_at	-1.874821	-6.260291	0.015554			
BM781103.V1.3_at	-1.590271	-6.252160	0.015815			
Foe1288.V1.3_at	-1.086282	-6.246331	0.016004			
BM734780.V1.3_at	-1.686861	-6.126850	0.020531	-1.177444	-4.430605	0.029708
BM781375.V1.3_at	-1.401878	-6.104504	0.021514	-0.885759	-3.996806	0.043572
WBC016G11_V1.3_at	-1.524048	-6.096714	0.021863	-0.964780	-3.998437	0.043572
WBC013E05_V1.3_at	-1.235319	-6.073394	0.022944			
WBC035E01_V1.3_at	-1.009758	-6.067899	0.023204	-0.657412	-4.093653	0.036940
Foe443.V1.3_at	-1.810221	-6.050102	0.024086			
WBC013A09_V1.3_at	-1.197534	-6.028120	0.025226	-0.798145	-4.162797	0.033380
WBC009H07_V1.3_at	-1.169165	-6.027141	0.025270			

Gene Name	M (24 hours)	T (24 hours)	Holm P (24 hours)	M (72 hours)	T (72 hours)	FDR P (72 hours)
WBC016A12_V1.3_at	-1.818692	-5.989753	0.027347			
WBC027H11_V1.3_at	-1.218607	-5.989121	0.027374			
WBC004G01_V1.3_at	-1.133747	-5.983072	0.027719			
BM735402.V1.3_at	-1.194590	-5.964250	0.028841			
BM735494.V1.3_at	-1.750520	-5.958587	0.029181			
WBC374.V1.3_at	-1.644790	-5.957986	0.029208			
WBC335.V1.3_at	-1.119690	-5.956705	0.029278			
WBC031B06_V1.3_at	-1.371020	-5.939056	0.030389	-1.002910	-4.502046	0.029145
WBC019B05_V1.3_at	-2.812821	-5.935107	0.030625			
BM734661.V1.3_at	-1.009540	-5.929543	0.030980			
WBC028G09_V1.3_at	-1.536631	-5.888696	0.033768			
WBC032H02_V1.3_at	-1.665465	-5.848697	0.036747	-1.094870	-3.983557	0.043957
WBC038B01_V1.3_at	-1.238551	-5.775724	0.042904			
WBC004G09_V1.3_at	-2.481126	-5.766468	0.043737			
WBC020F05_V1.3_at	-1.228488	-5.741651	0.046091			
WBC022C04_V1.3_at	-1.051865	-5.738198	0.046419			
WBC107.V1.3_s_at	-1.968199	-5.730559	0.047158			
Foe1075.V1.3_at	-0.962785	-5.729726	0.047226			
WBC048H02_V1.3_at	-0.939329	-5.728407	0.047345			
WBC018B05_V1.3_at	-0.925714	-5.703704	0.049903			
BM734452.V1.3_at	0.805204	5.725055	0.047672			
WBC039F12_V1.3_at	1.150275	5.734195	0.046805			
WBC012C10_V1.3_at	1.627067	5.750482	0.045237			
WBC013C09_V1.3_at	0.805300	5.766335	0.043737			
B1961941.V1.3_at	0.808670	5.772622	0.043176			
BM735286.V1.3_at	0.677464	5.796605	0.041035	0.447623	3.969701	0.043957
BM734632.V1.3_at	1.546635	5.799185	0.040822			
BM734654.V1.3_at	1.896641	5.824011	0.038717			
WBC008A12_V1.3_at	1.454425	5.843937	0.037111	0.953908	3.974301	0.043957
WBC327.V1.3_at	3.134368	5.849951	0.036661			
B1961872.V1.3_at	0.695445	5.879069	0.034458			
WBC033D12_V1.3_at	1.564444	5.889206	0.033742			
WBC031D02_V1.3_at	1.280462	5.903074	0.032769			
BM735386.V1.3_at	0.843738	5.936267	0.030560			
WBC014H06_V1.3_at	2.344460	6.078689	0.022696			
WBC024G08_V1.3_at	0.990922	6.081274	0.022580			
BM781237.V1.3_s_at	1.208673	6.145017	0.019767			
WBC007F03_V1.3_at	0.678768	6.158498	0.019221	0.555707	5.226559	0.024866
WBC032D03_V1.3_at	1.385989	6.179118	0.018412			
WBC030E04_V1.3_at	4.696429	6.196116	0.017773			
WBC024F08_V1.3_at	1.057724	6.288312	0.014675			
WBC028C09_V1.3_at	0.725926	6.362683	0.012587			
WBC011D03_V1.3_at	1.853309	6.382535	0.012088			
B1961620.V1.3_at	1.747623	6.437617	0.010796			
WBC012B04_V1.3_at	2.475044	6.447033	0.010591			
WBC020H01_V1.3_at	1.314322	6.459585	0.010327			
BM780906.V1.3_at	1.288912	6.480826	0.009891			
WBC012E05_V1.3_at	2.297892	6.506542	0.009388			
WBC028E11_V1.3_at	2.406940	6.523695	0.009065			
WBC031G11_V1.3_at	1.225760	6.622921	0.007403			
WBC024H07_V1.3_at	0.976787	6.623779	0.007392			
BM734844.V1.3_at	0.933292	6.629950	0.007305			
B1961539.V1.3_at	4.852518	6.661050	0.006860			
WBC025A06_V1.3_at	1.823785	6.667810	0.006769			
WBC020H11_V1.3_at	0.986342	6.678247	0.006629	0.632519	4.440903	0.029708
BM781394.V1.3_at	1.762617	6.681449	0.006588			
WBC001E10_V1.3_at	1.449566	6.698739	0.006365			
WBC039G08_V1.3_at	0.952917	6.714431	0.006167			
BM734531.V1.3_at	2.023074	6.721602	0.006080			
WBC038D08_V1.3_at	0.973751	6.723009	0.006065	0.739545	5.296198	0.024866

Gene Name	M (24 hours)	T (24 hours)	Holm P (24 hours)	M (72 hours)	T (72 hours)	FDR P (72 hours)
WBC040E12_V1.3_at	2.867191	6.757972	0.005652			
B1961932.V1.3_s_at	1.234657	6.798806	0.005206			
WBC008D09_V1.3_at	2.132599	6.847202	0.004729			
WBC036E08_V1.3_at	0.903370	6.917203	0.004114			
BM735585.V1.3_at	1.170140	6.927900	0.004028			
WBC027E07_V1.3_at	0.856915	6.949906	0.003858			
B1961880.V1.3_at	2.362559	6.989422	0.003569			
WBC21.V1.3_at	3.858556	7.040639	0.003228			
BM734862.V1.3_at	1.814033	7.048185	0.003181			
B1961932.V1.3_at	1.458519	7.135736	0.002677			
WBC038G11_V1.3_at	0.970456	7.150263	0.002603			
BM735519.V1.3_at	1.321178	7.203189	0.002348			
WBC014B05_V1.3_at	3.009994	7.237630	0.002196			
WBC001D02_V1.3_at	1.758208	7.274337	0.002044			
WBC027F05_V1.3_at	4.660849	7.282229	0.002013			
BM734694.V1.3_at	1.920448	7.314034	0.001893			
BM734933.V1.3_at	2.051080	7.334686	0.001820	1.052354	3.899225	0.048632
GI9717252-3M_at	2.344887	7.340340	0.001800	1.236716	4.010774	0.043572
WBC044E01_V1.3_at	1.317571	7.360577	0.001731	0.953823	5.524562	0.024866
WBC027B01_V1.3_at	0.925355	7.371553	0.001695			
WBC003D11_V1.3_at	4.056714	7.407465	0.001582			
WBC021E07_V1.3_at	0.996203	7.449580	0.001459			
BM781186.V1.3_at	2.960940	7.599579	0.001096			
BM781269.V1.3_at	5.802158	7.601829	0.001091			
WBC019C11_V1.3_at	1.276000	7.664242	0.000970			
WBC025E03_V1.3_at	2.105169	7.668296	0.000963			
WBC008A10_V1.3_at	5.312376	7.675685	0.000949			
BM734900.V1.3_at	2.168771	7.714757	0.000882			
BM735452.V1.3_at	1.455575	7.894775	0.000629			
WBC005F10_V1.3_at	1.513331	8.094985	0.000434			
WBC028D04_V1.3_at	2.350644	8.115434	0.000418			
WBC031F04_V1.3_at	2.689395	8.137599	0.000401	1.325124	4.155226	0.033380
BM781278.V1.3_at	0.846445	8.145422	0.000396			
GI9717252-3_at	2.268058	8.389991	0.000254	1.189076	4.557171	0.029004
BM735091.V1.3_at	2.927326	8.424147	0.000239			
BM735057.V1.3_s_at	0.903257	8.439540	0.000232			
WBC015B08_V1.3_at	1.759706	8.580595	0.000180			
WBC030C04_V1.3_at	2.989697	8.747470	0.000134	1.418361	4.302077	0.033199
BM734722.V1.3_at	1.873417	8.955619	0.000093	0.956808	4.742436	0.029004
BM780914.V1.3_at	2.022282	9.423418	0.000042			
BM735487.V1.3_at	0.940146	9.472548	0.000039			
BM734891.V1.3_at	1.763656	9.766923	0.000024	0.678177	3.896254	0.048632
WBC024G03_V1.3_at	2.694822	9.905797	0.000019			
WBC117.gRSP.V1.3_at	2.194570	10.473732	0.000008			
WBC017B09_V1.3_at				-0.819031	-5.281446	0.024866
WBC005E06_V1.3_at				-0.554386	-5.100535	0.026896
B1961499.V1.3_at				-0.407910	-4.924593	0.029004
WBC311.V1.3_at				-0.607729	-4.873480	0.029004
BM734795.V1.3_at				-1.446996	-4.750582	0.029004
BM781409.V1.3_at				-0.780927	-4.746039	0.029004
BM781438.V1.3_at				-1.044275	-4.523519	0.029004
BM781379.V1.3_at				-0.556041	-4.410744	0.030078
BM781319.V1.3_at				-1.102450	-4.335677	0.033199
WBC023F12_V1.3_at				-1.739066	-4.277504	0.033199
WBC021E02_V1.3_at				-0.771972	-4.269989	0.033199
WBC012E07_V1.3_at				-0.881844	-4.248284	0.033199
WBC043B10_V1.3_at				-0.800840	-4.233410	0.033199
WBC215.gRSP.V1.3_at				-1.002742	-4.199851	0.033199
WBC013E10_V1.3_at				-1.090284	-4.184730	0.033199
Foe146.V1.3_at				-0.733985	-3.945641	0.045654

Gene Name	M (24 hours)	T (24 hours)	Holm P (24 hours)	M (72 hours)	T (72 hours)	FDR P (72 hours)
WBC017C08_V1.3_at				0.889661	4.203909	0.033199
BM734511.V1.3_at				1.107206	4.241555	0.033199
Foe1092.V1.3_at				0.762973	4.291741	0.033199
B1961827.V1.3_at				0.712699	4.382743	0.031054
WBC038E02_V1.3_at				0.422022	4.521474	0.029004
B1961900.V1.3_at				0.559448	4.667569	0.029004
WBC027D09_V1.3_at				0.664437	5.274541	0.024866

TABLE 6

TWO GENES SELECTED

Genes		Sensitivity	Specificity	Success
Foe1216	BM734531	1	1	1
BM734933	WBC012A03	1	1	1
Foe1263	BM734531	1	1	1
BM735452	WBC003D11	1	1	1
WBC008A10	WBC020H11	1	1	1
BM781409	WBC019C11	1	1	1
WBC013E10	BM734844	1	1	1
WBC038A02	WBC032H02	1	1	1
BM734943	WBC005F10	1	1	1
WBC030E04	B1961438	1	1	1
BM781375	WBC031C11	1	1	1
WBC310	WBC309	1	1	1
WBC036E08	B1961932	1	1	1
WBC001F10	BM734722	1	1	1
BM734900	WBC21	1	1	1
BM735452	WBC038E02	1	1	1
WBC024B05	WBC047A01	1	1	1
WBC024H07	BM734780	1	1	1
B1961856	BM734862	1	1	1
BM734661	WBC030E04	1	1	1

TABLE 7

THREE GENES SELECTED

Genes			Sensitivity	Specificity	Success
BM781409	BM734632	BM781033	1	1	1
WBC018B05	WBC009F04	WBC012E07	1	1	1
WBC021E07	WBC013A09	Foe1324	1	1	1
WBC012E05	BM735286	WBC008A12	1	1	1
WBC008A10	WBC038G11	WBC038B01	1	1	1
Foe1263	WBC028D04	WBC012A03	1	1	1
WBC018B05	WBC009F04	WBC024H07	1	1	1
WBC008D09	WBC028D04	WBC039F12	1	1	1
B1961499	BM735091	WBC015B08	1	1	1
Foe1288	WBC038B01	WBC031C11	1	1	1
WBC035E01	BM781319	GI9717252	1	1	1
WBC024F08	WBC013A09	WBC031F04	1	1	1
BM781269	WBC018D03	B1961620	1	1	1
BM781278	B1961932	WBC014B05	1	1	1
WBC031F04	Foe1324	B1961941	1	1	1
BM734654	WBC335	B1961880	1	1	1
WBC009H07	BM734933	BM734661	1	1	1
B1961941	WBC025E03	WBC327	1	1	1
WBC018D03	WBC014H06	WBC011F05	1	1	1
BM734694	WBC005F01	WBC011D03	1	1	1

TABLE 8

FOUR GENES SELECTED

Genes				Sensitivity	Specificity	Success
BM780914	WBC030E04	WBC031C11	WBC005E06	1	1	1
WBC021E02	B1961438	BM734531	WBC310	1	1	1
WBC374	Foe1263	BM734452	BM781067	1	1	1
WBC030C11	B1961941	WBC009H07	WBC005F01	1	1	1
WBC038G11	WBC019B05	WBC027F05	WBC024B05	1	1	1
BM781278	WBC001D02	WBC033D12	WBC031D02	1	1	1
WBC043B10	WBC030C11	WBC007F03	WBC024H07	1	1	1
BM781067	WBC005F01	WBC048H02	BM781237	1	1	1
BM734511	WBC020H11	WBC039F12	WBC019B05	1	1	1
WBC964	B1961932	WBC031D02	WBC037C09	1	1	1
WBC013E05	WBC012C10	WBC035E01	BM781186	1	1	1
WBC001E10	BM781269	BM734943	BM735519	1	1	1
B1961900	WBC022C04	BM735286	WBC327	1	1	1
WBC013C09	WBC028E11	GI9717252	WBC019B05	1	1	1
BM781409	WBC024B05	WBC014H06	WBC036E08	1	1	1
WBC21	WBC018F03	BM781379	WBC037C09	1	1	1
BM734531	WBC374	BM735386	WBC030C11	1	1	1
BM734632	B1961827	WBC013C09	B1961900	1	1	1
WBC031B06	BM781103	WBC039G08	BM781186	1	1	1
WBC014G03	WBC018F03	BM734654	BM781033	1	1	1

TABLE 9

FIVE GENES SELECTED

Genes					Sensitivity	Specificity	Success
WBC007A08	WBC012E05	WBC018B05	BM781394	WBC040E12	1	1	1
WBC038E02	WBC025C03	WBC013E05	WBC004E04	WBC005D09	1	1	1
BM781379	WBC038D08	B1961499	BM781033	WBC022D03	1	1	1
WBC005D09	Foe1216	WBC311	B1961872	BM781379	1	1	1
WBC021E07	WBC311	WBC027H11	B1961932	BM734933	1	1	1
B1961827	WBC028C09	BM735487	WBC117	BM735057	1	1	1
B1961438	WBC030C11	WBC012E07	WBC001D02	BM735286	1	1	1
WBC21	WBC039D09	WBC014E06	WBC012E05	WBC009H07	1	1	1
WBC004G09	WBC311	WBC020F05	WBC024G03	WBC215	1	1	1
B1961438	WBC013A11	BM781278	BM734452	Foe443	1	1	1
WBC309	WBC039F12	WBC001E10	WBC027H11	BM780999	1	1	1
B1961539	BM734933	BM781067	BM781269	WBC038E02	1	1	1
BM734900	B1961932	WBC031G11	BM734780	BM734975	1	1	1
Foe443	WBC032D03	WBC030E04	WBC022D03	WBC001D02	1	1	1
Foe1263	WBC022B03	WBC040E12	WBC013E05	WBC009H07	1	1	1
Foe1288	BM734844	BM781033	WBC001F10	B1961932	1	1	1
WBC964	WBC005E06	WBC013C09	BM781033	WBC013E05	1	1	1
WBC030C11	WBC031G11	WBC009F04	WBC964	BM734719	1	1	1
WBC004E04	BM734943	WBC012B04	WBC031B06	WBC001F11	1	1	1
Foe146	Foe1317	WBC008D09	WBC020H11	WBC003D11	1	1	1

TABLE 10

SIX GENES SELECTED

Genes						Sensitivity	Specificity	Success
WBC035E01	Foe1075	WBC028C09	WBC013A09	WBC004E04	WBC014E06	1	1	1
WBC040E12	WBC005F10	BM735286	BM735452	WBC032H02	BM781319	1	1	1
Foe1317	WBC024B05	WBC027E07	BM781375	B1961539	WBC028G09	1	1	1
WBC001F10	WBC040E12	WBC022B03	WBC031C11	B1961499	BM734780	1	1	1
WBC017C08	BM734719	BM734891	GI9717252.3M	Foe1317	WBC031G11	1	1	1
WBC044E01	BM781409	WBC043B10	BM735452	BM781379	BM781033	1	1	1
WBC048H02	BM735091	WBC016A12	WBC012E05	WBC031F04	WBC012B04	1	1	1
WBC019B05	BM780999	BM734722	WBC023F12	WBC008A12	WBC012E05	1	1	1
WBC031F04	WBC038B01	B1961539	BM735386	WBC024F08	BM781278	1	1	1
BM734632	WBC020H01	WBC012B04	BM735452	WBC009H07	WBC018B05	1	1	1
WBC038E02	WBC044E01	WBC027H11	WBC038G11	BM781409	WBC031F04	1	1	1
WBC005D09	BM735091	BM734722	BM781394	WBC011F05	WBC374	1	1	1
WBC018B05	WBC018F03	WBC032D03	B1961499	WBC027F05	WBC117	1	1	1
Foe1324	B1961438	BM734632	WBC024F08	WBC019C11	WBC024G08	1	1	1
WBC004G09	WBC335	Foe1317	WBC038E02	B1961932	Foe1075	1	1	1
WBC007A08	WBC036E08	Foe146	BM781269	B1961900	WBC964	1	1	1
WBC335	WBC005F01	WBC327	BM734452	WBC016G11	BM735585	1	1	1
BM734862	GI9717252.3	WBC022C04	WBC018D03	Foe1263	WBC031D02	1	1	1
WBC007F03	BM734943	B1961932	WBC038A02	WBC028C09	WBC013E05	1	1	1
Foe1092	WBC030E04	BM781269	BM735386	WBC009F04	B1961856	1	1	1

TABLE 11

SEVEN GENES SELECTED

Genes							Sensitivity	Specificity	Success
B1961900	WBC017C08	BM734632	WBC028C09	BM735452	WBC004E04	WBC031F04	1	1	1
WBC027E07	WBC027H11	BM781233	WBC012E07	B1961872	WBC310	WBC005E06	1	1	1
WBC020H11	WBC040E12	WBC021E07	BM735402	WBC117	WBC018B05	B1961932	1	1	1
WBC014G03	BM781237_s	BM735487	WBC033A01	WBC019C11	WBC012E05	WBC215	1	1	1
WBC215	WBC014G03	BM734975	WBC031G11	WBC017B09	WBC013A09	BM735386	1	1	1
WBC018D03	WBC021E02	WBC027D09	WBC038D08	B1961620	WBC964	WBC027F05	1	1	1
BM734531	BM781379	BM781067	WBC015B08	WBC004G09	BM735091	BM734844	1	1	1
Foe1075	WBC008A10	WBC025C03	WBC035E01	BM735519	WBC013E10	BM734780	1	1	1
BM781067	BM780906	WBC21	WBC005E06	WBC028E11	BM734661	WBC031G11	1	1	1
WBC001F10	B1961872	WBC005E06	BM734722	BM735452	BM734900	WBC028C09	1	1	1
WBC007A08	WBC008D09	WBC044E01	BM781438	BM735519	WBC003D11	WBC031B06	1	1	1
WBC003D11	WBC038B01	WBC048H02	B1961620	Foe443	WBC310	WBC017B09	1	1	1
BM734661	WBC038B01	WBC036E08	WBC001F11	WBC309	BM735585	BM734975	1	1	1
WBC004G01	B1961827	WBC335	BM781416	WBC038A02	WBC022B03	WBC036E08	1	1	1
BM734891	WBC028E11	B1961941	BM735057	BM781438	WBC024H07	WBC015B08	1	1	1
BM781269	BM735494	WBC027H11	B1961941	WBC028C09	WBC032H02	WBC374	1	1	1
BM734975	WBC037C09	BM781103	WBC21	WBC030E04	WBC043B10	WBC311	1	1	1
Foe1324	WBC019B05	BM781269	WBC030C04	BM735402	BM734844	WBC018D03	1	1	1
WBC040E12	WBC005F01	B1961900	Foe1075	WBC027H11	WBC039G08	WBC023F12	1	1	1
WBC017C08	B1961539	B1961856	WBC004E04	BM781033	WBC001E10	BM781278	1	1	1

TABLE 12

EIGHT GENES SELECTED

Genes								Sensitivity	Specificity	Success
WBC025A06	WBC014B05	Foe1216	WBC039F12	BM734654	WBC020F05	Foe1324	WBC024F08	1	1	1
BM781033	WBC025A06	BM780906	BM735286	WBC335	WBC008A10	BM781067	WBC044E01	1	1	1
Foe1263	Foe146	WBC020H11	BM735487	B1961856	WBC033A01	WBC107	WBC025C03	1	1	1
BM734900	WBC025E03	WBC031F04	BM734452	WBC013A11	WBC048H02	WBC020F05	BM734844	1	1	1
WBC011F05	WBC033D12	WBC012E05	B1961438	BM734511	BM781033	WBC011D03	WBC022C04	1	1	1
WBC020H01	WBC044E01	BM735487	BM734654	B1961438	GI9717252.3M	WBC038D08	BM781233	1	1	1
WBC019B05	WBC005F01	Foe1288	BM734891	WBC025E03	WBC038E02	BM781409	WBC027H11	1	1	1
WBC011F05	Foe1216	WBC004E04	BM781319	WBC013A09	B1961620	WBC107	WBC33	1	1	1
B1961827	WBC001F11	BM781033	BM781233	WBC020H11	WBC008D09	BM735402	BM735585	1	1	1
WBC003D11	WBC039G08	WBC013C09	WBC023F12	WBC964	WBC019C11	WBC018B05	WBC030C04	1	1	1
WBC035E01	WBC025A06	WBC011F05	BM734943	WBC964	BM781438	BM734933	WBC038B01	1	1	1
BM781103	WBC024F08	BM735402	WBC327	BM781416	B1961856	WBC038A02	WBC024G03	1	1	1
BM781067	WBC025A06	WBC038A02	WBC014H06	BM781319	B1961880	WBC311	WBC007F03	1	1	1
WBC374	WBC009F04	WBC038A02	B1961539	WBC039D09	WBC019B05	BM734943	WBC016A12	1	1	1
WBC013E10	B1961932	Foe148	WBC012E05	WBC309	BM734943	BM734975	B1961941	1	1	1
WBC024G03	BM780999	WBC009F04	BM781233	BM735585	WBC020F05	B1961499	WBC014E06	1	1	1
WBC025B03	BM735585	WBC001F10	WBC003D11	WBC022B03	WBC038A02	Foe1324	B1961539	1	1	1
GI9717252.3M	WBC21	WBC013E10	WBC032D03	WBC031D02	WBC022D03	BM734632	BM735402	1	1	1
WBC013E10	BM781237	WBC018D03	BM780914	WBC027E07	WBC027B01	BM734891	Foe1216	1	1	1
WBC028C09	BM735519	WBC013E10	WBC038G11	BM781233	WBC027H11	WBC011F05	B1961620	1	1	1

TABLE 13

NINE GENES SELECTED

Genes									Sensitivity	Specificity	Success
BM734719	WBC030C11	BM734654	WBC014G03	WBC013C09	WBC031F04	WBC028C09	BM735494	WBC21	1	1	1
BM735057	BM781379	B1961499	WBC031G11	WBC033D12	WBC030E04	WBC016G11	BM734900	BM734694	1	1	1
BM781269	WBC031D02	WBC013C09	WBC014H06	Foe1324	WBC008A10	BM734661	WBC215	WBC005D09	1	1	1
BM781233	WBC014E06	WBC327	WBC007A08	B1961932	BM780906	B1961900	WBC004E04	BM735286	1	1	1
WBC025A06	WBC21	BM781233	BM781278	WBC310	BM781394	WBC019B05	WBC107	WBC012E07	1	1	1
BM781416	WBC020H01	WBC374	BM734943	BM781394	WBC027B01	WBC024H07	WBC027F05	WBC027D09	1	1	1
WBC016G11	BM734780	WBC024H07	WBC030C11	B1961941	WBC022B03	WBC019C11	WBC024G08	WBC309	1	1	1
WBC038A02	WBC017C08	BM781416	WBC030C11	WBC027H11	WBC021E02	BM781237	WBC033D12	BM781233	1	1	1
WBC008A12	WBC037C09	BM781375	WBC009H07	WBC012E05	WBC030C11	BM734891	WBC016G11	WBC311	1	1	1
WBC335	WBC025C03	WBC032D03	WBC001F11	WBC374	WBC020H11	WBC007F03	WBC017B09	WBC005E06	1	1	1
B1961932	BM734975	B1961856	WBC004G01	WBC013E10	BM781409	BM734900	WBC016A12	WBC107	1	1	1
WBC038G11	WBC048H02	B1961856	WBC008A10	WBC024H07	WBC014E06	Foe1216	B1961941	BM781379	1	1	1
WBC311	B1961880	WBC015B08	BM735386	WBC374	WBC030E04	WBC024F08	WBC008D09	WBC018D03	1	1	1
WBC018F03	BM735494	WBC025B03	BM734943	BM734722	Foe148	WBC018B05	WBC040E12	WBC031F04	1	1	1
BM781233	BM734632	WBC030C04	BM781394	BM734694	BM734780	BM781278	B1961872	WBC019C11	1	1	1
WBC033D12	Foe1317	WBC009H07	B1961856	BM781186	WBC327	WBC005F01	WBC037C09	WBC012E05	1	1	1
WBC023F12	WBC025C03	WBC044E01	WBC001D02	WBC009H07	BM781409	BM781103	BM781067	WBC008A10	1	1	1
WBC030E04	WBC335	B1961438	WBC028C09	BM735487	WBC018F03	WBC030C04	WBC038E02	WBC031D02	1	1	1
BM734780	WBC013C09	B1961438	WBC023F12	WBC014E06	WBC011F05	BM734943	B1961872	WBC028C09	1	1	1
WBC028E11	B1961880	Foe148	WBC028G09	WBC031G11	BM781379	BM781067	WBC327	BM734694	1	1	1

TABLE 14

TEN GENES SELECTED

Genes	Sensitivity	Specificity	Success
WBC031B06; WBC031C11; WBC007F03; Foe1092; WBC33; WBC031F04; WBC005E06; B1961856; B1961499; WBC21	1	1	1
WBC027B01; BM734891; BM781375; WBC030E04; WBC012A03; WBC011D03; WBC024B05; WBC014G03; WBC031B06; GI9717252.3M	1	1	1
WBC011D03; WBC009F04; BM781269; WBC027B01; WBC025B03; WBC022B03; B1961872; WBC014E06; WBC031D02; BM781379	1	1	1
WBC025E03; WBC005F10; WBC024G08; BM734780; WBC014G03; WBC001D02; WBC008D09; WBC311; WBC107; BM781186	1	1	1
BM781103; WBC048H02; WBC038D08; WBC011D03; WBC020H01; BM734722; WBC028G09; BM734632; WBC012A03; BM734452	1	1	1
WBC008A10; WBC024H07; WBC044E01; WBC036E08; WBC030C11; BM781103; WBC009F04; BM780914; WBC025E03; WBC335	1	1	1
WBC001E10; WBC036E08; BM781103; Foe1075; WBC019B05; WBC024G08; BM735494; WBC022B03; WBC009F04; B1961438	1	1	1
WBC022C04; WBC012C10; WBC027B01; BM735519; BM781409; BM734632; BM781233; BM735286; WBC024G03; WBC043B10	1	1	1
BM781233; BM734719; BM781237; WBC022B03; B1961856; BM735519; WBC013E10; B1961932; WBC008D09; BM734862	1	1	1
WBC035E01; WBC032H02; WBC013E10; BM734943; BM781416; WBC001D02; WBC012E07; BM734661; WBC024F08; BM735057	1	1	1
WBC017B09; WBC038B01; Foe148; WBC023F12; WBC013E05; WBC012C10; WBC018D03; BM734780; WBC001E10; WBC005F01	1	1	1
WBC031D02; WBC33; WBC030C04; BM781416; WBC012E05; Foe1092; BM780906; WBC003D11; WBC036E08; WBC024G08	1	1	1
WBC039G08; WBC013E10; WBC016A12; BM781067; WBC001F10; WBC007F03; WBC022B03; WBC017B09; WBC020H01; BM735494	1	1	1
BM735452; WBC027E07; WBC037C09; B1961872; WBC016G11; WBC027F05; WBC024F08; WBC020H01; WBC014B05; WBC007F03	1	1	1
WBC011D03; WBC019C11; WBC021E02; WBC001F11; WBC004E04; WBC964; WBC015B08; WBC033D12; WBC008D09; WBC007A08	1	1	1
WBC028C09; BM734722; B1961900; BM734943; WBC024G08; WBC001E10; BM735286; WBC008A10; WBC019C11; WBC027E07	1	1	1
BM734780; BM734719; BM734933; BM735286; WBC008D09; WBC012E05; WBC039F12; WBC027E07; Foe1288; Foe1263	1	1	1
BM781233; WBC003D11; BM734780; B1961620; WBC020F05; WBC019B05; BM781103; B1961856; BM781394; WBC311	1	1	1
B1961932; WBC003D11; WBC025C03; Foe1075; Foe1263; WBC014B05; WBC011D03; B1961932; BM781394; BM734943	1	1	1
B1961499; WBC038A02; WBC014B05; WBC036E08; BM734900; WBC007A08; WBC014G03; B1961539; WBC007F03; WBC020H11	1	1	1

TABLE 15

TWELVE GENES SELECTED

Genes	Sensitivity	Specificity	Success
WBC014E06; WBC037C09; BM781278; WBC005F01; B1961856; BM735487; B1961880; WBC013A09; BM781103; WBC012E05; B1961499; WBC028C09	1	1	1
WBC027E07; WBC038E02; BM781416; BM781394; BM735091; WBC020H01; BM734975; BM734694; WBC001F10; B1961880; BM735585; Foe1092	1	1	1
B1961620; B1961932; BM781278; WBC028C09; BM735091; BM734654; WBC014E06; WBC21; BM781379; WBC012E07; BM781394; BM734862	1	1	1
WBC013A09; WBC038A02; Foe1075; WBC032H02; BM734632; WBC040E12; WBC025E03; Foe1092; BM735519; B1961438; WBC374; WBC030C11	1	1	1
BM734719; Foe1092; BM781438; Foe443; WBC039G08; BM735091; Foe1288; WBC016G11; BM734844; BM781233; BM735494; WBC047A01	1	1	1
Foe1075; WBC001E10; Foe1216; WBC215; WBC028E11; WBC004E04; BM781379; WBC024G08; B1961932; B1961880; WBC008A10; WBC031D02	1	1	1
WBC117; WBC031C11; WBC028C09; WBC048H02; WBC020H11; BM734531; WBC024F08; BM734694; BM781394; WBC016G11; BM735057; WBC005D09	1	1	1
WBC008A12; B1961499; BM781237; WBC117; WBC030E04; B1961620; Foe443; BM781375; WBC005F01; BM734975; WBC028E11; Foe146	1	1	1
WBC037C09; WBC017B09; BM734452; WBC005F01; BM781233; Foe148; BM735494; WBC027F05; BM735402; WBC033D12; BM734862; WBC019C11	1	1	1
BM734844; Foe1324; Foe148; WBC027B01; WBC009F04; WBC004E04; WBC309; WBC038D08; WBC027E07; BM734452; Foe1092; B1961900	1	1	1
B1961856; BM734862; BM735519; BM734900; WBC023F12; B1961620; BM781186; BM734933; WBC011F05; WBC014E06; BM781416; WBC007F03	1	1	1
WBC001D02; BM781438; BM734511; BM734452; WBC036E08; BM734632; BM734694; B1961932; WBC022D03; BM734531; WBC011D03; WBC023F12	1	1	1
WBC011F05; Foe1317; Foe1092; WBC024G03; WBC004G09; WBC012C10; B1961438; BM735585; WBC003D11; WBC009F04; BM734722; BM781237	1	1	1
BM781379; BM734891; WBC015B08; Foe146; WBC001F11; WBC013A11; WBC016A12; WBC033D12; WBC374; WBC310; WBC013E10; WBC038A02	1	1	1
WBC013C09; WBC014H06; BM781438; BM734661; WBC001F11; B1961827; WBC013E10; WBC036E08; WBC013A11; WBC005D09; BM735057; WBC031C11	1	1	1
WBC005D09; BM734654; WBC044E01; BM781233; WBC215; WBC012B04; WBC024B05; BM735452; BM735091; B1961539; BM734661; WBC964	1	1	1
B1961856; BM781067; B1961941; WBC327; BM735386; BM734694; WBC038A02; WBC024G03; WBC018D03; GI9717252.3M; BM780914; WBC021E07	1	1	1
BM734933; BM734661; BM734900; WBC001E10; WBC017B09; WBC004G01; WBC374; WBC039G08; WBC327; BM735585; WBC012B04; BM781186	1	1	1
WBC021E07; B1961872; BM735091; WBC21; WBC032H02; WBC33; WBC011D03; BM781416; BM734933; Foe1324; WBC005D09; WBC030C11	1	1	1
WBC021E02; B1961932; BM734452; BM734694; WBC009F04; WBC027E07; BM780914; BM734943; WBC024G03; WBC038G11; WBC004G09; WBC027H11	1	1	1

TABLE 16

THIRTEEN GENES SELECTED

Genes	Sensitivity	Specificity	Success
WBC335; WBC020H01; BM734891; WBC018F03; WBC014E06; WBC039F12; WBC311; Foe1288; BM735494; WBC035E01; WBC030C11; WBC020H11; WBC008D09	1	0.91	0.93
WBC038B01; GI9717252.3M; WBC012E05; BM781394; BM734661; WBC21; BM735402; WBC008A12; Foe1092; BM734933; BM781103; WBC020F05; BM781416	1	0.73	0.8
BM734694; B1961620; WBC011F05; BM735487; WBC036E08; WBC023F12; WBC038D08; WBC033D12; WBC004G09; BM735519; WBC020H11; WBC009H07; BM781278	0.75	0.73	0.73
WBC018F03; WBC037C09; WBC012B04; WBC013E05; WBC008A10; BM781409; WBC024B05; WBC020H01; B1961620; WBC028E11; WBC040E12; BM735585; WBC309	1	0.55	0.67
WBC008A10; WBC028G09; WBC031B06; BM781186; WBC038E02; WBC030E04; WBC025E03; WBC013E05; WBC027E07; Foe1324; WBC013C09; WBC021E02; WBC018F03	0.25	0.73	0.6
WBC027F05; WBC964; WBC008D09; WBC019B05; WBC020H01; WBC004E04; WBC028G09; BM734661; WBC030C04; BM781409; WBC027E07; WBC038E02; WBC001E10	1	0.09	0.33
Foe443; WBC374; WBC032D03; WBC33; WBC020H01; BM734862; B1961880; WBC013E05; WBC017B09; BM734891; WBC028C09; BM735057; BM734661	1	0.09	0.33
Foe1263; BM734780; WBC031B06; WBC014E06; WBC036E08; WBC009F04; WBC025B03; B1961872; BM734891; BM735494; WBC014B05; WBC017B09; BM781438	1	0.09	0.33
WBC024G08; BM734511; BM734452; BM734632; BM734844; WBC024F08; WBC311; WBC038A02; WBC023F12; WBC027D09; WBC009H07; WBC021E07; WBC021E02	1	0.09	0.33
WBC022D03; WBC107; BM734943; WBC001E10; WBC011D03; WBC001F10; WBC024H07; BM735452; B1961856; BM781269; WBC004E04; WBC023F12; Foe1324	1	0.09	0.33
B1961872; WBC215; BM735402; BM781375; WBC018F03; WBC033D12; WBC024H07; BM781379; GI9717252.3M; WBC032H02; WBC013A11; WBC005F10; WBC009H07	1	0.09	0.33
WBC024G03; B1961932; BM735494; WBC035E01; WBC012B04; WBC024H07; BM734862; WBC004G01; B1961620; BM734975; WBC019B05; BM734719; BM780914	1	0.09	0.33
WBC038B01; BM780914; WBC024H07; GI9717252.3; WBC020F05; WBC016G11; WBC011D03; WBC001F11; BM781269; WBC031B06; WBC027H11; BM735494; WBC011F05	1	0.09	0.33
BM735402; BM735494; B1961932; BM734661; WBC003D11; B1961941; WBC014G03; WBC017B09; BM781409; WBC021E07; WBC030C04; B1961620; BM781103	1	0.09	0.33
WBC024B05; WBC031F04; BM780906; GI9717252.3M; BM734719; WBC038B01; BM781409; BM734933; B1961827; B1961932; BM735494; WBC031C11; WBC013A11	1	0.09	0.33
WBC003D11; WBC038A02; WBC018F03; WBC024G08; WBC018B05; WBC107; BM734531; Foe1216; BM781409; BM781186; BM735452; WBC038D08; WBC031B06	1	0.09	0.33
WBC024G03; B1961827; B1961880; WBC016G11; BM781409; Foe146; WBC040E12; WBC019C11; BM735091; BM781186; WBC033A01; WBC008D09; BM780999	1	0.09	0.33
WBC012B04; WBC039D09; WBC022D03; WBC038D08; WBC009H07; BM734452; WBC022C04; WBC038A02; WBC027E07; WBC374; Foe146; WBC117; Foe1317	1	0.09	0.33
Foe1075; WBC024G03; B1961900; WBC311; BM781269; WBC310; WBC027B01; BM781186; WBC017B09; WBC038D08; WBC008A12; B1961880; B1961620	1	0.09	0.33
WBC024F08; WBC020F05; WBC014H06; BM734844; BM735487; Foe1317; BM734654; WBC012E05; WBC012E07; WBC008D09; WBC037C09; BM734632; WBC032H02	1	0.09	0.33

TABLE 17

ENDOTOXEMIA MARKER GENE ONTOLOGY

Gene Name	Cellular location	Pathway	Molecular function
B1961438.V1.3_at	NA	NA	NA
B1961499.V1.3_at	Cytoplasm	Translation initiation activity	regulation of translational initiation
B1961539.V1.3_at	NA	inflammatory response	signal transducer activity
B1961620.V1.3_at	NA	NA	NA
B1961827.V1.3_at	Arp2/3 protein complex	structural constituent of cytoskeleton	cell motility
B1961856.V1.3_at	NA	NA	NA
B1961872.V1.3_at	NA	NA	NA
B1961880.V1.3_at	extracellular	negative regulation of membrane protein ectodomain proteolysis; positive *regulation of cell proliferation*	metalloendopeptidase inhibitor activity
B1961900.V1.3_at	NA	NA	NA
B1961932.V1.3_at	membrane	inflammatory response	interleukin-4 receptor activity
B1961932.V1.3_s_at	membrane	inflammatory response	interleukin-4 receptor activity
B1961941.V1.3_at		glycolysis	fructose-bisphosphate aldolase activity
BM734452.V1.3_at	Integral to plasma membrane	NA	inflammatory response; phagocytosis
BM734511.V1.3_at	NA	NA	NA
BM734531.V1.3_at	NA	NA	NA
BM734632.V1.3_at	NA	NA	NA
BM734654.V1.3_at	NA	NA	NA
BM734661.V1.3_at	cytoplasm	protein modification	
BM734694.V1.3_at	membrane	protein amino acid phosphorylation	protein-tyrosine kinase activity
BM734719.V1.3_at	NA	NA	NA

Gene Name	Cellular location	Pathway	Molecular function
BM734722.V1.3_at	NA	NA	NA
BM734780.V1.3_at	cytoplasm	JAK-STAT cascade	transcription factor activity
BM734795	Nucleus, immune synapse	Granzyme A activity, protein binding	Immune response
BM734844.V1.3_at	membrane	transferase activity	biosynthesis
BM734862.V1.3_at	membrane	humoral immune response	receptor activity
BM734891.V1.3_at	NA	NA	NA
BM734900.V1.3_at	extracellular space	proteolysis and peptidolysis	collagenase activity
BM734933.V1.3_at	NA	NA	calcium ion binding
BM734943.V1.3_at	NA	NA	NA
BM734975.V1.3_at	Plasma membrane	signal transduction	GTP binding
BM735057.V1.3_s_at	extracellular space	inflammatory response	chemokine
BM735091.V1.3_at	cytoplasm	NA	serine-type endopeptidase inhibitor activity
BM735286.V1.3_at	cytoplasm	iron ion homeostasis	ferric iron binding
BM735386.V1.3_at	NA	NA	NA
BM735402.V1.3_at	NA	NA	NA
BM735452.V1.3_at	NA	NA	NA
BM735487.V1.3_at	NA	NA	NA
BM735494.V1.3_at	Plasma membrane	signal transduction	immune response
BM735519.V1.3_at	NA	NA	NA
BM735585.V1.3_at	membrane	immunoglobulin secretion	NA
BM780906.V1.3_at	NA	NA	NA
BM780914.V1.3_at	NA	NA	NA
BM780999.V1.3_at	nucleus	chromatin remodelling	NA
BM781033.V1.3_at	nucleus	DNA metabolism	single-stranded DNA binding
BM781067.V1.3_at	membrane	positive regulation of T-cell proliferation	T-cell receptor binding

Gene Name	Cellular location	Pathway	Molecular function
BM781103.V1.3_at	cytoplasm	proteolysis and peptidolysis	cathepsin H activity
BM781186.V1.3_at	membrane	NA	NA
BM781233.V1.3_at	cytoplasm	translational elongation	translation elongation factor activity
BM781237.V1.3_s_at	nucleus	cytokinesis	cell cycle
BM781269.V1.3_at	membrane	immune response	interleukin-1, Type II, blocking receptor activity
BM781278.V1.3_at	NA	NA	NA
BM781319.V1.3_at		G1/S transition of mitotic cell cycle	NA
BM781375.V1.3_at	NA	protein kinase C activation	protein kinase C activity
BM781379.V1.3_at	cytoplasm	protein-tyrosine kinase activity	intracellular signalling
BM781394.V1.3_at	NA	NA	NA
BM781409.V1.3_at	NA	NA	NA
BM781416.V1.3_at	NA	NA	NA
BM781438.V1.3_at	integral to membrane	insulin-like growth factor receptor activity	neurogenesis
Foe1075.V1.3_at	*cytoplasm*	*regulation of translational initiation*	*translation initiation factor activity*
Foe1092.V1.3_at	NA	NA	NA
Foe1216.V1.3_at	nucleus	regulation of transcription from Pol II promoter	transcription coactivator activity
Foe1263.V1.3_at	NA	NA	NA
Foe1288.V1.3_at	NA	NA	NA
Foe1317.V1.3_at		fatty acid metabolism	oxidoreductase activity
Foe1324.V1.3_at	nucleus	nucleosome assembly	DNA binding
Foe146.V1.3_at	NA	NA	NA
Foe148.V1.3_at	golgi apparatus	glycoprotein 6-alpha-L-fucosyltransferase activity	oligosaccharide biosynthesis
Foe443.V1.3_at	NA	subtilase activity	proteolysis
GI9717252-3_at	membrane	detection of pathogenic bacteria	lipopolysaccharide binding

Gene Name	Cellular location	Pathway	Molecular function
GI9717252-3M_at	membrane	detection of pathogenic bacteria	lipopolysaccharide binding
WBC001D02_V1.3_at	membrane	potassium ion transport	voltage-gated potassium channel activity
WBC001E10_V1.3_at	NA	NA	NA
WBC001F10_V1.3_at	NA	protein amino acid dephosphorylation	protein tyrosine phosphatase activity
WBC001F11_V1.3_at	Nucleus	cell cycle	regulation of transcription
WBC003D11_V1.3_at	NA	NA	NA
WBC004E04_V1.3_at	Nucleus	NA	NA
WBC004G01_V1.3_at	NA	NA	NA
WBC004G09_V1.3_at	NA	NA	NA
WBC005D09_V1.3_at	NA	NA	NA
WBC005E06_V1.3_at	Nucleus	NA	DNA binding
WBC005F01_V1.3_at	NA	protein amino acid phosphorylation	protein serine/threonine kinase activity
WBC005F10_V1.3_at	NA	NA	Receptor activity
WBC007A08_V1.3_at	NA	NA	NA
WBC007F03_V1.3_at	Nucleus	Transcription, glycolysis	phosphopyruvate hydratase activity
WBC008A10_V1.3_at	extracellular	proteolysis and peptidolysis	neutrophil collagenase activity
WBC008A12_V1.3_at	NA	electron transport	electron transporter activity
WBC008D09_V1.3_at	membrane	cation transport	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism
WBC009F04_V1.3_at	membrane	cell adhesion	protein binding
WBC009H07_V1.3_at	nucleus	NA	helicase activity
WBC011D03_V1.3_at	nucleus	cell cycle	calmodulin binding
WBC011F05_V1.3_at	NA	NA	NA
WBC012A03_V1.3_at	NA	NA	NA
WBC012B04_V1.3_at	Type I membrane protein	NA	calcium ion binding

Gene Name	Cellular location	Pathway	Molecular function
WBC012C10_V1.3_at	membrane	potassium ion transport	inward rectifier potassium channel activity
WBC012E05_V1.3_at	NA	NA	NA
WBC012E07_V1.3_at	Plasma membrane	Structural molecule activity	cell adhesion
WBC013A09_V1.3_at	membrane	humoral immune response	beta-galactoside alpha-2,6-sialyltransferase activity
WBC013A11_V1.3_at	nucleus	nucleosome assembly	NA
WBC013C09_V1.3_at	membrane	hemocyte development	NA
WBC013E05_V1.3_at	membrane	immune response	NA
WBC013E10_V1.3_at	NA	NA	NA
WBC014B05_V1.3_at	NA	anti-apoptosis	NA
WBC014E06_V1.3_at	NA	NA	NA
WBC014G03_V1.3_at	Nucleus	nucleotide binding	mRNA processing
WBC014H06_V1.3_at	membrane	NA	G-protein coupled receptor activity
WBC015B08_V1.3_at	cytoplasm	kinase, transferase and transporter activity	lipid metabolism and molecular transport
WBC016A12_V1.3_at	NA	NA	NA
WBC016G11_V1.3_at	nucleus	DNA replication	DNA-dependent ATPase activity
WBC017B09_V1.3_at	Integral to membrane	intracellular signalling cascade	DNA binding
WBC017C08_V1.3_at	NA	NA	NA
WBC018B05_V1.3_at	nucleus	negative regulation of transcription from Pol II promoter	transcription corepressor activity
WBC018D03_V1.3_at	NA	NA	NA
WBC018F03_V1.3_at	membrane	cell adhesion	receptor activity
WBC019B05_V1.3_at	NA	NA	NA
WBC019C11_V1.3_at	extracellular	humoral immune response	
WBC020F05_V1.3_at	cytoplasm	regulation of translational initiation	translation initiation factor activity
WBC020H01_V1.3_at	cytoplasm	antimicrobial humoral response (sensu Vertebrata)	MAP kinase kinase activity

Gene Name	Cellular location	Pathway	Molecular function
WBC020H11_V1.3_at	nucleus	transcription from Pol II promoter	transcription factor activity
WBC021E02_V1.3_at	NA	NA	NA
WBC021E07_V1.3_at	Nucleus	intracellular signalling cascade	Transcription factor activity
WBC022B03_V1.3_at	NA	NA	T-cell receptor binding
WBC022C04_V1.3_at	Cytoplasmic and nuclear	Binds to caspase 1	Negative regulation of caspase
WBC022D03_V1.3_at	NA	NA	NA
WBC023F12_V1.3_at	NA	NA	NA
WBC024B05_V1.3_at	membrane, cytoskeleton	NA	structural
WBC024F08_V1.3_at	NA	NA	NA
WBC024G03_V1.3_at	Extracellular	NA	inhibition of proteases
WBC024G08_V1.3_at	NA	NA	NA
WBC024H07_V1.3_at	membrane	cell surface receptor linked signal transduction	interferon-gamma receptor activity
WBC025A06_V1.3_at	NA	NA	NA
WBC025B03_V1.3_at			receptor activity
WBC025C03_V1.3_at	NA	Cell cycle	Protein binding
WBC025E03_V1.3_at	nucleus	skeletal development	DNA binding
WBC027B01_V1.3_at	NA	NA	NA
WBC027D09_V1.3_at	Na	NA	NA
WBC027E07_V1.3_at	membrane	cell surface receptor linked signal transduction	protein tyrosine phosphatase activity
WBC027F05_V1.3_at	extracellular	proteolysis and peptidolysis	neutrophil collagenase activity
WBC027H11_V1.3_at	cytoplasm	protein biosynthesis	structural constituent of ribosome
WBC028C09_V1.3_at	cytoplasm	NA	endocytosis
WBC028D04_V1.3_at	NA	NA	NA
WBC028E11_V1.3_at	cytoplasm	signal transduction	signal transducer activity
WBC028G09_V1.3_at	NA	NA	NA
WBC030C04_V1.3_at	NA	NA	NA
WBC030C11_V1.3_at	cytoplasm	protein ubiquitination	ubiquitin-protein ligase activity
WBC030E04_V1.3_at	extracellular	proteolysis and peptidolysis	interstitial collagenase activity

Gene Name	Cellular location	Pathway	Molecular function
WBC031B06_V1.3_at	endosomes, lysosomes, plasma membrane	NA	receptor activity
WBC031C11_V1.3_at	cytoplasm	protein biosynthesis	structural constituent of ribosome
WBC031D02_V1.3_at	membrane	actin cytoskeleton organization and biogenesis	cytoskeletal adaptor activity
WBC031F04_V1.3_at	NA	NA	NA
WBC031G11_V1.3_at	membrane	carbohydrate transport	glucose transporter activity
WBC032D03_V1.3_at	NA	NA	NA
WBC032H02_V1.3_at	NA	NA	NA
WBC033A01_V1.3_at	nucleus	regulation of transcription, DNA-dependent	transcription factor activity
WBC033D12_V1.3_at	NA	NA	NA
WBC035E01_V1.3_at	NA	NA	mRNA processing
WBC036E08_V1.3_at	Plasma membrane	phospholipase activity	skeletal development
WBC037C09_V1.3_at	NA	NA	NA
WBC038A02_V1.3_at	cytoplasm	protein biosynthesis	structural constituent of ribosome
WBC038B01_V1.3_at	cytoplasm	protein biosynthesis	structural constituent of ribosome
WBC038D08_V1.3_at	NA	NA	NA
WBC038E02_V1.3_at	Integral to plasma membrane	protein amino acid phosphorylation	protein-tyrosine kinase activity
WBC038G11_V1.3_at	NA	NA	NA
WBC039D09_V1.3_at	NA	ubiquitin cycle	ubiquitin conjugating enzyme activity
WBC039F12_V1.3_at	Plasma membrane	NA	cell adhesion
WBC039G08_V1.3_at	NA	NA	NA
WBC040E12_V1.3_at	integral to membrane	NA	NA
WBC043B10_V1.3_at	nucleus	DNA replication initiation	DNA binding
WBC044E01_V1.3_at	cytoplasm	purine catabolism	dihydropyrimidine dehydrogenase (NADP+) activity

Gene Name	Cellular location	Pathway	Molecular function
WBC047A01_V1.3_at	nucleus	negative regulation of transcription from Pol II promoter	DNA binding
WBC048H02_V1.3_at	NA	protein kinase C activation	protein kinase C binding
WBC107.V1.3_s_at	NA	NA	NA
WBC117.gRSP.V1.3_at	NA	NA	NA
WBC21.V1.3_at	NA	NA	NA
WBC215.gRSP.V1.3_at	Nucleus	Cell proliferation	phosphoprotein phosphatase activity
WBC309.V1.3_at	NA	NA	NA
WBC310.V1.3_at	Nucleus, cytoplasm	transcription	regulation of transcription
WBC311.V1.3_at	nucleus	cell surface receptor linked signal transduction	DNA binding activity
WBC327.V1.3_at	membrane	starch catabolism	catalytic activity
WBC33.gRSP.V1.3_at	NA	NA	NA
WBC335.V1.3_at	cytoplasm (cytoskeleton)	NA	structural molecule activity
WBC374.V1.3_at	NA	NA	NA
WBC964.gRSP.V1.3_at	NA	NA	NA

WHAT IS CLAIMED IS:

1. A method for diagnosing the presence of an endotoxemia-related condition in a test subject, comprising detecting in the test subject aberrant expression of at least one endotoxemia marker gene that is expressed in cells of the immune system and that 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, 6, 7, 9, 10, 11, 13, 15, 16, 17, 18, 19, 21, 23, 25, 26, 27, 29, 31, 33, 35, 37, 38, 39, 41, 42, 43, 44, 45, 47, 49, 50, 52, 54, 56, 58, 60, 61, 63, 64, 66, 67, 68, 69, 70, 71, 73, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 86, 88, 90, 92, 93, 94, 96, 98, 100, 101, 102, 103, 104, 106, 107, 109, 110, 111, 113, 114, 115, 117, 119, 121, 122, 123, 124, 125, 126, 128, 130, 132, 134, 136, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 158, 160, 162, 164, 166, 168, 169, 170, 172, 173, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 193, 194, 195, 197, 199, 201, 203, 205, 206, 207, 209, 210, 211, 212, 214, 215, 216, 218, 220, 222, 223, 224, 225, 227, 229, 231, 233, 235, 236, 237, 239, 240, 242, 244, 245, 246, 248, 250, 252, 254, 255, 257, 259 260, 262, 264, 266, 268, 269, 270, 271, 272, 274, 276, 278, 279, 280, 282, 284, 286, 288, 290, 292, 294, 296,.298, 300, 302, 304, 305, 306, 307, 309, 311, 312, 314, 315, 316, 318, 320 321, 323 or 325, 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, 8, 12, 14, 20, 22, 24, 28, 30, 32, 34, 36, 40, 46, 48, 51, 53, 55, 57, 59, 62, 65, 72, 74, 78, 85, 87, 89, 91, 95, 97, 99, 105, 108, 112, 116, 118, 120, 127, 129, 131, 133, 135,138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 159, 161, 163, 165, 167, 171, 175, 177, 179, 181, 183, 185, 187, 189, 191, 196, 198, 200, 202, 204, 208, 213, 217, 219, 221, 226, 228, 230, 232, 234, 236, 238, 241, 243, 247, 249, 251, 253, 256, 258, 261, 263, 265, 267, 273, 275, 277, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324 or 326; (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, 8, 12, 14, 20, 22, 24, 28, 30, 32, 34, 36, 40, 46, 48, 51, 53, 55, 57, 59, 62, 65, 72, 74, 78, 85, 87, 89, 91, 95, 97, 99, 105, 108, 112, 116, 118, 120, 127, 129, 131, 133, 135,138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 159, 161, 163, 165, 167, 171, 175, 177, 179, 181, 183, 185, 187, 189, 191, 196, 198, 200, 202, 204, 208, 213, 217, 219, 221, 226, 228, 230, 232, 234, 236, 238, 241, 243, 247, 249, 251, 253, 256, 258, 261, 263, 265, 267, 273, 275, 277, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324 or 326, 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 detecting aberrant expression of an endotoxemia 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, 6, 7, 9, 10, 11, 13, 15, 16, 17, 18, 19, 21, 23, 25, 26, 27, 29, 31, 33, 35, 37, 38, 39, 41, 42, 43, 44, 45, 47, 49, 50, 52, 54, 56, 58, 60, 61, 63, 64, 66, 67, 68, 69, 70, 71, 73, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 86, 88, 90, 92, 93, 94, 96, 98, 100, 101, 102, 103, 104, 106, 107, 109, 110, 111, 113, 114, 115, 117, 119, 121, 122, 123, 124, 125, 126, 128, 130, 132, 134, 136, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 158, 160, 162, 164, 166, 168, 169, 170, 172, 173, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 193, 194, 195, 197, 199, 201, 203, 205, 206, 207, 209, 210, 211, 212, 214, 215, 216, 218, 220, 222, 223, 224, 225, 227, 229, 231, 233, 235, 236, 237, 239, 240, 242, 244, 245, 246, 248, 250, 252, 254, 255, 257, 259 260, 262, 264, 266, 268, 269, 270, 271, 272, 274, 276, 278, 279, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 305, 306, 307, 309, 311, 312, 314, 315, 316, 318, 320 321, 323 or 325, 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, 12, 14, 20, 22, 24, 28, 30, 32, 34, 36, 40, 46, 48, 51, 53, 55, 57, 59, 62, 65, 72, 74, 78, 85, 87, 89, 91, 95, 97, 99, 105, 108, 112, 116, 118, 120, 127, 129, 131, 133, 135,138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 159, 161, 163, 165, 167, 171, 175, 177, 179, 181, 183, 185, 187, 189, 191, 196, 198, 200, 202, 204, 208, 213, 217, 219, 221, 226, 228, 230, 232, 234, 236, 238, 241, 243, 247, 249, 251, 253, 256, 258, 261, 263, 265, 267, 273, 275, 277, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324 or 326; (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, 12, 14, 20, 22, 24, 28, 30, 32, 34, 36, 40, 46, 48, 51, 53, 55, 57, 59, 62, 65, 72, 74, 78, 85, 87, 89, 91, 95, 97, 99, 105, 108, 112, 116, 118, 120, 127, 129, 131, 133, 135,138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 159, 161, 163, 165, 167, 171, 175, 177, 179, 181, 183, 185, 187, 189, 191, 196, 198, 200, 202, 204, 208, 213, 217, 219, 221, 226, 228, 230, 232, 234, 236, 238, 241, 243, 247, 249, 251, 253, 256, 258, 261, 263, 265, 267, 273, 275, 277, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324 or 326; 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 an endotoxemia 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, 8, 12, 14, 20, 22, 24, 28, 30, 32, 34, 36, 40, 46, 48, 51, 53, 55, 57, 59, 62, 65, 72, 74, 78, 85, 87, 89, 91, 95, 97, 99, 105, 108, 112, 116, 118,

120, 127, 129, 131, 133, 135,138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 159, 161, 163, 165, 167, 171, 175, 177, 179, 181, 183, 185, 187, 189, 191, 196, 198, 200, 202, 204, 208, 213, 217, 219, 221, 226, 228, 230, 232, 234, 236, 238, 241, 243, 247, 249, 251, 253, 256, 258, 261, 263, 265, 267, 273, 275, 277, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324 or 326; (ii) a polypeptide comprising a portion of the sequence set forth in any one of SEQ ID NO: 2, 8, 12, 14, 20, 22, 24, 28, 30, 32, 34, 36, 40, 46, 48, 51, 53, 55, 57, 59, 62, 65, 72, 74, 78, 85, 87, 89, 91, 95, 97, 99, 105, 108, 112, 116, 118, 120, 127, 129, 131, 133, 135,138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 159, 161, 163, 165, 167, 171, 175, 177, 179, 181, 183, 185, 187, 189, 191, 196, 198, 200, 202, 204, 208, 213, 217, 219, 221, 226, 228, 230, 232, 234, 236, 238, 241, 243, 247, 249, 251, 253, 256, 258, 261, 263, 265, 267, 273, 275, 277, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324 or 326, 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, 8, 12, 14, 20, 22, 24, 28, 30, 32, 34, 36, 40, 46, 48, 51, 53, 55, 57, 59, 62, 65, 72, 74, 78, 85, 87, 89, 91, 95, 97, 99, 105, 108, 112, 116, 118, 120, 127, 129, 131, 133, 135,138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 159, 161, 163, 165, 167, 171, 175, 177, 179, 181, 183, 185, 187, 189, 191, 196, 198, 200, 202, 204, 208, 213, 217, 219, 221, 226, 228, 230, 232, 234, 236, 238, 241, 243, 247, 249, 251, 253, 256, 258, 261, 263, 265, 267, 273, 275, 277, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324 or 326; and (iv) a polypeptide comprising a portion of the sequence set forth in any one of SEQ ID: 2, 8, 12, 14, 20, 22, 24, 28, 30, 32, 34, 36, 40, 46, 48, 51, 53, 55, 57, 59, 62, 65, 72, 74, 78, 85, 87, 89, 91, 95, 97, 99, 105, 108, 112, 116, 118, 120, 127, 129, 131, 133, 135,138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 159, 161, 163, 165, 167, 171, 175, 177, 179, 181, 183, 185, 187, 189, 191, 196, 198, 200, 202, 204, 208, 213, 217, 219, 221, 226, 228, 230, 232, 234, 236, 238, 241, 243, 247, 249, 251, 253, 256, 258, 261, 263, 265, 267, 273, 275, 277, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324 or 326, 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 endotoxemia 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 lacking an endotoxemia-related condition, 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 an endotoxemia-related condition in the test subject.

5. A method according to claim 4, further comprising diagnosing the presence, stage or degree of an endotoxemia-related condition 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.

6. A method according to claim 5, wherein the presence of endotoxemia-related condition is determined by detecting an increase in the level or functional activity of at least one endotoxemia 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, 5, 6, 7, 9, 10, 11, 13, 15, 16, 17, 18, 19, 21, 23, 25, 26, 27, 29, 31, 33, 35, 37, 38, 39, 41, 42, 43, 44, 45, 47, 49, 50, 52, 54, 56, 58, 60, 61, 63, 64, 66, 67, 68, 69, 70, 71, 73, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 86, 88, 90, 92, 93, 94, 96, 98, 100, 101, 102, 103, 104, 106, 107, 109, 110, 111, 113, 114, 115, 117, 119, 121, 122, 123, 124, 125, 126, 128, 130, 132, 134, 136, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 158, 160, 162, 164, 166, 168, 169, 170, 172, 173, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 193, 194, 195, 197, 199, 201, 203, 205, 206, 207, 209, 210, 211, 212, 214, 215, 216, 218, 220, 222, 223, 224, 225, 227, 229, 231, 233, 235, 236, 237, 239, 240, 242, 244, 245, 246, 248, 250, 252, 254, 255, 257, 259 260, 262, 264, 266, 268, 269, 270, 271, 272, 274, 276, 278, 279, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 305, 306, 307, 309, 311, 312, 314, 315, 316, 318, 320 321, 323 or 325, 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, 12, 14, 20, 22, 24, 28, 30, 32, 34, 36, 40, 46, 48, 51, 53, 55, 57, 59, 62, 65, 72, 74, 78, 85, 87, 89, 91, 95, 97, 99, 105, 108, 112, 116, 118, 120, 127, 129, 131, 133, 135,138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 159, 161, 163, 165, 167, 171, 175, 177, 179, 181, 183, 185, 187, 189, 191, 196, 198, 200, 202, 204, 208, 213, 217, 219, 221, 226, 228, 230, 232, 234, 236, 238, 241, 243, 247, 249, 251, 253, 256, 258, 261, 263, 265, 267, 273, 275, 277, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324 or 326; (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, 12, 14, 20, 22, 24, 28, 30, 32, 34, 36, 40, 46, 48, 51, 53, 55, 57, 59, 62, 65, 72, 74, 78, 85, 87, 89, 91, 95, 97, 99, 105, 108, 112, 116, 118, 120, 127, 129, 131, 133, 135,138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 159, 161, 163, 165, 167, 171, 175, 177, 179, 181, 183, 185, 187, 189, 191, 196, 198, 200, 202, 204, 208, 213, 217, 219, 221, 226, 228, 230, 232, 234, 236, 238, 241, 243, 247, 249, 251, 253, 256, 258, 261, 263, 265, 267, 273, 275, 277, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324 or 326, 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 an endotoxemia-related condition 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.

8. A method according to claim 7, wherein the presence of an endotoxemia-related condition is determined by detecting a decrease in the level or functional activity of at least one endotoxemia 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, 6, 7, 11, 13, 15, 16, 17, 18, 19, 21, 25, 26, 35, 37, 38, 41, 42, 43, 44, 50, 52, 54, 58, 60, 63, 64, 69, 70, 71, 73, 77, 79, 80, 81, 82, 83, 86, 92, 93, 96, 98, 100, 101, 102, 103, 104, 106, 115, 117, 128, 134, 137, 141, 143, 153, 155, 158, 162, 164, 166, 174, 182, 186, 188, 190, 195, 197, 199, 201, 205, 206, 207, 209, 210, 211, 214, 215, 216, 222, 223, 240, 244, 246, 248, 259, 260, 269, 272, 280, 282, 284, 286, 290, 298, 300, 302, 305, 306, 307, 309, 312, 314, 315, 316, 318, 320, 321, 323, 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: 8, 12, 14, 20, 22, 36, 51, 53, 55, 59, 65, 72, 74, 78, 87, 97, 99, 105, 116, 118, 129, 135, 138, 142, 144, 154, 156, 159, 163, 165, 167, 175, 183, 187, 189, 191, 196, 198, 200, 202, 208, 217, 241, 247, 249, 261, 273, 281, 283, 285, 287, 291, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324; (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: 8, 12, 14, 20, 22, 36, 51, 53, 55, 59, 65, 72, 74, 78, 87, 97, 99, 105, 116, 118, 129, 135, 138, 142, 144, 154, 156, 159, 163, 165, 167, 175, 183, 187, 189, 191, 196, 198, 200, 202, 208, 217, 241, 247, 249, 261, 273, 281, 283, 285, 287, 291, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324, 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 an endotoxemia-related condition 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 two endotoxemia marker genes.

12. A method according to claim 4, comprising measuring the level or functional activity of individual expression products of at least one level one correlation endotoxemia 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: 11, 23, 29, 35, 43, 44, 68, 81, 82, 84, 104, 105, 107, 119, 130, 136, 147, 155, 174, 192, 193, 245, 254, 255, 262, 264, 270, 271, 279, 296, or 325, 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: 12, 24, 30, 36, 85, 108, 120, 131, 148, 156, 175, 256, 263, 265, 297, or 326; (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: 12, 24, 30, 36, 85, 108, 120, 131, 148, 156, 175, 256, 263, 265, 297, or 326, 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 one level two correlation endotoxemia 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: 1, 7, 9, 10, 17, 18, 21, 25, 26, 33, 54, 61, 64, 79, 80, 90, 94, 115, 117, 121, 122, 125, 126, 143, 160, 162, 164, 172, 173, 178, 184, 186, 194, 199, 205, 206, 225, 229, 242, 244, 252, 257, 259, 274, 276, 282, 284, 288, 294, 306, 316, or 318, 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, 22, 34, 55, 62, 65, 91, 95, 116, 118, 127, 144, 161, 163, 165, 179, 185, 187, 200, 226, 230, 243, 253, 258, 275, 277, 283, 285, 289, 295, 317, or 319, (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, 22, 34, 55, 62, 65, 91, 95, 116, 118, 127, 144, 161, 163, 165, 179, 185, 187, 200, 226, 230, 243, 253, 258, 275, 277, 283, 285, 289, 295, 317, or 319, 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 one level three correlation endotoxemia 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: 3, 4, 5, 6,

13, 15, 16, 27, 31, 37, 38, 39, 41, 42, 45, 47, 49, 52, 56, 58, 63, 66, 67, 69, 70, 71, 77, 83, 86, 88, 96, 98, 100, 101, 106, 109, 110, 111, 113, 114, 128, 132, 134, 137, 139, 141, 145, 149, 151, 153, 157, 158, 166, 168, 169, 176, 180, 188, 190, 197, 203, 207, 209, 210, 211, 214, 215, 218, 220, 222, 223, 224, 231, 233, 236, 237, 239, 240, 241, 246, 250, 260, 266, 268, 269, 272, 278, 280, 286, 290, 292, 300, 304, 309, 312, 314, 315, 321, or 323, 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: 14, 28, 32, 40, 46, 48, 53, 57, 59, 72, 78, 87, 89, 97, 99, 112, 129, 133, 135, 138, 140, 142, 146, 150, 152, 154, 159, 167, 177, 181, 189, 191, 198, 204, 208, 219, 221, 232, 234, 238, 247, 251, 261, 267, 273, 281, 287, 291, 293, 301, 310, 313, 322, or 324; (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: 14, 28, 32, 40, 46, 48, 53, 57, 59, 72, 78, 87, 89, 97, 99, 112, 129, 133, 135, 138, 140, 142, 146, 150, 152, 154, 159, 167, 177, 181, 189, 191, 198, 204, 208, 219, 221, 232, 234, 238, 247, 251, 261, 267, 273, 281, 287, 291, 293, 301, 310, 313, 322, or 324, 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 one level four correlation endotoxemia 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: 19, 50, 60, 73, 75, 92, 93, 102, 103, 123, 124, 170, 182, 195, 201, 212, 216, 227, 235, 248, 298, 302, 305, 307, 311, or 320, 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, 51, 74, 76, 171, 183, 196, 202, 213, 217, 228, 249, 299, 303, or 308; (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, 51, 74, 76, 171, 183, 196, 202, 213, 217, 228, 249, 299, 303, or 308, 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, wherein the biological sample comprises blood.

17. A method according to claim 4, wherein the biological sample comprises peripheral blood.

18. A method according to claim 4, wherein the biological sample comprises leukocytes.

19. A method according to claim 4, wherein the expression product is a RNA molecule.

20. A method according to claim 4, wherein the expression product is a polypeptide.

21. A method according to claim 4, wherein the expression product is the same as the corresponding expression product.

22. A method according to claim 4, wherein the expression product is a variant of the corresponding expression product.

23. 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 an endotoxemia marker polynucleotide.

24. A method according to claim 23, 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.

25. A method according to claim 23, wherein the nucleic acid probe is immobilized on a solid or semi-solid support.

26. A method according to claim 23, wherein the nucleic acid probe forms part of a spatial array of nucleic acid probes.

27. A method according to claim 23, wherein the level of nucleic acid probe that is bound to the target RNA or to the DNA copy is measured by hybridization.

28. A method according to claim 23, 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.

29. A method according to claim 23, 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.

30. A method according to claim 23, wherein the probe for detecting the endotoxemia marker polynucleotide comprises a sequence as set forth in any one of SEQ ID NO: 327-2317.

31. A method according to claim 23, 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.

32. A method according to claim 23, wherein the measured level of the target polypeptide is normalized to the level of a reference polypeptide that is present in the same sample.

33. A method according to claim 23, wherein the antigen-binding molecule is immobilized on a solid or semi-solid support.

34. A method according to claim 23, wherein the antigen-binding molecule forms part of a spatial array of antigen-binding molecule.

35. A method according to claim 23, wherein the level of antigen-binding molecule that is bound to the target polypeptide is measured by immunoassay.

36. 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.

37. A method according to claim 36, 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.

38. 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.

39. A method according to claim 38, wherein the base station is further caused to provide a diagnosis for the presence, absence or degree of an endotoxemia-related condition.

40. A method according to claim 38, wherein the base station is further caused to transfer an indication of the diagnosis to the end station *via* the communications network.

41. A method according to claim 1, wherein detection of the aberrant expression is indicative of the presence or risk of an endotoxemia-related condition.

42. A method according to claim 1, wherein the test subject is a horse.

43. A method for treating, preventing or inhibiting the development of an endotoxemia-related condition in a subject, the method comprising detecting aberrant expression of at least one endotoxemia 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 the endotoxemia-related condition in the subject, wherein the endotoxemia marker gene is expressed in cells of the immune system and 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, 6, 7, 9, 10, 11, 13, 15, 16, 17, 18, 19, 21, 23, 25, 26, 27, 29, 31, 33, 35, 37, 38, 39, 41, 42, 43, 44, 45, 47, 49, 50, 52, 54, 56, 58, 60, 61, 63, 64, 66, 67, 68, 69, 70, 71, 73, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 86, 88, 90, 92, 93, 94, 96, 98, 100, 101, 102, 103, 104, 106, 107, 109, 110, 111, 113, 114, 115, 117, 119, 121, 122, 123, 124, 125, 126, 128, 130, 132, 134, 136, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 158, 160, 162, 164, 166, 168, 169, 170, 172, 173, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 193, 194, 195, 197, 199,

201, 203, 205, 206, 207, 209, 210, 211, 212, 214, 215, 216, 218, 220, 222, 223, 224, 225, 227, 229, 231, 233, 235, 236, 237, 239, 240, 242, 244, 245, 246, 248, 250, 252, 254, 255, 257, 259 260, 262, 264, 266, 268, 269, 270, 271, 272, 274, 276, 278, 279, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 305, 306, 307, 309, 311, 312, 314, 315, 316, 318, 320 321, 323 or 325; 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, 8, 12, 14, 20, 22, 24, 28, 30, 32, 34, 36, 40, 46, 48, 51, 53, 55, 57, 59, 62, 65, 72, 74, 78, 85, 87, 89, 91, 95, 97, 99, 105, 108, 112, 116, 118, 120, 127, 129, 131, 133, 135,138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 159, 161, 163, 165, 167, 171, 175, 177, 179, 181, 183, 185, 187, 189, 191, 196, 198, 200, 202, 204, 208, 213, 217, 219, 221, 226, 228, 230, 232, 234, 236, 238, 241, 243, 247, 249, 251, 253, 256, 258, 261, 263, 265, 267, 273, 275, 277, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324 or 326; (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, 8, 12, 14, 20, 22, 24, 28, 30, 32, 34, 36, 40, 46, 48, 51, 53, 55, 57, 59, 62, 65, 72, 74, 78, 85, 87, 89, 91, 95, 97, 99, 105, 108, 112, 116, 118, 120, 127, 129, 131, 133, 135,138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 159, 161, 163, 165, 167, 171, 175, 177, 179, 181, 183, 185, 187, 189, 191, 196, 198, 200, 202, 204, 208, 213, 217, 219, 221, 226, 228, 230, 232, 234, 236, 238, 241, 243, 247, 249, 251, 253, 256, 258, 261, 263, 265, 267, 273, 275, 277, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324 or 326, 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.

44. An isolated endotoxemia 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, 5, 6, 7, 9, 10, 11, 13, 15, 16, 17, 18, 19, 21, 23, 25, 26, 27, 29, 31, 33, 35, 37, 38, 39, 41, 42, 43, 44, 45, 47, 49, 50, 52, 54, 56, 58, 60, 61, 63, 64, 66, 67, 68, 69, 70, 71, 73, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 86, 88, 90, 92, 93, 94, 96, 98, 100, 101, 102, 103, 104, 106, 107, 109, 110, 111, 113, 114, 115, 117, 119, 121, 122, 123, 124, 125, 126, 128, 130, 132, 134, 136, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 158, 160, 162, 164, 166, 168, 169, 170, 172, 173, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 193, 194, 195, 197, 199, 201, 203, 205, 206, 207, 209, 210, 211, 212, 214, 215, 216, 218, 220, 222, 223, 224, 225, 227, 229, 231, 233, 235, 236, 237, 239, 240, 242, 244, 245, 246, 248, 250, 252, 254, 255, 257, 259 260, 262, 264, 266, 268, 269, 270, 271, 272, 274, 276, 278, 279, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 305, 306, 307, 309, 311, 312, 314, 315, 316, 318, 320 321, 323 or 325, or a complement thereof; (b) a polynucleotide comprising a

portion of the sequence set forth in any one of SEQ ID NO: 1, 3, 4, 5, 6, 7, 9, 10, 11, 13, 15, 16, 17, 18, 19, 21, 23, 25, 26, 27, 29, 31, 33, 35, 37, 38, 39, 41, 42, 43, 44, 45, 47, 49, 50, 52, 54, 56, 58, 60, 61, 63, 64, 66, 67, 68, 69, 70, 71, 73, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 86, 88, 90, 92, 93, 94, 96, 98, 100, 101, 102, 103, 104, 106, 107, 109, 110, 111, 113, 114, 115, 117, 119, 121, 122, 123, 124, 125, 126, 128, 130, 132, 134, 136, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 158, 160, 162, 164, 166, 168, 169, 170, 172, 173, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 193, 194, 195, 197, 199, 201, 203, 205, 206, 207, 209, 210, 211, 212, 214, 215, 216, 218, 220, 222, 223, 224, 225, 227, 229, 231, 233, 235, 236, 237, 239, 240, 242, 244, 245, 246, 248, 250, 252, 254, 255, 257, 259 260, 262, 264, 266, 268, 269, 270, 271, 272, 274, 276, 278, 279, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 305, 306, 307, 309, 311, 312, 314, 315, 316, 318, 320 321, 323 or 325, 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: 1, 3, 4, 5, 6, 7, 9, 10, 11, 13, 15, 16, 17, 18, 19, 21, 23, 25, 26, 27, 29, 31, 33, 35, 37, 38, 39, 41, 42, 43, 44, 45, 47, 49, 50, 52, 54, 56, 58, 60, 61, 63, 64, 66, 67, 68, 69, 70, 71, 73, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 86, 88, 90, 92, 93, 94, 96, 98, 100, 101, 102, 103, 104, 106, 107, 109, 110, 111, 113, 114, 115, 117, 119, 121, 122, 123, 124, 125, 126, 128, 130, 132, 134, 136, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 158, 160, 162, 164, 166, 168, 169, 170, 172, 173, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 193, 194, 195, 197, 199, 201, 203, 205, 206, 207, 209, 210, 211, 212, 214, 215, 216, 218, 220, 222, 223, 224, 225, 227, 229, 231, 233, 235, 236, 237, 239, 240, 242, 244, 245, 246, 248, 250, 252, 254, 255, 257, 259 260, 262, 264, 266, 268, 269, 270, 271, 272, 274, 276, 278, 279, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 305, 306, 307, 309, 311, 312, 314, 315, 316, 318, 320 321, 323 or 325, 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.

45. A nucleic acid construct comprising an endotoxemia marker polynucleotide according to claim 44, in operable connection with a regulatory element that is operable in a host cell.

46. An isolated host cell containing a nucleic acid construct according to claim 45.

47. A probe comprising a nucleotide sequence that hybridizes under at least low stringency conditions to a polynucleotide according to claim 44.

48. A probe according to claim 47, consisting essentially of a nucleic acid sequence that 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, 8, 12, 14, 20, 22, 24, 28, 30, 32, 34, 36, 40, 46, 48, 51, 53, 55, 57, 59, 62, 65, 72, 74, 78, 85, 87, 89, 91, 95, 97, 99, 105, 108, 112,

116, 118, 120, 127, 129, 131, 133, 135,138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 159, 161, 163, 165, 167, 171, 175, 177, 179, 181, 183, 185, 187, 189, 191, 196, 198, 200, 202, 204, 208, 213, 217, 219, 221, 226, 228, 230, 232, 234, 236, 238, 241, 243, 247, 249, 251, 253, 256, 258, 261, 263, 265, 267, 273, 275, 277, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324 or 326, wherein the portion is at least 15 nucleotides in length.

49. A probe according to claim 47, wherein the probe comprises 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, 8, 12, 14, 20, 22, 24, 28, 30, 32, 34, 36, 40, 46, 48, 51, 53, 55, 57, 59, 62, 65, 72, 74, 78, 85, 87, 89, 91, 95, 97, 99, 105, 108, 112, 116, 118, 120, 127, 129, 131, 133, 135,138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 159, 161, 163, 165, 167, 171, 175, 177, 179, 181, 183, 185, 187, 189, 191, 196, 198, 200, 202, 204, 208, 213, 217, 219, 221, 226, 228, 230, 232, 234, 236, 238, 241, 243, 247, 249, 251, 253, 256, 258, 261, 263, 265, 267, 273, 275, 277, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324 or 326; under at least low stringency conditions, wherein the portion is at least 15 nucleotides in length.

50. A probe according to claim 47, wherein the probe 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, 6, 7, 9, 10, 11, 13, 15, 16, 17, 18, 19, 21, 23, 25, 26, 27, 29, 31, 33, 35, 37, 38, 39, 41, 42, 43, 44, 45, 47, 49, 50, 52, 54, 56, 58, 60, 61, 63, 64, 66, 67, 68, 69, 70, 71, 73, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 86, 88, 90, 92, 93, 94, 96, 98, 100, 101, 102, 103, 104, 106, 107, 109, 110, 111, 113, 114, 115, 117, 119, 121, 122, 123, 124, 125, 126, 128, 130, 132, 134, 136, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 158, 160, 162, 164, 166, 168, 169, 170, 172, 173, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 193, 194, 195, 197, 199, 201, 203, 205, 206, 207, 209, 210, 211, 212, 214, 215, 216, 218, 220, 222, 223, 224, 225, 227, 229, 231, 233, 235, 236, 237, 239, 240, 242, 244, 245, 246, 248, 250, 252, 254, 255, 257, 259 260, 262, 264, 266, 268, 269, 270, 271, 272, 274, 276, 278, 279, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 305, 306, 307, 309, 311, 312, 314, 315, 316, 318, 320 321, 323 or 325, under at least low stringency conditions, wherein the portion is at least 15 nucleotides in length.

51. A probe according to claim 47, comprising a sequence as set forth in any one of SEQ ID NO: 145-2150.

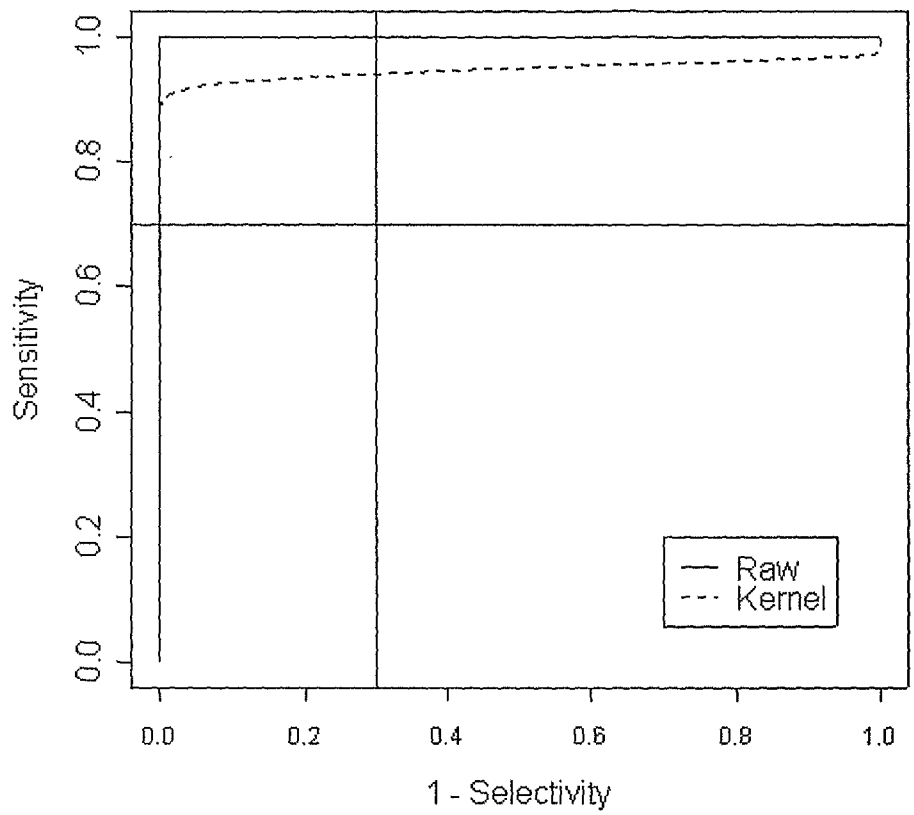
52. A solid or semi-solid support comprising at least one probe according to claim 47 immobilized thereon.

53. Use of one or more endotoxemia marker polynucleotides according to claim 44, or the use of one or more probes according to claim 47, or the use of one or more endotoxemia marker polypeptides 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, 8, 12, 14, 20, 22, 24, 28, 30, 32, 34, 36, 40, 46, 48, 51, 53, 55, 57, 59, 62, 65, 72, 74, 78, 85, 87, 89, 91, 95, 97, 99, 105, 108, 112, 116, 118, 120, 127, 129, 131, 133, 135,138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 159, 161, 163, 165, 167, 171, 175, 177, 179, 181, 183, 185, 187, 189, 191, 196, 198, 200, 202, 204, 208, 213, 217, 219, 221, 226, 228, 230, 232, 234, 236, 238, 241, 243, 247, 249, 251, 253, 256, 258, 261, 263, 265, 267, 273, 275, 277, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324 or 326; (ii) a polypeptide comprising an amino acid sequence that shares at least 50% sequence similarity with a polypeptide expression product of an endotoxemia marker gene that comprises a sequence set forth in any one of SEQ ID NO: 2, 8, 12, 14, 20, 22, 24, 28, 30, 32, 34, 36, 40, 46, 48, 51, 53, 55, 57, 59, 62, 65, 72, 74, 78, 85, 87, 89, 91, 95, 97, 99, 105, 108, 112, 116, 118, 120, 127, 129, 131, 133, 135,138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 159, 161, 163, 165, 167, 171, 175, 177, 179, 181, 183, 185, 187, 189, 191, 196, 198, 200, 202, 204, 208, 213, 217, 219, 221, 226, 228, 230, 232, 234, 236, 238, 241, 243, 247, 249, 251, 253, 256, 258, 261, 263, 265, 267, 273, 275, 277, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324 or 326; (iii) a portion of the polypeptide according to (i) or (ii) wherein the portion comprises at least 5 contiguous amino acid residues of that polypeptide; (iv) a polypeptide comprising an amino acid sequence that shares at least 30% similarity with at least 15 contiguous amino acid residues of the polypeptide according to (i) or (ii); and (iv) a polypeptide comprising a portion of the polypeptide according to (i) or (ii), wherein the portion comprises at least 5 contiguous amino acid residues of the polypeptide according to (i) or (ii) and is immuno-interactive with an antigen-binding molecule that is immuno-interactive with a sequence of (i), (ii) or (iii), or the use of one or more antigen-binding molecules that are immuno-interactive with a said endotoxemia marker polypeptide, in the manufacture of a kit for diagnosing the presence of an endotoxemia-related condition in a subject.

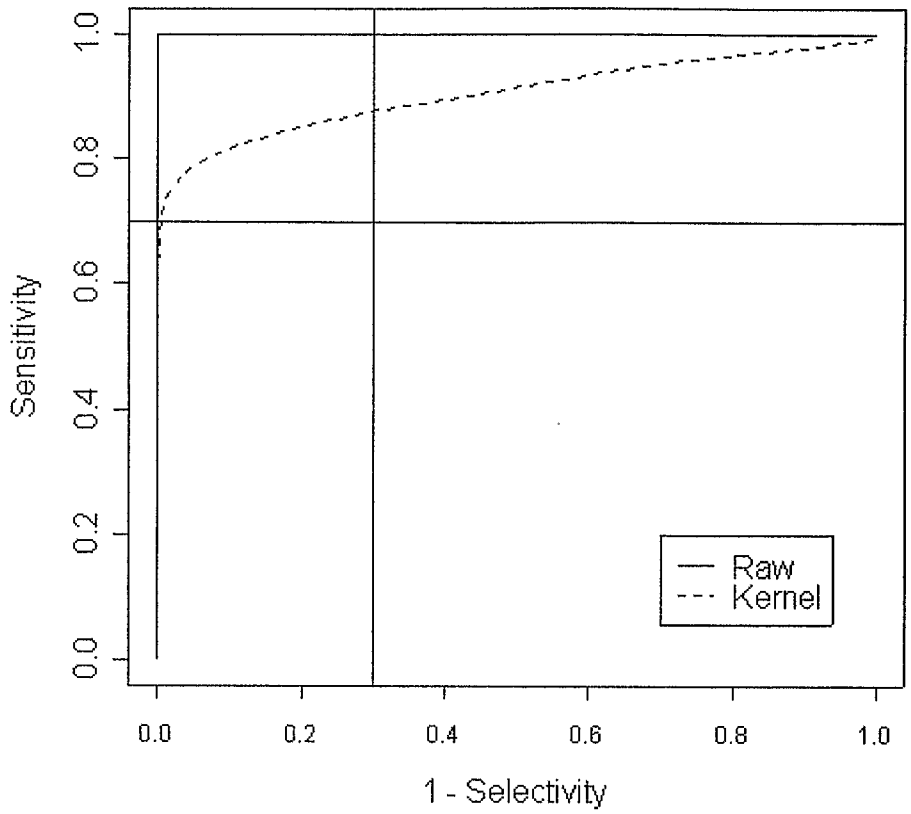
54. A method for diagnosing the presence of an endotoxemia-related condition in a test subject, comprising detecting in the test subject aberrant expression of at least one endotoxemia marker polynucleotide that is expressed in cells of the immune system and that is selected from the group consisting 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, 6, 7, 9, 10, 11, 13, 15, 16, 17, 18, 19, 21, 23, 25, 26, 27, 29, 31, 33, 35, 37, 38, 39, 41, 42, 43, 44, 45, 47, 49, 50, 52, 54, 56, 58, 60, 61, 63, 64, 66, 67, 68, 69, 70, 71, 73, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 86, 88, 90, 92, 93, 94, 96, 98, 100, 101, 102, 103, 104, 106, 107, 109, 110, 111, 113, 114, 115, 117, 119, 121, 122, 123, 124, 125, 126, 128, 130, 132, 134, 136, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 158, 160, 162, 164, 166, 168, 169, 170, 172, 173, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 193, 194, 195, 197, 199, 201, 203, 205, 206, 207, 209, 210, 211, 212, 214, 215, 216, 218, 220, 222, 223, 224, 225, 227, 229, 231, 233, 235, 236,

237, 239, 240, 242, 244, 245, 246, 248, 250, 252, 254, 255, 257, 259 260, 262, 264, 266, 268, 269, 270, 271, 272, 274, 276, 278, 279, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 305, 306, 307, 309, 311, 312, 314, 315, 316, 318, 320 321, 323 or 325, 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, 12, 14, 20, 22, 24, 28, 30, 32, 34, 36, 40, 46, 48, 51, 53, 55, 57, 59, 62, 65, 72, 74, 78, 85, 87, 89, 91, 95, 97, 99, 105, 108, 112, 116, 118, 120, 127, 129, 131, 133, 135,138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 159, 161, 163, 165, 167, 171, 175, 177, 179, 181, 183, 185, 187, 189, 191, 196, 198, 200, 202, 204, 208, 213, 217, 219, 221, 226, 228, 230, 232, 234, 236, 238, 241, 243, 247, 249, 251, 253, 256, 258, 261, 263, 265, 267, 273, 275, 277, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324 or 326; (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, 12, 14, 20, 22, 24, 28, 30, 32, 34, 36, 40, 46, 48, 51, 53, 55, 57, 59, 62, 65, 72, 74, 78, 85, 87, 89, 91, 95, 97, 99, 105, 108, 112, 116, 118, 120, 127, 129, 131, 133, 135,138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 159, 161, 163, 165, 167, 171, 175, 177, 179, 181, 183, 185, 187, 189, 191, 196, 198, 200, 202, 204, 208, 213, 217, 219, 221, 226, 228, 230, 232, 234, 236, 238, 241, 243, 247, 249, 251, 253, 256, 258, 261, 263, 265, 267, 273, 275, 277, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 308, 310, 313, 317, 319, 322, 324 or 326, 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.



0 Hours versus 24 Hours

FIGURE 1



0 Hours versus 72 Hours

FIGURE 2

INTERNATIONAL SEARCH REPORT

International application No.
PCT/AU2006/000970

A. CLASSIFICATION OF SUBJECT MATTER

Int. Cl.

C12Q 1/68 (2006.01)

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
WPIDS, CA, BIOSIS, MEDLINE, AGRICOLA, BIOTECHABS. Keywords: endotoxemia, laminitis, septic shock, sepsis, gene, marker, profile, screen, identify, determine.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 2003/0194752 A1 (ANDERSON, S. J. et.al.) 16 October 2003. (see paragraphs 9, 10, 62 – 72, 90, 94 and Claims)	1 - 43
X	DE 10315031 A1 (SIRS-Lab GmbH) 14 October 2004 (see paragraphs 21 – 29)	1 - 43
P,X	DE 102004015605 A1 (SIRS-Lab GmbH) 20 October 2005 (see paragraphs 20 – 43 and Claims)	1 - 43
X	WO 2004044556 A2 (BECTON, DICKINSON AND COMPANY) 27 May 2004. (see paragraphs 9, 12 – 22 and Claims)	1 - 43

[X] Further documents are listed in the continuation of Box C

[X] See patent family annex

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
08 August 2006	30 AUG 2006
Name and mailing address of the ISA/AU	Authorized officer
AUSTRALIAN PATENT OFFICE PO BOX 200, WODEN ACT 2606, AUSTRALIA E-mail address: pct@ipaustralia.gov.au Facsimile No. (02) 6285 3929	**Alistair Bestow** Telephone No : (02) 6283 2450

INTERNATIONAL SEARCH REPORT

International application No.
PCT/AU2006/000970

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.: **44 – 53.**
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
The invention relates to methods of diagnosing endotoxemia related condition by detecting certain marker genes. (p. 5 line 2 - p. 17 line 16 and Examples.) The above claims are to specific polynucleotides and variants thereof, most of which (if not all) are known (eg SEQ ID 35 was available in 1993 as Accession No. X68969, and SEQ ID 132 was available in 2000 as Accession No. AF076642), and are not limited to the technical features of the invention, and therefore no meaningful search can be carried out on these claims.

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	MARSHALL, J. C., et. al. (May 2003) Measures, markers, and mediators: Toward a staging system for clinical sepsis. A Report of the Fifth Toronto Sepsis Roundtable, Toronto, Ontario, Canada October 25-26, 2000. *Critical Care Medicine* 31(5):1560-7. (see Abstract, Table 2, p.1561 col. 2 line 22 – p. 1563, col. 1 line 24)	1 - 43
X	GIBOT, S., et. al. (August 2004) Soluble form of the Triggering Receptor Expressed on Myeloid Cells-1 as a Marker of Microbial Infection. *Clinical Medicine and Research* 2(3):181-7. (see Abstract, p. 182-3, Conclusion)	1 - 43
X	LAYSECA-ESPINOSA, E., et. al. (October 2002) Expression of CD64 as a potential marker of neonatal sepsis. *Pediatric Allergy and Immunology* 13(5):319-27. (see Abstract, p. 319 col. 1 line 1 – p. 320 col. 1 line 31, and p. 324 Discussion)	1 - 43
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INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No.
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This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document Cited in Search Report		Patent Family Member					
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Due to data integration issues this family listing may not include 10 digit Australian applications filed since May 2001.

END OF ANNEX