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(54) **CA125 GENE AND ITS USE FOR DIAGNOSTIC AND THERAPEUTIC INTERVENTIONS**

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(57) **ABSTRACT**

The CA125 gene has been cloned and multiple repeat sequences as well as the carboxy terminus have been identified. The CA125 molecule comprises three major domains: an extracellular amino terminal domain (Domain 1); a large multiple repeat domain (Domain 2); and a carboxy terminal domain (Domain 3) which includes a transmembrane anchor with a short cytoplasmic domain. The amino terminal domain is dominated by its capacity for O-glycosylation and its resultant richness in serine and threonine residues. An amino terminal extension is presented, which comprises four genomic exons. The molecular structure is dominated by a repeat domain comprising 156 amino acid repeat units, which encompass the epitope binding sites. More than 60 repeat units have been identified, sequenced, and contiguously placed in the CA125 domain structure. More specifically, this invention is directed to a CA125 cDNA sequence which can be introduced into animal or human cells to achieve transcription or expression of the cDNA.

CA125 GENE AND ITS USE FOR DIAGNOSTIC AND THERAPEUTIC INTERVENTIONS

[0001] This application is a continuation-in-part of U.S. Provisional Application Ser. No. 60/284,175 filed Apr. 17, 2001, U.S. Provisional Application Ser. No. 60/299,380 filed Jun. 19, 2001, U.S. Non-Provisional application Ser. No. 09/965,738 filed Sep. 27, 2001, and U.S. Provisional Application Ser. No. 60/345,180. This application is a continuation-in-part of provisional application 60/427,045 (filed Nov. 15, 2002), all of which are hereby specifically incorporated by reference. Applicants hereby specifically claims the benefit of these prior filed applications under 35 U.S.C. §119(e), and 120.

BACKGROUND OF THE INVENTION

[0002] The present invention relates generally to the cloning, identification, and expression of the CA125 gene's glycosylated amino terminal domain, the multiple repeat domain, and the carboxy terminal domain in vitro and, more specifically, to the use of recombinant CA125 with epitope binding sites for diagnostic and therapeutic purposes. Additionally, the genomic DNA, a molecule encoding a 5' upstream region of CA125 and a genomic DNA sequence for the amino terminal, extra cellular repeats and carboxy terminal of CA125 has been determined.

[0003] CA125 is an antigenic determinant located on the surface of ovarian carcinoma cells with essentially no expression in normal adult ovarian tissue. Elevated in the sera of patients with ovarian adenocarcinoma, CA125 has played a critical role for more than 15 years in the management of these patients relative to their response to therapy and also as an indicator of recurrent disease.

[0004] It is well established that CA125 is not uniquely expressed in ovarian carcinoma, but is also found in both normal secretory tissues and other carcinomas (i.e., pancreas, liver, colon) [Hardardottir H et al., Distribution of CA125 in embryonic tissue and adult derivatives of the fetal periderm, *Am J Obstet. Gynecol.* 163; 6(1):1925-1931 (1990); Zurawski V R et al., Tissue distribution and characteristics of the CA125 antigen, Cancer Rev. 11-12:102-108 (1988); and O'Brien T J et al., CA125 antigen in human amniotic fluid and fetal membranes, *Am J Obstet Gynecol.* 155:50-55, (1986); Nap M et al., Immunohistochemical characterization of 22 monoclonal antibodies against the CA125 antigen: 2nd report from the ISOBM TD-1 workshop, Tumor Biology 17:325-332 (1996)]. Notwithstanding, CA125 correlates directly with the disease status of affected patients (i.e., progression, regression, and no change), and has become the "gold standard" for monitoring patients with ovarian carcinoma [Bast R C et al., A radioimmunoassay using a monoclonal antibody to monitor the course of epithelial ovarian cancer, *N Engl J Med.* 309:883-887 (1983); and Bon G C et al., Serum tumor marker immunoassays in gynecologic oncology: Establishment of reference values, *Am J. Obstet. Gynecol.* 174:107-114 (1996)]. CA125 is especially useful in post-menopausal patients where endometrial tissue has become atrophic and, as a result, is not a major source of normal circulating CA125.

[0005] During the mid 1980's, the inventor of the present invention and others developed M11, a monoclonal antibody to CA125. M11 binds to a dominant epitope on the repeat structure of the CA125 molecule [O'Brien T J et al., New monoclonal antibodies identify the glycoprotein carrying the CA125 epitope, *Am J Obstet Gynecol* 165:1857-64 (1991)]. More recently, the inventor and others developed a purification and stabilization scheme for CA125, which allows for the accumulation of highly purified high molecular weight CA125 [O'Brien T J et al., More than 15 years of CA125: What is known about the antigen, its structure and its function, *Int J Biological Markers* 13(4):188-195 (1998)].

[0006] Considerable progress has been made over the years to further characterize the CA125 molecule, its structure and its function. The CA125 molecule is a high molecular weight glycoprotein with a predominance of O-linked sugar side chains. The native molecule exists as a very large complex (~2-5 million daltons). The complex appears to be composed of an epitope containing CA125 molecule and binding proteins which carry no CA125 epitopes. The CA125 molecule is heterogenous in both size and charge, most likely due to continuous deglycosylation of the side chains during its lifespan in bodily fluids. The core CA125 subunit is in excess of 200,000 daltons, and retains the capacity to bind both OC125 and M11 class antibodies.

[0007] Despite the advances in detection and quantitation of serum tumor markers like CA125, the majority of ovarian cancer patients are still diagnosed at an advanced stage of the disease—Stage III or IV. Further, the management of patients' responses to treatment and the detection of disease recurrence remain major problems. There, thus, remains a need to significantly improve and standardize current CA125 assay systems. Further, the development of an early indicator of risk of ovarian cancer will provide a useful tool for early diagnosis and improved prognosis.

SUMMARY OF THE INVENTION

[0008] Thus, it is an object of the present invention to provide a recombinant CA125 cDNA molecule which can be introduced into animals or human cells to achieve transcription or expression of the cDNA. The utility of knowing the DNA sequence of a specific gene is that a recombinant protein can be produced which can be used as an easily renewable source of that gene or a portion of the gene. Producing and purifying recombinant protein is easier and can produce greater quantities of protein than purifying native protein from patients. The recombinant protein can then be used to produce antibodies to the gene, both polyclonal and monoclonal. The recombinant protein can also be used as a positive control in test kits and experiments.

[0009] The genomic sequence for CA125 and a 5' upstream region has been determined. A DNA sequence showing the 5' upstream region and the amino terminal portion of the CA125 molecule is set out in Table 1 and SEQ ID NO: 1. The extracellular amino terminal domain is made of exons: Exon 1 from 2205-11679; Exon 2 from 13464-13570; Exon 3 from 16177-34419; Exon 4 from 34575-38024; Exon 5 from 38689-38800; Exon 6 from 40578-45257; Exon 7 from 47360-47395; Exon 8 from 52407-52442; Exon 9 from 52686-52744 as set out in SEQ ID NO: 1. A DNA sequence showing the extracellular repeat portion of the CA125 molecule is set out in Table 2 and SEQ ID NO: 2. The genomic repeats are made of exons: Exon R1 from 1-130; Exon R2 from 442-510; Exon R3 from 5479-5652; Exon R4 from 6301-6334; Exon R5 from 6593-6657; Exon R1 from 7558-7683; Exon R2 from 8216-8284; Exon R3 from 8877-9050; Exon R4 from 9380-9413; Exon R5 from 9675-9739; Exon R1 from 10201-10291; Exon R2 from 10524-10592; Exon

R3 from 11200-11373; Exon R4 from 11722-11755; Exon R5 from 12016-12036; Exon R1 from 12169-12295; Exon R2 from 12532-12600; Exon R3 from 13219-13392; Exon R4 from 13723-13756; Exon R5 from 14016-14077; Exon R1 from 15001-15126; Exon R2 from 15367-15435; Exon R1 from 15648-15773; Exon R2 from 16002-16070; Exon R3 from 16653-16826; Exon R4 from 17158-17191; Exon R5 from 17453-17517; Exon R1 from 18532-18657; Exon R2 from 18888-18956; Exon R3 from 19633-19806; Exon R4 from 20141-20176; Exon R5 from 20387-20449; Exon R1 from 21609-21731; Exon R2 from 21940-22008; Exon R3 from 22605-22778; Exon R4 from 23109-23142; Exon R1 from 29046-29168; Exon R2 from 29266-29334; Exon R3 from 33917-34090; Exon R4 from 36702-36734; Exon R5 from 38270-38320; Exon R1 from 39104-39224; Exon R2 from 39315-39383; Exon R3 from 39532-39705; Exon R4 from 41862-41992. A DNA sequence showing the carboxy terminal domain of the CA125 molecule is set out in Table 3 and SEQ ID NO: 3. The carboxy terminal portion is made of exons: Exon C1 from 1-66; Exon C2 from 1802-1947; Exon C3 from 4198-4350; Exon C4, from 4679-4747; Exon C5 from 6811-6978; Exon C6 from 11232-11270; Exon C7 from 11594-11677; Exon C8 from 14095-14187 as set out in SEQ ID NO: 3. A full length cDNA molecule for CA125 is set out in Table 4 and SEQ ID NO: 4. A CA125 protein is set out in Table 5 and SEQ ID NO: 5.

[0010] Now that the DNA sequence which encodes CA125 has been discovered known synthetic methods can be employed to prepare DNA molecules containing portions of the sequence. Conventional cloning vehicles, such as plasmids, viruses, or bacteria phages can be modified using known methods so as to produce novel cloning vehicles which contain cDNA encoding, CA125, analogs or mutants thereof. Similarly, such cloning vehicles can be modified or engineered so that they contain DNA molecules from Table 4 and SEQ ID NO: 4 or segments substantially similar thereto. The DNA molecule inserted may be made by various methods including enzymatic or chemical synthesis.

[0011] The CA125 gene has been cloned and multiple repeat sequences as well as the glycosylated amino terminal and the carboxy terminus have been identified. CA125 requires a transcript of more than 35,000 bases and occupies approximately 150,000 by on chromosome 19p 13.2. The CA125 molecule comprises three major domains: an extracellular amino terminal domain (Domain 1); a large multiple repeat domain (Domain 2); and a carboxy terminal domain (Domain 3) which includes a transmembrane anchor with a short cytoplasmic domain. The amino terminal domain is assembled by combining five genomic exons, four very short amino terminal sequences and one extraordinarily large exon. This domain is dominated by its capacity for O-glycosylation and its resultant richness in serine and threonine residues. Additionally, an amino terminal extension is present, which comprises four genomic exons. Analysis of the amino terminal extension revealed that its amino acid composition is consistent with the amino acid composition of the amino terminal domain.

[0012] Perhaps even more significantly, the multiple repeat domains of CA125 or other domains could also be used for the development of a potential vaccine for patients with ovarian cancer. In order to induce cellular and humoral immunity in humans to CA125, murine antibodies specific for CA125 were utilized in anticipation of patient production of anti-ideotypic antibodies, thus indirectly allowing the induction of an immune response to the CA125 molecule. With the availability of recombinant CA125, especially domains which encompass epitope binding sites for known murine antibodies, it will be feasible to more directly stimulate patients' immune systems to CA125 and, as a result, extend the life of ovarian carcinoma patients.

[0013] The recombinant CA125 of the present invention may also be used to develop therapeutic targets. Molecules like CA125, which are expressed on the surface of tumor cells, provide potential targets for immune stimulation, drug delivery, biological modifier delivery or any agent which can be specifically delivered to ultimately kill the tumor cells. Humanized or human antibodies to CA125 epitopes could be used to deliver all drug or toxic agents including radioactive agents to mediate direct killing of tumor cells. Natural ligands having a natural binding affinity for domains on the CA125 molecule could also be utilized to deliver therapeutic agents to tumor cells.

[0014] CA125 expression may further provide a survival or metastatic advantage to ovarian tumor cells. Antisense oligonucleotides derived from the CA125 repeat sequences could be used to down-regulate the expression of CA125. Further, antisense therapy could be used in association with a tumor cell delivery system of the type described above.

[0015] Recombinant domains of the CA125 molecule also have the potential to identify small molecules, which bind to individual domains of the CA125 molecule. These small molecules could also be used as delivery agents or as biological modifiers.

[0016] In another aspect of the present invention, an isolated nucleic acid of the CA125 gene is disclosed, which comprises a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequences set forth in SEQ ID NOS: 1, 2, 3 and 4; (b) a nucleotide sequence having at least 70% sequence identity to any one of the sequences in (a); (c) a degenerate variant of any one of (a) to (b); and (d) a fragment of any one of (a) to (c).

[0017] In another aspect of the present invention, an isolated nucleic acid of the CA125 gene, comprising a sequence that encodes a polypeptide with the amino acid sequence selected from the group consisting of: (a) the amino acid sequences set forth in SEQ ID NO: 5; (b) an amino acid sequence having at least 50% sequence identity to any one of the sequences in (a); (c) a conservative variant of any one of (a) to (b); and (d) a fragment of any one of (a) to (c).

[0018] The vector may be a cloning vector, a shuttle vector, or an expression vector. A cultured cell comprising the vector is also contemplated.

[0019] More specifically, this invention relates to a purified antibody that selectively binds to an epitope in the CA125 protein of SEQ ID NO: 5. Similarly, the purified antibody selectively binds to an amino acid sequence having at least 50% sequence identity to said sequence; the purified antibody selectively binds to an amino acid sequence having at least 60% sequence identity to said sequence; the purified antibody selectively binds to an amino acid sequence having at least 70% sequence identity to said sequence; the purified antibody selectively binds to an amino acid sequence having at least 80% sequence identity to said sequence; and the purified antibody selectively binds to an amino acid sequence having at least 90% sequence identity to said sequence. Additionally,

purified antibody can be a conservative variant of the amino acid sequence set forth in SEQ ID NO: 5 or a fragment thereof.

DETAILED DESCRIPTION OF THE INVENTION

[0020] In accordance with the present invention, conventional molecular biology, microbiology, and recombinant DNA techniques may be used that will be apparent to those skilled in the relevant art. Such techniques are explained fully in the literature (see, e.g., Maniatis, Fritsch & Sambrook, "Molecular Cloning: A Laboratory Manual (1982); "DNA Cloning: A Practical Approach," Volumes I and II (D. N. Glover ed. 1985); "Oligonucleotide Synthesis" (M. J. Gait ed. 1984); "Nucleic Acid Hybridization" (B. D. Hames & S. J. Higgins eds. (1985)); "Transcription and Translation" (B. D. Hames & S. J. Higgins eds. (1984)); "Animal Cell Culture" (R. I. Freshney, ed. (1986)); "Immobilized Cells And Enzymes" (IRL Press, (1986)); and B. Perbal, "A Practical Guide To Molecular Cloning" (1984)).

[0021] Therefore, if appearing herein, the following terms shall have the definitions set out below.

[0022] A "vector" is a replicon, such as plasmid, phage or cosmid, to which another DNA segment may be attached so as to bring about the replication of the attached segment.

[0023] A "DNA molecule" refers to the polymeric form of deoxyribonucleotides (adenine, guanine, thymine, or cytosine) in either single stranded form, or a double-stranded helix. This term refers only to the primary and secondary structure of the molecule, and does not limit it to any particular tertiary forms. Thus, this term includes double-stranded DNA found, inter alia, in linear DNA molecules (e.g., restriction fragments), viruses, plasmids, and chromosomes.

[0024] As used herein, the term "gene" shall mean a region of DNA encoding a polypeptide chain.

[0025] "Messenger RNA" or "mRNA" shall mean an RNA molecule that encodes for one or more polypeptides.

[0026] "DNA polymerase" shall mean an enzyme which catalyzes the polymerization of deoxyribonucleotide triphosphates to make DNA chains using a DNA template.

[0027] "Reverse transcriptase" shall mean an enzyme which catalyzes the polymerization of deoxy- or ribonucleotide triphosphates to make DNA or RNA chains using an RNA or DNA template.

[0028] "Complementary DNA" or "cDNA" shall mean the DNA molecule synthesized by polymerization of deoxyribonucleotides by an enzyme with reverse transcriptase activity.

[0029] An "isolated nucleic acid" is a nucleic acid the structure of which is not identical to that of any naturally occurring nucleic acid or to that of any fragment of a naturally occurring genomic nucleic acid spanning more than three separate genes. The term therefore covers, for example, (a) a DNA which has the sequence of part of a naturally occurring genomic DNA molecule but is not flanked by both of the coding sequences that flank that part of the molecule in the genome of the organism in which it naturally occurs; (b) a nucleic acid incorporated into a vector or into the genomic DNA of a prokaryote or eukaryote in a manner such that the resulting molecule is not identical to any naturally occurring vector or genomic DNA; (c) a separate molecule such as a cDNA, a genomic fragment, a fragment produced by polymerase chain reaction (PCR), or a restriction fragment; and (d) a recombinant nucleotide sequence that is part of a hybrid gene, i.e., a gene encoding a fusion protein.

[0030] "Oligonucleotide", as used herein in referring to the probes or primers of the present invention, is defined as a molecule comprised of two or more deoxy- or ribonucleotides, preferably more than ten. Its exact size will depend upon many factors which, in turn, depend upon the ultimate function and use of the oligonucleotide.

[0031] "DNA fragment" includes polynucleotides and/or oligonucleotides and refers to a plurality of joined nucleotide units formed from naturally-occurring bases and cyclofuranosyl groups joined by native phosphodiester bonds. This term effectively refers to naturally-occurring species or synthetic species formed from naturally-occurring subunits. "DNA fragment" also refers to purine and pyrimidine groups and moieties which function similarly but which have non naturally-occurring portions. Thus, DNA fragments may have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species. They may also contain altered base units or other modifications, provided that biological activity is retained. DNA fragments may also include species which include at least some modified base forms. Thus, purines and pyrimidines other than those normally found in nature may be so employed. Similarly, modifications on the cyclofuranose portions of the nucleotide subunits may also occur as long as biological function is not eliminated by such modifications.

[0032] "Primer" shall refer to an oligonucleotide, whether occurring naturally or produced synthetically, which is capable of acting as a point of initiation of synthesis when placed under conditions in which synthesis of a primer extension product, which is complementary to a nucleic acid strand, is induced, i.e., in the presence of nucleotides and an inducing agent such as a DNA polymerase and at a suitable temperature and pH. The primer may be either single-stranded or double-stranded and must be sufficiently long to prime the synthesis of the desired extension product in the presence of the inducing agent. The exact length of the primer will depend upon many factors, including temperature, the source of primer and the method used. For example, for diagnostic applications, depending on the complexity of the target sequence, the oligonucleotide primer typically contains 10-25 or more nucleotides, although it may contain fewer nucleotides.

[0033] The primers herein are selected to be "substantially" complementary to different strands of a particular target DNA sequence. This means that the primers must be sufficiently complementary to hybridize with their respective strands. Therefore, the primer sequence need not reflect the exact sequence of the template. For example, a non-complementary nucleotide fragment may be attached to the 5' end of the primer, with the remainder of the primer sequence being complementary to the strand. Alternatively, non-complementary bases or longer sequences can be interspersed into the primer, provided that the primer sequence has sufficient complementarity with the sequence or hybridize therewith and thereby form the template for the synthesis of the extension product.

[0034] As used herein, the term "hybridization" refers generally to a technique wherein denatured RNA or DNA is combined with complementary nucleic acid sequence which is either free in solution or bound to a solid phase. As recognized by one skilled in the art, complete complementarity between the two nucleic acid sequences is not a pre-requisite for hybridization to occur. The technique is ubiquitous in

molecular genetics and its use centers around the identification of particular DNA or RNA sequences within complex mixtures of nucleic acids.

[0035] As used herein, "restriction endonucleases" and "restriction enzymes" shall refer to bacterial enzymes which cut double-stranded DNA at or near a specific nucleotide sequence.

[0036] "Purified polypeptide" refers to any peptide generated from CA125 either by proteolytic cleavage or chemical cleavage.

[0037] "Degenerate variant" refers to any amino acid variation in the repeat sequence, which fulfills the homology exon structure and conserved sequences and is recognized by the M11, OC125 and ISOBM series of antibodies.

[0038] "Fragment" refers to any part of the CA125 molecule identified in a purification scheme.

[0039] "Conservative variant antibody" shall mean any antibody that fulfills the criteria of M11, OC125 or any of the ISOBM antibody series.

[0040] "Homology" refers to similarity based on identical base matches in alignment. When two sequences are identical there is a 100% homology, as base matches differ in alignment the homology between two sequences is reduced.

[0041] The CA125 gene has been cloned and multiple repeat sequences as well as the carboxy terminus have been identified. The cDNA for the CA125. gene is set out in SEQ ID NO: 4. The CA125 molecule comprises three major domains: an extracellular amino terminal domain (Domain 1); a large multiple repeat domain (Domain 2); and a carboxy terminal domain (Domain 3) which includes a transmembrane anchor with a short cytoplasmic domain. The amino terminal domain is assembled by combining five genomic exons, four very short amino terminal sequences and one extraordinarily large exon. This domain is dominated by its capacity for O-glycosylation and its resultant richness in serine and threonine residues. Additionally, an amino terminal extension is present, which comprises four genomic exons. The amino acid composition of the amino terminal extension was found to be consistent with the amino acid composition of the amino terminal domain. The molecular structure is dominated by a repeat domain comprising 156 amino acid repeat units, which encompass the epitope binding sites. More than 60 repeat units have been identified, sequenced, and contiguously placed in the CA125 domain structure. The repeat units encompass an interactive disulfide bridged C-enclosure and the site of OC125 and M11 binding. The repeat sequences demonstrated 70-85% homology to each other. Expression of the repeats was demonstrated in *E. coli*. The CA125 molecule is anchored at its carboxy terminal through a transmembrane domain and a short cytoplasmic tail. The carboxy terminal also contains a proteolytic cleavage site approximately 50 amino acids upstream from the transmembrane domain, which allows for proteolytic cleavage and release of the CA125 molecule. Any one of the repeat domains has the potential for use as a new gold standard for detecting and monitoring the presence of the CA125 antigen. Further, the repeat domains or other domains, especially the c-terminal to the repeat domain also provide a basis for the development of a vaccine, which would be useful for the treatment of ovarian cancer and other carcinomas where CA125 is elevated.

[0042] The DNA sequences of the present invention can also be characterized as encoding the amino acid sequence equivalents of the amino acid sequence, equivalents, as used in this context, include peptides of substantially similar length and amino acid identity to those disclosed, but having conservative amino acid substitution at a non-critical residue position. A conservative amino acid substitution is a substitution in which an amino acid residue is replaced with an amino acid residue of differing identity, but whose R group can be characterized by chemically similar. Four common categories include: polor but uncharged R groups; positively charged R groups; negatively charged R groups; and, hydrophobic R groups. A preferred conservative substitution involves the substitution of a second hydrophobic residue for a fir hydrophobic residue, the first and second hydrophobic residues differing primarily in the size of the R group. The hydrophobic residue would be predicted to be located internally in the folded peptide structure and the mild pertubatim caused only by a change in the size of an R group at an internally located which would not alter the antigenecity of R protein. More specifically, two nucleic acid molecules are substantially equivalent if they have at least about 70% homology.

[0043] The isolated cDNA sequences (Table 4 and SEQ ID NO: 4) of the present invention can be inserted into an expression vector. Such vectors contain all necessary regulatory signals to promote the expression of a DNA sequence of interest. Expression vectors are typically either prokaryote or eukaryote specific. Expression vectors can be introduced into either prokaryote or eukaryote cells to produce CA125 proteins or portions thereof. The isolated cDNA sequence as shown in Table 4 was expressed to provide the CA125 molecule set out in Table 5 and SEQ ID NO: 5. The expressed CA125 is a polypeptide with the amino acid sequence set forth in SEQ ID NO: 5; an amino acid sequence having at least 50% sequence identity to the sequence, a conservative for variant or a fragment of any of the above. Two polypeptide sequences are substantially equivalent if there is at least 50% sequence homology and substantial similar physical characteristics. However, in practice, a portion of an isolated nucleic acid molecule set out in SEQ ID NO: 4 is expressed to obtain a fragment of the CA125 molecule. This fragment is then purified to obtain an isolated CA125 fragment.

[0044] In certain embodiments, "purified" refers to a polypeptide composition which has been subjected to fractionation to remove various nonprotein components such as other cellular components. Various techniques suitable for use in protein purification are known to those skilled in the relevant art. These techniques include, for example, precipitation with ammonium sulphate, PEG, antibodies and the like or by heat denaturation, followed by centrifugation; chromatography steps such as ion exchange, gel filtration, reverse phase, hydroxylapatite and affinity chromatography; isoelectric focusing; gel electrophoresis; and combination of such techniques. Similarly, a "purification scheme" is a technique or system to remove various nonprotein components such as other cellular components from the expressed protein. Various techniques suitable for use in protein purification are known to those skilled in the relevant art. These techniques include, for example, precipitation with ammonium sulphate, PEG, antibodies and the like or by heat denaturation, followed by centrifugation; chromatography steps such as ion exchange, gel filtration, reverse phase, hydroxylapatite and affinity chromatography; isoelectric focusing; gel electrophoresis; and combination of such techniques.

[0045] The genomic DNA and a full-length cDNA sequence of human CA125 has been determined. Addition-

ally, a nucleic acid molecule encoding a 5' upstream region of the CA125 gene has been determined. cDNA is expressed with the use of an expression vector. An expression vector is a carrying vector that has an inducer for expression built into the vector. Different vectors use different inducers. The cDNA is ligased into the expression vector using restriction digest sites designed in the vector. The cDNA must be ligased in the sense direction and in the correct reading frame for expression to occur. Once the cDNA is ligased into the expression vector, the construct is transformed into a cell. In the preferred embodiment, we use *E-Coli* bacteria, but the transformation can be done with yeast, mammalian cells, plants cells, etc. The transformed cells are then grown in culture and protein production is induced with the an inducing agent for the expression vector. In the preferred embodiment, we use the pQE-30 expression vector and induce with IPTG. Once induction has occurred, the cells are harvested and the protein is purified. It should be noted that some expression vectors add tags to the recombinant protein to aid in purification. For example, pQE-30 adds a His-Tag which binds to nickel to aid in purification. Once cells have been successfully transformed, a small aliquot can be frozen and stored for future use.

[0046] With a cDNA sequence, one skilled in the art has an easily renewable source of purified CA125. Portions of this cDNA sequence can be expressed to make CA125 polypeptides and these polypeptides can be used to make monoclonal antibodies. These monoclonal antibodies can be made by one skilled in the art to portions of the protein which heretofore do not have any monoclonal antibodies, such as the amino terminal sequence.

[0047] More specifically, the purified antibodies are made by the following process: the recombinant protein is injected into an animal (usually a mouse, but other animals can be used). The animal's B-lymphocytes produce antibodies to the protein. Each activated B lymphocyte forms a clone of cells in spleen or lymph nodes, with each cell of the clone producing identical antibody. These spleen cells are then harvested and fused with myeloma cells to produce hybridomas. These hybridomas are immortal and produce only one type of antibody. The hybridomas are selected from cells that did not fuse by selective media. The hybidomas can then be grown in large quantities to produce large quantities of monoclonal antibodies.

[0048] Therapeutic Targets: Molecules, which are expressed on the surface of tumor cells as CA125 is, offer potential targets for immune stimulation, drug delivery, biological modifier delivery or any agent which can be specifically delivered to ultimately kill the tumor cells. CA125 offers such potential as a target: 1) Antibodies to CA125 epitopes or newly described potential epitopes: Most especially humanized or human antibodies to CA125 which could directly activate the patients' immune system to attack and kill tumor cells. Antibodies could be used to deliver all drug or toxic agents, including radioactive agents to mediate direct killing of tumor cells. 2) Natural ligands: Under normal circumstances, molecules are bound to the CA125 molecule e.g. a 50 k dalton protein which does not contain CA125 epitopes co-purifies with CA125. Such a molecule, which might have a natural binding affinity for domains on the CA125 molecule, could also be utilized to deliver therapeutic agents to tumor cells.

[0049] Anti-sense therapy: CA125 expression may provide a survival or metastatic advantage to ovarian tumor cells as such antisense oligonucleotide derived from the CA125 sequence could be used to down-regulate the expression of CA125. Antisense therapy could be used in association with a tumor cell delivery system such as described above.

[0050] Small Molecules: Recombinant domains of CA125 also offer the potential to identify small molecules which bind to individual domains of the molecule. Small molecules either from combinatorial chemical libraries or small peptides can also be used as delivery agents or as biological modifiers.

[0051] Transgenic Animals/Transformed: CA125 and genomic DNA can be used to develop transgenic animal models and can be used under low stringency conditions, to clone CA125 cDNAs and genomic DNAs of other animal species. The CA125 cDNA can be used to prepare stable transformants. The bacterial cells could be transformed with CA125 cDNA to include these genes.

Example 1

[0052] Expression of 6×His-tagged CA125 repeat in *E. coli*: The open reading frame of the CA125 repeat was amplified by PCR with the 5' sense primer 1 (5'-ACCGGATCCATGGGCCACACAGAGCCTGGCCC-3') (SEQ ID NO: 6) and the 3' antisense primer 2 (5'-TGTAAGCTTAGGCAGGGAGGATGGAGTCC-3') (SEQ ID NO: 7). The open reading frame of the CA125 repeat constitutes a portion of the isolated nucleic acid molecule set out in SEQ ID NO: 4. PCR was performed in a reaction mixture consisting of ovarian tumor cDNA derived from 50 ng of mRNA, 5 μmol each of sense and antisense primers for the CA125 repeat, 0.2 mmol of dNTPs, and 0.625 U of Taq polymerase in 1× buffer in a final volume of 25 μl. This mixture was subjected to 1 minute of denaturation at 95° C. followed by 30 cycles of PCR consisting of the following: denaturation for 30 seconds at 95° C., 30 seconds of annealing at 62° C., and 1 minute of extension at 72° C. with an additional 7 minutes of extension on the last cycle. The product was electrophoresed through a 2% agarose gel for separation, the PCR product was purified and digested with the restriction enzymes BamHI and HindIII. This digested PCR product was ligated into the expression vector pQE-30, which had also been digested with BamHI and HindIII. The ligation reaction consisted of 1 ul of 10× ligation buffer, 1 ul of 10× bovine serum albumin (BSA), 1 ul of T4 ligase enzyme, and 7 ul of digested PCR product. The reaction went overnight at 15° C. This clone would allow for expression of recombinant amino-terminal 6×His-tagged CA125 repeat. The construct was then transformed into JM109 *E. coli* cells. The transformation reaction consisted of 5 ul of ligation reaction and 50 ul of cells. The reaction was mixed gently and then incubated on ice for 30 minutes. The reaction was then heat shocked at 42° C. for 45 seconds in a water bath before being returned to ice for 2 minutes. 500 ul of LB broth media were added and the mixture was incubated at 37° C. for 1 hour. At the end of 1 hour the cells were spun down in a microfuge at 4,000×g for 5 minutes and approximately 450 ul of media was removed. The cells were resuspended in the remaining 100 ul of media, transferred to a LAIX plate, and incubated overnight at 37° C. White colonies were picked from the plate and cultured in 5 ml LB broth media to determine if the transformation was successful. Transformed *E. coli* were grown in 1 L cultures to an OD_{600} of 1.5-2.0 at 37° C. and were induced with IPTG (0.1 mM) for 4-6 hours at 25° C. to produce recombinant protein. Whole *E. coli* lysate was electrophoresed through a denaturing 12%

polyacrylamide gel and Coomassie stained to detect highly expressed proteins. His-tagged proteins were purified under denaturing conditions using Ni-NTA agarose metal chelating affinity chromatography available from Qiagen according to the manufacturer's instructions. Cells are spun down to remove liquid LB broth media. The cells are then resuspended in 40 ml of 8M Urea lysis buffer (pH 8.0) and incubated with agitation overnight at room temperature. The mixture is then spun down and the lysate is removed. The lysate is then incubated with Ni-NTA agarose beads with agitation overnight at room temperature. The beads are pelleted and the supernatant is removed. The beads are then washed twice in lysis buffer pH 8.0 plus Triton X, three times with lysis buffer pH 6.3 plus Triton X, and four times with lysis buffer pH 6.3 without Triton X. The protein is then eluted from the beads with lysis buffer pH4.2 plus 25 mM EDTA incubated overnight with agitation at room temperature. The beads are pelleted and the supernatant containing the recombinant protein is removed. The supernatant is then dialyzed twice in 0.2× PBS to remove the urea and freeze dried for storage. 1 L of culture produced 2.4 mg of recombinant protein.

[0053] It should be understood that various changes and modifications to the presently preferred embodiments described herein will be apparent to those skilled in the art. Such changes and modifications can be made without departing from the spirit and scope of the present invention and without diminishing its attendant advantages.

TABLE 1

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

```
   1 GGTGCGCACC ACTATGTCTG GCTAATTTTT GTATTTTTTT GTAGAGACAT
  51 GGTTTCACCA TGTTGGCCAG GCTGGTCTCG AATTCCTGAC TTCAAGTAAT
 101 CCACCCACCT CAGCCTCCCA AAGTGCTGGG ATTACAAGCA TGAGCCACCA
 151 TGCATGGCCT AAAGCTTCTT TTAAAGCCAC CAAGTCCCTT CCCATGTTAG
 201 CCCACTAATC CATGGGTTAG TCATGAATGG ATTAATCTAT TCATACGGAC
 251 AGAGCCCTCA TCACCCAATC ACCTCTTAAA GGCCCCACCT CTCAATACTG
 301 CCACACTGGG GATTAAGTTT CAACAGAGTT TTGGAGGGGA CATTCAAATC
 351 ATAGTAATGC CCAAAGTGAA AAATCTTCCC TGCACTTTTC CCTCAACAAA
 401 AACAGCCAGA GATAGTGAGC TGCCAGGAAA TTCTTTTTTT TTTCCTCTTC
 451 TGTCCTAAAT CAGCATCGCT AGACCTTTAC ATGATTCAAC CTCATCTTCT
 501 TCACCCTCTG GGTCATGAAA TTTTATTTAT TTATTTATTA TTTTCTTGGG
 551 ACAGACTCTG GCTCTGTCGC CCAGGCTGAA GTGCAGTGGT GTGATCTTGG
 601 CTCACTGCAA CCTCCGCCTC CCGGGTTCAA GCGATTCTCC TGCCTCAGCC
 651 TCCTGAGTAG CTGGGATTAC AGGTGGGCGC CACCACACCC AGCTAATTTT
 701 TTGTATTTTT AGTAGAGATG GGGTTTCACC ATATTAGCCA GGATGGTCTC
 751 CATCTCTTGA CCTCGTGATC TGCCCACCTC AGCCTCCCAA AATGCTGGGA
 801 TTACAGGCAT GAGACACCAC GCCCAGCAGG CCAGGGTCAT GAGATTTTAA
 851 TCAAGAGCAA CTTCCACTGA TTCCTGAGAG TGCATCTGTG GGCCCCTGCT
 901 CTGATCTGAA CAGAAGTGCC GTGTCTTCTC TGACCTCCAC TTCTCAATTC
 951 AAGAGCCTTA GTATCTGCCA GTATCACACA CTGAGCATTA GCTCCATCTC
1001 ATGGGGGTGT AGGTAGGGGC TCTATCTGCA TCTTTCTTTC TTTTTTTCTT
1051 TCTTTCCCTT CCTCCCTTCC TCACTCCCTC GGTCCTCTCT TTCTTTCCTT
1101 TTCTTTCTTC CTTCCTCCCT TCCTCCCTCC CTCCCTCTCT CTTTCTCTCT
1151 TTCTTTCTTT CCTTCTTTCT TTCTTTCTCT CTTCCTTCCC TCCCTCCCTC
1201 CTTCCTTCCT TTCTCTTTCT TTCTCTTTCT TTCTTTTTTT CCTTCCTTCC
1251 TTCCTTCTTT CTCTTTCTCT CCCTCCCTTC CTTCCTTCCT TCCTTCCTTC
1301 CTTCCTTTCT TTCTTTCTTT CTTTCTTTCT TTCTTTCTTT CTTTCTTTCT
1351 TTCTTTCTTC CTTCCTTCCT TCCTTCCTTC CTTCCTTCCT TCCTTCCTTT
```

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)					
1401	CTTTTCTTTC	TTTCTCTTTC	TTTTTGAGAC	AGAGCTCTTA	TTACCCATGC
1451	TGGAGTGCAG	TGGTGTGACC	TTGGCTTACT	GCAACATCTG	CCTCCTAGGG
1501	TCAAGTGATT	CTCCTGCCTC	AGCCTCCTAA	GTAGCTGGGA	TTACAGACAC
1551	ATGCCACCAC	ACCCAATATT	TATTTTTATT	AAAATTTTTT	TTAAAATTAT
1601	TTTTAAAAAA	TTAAAAATAA	TTTTGTATTT	TTAGTAGAGA	CGGGGTTTCT
1651	CCATGTTGGT	CAGGCTGATC	TCAAACTCCC	AACCTCAGGT	GATCCTCCCA
1701	CCTCACCTCC	CAAAGTGCTG	GGATTACAGG	CATGAGCCAC	CGTGCCCAGC
1751	CTGGTTCCTG	GTTTCTAAGA	CATCACACAC	ACACACACAC	ACACACACAC
1801	ACACTCACAC	ACTCAGAGAG	AGAGAGAGAG	AGAGGATCAT	TAAGACATGA
1851	TACACTAAGA	AATTCTATTC	TGCAGACACT	GAGAATCCGT	TAAAAAGTTT
1901	GAAGGGAAGA	ATTGAGATCA	TCAGGTGTTT	ATTTGAGGAA	ATTGTCTGTG
1951	GTTGAACTAT	CCTTTCCTTT	CTCTCCCTGA	GATTTGGTCT	TCTCAATTAG
2001	AAGCGTTGCA	CAATTCCCCC	AACCTCCATA	CATACGGCAG	CTCTTCTAGA
2051	CACAGGTTTT	CCCAGGTCAA	ATGCGGGGAC	CCCAGCCATA	TCTCCCACCC
2101	TGAGAAATTT	TGGAGTTTCA	GGGAGCTCAG	AAGCTCTGCA	GAGGCCACCC
2151	TCTCTGAGGG	GATTCTTCTT	AGACCTCCAT	CCAGAGGCAA	ATGTTGACCT
			Exon 1		
2201	GTCCATGCTG	AAACCCTCAG	GCCTTCCTGG	GTCATCTTCT	CCCACCCGCT
2251	CCTTGATGAC	AGGGAGCAGG	AGCACTAAAG	CCACACCAGA	AATGGATTCA
2301	GGACTGACAG	GAGCCACCTT	GTCACCTAAG	ACATCTACAG	GTGCAATCGT
2351	GGTGACAGAA	CATACTCTGC	CCTTTACTTC	CCCAGATAAG	ACCTTGGCCA
2401	GTCCTACATC	TTCGGTTGTG	GGAAGAACCA	CCCAGTCTTT	GGGGGTGATG
2451	TCCTCTGCTC	TCCCTGAGTC	AACCTCTAGA	GGAATGACAC	ACTCCGAGCA
2501	AAGAACCAGC	CCATCGCTGA	GTCCCCAGGT	CAATGGAACT	CCCTCTAGGA
2551	ACTACCCTGC	TACAAGCATG	GTTTCAGGAT	TGAGTTCCCC	AAGGACCAGG
2601	ACCAGTTCCA	CAGAAGGAAA	TTTTACCAAA	GAAGCATCTA	CATACACACT
2651	CACTGTAGAG	ACCACAAGTG	GCCCAGTCAC	TGAGAAGTAC	ACAGTCCCCA
2701	CTGAGACCTC	AACAACTGAA	GGTGACAGCA	CAGAGACCCC	CTGGGACACA
2751	AGATATATTC	CTGTAAAAAT	CACATCTCCA	ATGAAAACAT	TTGCAGATTC
2801	AACTGCATCC	AAGGAAAATG	CCCCAGTGTC	TATGACTCCA	GCTGAGACCA
2851	CAGTTACTGA	CTCACATACT	CCAGGAAGGA	CAAACCCATC	ATTTGGGACA
2901	CTTTATTCTT	CCTTCCTTGA	CCTATCACCT	AAAGGGACCC	CAAATTCCAG
2951	AGGTGAAACA	AGCCTGGAAC	TGATTCTATC	AACCACTGGA	TATCCCTTCT
3001	CCTCTCCTGA	ACCTGGCTCT	GCAGGACACA	GCAGAATAAG	TACCAGTGCG
3051	CCTTTGTCAT	CATCTGCTTC	AGTTCTCGAT	AATAAAATAT	CAGAGACCAG
3101	CATATTCTCA	GGCCAGAGTC	TCACCTCCCC	TCTGTCTCCT	GGGGTGCCCG

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)	
3151	AGGCCAGAGC CAGCACAATG CCCAACTCAG CTATCCCTTT TTCCATGACA
3201	CTAAGCAATG CAGAAACAAG TGCCGAAAGG GTCAGAAGCA CAATTTCCTC
3251	TCTGGGGACT CCATCAATAT CCACAAAGCA GACAGCAGAG ACTATCCTTA
3301	CCTTCCATGC CTTCGCTGAG ACCATGGATA TACCCAGCAC CCACATAGCC
3351	AAGACTTTGG CTTCAGAATG GTTGGGAAGT CCAGGTACCC TTGGTGGCAC
3401	CAGCACTTCA GCGCTGACAA CCACATCTCC ATCTACCACT TTAGTCTCAG
3451	AGGAGACCAA CACCCATCAC TCCACGAGTG GAAAGGAAAC AGAAGGAACT
3501	TTGAATACAT CTATGACTCC ACTTGAGACC TCTGCTCCTG GAGAAGAGTC
3551	CGAAATGACT GCCACCTTGG TCCCCACTCT AGGTTTTACA ACTCTTGACA
3601	GCAAGATCAG AAGTCCATCT CAGGTCTCTT CATCCCACCC AACAAGAGAG
3651	CTCAGAACCA CAGGCAGCAC CTCTGGGAGG CAGAGTTCCA GCACAGCTGC
3701	CCACGGGAGC TCTGACATCC TGAGGGCAAC CACTTCCAGC ACCTCAAAAG
3751	CATCATCATG GACCAGTGAA AGCACAGCTC AGCAATTTAG TGAACCCCAG
3801	CACACACAGT GGGTGGAGAC AAGTCCTAGC ATGAAAACAG AGAGACCCCC
3851	AGCATCAACC AGTGTGGCAG CCCCTATCAC CACTTCTGTT CCCTCAGTGG
3901	TCTCTGGCTT CACCACCCTG AAGACCAGCT CCACAAAAGG GATTTGGCTT
3951	GAAGAAACAT CTGCAGACAC ACTCATCGGA GAATCCACAG CTGGCCCAAC
4001	CACCCATCAG TTTGCTGTTC CCACTGGGAT TTCAATGACA GGAGGCAGCA
4051	GCACCAGGGG AAGCCAGGGC ACAACCCACC TACTCACCAG AGCCACAGCA
4101	TCATCTGAGA CATCCGCAGA TTTGACTCTG GCCACGAACG GTGTCCCAGT
4151	CTCCGTGTCT CCAGCAGTGA GCAAGACGGC TGCTGGCTCA AGTCCTCCAG
4201	GAGGGACAAA GCCATCATAT ACAATGGTTT CTTCTGTCAT CCCTGAGACA
4251	TCATCTCTAC AGTCCTCAGC TTTCAGGGAA GGAACCAGCC TGGGACTGAC
4301	TCCATTAAAC ACTAGACATC CCTTCTCTTC CCCTGAACCA GACTCTGCAG
4351	GACACACCAA GATAAGCACC AGCATTCCTC TGTTGTCATC TGCTTCAGTT
4401	CTTGAGGATA AAGTGTCAGC GACCAGCACA TTCTCACACC ACAAAGCCAC
4451	CTCATCTATT ACCACAGGGA CTCCTGAAAT CTCAACAAAG ACAAAGCCCA
4501	GCTCAGCCGT TCTTTCCTCC ATGACCCTAA GCAATGCAGC AACAAGTCCT
4551	GAAAGAGTCA GAAATGCAAC TTCCCCTCTG ACTCATCCAT CTCCATCAGG
4601	GGAAGAGACA GCAGGGAGTG TCCTCACTCT CAGCACCTCT GCTGAGACTA
4651	CAGACTCACC TAACATCCAC CCAACTGGGA CACTGACTTC AGAATCGTCA
4701	GAGAGTCCTA GCACTCTCAG CCTCCCAAGT GTCTCTGGAG TCAAAACCAC
4751	ATTTTCTTCA TCTACTCCTT CCACTCATCT ATTTACTAGT GGAGAAGAAA
4801	CAGAGGAAAC TTCGAATCCA TCTGTGTCTC AACCTGAGAC TTCTGTTTCC
4851	AGAGTAAGGA CCACCTTGGC CAGCACCTCT GTCCCTACCC CAGTATTCCC
4901	CACCATGGAC ACCTGGCCTA CACGTTCAGC TCAGTTCTCT TCATCCCACC
4951	TAGTGAGTGA GCTCAGAGCT ACGAGCAGTA CCTCAGTTAC AAACTCAACT

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)	
5001	GGTTCAGCTC TTCCTAAAAT ATCTCACCTC ACTGGGACGG CAACAATGTC
5051	ACAGACCAAT AGAGACACGT TTAATGACTC TGCTGCACCC CAAAGCACAA
5101	CTTGGCCAGA GACTAGTCCC AGATTCAAGA CAGGGTTACC TTCAGCAACA
5151	ACCACTGTTT CAACCTCTGC CACTTCTCTC TCTGCTACTG TAATGGTCTC
5201	TAAATTCACT TCTCCAGCAA CTAGTTCCAT GGAAGCAACT TCTATCAGGG
5251	AACCATCAAC AACCATCCTC ACAACAGAGA CCACGAATGG CCCAGGCTCT
5301	ATGGCTGTGG CTTCTACCAA CATCCCAATT GGAAAGGGCT ACATTACTGA
5351	AGGAAGATTG GACACAAGCC ATCTGCCCAT TGGAACCACA GCTTCCTCTG
5401	AGACATCTAT GGATTTTACC ATGGCCAAAG AAAGTGTCTC AATGTCAGTA
5451	TCTCCATCTC AGTCCATGGA TGCTGCTGGC TCAAGCACTC CAGGAAGGAC
5501	AAGCCAATTC GTTGACACAT TTTCTGATGA TGTCTATCAT TTAACATCCA
5551	GAGAAATTAC AATACCTAGA GATGGAACAA GCTCAGCTCT GACTCCACAA
5601	ATGACTGCAA CTCACCCTCC ATCTCCTGAT CCTGGCTCTG CTAGAAGCAC
5651	CTGGCTTGGC ATCTTGTCCT CATCTCCTTC TTCTCCTACT CCCAAAGTCA
5701	CAATGAGCTC CACATTTTCA ACTCAGAGAG TCACCACAAG CATGATAATG
5751	GACACAGTTG AAACTAGTCG GTGGAACATG CCCAACTTAC CTTCCACGAC
5801	TTCCTTGACA CCAAGTAATA TTCCAACAAG TGGTGCCATA GGAAAAAGCA
5851	CCCTGGTTCC CTTGGACACT CCATCTCCAG CCACATCATT GGAGGCATCA
5901	GAAGGGGGAC TTCCAACCCT CAGCACCTAC CCTGAATCAA CAAACACACC
5951	CAGCATCCAC CTCGGAGCAC ACGCTAGTTC AGAAAGTCCA AGCACCATCA
6001	AACTTACCAT GGCTTCAGTA GTAAAACCTG GCTCTTACAC ACCTCTCACC
6051	TTCCCCTCAA TAGAGACCCA CATTCATGTA TCAACAGCCA GAATGGCTTA
6101	CTCTTCTGGG TCTTCACCTG AGATGACAGC TCCTGGAGAG ACTAACACTG
6151	GTAGTACCTG GGACCCCACC ACCTACATCA CCACTACGGA TCCTAAGGAT
6201	ACAAGTTCAG CTCAGGTCTC TACACCCCAC TCAGTGAGGA CACTCAGAAC
6251	CACAGAAAAC CATCCAAAGA CAGAGTCCGC CACCCCAGCT GCTTACTCTG
6301	GAAGTCCTAA AATCTCAAGT TCACCCAATC TCACCAGTCC GGCCACAAAA
6351	GCATGGACCA TCACAGACAC AACTGAACAC TCCACTCAAT TACATTACAC
6401	AAAATTGGCA GAAAAATCAT CTGGATTTGA GACACAGTCA GCTCCAGGAC
6451	CTGTCTCTGT AGTAATCCCT ACCTCCCCTA CCATTGGAAG CAGCACATTG
6501	GAACTAACTT CTGATGTCCC AGGGGAACCC CTGGTCCTTG CTCCCAGTGA
6551	GCAGACCACA ATCACTCTCC CCATGGCAAC ATGGCTGAGT ACCAGTTTGA
6601	CAGAGGAAAT GGCTTCAACA GACCTTGATA TTTCAAGTCC AAGTTCACCC
6651	ATGAGTACAT TTGCTATTTT TCCACCTATG TCCACACCTT CTCATGAACT
6701	TTCAAAGTCA GAGGCAGATA CCAGTGCCAT TAGAAATACA GATTCAACAA
6751	CGTTGGATCA GCACCTAGGA ATCAGGAGTT TGGGCAGAAC TGGGGACTTA

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)	
6801	ACAACTGTTC CTATCACCCC ACTGACAACC ACGTGGACCA GTGTGATTGA
6851	ACACTCAACA CAAGCACAGG ACACCCTTTC TGCAACGATG AGTCCTACTC
6901	ACGTGACACA GTCACTCAAA GATCAAACAT CTATACCAGC CTCAGCATCC
6951	CCTTCCCATC TTACTGAAGT CTACCCTGAG CTCGGGACAC AAGGGAGAAG
7001	CTCCTCTGAG GCAACCACTT TTTGGAAACC ATCTACAGAC ACACTGTCCA
7051	GAGAGATTGA GACTGGCCCA ACAAACATTC AATCCACTCC ACCCATGGAC
7101	AACACAACAA CAGGGAGCAG TAGTAGTGGA GTCACCCTGG GCATAGCCCA
7151	CCTTCCCATA GGAACATCCT CCCCAGCTGA GACATCCACA AACATGGCAC
7201	TGGAAAGAAG AAGTTCTACA GCCACTGTCT CTATGGCTGG GACAATGGGA
7251	CTCCTTGTTA CTAGTGCTCC AGGAAGAAGC ATCAGCCAGT CATTAGGAAG
7301	AGTTTCCTCT GTCCTTTCTG AGTCAACTAC TGAAGGAGTC ACAGATTCTA
7351	GTAAGGGAAG CAGCCCAAGG CTGAACACAC AGGGAAATAC AGCTCTCTCC
7401	TCCTCTCTTG AACCCAGCTA TGCTGAAGGA AGCCAGATGA GCACAAGCAT
7451	CCCTCTAACC TCATCTCCTA CAACTCCTGA TGTGGAATTC ATAGGGGGCA
7501	GCACATTTTG GACCAAGGAG GTCACCACAG TTATGACCTC AGACATCTCC
7551	AAGTCTTCAG CAAGGACAGA GTCCAGCTCA GCTACCCTTA TGTCCACAGC
7601	TTTGGGAAGC ACTGAAAATA CAGGAAAAGA AAAACTCAGA ACTGCCTCTA
7651	TGGATCTTCC ATCTCCAACT CCATCAATGG AGGTGACACC ATGGATTTCT
7701	CTCACTCTCA GTAATGCCCC CAATACCACA GATTCACTTG ACCTCAGCCA
7751	TGGGGTGCAC ACCAGCTCTG CAGGGACTTT GGCCACTGAC AGGTCATTGA
7801	ATACTGGTGT CACTAGAGCC TCCAGATTGG AAAACGGCTC TGATACCTCT
7851	TCTAAGTCCC TGTCTATGGG AAACAGCACT CACACTTCCA TGACTTACAC
7901	AGAGAAGAGT GAAGTGTCTT CTTCAATCCA TCCCCGACCT GAGACCTCAG
7951	CTCCTGGAGC AGAGACCACT TTGACTTCCA CTCCTGGAAA CAGGGCCATA
8001	AGCTTAACAT TGCCTTTTTC ATCCATTCCA GTGGAAGAAG TCATTTCTAC
8051	AGGCATAACC TCAGGACCAG ACATCAACTC AGCACCCATG ACACATTCTC
8101	CCATCACCCC ACCAACAATT GTATGGACCA GTACAGGCAC AATTGAACAG
8151	TCCACTCAAC CACTACATGC AGTTTCTTCA GAAAAAGTTT CTGTGCAGAC
8201	ACAGTCAACT CCATATGTCA ACTCTGTGGC AGTGTCTGCT TCCCCTACCC
8251	ATGAGAATTC AGTCTCTTCT GGAAGCAGCA CATCCTCTCC ATATTCCTCA
8301	GCCTCACTTG AATCCTTGGA TTCCACAATC AGTAGGAGGA ATGCAATCAC
8351	TTCCTGGCTA TGGGACCTCA CTACATCTCT CCCCACTACA ACTTGGCCAA
8401	GTACTAGTTT ATCTGAGGCA CTGTCCTCAG GCCATTCTGG GGTTTCAAAC
8451	CCAAGTTCAA CTACGACTGA ATTTCCACTC TTTTCAGCTG CATCCACATC
8501	TGCTGCTAAG CAAAGAAATC CAGAAACAGA GACCCATGGT CCCCAGAATA
8551	CAGCCGCGAG TACTTTGAAC ACTGATGCAT CCTCGGTCAC AGGTCTTTCT
8601	GAGACTCCTG TGGGGGCAAG TATCAGCTCT GAAGTCCCTC TTCCAATGGC

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)	
8651	CATAACTTCT AGATCAGATG TTTCTGGCCT TACATCTGAG AGTACTGCTA
8701	ACCCGAGTTT AGGCACAGCC TCTTCAGCAG GGACCAAATT AACTAGGACA
8751	ATATCCCTGC CCACTTCAGA GTCTTTGGTT TCCTTTAGAA TGAACAAGGA
8801	TCCATGGACA GTGTCAATCC CTTTGGGGTC CCATCCAACT ACTAATACAG
8851	AAACAAGCAT CCCAGTAAAC AGCGCAGGTC CACCTGGCTT GTCCACAGTA
8901	GCATCAGATG TAATTGACAC ACCTTCAGAT GGGGCTGAGA GTATTCCCAC
8951	TGTCTCCTTT TCCCCCTCCC CTGATACTGA AGTGACAACT ATCTCACATT
9001	TCCCAGAAAA GACAACTCAT TCATTTAGAA CCATTTCATC TCTCACTCAT
9051	GAGTTGACTT CAAGAGTGAC ACCTATTCCT GGGGATTGGA TGAGTTCAGC
9101	TATGTCTACA AAGCCCACAG GAGCCAGTCC CTCCATTACA CTGGGAGAGA
9151	GAAGGACAAT CACCTCTGCT GCTCCAACCA CTTCCCCCAT AGTTCTCACT
9201	GCTAGTTTCA CAGAGACCAG CACAGTTTCA CTGGATAATG AAACTACAGT
9251	AAAAACCTCA GATATCCTTG ACGCACGGAA AACAAATGAG CTCCCCTCAG
9301	ATAGCAGTTC TTCTTCTGAT CTGATCAACA CCTCCATAGC TTCTTCAACT
9351	ATGGATGTCA CTAAAACAGC CTCCATCAGT CCCACTAGCA TCTCAGGAAT
9401	GACAGCAAGT TCCTCCCCAT CTCTCTTCTC TTCAGATAGA CCCCAGGTTC
9451	CCACATCTAC AACAGAGACA AATACAGCCA CCTCTCCATC TGTTTCCAGT
9501	AACACCTATT CTCTTGATGG GGGCTCCAAT GTGGGTGGCA CTCCATCCAC
9551	TTTACCACCC TTTACAATCA CCCACCCTGT CGAGACAAGC TCGGCCCTAT
9601	TAGCCTGGTC TAGACCAGTA AGAACTTTCA GCACCATGGT CAGCACTGAC
9651	ACTGCCTCCG GAGAAAATCC TACCTCTAGC AATTCTGTGG TGACTTCTGT
9701	TCCAGCACCA GGTACATGGA CCAGTGTAGG CAGTACTACT GACTTACCTG
9751	CCATGGGCTT TCTCAAGACA AGTCCTGCAG GAGAGGCACA CTCACTTCTA
9801	GCATCAACTA TTGAACCAGC CACTGCCTTC ACTCCCCATC TCTCAGCAGC
9851	AGTGGTCACT GGATCCAGTG CTACATCAGA AGCCAGTCTT CTCACTACGA
9901	GTGAAAGCAA AGCCATTCAT TCTTCACCAC AGACCCCAAC TACACCCACC
9951	TCTGGAGCAA ACTGGGAAAC TTCAGCTACT CCTGAGAGCC TTTTGGTAGT
10001	CACTGAGACT TCAGACACAA CACTTACCTC AAAGATTTTG GTCACAGATA
10051	CCATCTTGTT TTCAACTGTG TCCACGCCAC CTTCTAAATT TCCAAGTACG
10101	GGGACTCTGT CTGGAGCTTC CTTCCCTACT TTACTCCCGG ACACTCCAGC
10151	CATCCCTCTC ACTGCCACTG AGCCAACAAG TTCATTAGCT ACATCCTTTG
10201	ATTCCACCCC ACTGGTGACT ATAGCTTCGG ATAGTCTTGG CACAGTCCCA
10251	GAGACTACCC TGACCATGTC AGAGACCTCA AATGGTGATG CACTGGTTCT
10301	TAAGACAGTA AGTAACCCAG ATAGGAGCAT CCCTGGAATC ACTATCCAAG
10351	GAGTAACAGA AAGTCCACTC CATCCTTCTT CCACTTCCCC CTCTAAGATT
10401	GTTGCTCCAC GGAATACAAC CTATGAAGGT TCGATCACAG TGGCACTTTC

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)					
10451	TACTTTGCCT	GCGGGAACTA	CTGGTTCCCT	TGTATTCAGT	CAGAGTTCTG
10501	AAAACTCAGA	GACAACGGCT	TTGGTAGACT	CATCAGCTGG	GCTTGAGAGG
10551	GCATCTGTGA	TGCCACTAAC	CACAGGAAGC	CAGGGTATGG	CTAGCTCTGG
10601	AGGAATCAGA	AGTGGGTCCA	CTCACTCAAC	TGGAACCAAA	ACATTTTCTT
10651	CTCTCCCTCT	GACCATGAAC	CCAGGTGAGG	TTACAGCCAT	GTCTGAAATC
10701	ACCACGAACA	GACTGACAGC	TACTCAATCA	ACAGCACCCA	AAGGGATACC
10751	TGTGAAGCCC	ACCAGTGCTG	AGTCAGGCCT	CCTAACACCT	GTCTCTGCCT
10801	CCTCAAGCCC	ATCAAAGGCC	TTTGCCTCAC	TGACTACAGC	TCCCCCAACT
10851	TGGGGGATCC	CACAGTCTAC	CTTGACATTT	GAGTTTTCTG	AGGTCCCAAG
10901	TTTGGATACT	AAGTCCGCTT	CTTTACCAAC	TCCTGGACAG	TCCCTGAACA
10951	CCATTCCAGA	CTCAGATGCA	AGCACAGCAT	CTTCCTCACT	GTCCAAGTCT
11001	CCAGAAAAAA	ACCCAAGGGC	AAGGATGATG	ACTTCCACAA	AGGCCATAAG
11051	TGCAAGCTCA	TTTCAATCAA	CAGGTTTTAC	TGAAACCCCT	GAGGGATCTG
11101	CCTCCCCTTC	TATGGCAGGG	CATGAACCCA	GAGTCCCCAC	TTCAGGAACA
11151	GGGGACCCTA	GATATGCCTC	AGAGAGCATG	TCTTATCCAG	ACCCAAGCAA
11201	GGCATCATCA	GCTATGACAT	CGACCTCTCT	TGCATCAAAA	CTCACAACTC
11251	TCTTCAGCAC	AGGTCAAGCA	GCAAGGTCTG	GTTCTAGTTC	CTCTCCCATA
11301	AGCCTATCCA	CTGAGAAAGA	AACAAGCTTC	CTTTCCCCCA	CTGCATCCAC
11351	CTCCAGAAAG	ACTTCACTAT	TTCTTGGGCC	TTCCATGGCA	AGGCAGCCCA
11401	ACATATTGGT	GCATCTTCAG	ACTTCAGCTC	TGACACTTTC	TCCAACATCC
11451	ACTCTAAATA	TGTCCCAGGA	GGAGCCTCCT	GAGTTAACCT	CAAGCCAGAC
11501	CATTGCAGAA	GAAGAGGGAA	CAACAGCTGA	AACACAGACG	TTAACCTTCA
11551	CACCATCTGA	GACCCCAACA	TCCTTGTTAC	CTGTCTCTTC	TCCCACAGAA
11601	CCCACAGCCA	GAAGAAAGAG	TTCTCCAGAA	ACATGGGCAA	GCTCTATTTC
11651	AGTTCCTGCC	AAGACCTCCT	TGGTTGAAAG	TAAGAATGCC	CTGCTCCTTC
11701	CCCAAGTGTG	CTGGGGATGA	ATCTGGAAAT	AAACTACATC	TTTTTTATTT
11751	TTTAAACTTT	TATATTTGAA	AATATAAATA	TTTTAGGTTC	AGGGAACATG
11801	TGCAGGTTTG	TTATATAGGT	AAATTGCATG	TCATGGGGGC	TTGGGGTACA
11851	GATTACATCA	TCAGCCAGGT	AATAAGCCTA	GTACCTGATC	AGTAGATTTT
11901	TTTTAATCCT	CTCCCTCCTC	CCAGCCTCCA	CCCTCAATTC	ACATGTCTCC
11951	ATGTGTACTC	AAGGTTTAAT	TCCCACTTAT	GAGTGAGAAC	ATGCGGTATT
12001	TGTAAACTAC	ATCTTTATTT	TTGCTAACCT	CGAACTGAAA	TTTAGCATTT
12051	GTTTTATTGA	TGAATAGAGG	TAACAAAACA	AACCACATTA	ATCCTAGCAG
12101	TGCCTGTGCC	TTTGCCAACA	ACAGAAATTC	CGGACACTTT	CATATCCTAT
12151	GACAATTGTT	GCAAGCACTT	TTAAAAATCA	TGTACGACTT	TATTCATAAT
12201	TATAGTGGTT	ATTAGGCTTT	TCAATAGATC	TTATTTTATG	AGTTAGTAAA
12251	ATAAGTGCCT	GTATTATTGT	ATTACATTTG	TTTATTAAGA	TCTTGATAAC

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)
12301 AACATTTCAA TATAATCATT TCCTTTGTTT TTTAAATTTT AGATTCAGGG
12351 GTATATGTGC AGGTTTGTTA CGTGGATATA CTGCATAATG ATGAGGTTTG
12401 GCTTCTAGTG AACCCATCAG CCAAATAGTG AATGTTGTGC CCAATAAGTA
12451 GTTTTTCAAT CCTCACTTCA CTCCCAGCCT CCTCTATTTT GGAGTCCCAG
12501 TGTCTATTAT TTCTATCTTT ATGTCCACAT GTACCCATTG GTTAGCTCCC
12551 ACTTATAAGT GAGAATGTGC AGTATTTAAT TTTCTGTTTT TGAGTTATTT
12601 TGCTTAGGTT GATGGCCTTC AGCTCCAGCC ACGTTGCTTT AAAGAACATG
12651 ATTTCATTCT TTTTTATGGC TGCATAGTAC TCCGAGGTGT ATGTGTACCA
12701 GATTTTCTTT ATCCACAATG ATTTCCTTTG TAATCTAATA TTTTATATTG
12751 TTATTTTATG TTTTATTCTA TATTTTTATT TTAATTTATA AAGGAATTCA
12801 TATGGTTCAC AAGCCTGTCA AAGGGACCTA TAATAAAAAG AGGTTAAGAA
12851 TCCATGCTCT AAACAGAATA TTACTCCATT TTATTTCATT TATTTTTAAA
12901 GAGACAGTCT CACTCTGTCA TCCAGGCTGG AGTACAGTGG AGTGATCATA
12951 GCTCATTGCA ACCCTGAACT CTTGGGCACA AGCAATTCTC CTGCTTCATC
13001 CTCCAGAGGA GCTGGGACTA CAGGTGCACA TCACCATGCC CAGCTAGTTT
13051 TAAAAATTAT TTTGTAGAGA TGGTGTCTCA CTATCCTACC CAGGCTGGTC
13101 TCAAACTCCT GGGCTCAGGC AATCCTCCCA CTTTGACCTC CCAAAGTGTT
13151 GAGATTACAG GGGCAAGCCA CTGTGCCTGG CCACTTGTCA CATTTTAATT
13201 TGTGATTACT TATAAAATGA ACCCCTTCCC ATCTGAGATC TGTCAGTCTT
13251 TCTGGTGACG GTGCCTGGTG TCTGCTTTCT ACCATGTCCT GTTAGACTAG
13301 TGTTTGATGG GAGGTCACCT GGGCAGCTGT CCAGCTCACT CACTGGGCTC
13351 TAGAGCCTCT GAGTTGAAGC AAAATAGAAA GATCAGTCAA TGTAAAGAAA
13401 GCTCAAAAAC TGACATTCTG AAGTAATGGA TAGCTAAACC TTCCTATTGC
Exon 2
13451 CCTTTTCTTT CAGCAACTGA TGGAACGCTA GTGACCACCA TAAAGATGTC
13501 AAGCCAGGCA GCACAAGGAA ATTCCACGTG GCCTGCCCCA GCAGAGGAGA
13551 CGGGGACCAG TCCAGCAGGT AAATATAGAC CTTGTTTCCA TTTCTGCTCT
13601 GCTAATGCCA CCCAAGCCTT TCTTTTCTTT TCTTTTCTTT TCTTTTCTTT
13651 TCTTTTCTTT TCTTTTCTTT CTCTCCCTTT CTTTCTTTCT TTCTTTCTTT
13701 CTTTCTTTCT TTCTTTCTTT CTTTCTTTCT CTTTCTTTCT TTCTTTCTTT
13751 CTTTCTTTCT TTCTTTCTTT CTTTCTTTCT CTTTCTTTCT TCTTTCTCTC
13801 TCTCTCTTTC TTTCTTTCTC TTGTTCTTTT TAAATTTTTT ATTTTTTTAC
13851 TTAATTTTTT TCACCCAAGC CTTAAGGCCA GTTTGGACCA GATAGTGAGA
13901 CCCCACCTCT ATAAAAAAAA TTTTTAAAAA AAAAATAAGT TGGGCATCGT
13951 GCAGGCCTGT AGTCCCTGCT ACTCGAGAGG CCAAGGTGGG AGGACAGCTT
14001 GCTGCTGACT AAAAGTGCTG CTTATTGATT CTGGGAAGAA AAAATATACA

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)
14051 AGGCTTCAGT TTCATTATTT TATAAGTAAA TGCTAGCAAC TTTTCCTTTC
14101 TTTCTCTCTT TCTCTCTTCC TCTCTTTCTC TCCTCTCCTT CTCTTCTCTC
14151 TCTCTCTCTC TCTCTCTCTC TTTCTCTCTC CTCTCCTTCT CTTCTCTTCT
14201 TTCTCTCTCT CTCTCTTTCA TTTATTTTTG AGACATGGTC TCATTCTGTC
14251 ACCCAGGCTG GAGTACAGTG GTGTATATTT ACTGCAGTAC TCACTGTACT
14301 CACTGCAGCC TCAAATTCCT GGGCTCAAGC TATCCTCTCA CCTCAGCCTC
14351 CTGAGTAGCT GGGCAGCAGT CCAGCTCACT CACTGGGCTC TAGAGCCTCT
14401 GTGCTATGCC CAGCTTATTG TTGTTGTTTT TTTAAATTTT TTTTTTTGTA
14451 CAGATGGGGT CTCACTATGT GGCCCAAGGT GGTCTTAAAC TCCTGGCTCC
14501 AAGAGATCCT CCCACCTCAG CCTCCCAAAG TGCAGGGATT ACAGGTGTGA
14551 GCCACTGTGC CCAGCCTAGA CAGCATTTTT TTTTTTTGAA ACAGGGTCTC
14601 CCTCTGTTGC CCAGGCTGGA GTGCAATGGC GTGTTCATGG TTCACTGCAG
14651 CCTCAGCCTC CTCAGTCTCA AGCAATCCTC CAACTTCAGC CTCCCCCAAC
14701 AGCTAGAACT GCAGGTGATC ATCACCAATT AGCCTGGTTA ATTGTGTGTG
14751 TATTTCTTAA ATTTTTTGTA GAGATAGTTC TCACTATATT GCTTGGGCTG
14801 GTCTCAAACT CCTGGACTCA AGTGATTCAC CTACCTCGGC CTCCCTAAGC
14851 ACTGGGATTA CAGGCTTGAG CCACCACACC CGGCAAGGAC TAGGTTTTAA
14901 AATAGGTTCC TAGGCTGGGT GTGGTGGCTT ACGCCCGTAA TCCCAGCACT
14951 TTGGGAGGCT GAGGTGGGCG GATCACGAGG TCAGGAGTTT GAGACCAGCC
15001 TGGCCAACAT AGTGAAACCC TGTCTCTACT AAAAATACAA AAAATTAGCT
15051 GGGCATAGTG GCACACACCT GTAATCCCAG CTACTCGGGA GGCTGAGGAA
15101 GGAGAATCAC TTGAACCTGG GAGGCGGAGG TTGCAGTGAG CCGAGATCAT
15151 GCCATTGCTC TCCAGCCTGG GTGACAGAGC AAGACTCCAT CTAAAAAAAA
15201 AAAAAAAAGT TCCTTTGACT TCTTGACACT CTTCTCTGAG GATATTGATC
15251 ATTTTTCCCC AATAGATGTT ACTAATTGAA CACTTCTGTT GCTTCAACTT
15301 ACTAATTTAC ATGATCAATA GCCAATTAAT TCAGCAGGAG AGAATGCTAC
15351 AGAGTCGATT CTTTCTGTAC TTTCTTCTGC TCCAGAGTGA AGGATCTTTC
15401 TAAATCAGAG ACCATCACTG TGTTCACAGG GAGGGCCTAG GTGAACCTGA
15451 GATGGCAAAT GTTGCGTTTG TTCTACGGAA GAAGGGATTA TGGGTTGAAG
15501 TCCTTGGCAG TGCCAAATTG CTTAGAAAAA TGTGAAATAT GGTCCCTAGG
15551 AGTGCTCTTG GGATGTCACA TTTTTCTCAC TCCTTTGACA GGTAGATGTT
15601 ATTTTCCTGA AGGCCAGGGA AAGGATTCAG AGGGAGGAAT GAATTTGAAA
15651 GAAAATGAAG GTGACGAGAA AGAATGAGCT CATCTCCCTT ATCCTCTTTC
15701 TTCTCAAATC CTTAAGTAGC TTTGCAGTGA ACTAAGATTT GGGGGAACCT
15751 AGAGGAGGCT GAAAGTTGGA AGCTGAAATT GGCTTAGCAA GGGCAAGCTC
15801 CAAAGACAAA AGTGGAAATA GTTTGGGGGT AGCCTTTTGC ATGGGTGAAA
15851 TCCTGGTTCA TCACATCCTC CCTTATGCAA AGAGCCCTTT TATATGGGGC

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)
15901 ATGGGGAAAA ACTGAGCTAA AGGTGATAAT TTCTCCTGAG CAAGCCAGAT
15951 GGTCAAAGCT CTAACTTCAC CATCTCCCTT GGAATGTTTA ATGTGTTCCC
16001 TGGTGTCCAG AGGCTTAACG TGTGAGAATT AAAAGCTCAA CATTTTCTTT
16051 CCCAGGGAAG GAGGAAATAG TTTTAATTGA AATCCCGGGA GGAAATGAAT
16101 GATAGTGTCA AACCAAAAAA CTTCATCTTC TGTACCACTT GCATATACTC
Exon 3
16151 CACTGACTTA CTTTCTAATC ACAGGCACAT CCCCAGGAAG CCCAGAAATG
16201 TCTACCACTC TCAAAATCAT GAGCTCCAAG GAACCCGGCA TCAGCCCAGA
16251 GATCAGGTCC ACTGTGAGAA ATTCTCCTTG GAAGACTCCA GAAACAACTG
16301 TTCCCATGGA GACCACAGTG GAACCAGTCA CCCTTCAGTC CACAGCCCTA
16351 GGAAGTGGCA GCACCAGCAT CTCTCACCTG CCCACAGGAA CCACATCACC
16401 AACCAAGTCA CCAACAGAAA ATATGTTGGC TACAGAAAGG GTCTCCCTCT
16451 CCCCATCCCC ACCTGAGGCT TGGACCAACC TTTATTCTGG AACTCCAGGA
16501 GGGACCAGGC AGTCACTGGC CACAATGTCC TCTGTCTCCC TAGAGTCACC
16551 AACTGCTAGA AGCATCACAG GGACTGGTCA GCAAAGCAGT CCAGAACTGG
16601 TTTTAAAGAC AACTGGAATG GAATTCTCTA TGTGGCATGG CTCTACTGGA
16651 GGGACCACAG GGGACACACA TGTCTCTCTG AGCACATCTT CCAATATCCT
16701 TGAAGACCCT GTAACCAGCC CAAACTCTGT GAGCTCATTG ACAGATAAAT
16751 CCAAACATAA AACCGAGACA TGGGTCAGCA CCACAGCCAT TCCCTCCACT
16801 GTCCTGAATA ATAAGATAAT GGCAGCTGAA CAACAGACAA GTCGATCTGT
16851 GGATGAGGCT TATTCATCAA CTAGTTCTTG GTCAGATCAG ACATCTGGGA
16901 GTGACATCAC CCTTGGTGCA TCTCCTGATG TCACAAACAC ATTATACATC
16951 ACCTCCACAG CACAAACCAC CTCACTAGTA TCTCTGCCCT CTGGAGACCA
17001 AGGCATTACA AGCCTCACCA ATCCCTCAGG AGGAAAAACA AGCTCTGCAT
17051 CATCTGTCAC ATCTCCTTCA ATAGGGCTTG AGACTCTGAT GGCCAATGTA
17101 AGTGCAGTGA CAAGTGACAT TGCCCCTACT GCTGGGCATC TATCTCAGAC
17151 TTCATCTCCT GCGGAAGTGA GCATCCTGGA CATAACCACA GCTCCTACTC
17201 CAGGTATCTC CACCACCATC ACCACCATGG GAACCAACTC AATCTCAACT
17251 ACCACACCCA ACCCAGAAGT GGGTATGAGT ACCATGGACA GCACCCCGGC
17301 CACAGAGAGG CACACAACTT CTACAGAACA CCCTTCCACC TGGTCTTCCA
17351 CAGCTGCATC AGATTCCTGG ACTGTCACAG ACATGACTTC AAACTTGAAA
17401 GTTGCAAGAT CTCCTGGAAC AATTTCCACA ATGCATACAA CTTCATTCTT
17451 AGCCTCAAGC ACTGAATTAG ACTCCATGTC TACTCCCCAT GGCCGTATAA
17501 CTGTCATTGG AACCAGCCTG GTCACTCCAT CCTCTGATGC TTCAGCTGTA
17551 AAGACAGAGA CCAGTACAAG TGAAAGAACA TTGAGTCCTT CAGACACAAC
17601 TGCATCTACT CCCATCTCAA CTTTTTCTCG TGTCCAGAGG ATGAGCATCT

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)	
17651	CAGTTCCTGA CATTTTAAGT ACAAGTTGGA CTCCCAGTAG TACAGAAGCA
17701	GAAGATGTGC CTGTTTCAAT GGTTTCTACA GATCATGCTA GTACAAAGAC
17751	TGACCCAAAT ATGCCCCTGT CCACTTTTCT GTTTGATTCT CTGTCCACTC
17801	TTGACTGGGA CACTGGGAGA TCTCTGTCAT CAGCCACAGC CACTACCTCA
17851	GCTCCTCAGG GGGCCACAAC TCCCCAAGAA CTCACTTTGG AAACCATGAT
17901	CAGCCCAGCT ACCTCACAGT TGCCCTTCTC TATAGGGCAC ATTACAAGTG
17951	CAGTCATACC AGCTGCAATG GCAAGGAGCT CTGGAGTTAC TTTTTCAAGA
18001	CCAGATCCCA CAAGCAAAAA GGCAGAGCAG ACTTCCACTC AGCTTCCCAC
18051	CACCACTTCT GCACATCCAG AGCAGGTGCC CAGATCAGCA GCAACAACTC
18101	TGGATGTGAT CCCACACACA GCAAAAACTC CAGATGCAAC TTTTCAGAGA
18151	CAAGGGCAGA CAGCTCTTAC AACAGAGGCA AGAGCTACAT CTGACTCCTG
18201	GAATGAGAAA GAAAAATCAA CCCCAAGTGC ACCTTGGATC ACTGAGATGA
18251	TGAATTCTGT CTCAGAAGAT ACCATCAAGG AGGTTACCAG CTCCTCCAGT
18301	GTGTTAAGGA CCCTGAATAC GCTGGACATA AACTTGGAAT CTGGGACGAC
18351	TTCATCCCCA AGTTGGAAAA GCAGCCCATA TGAGAGAATT GCCCCTTCTG
18401	AGTCTACCAC AGACAAAGAG GCAATTCACC CTTCTACAAA CACAGTAGAG
18451	ACCACTGGCT GGGTCACAAG TTCCGAACAT GCTTCTCATT CCACTATCCC
18501	AGCCCACTCA GCGTCATCCA AACTCACATC TCCAGTGGTT ACAACCTCCA
18551	CCAGGGAACA AGCAATAGTT TCTATGTCAA CAACCACATG GCCAGAGTCT
18601	ACAAGGGCTA GAACAGAGCC TAATTCCTTC TTGACTATTG AACTGAGGGA
18651	CGTCAGCCCT TACATGGACA CCAGCTCAAC CACACAAACA AGTTTTATCT
18701	CTTCCCCAGG TTCCACTGCG ATCACCAAGG GGCCTAGAAC AGAAATTACC
18751	TCCTCTAAGA GAATATCCAG CTCATTCCTT GCCCAGTCTA TGAGGTCGTC
18801	AGACAGCCCC TCAGAAGCCA TCTCCAGGCT GTCTAACTTT CCTGCCATGA
18851	CAGAATCTGG AGGAATGATC CTTGCTATGC AAACAAGTCC ACCTGGCGCT
18901	ACATCACTAA GTGCACCTAC TTTGGATACA TCAGCCACAG CCTCCTGGAC
18951	AGGGACTCCA CTGGCTACGA CTCAGAGATT TACATACTCA GAGAAGACCA
19001	CTCTCTTTAG CAAAGGTCCT GAGGATACAT CACAGCCAAG CCCTCCCTCT
19051	GTGGAAGAAA CCAGCTCTTC CTCTTCCCTG GTACCTATCA ATGCTACAAC
19101	CTCGCCTTCC AATATTTTGT TGACATCACA AGGGCACAGT CCCTCCTCTA
19151	CTCCACCTGT GACCTCAGTT TTCTTGTCTG AGACCTCTGG CCTGGGGAAG
19201	ACCACAGACA TGTCGAGGAT AAGCTTGGAA CCTGGCACAA GTTTACCTCC
19251	CAATTTGAGC AGTACAGCAG GTGAGGCGTT ATCCACTTAT GAAGCCTCCA
19301	GAGATACAAA GGCAATTCAT CATTCTGCAG ACACAGCAGT GACGAATATG
19351	GAGGCAACCA GTTCTGAATA TTCTCCTATC CCAGGCCATA CAAAGCCATC
19401	CAAAGCCACA TCTCCATTGG TTACCTCCCA CATCATGGGG GACATCACTT
19451	CTTCCACATC AGTATTTGGC TCCTCCGAGA CCACAGAGAT TGAGACAGTG

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)
19501 TCCTCTGTGA ACCAGGGACT TCAGGAGAGA AGCACATCCC AGGTGGCCAG
19551 CTCTGCTACA GAGACAAGCA CTGTCATTAC CCATGTGTCT AGTGGTGATG
19601 CTACTACTCA TGTCACCAAG ACACAAGCCA CTTTCTCTAG CGGAACATCC
19651 ATCTCAAGCC CTCATCAGTT TATAACTTCT ACCAACACAT TTACAGATGT
19701 GAGCACCAAC CCCTCCACCT CTCTGATAAT GACAGAATCT TCAGGAGTGA
19751 CCATCACCAC CCAAACAGGT CCTACTGGAG CTGCAACACA GGGTCCATAT
19801 CTCTTGGACA CATCAACCAT GCCTTACTTG ACAGAGACTC CATTAGCTGT
19851 GACTCCAGAT TTTATGCAAT CAGAGAAGAC CACTCTCATA AGCAAAGGTC
19901 CCAAGGATGT GTCCTGGACA AGCCCTCCCT CTGTGGCAGA AACCAGCTAT
19951 CCCTCTTCCC TGACACCTTT CTTGGTCACA ACCATACCTC CTGCCACTTC
20001 CACGTTACAA GGGCAACATA CATCCTCTCC TGTTTCTGCG ACTTCAGTTC
20051 TTACCTCTGG ACTGGTGAAG ACCACAGATA TGTTGAACAC AAGCATGGAA
20101 CCTGTGACCA ATTCACCTCA AAATTTGAAC AATCCATCAA ATGAGATACT
20151 GGCCACTTTG GCAGCCACCA CAGATATAGA GACTATTCAT CCTTCCATAA
20201 ACAAAGCAGT GACCAATATG GGGACTGCCA GTTCAGCACA TGTACTGCAT
20251 TCCACTCTCC CAGTCAGCTC AGAACCATCT ACAGCCACAT CTCCAATGGT
20301 TCCTGCCTCC AGCATGGGGG ACGCTCTTGC TTCTATATCA ATACCTGGTT
20351 CTGAGACCAC AGACATTGAG GGAGAGCCAA CATCCTCCCT GACTGCTGGA
20401 CGAAAAGAGA ACAGCACCCT CCAGGAGATG AACTCAACTA CAGAGTCAAA
20451 CATCATCCTC TCCAATGTGT CTGTGGGGGC TATTACTGAA GCCACAAAAA
20501 TGGAAGTCCC CTCTTTTGAT GCAACATTCA TACCAACTCC TGCTCAGTCA
20551 ACAAAGTTCC CAGATATTTT CTCAGTAGCC AGCAGTAGAC TTTCAAACTC
20601 TCCTCCCATG ACAATATCTA CCCACATGAC CACCACCCAG ACAGGGTCTT
20651 CTGGAGCTAC ATCAAAGATT CCACTTGCCT TAGACACATC AACCTTGGAA
20701 ACCTCAGCAG GGACTCCATC AGTGGTGACT GAGGGGTTTG CCCACTCAAA
20751 AATAACCACT GCAATGAACA ATGATGTCAA GGACGTGTCA CAGACAAACC
20801 CTCCCTTTCA GGATGAAGCC AGCTCTCCCT CTTCTCAAGC ACCTGTCCTT
20851 GTCACAACCT TACCTTCTTC TGTTGCTTTC ACACCGCAAT GGCACAGTAC
20901 CTCCTCTCCT GTTTCTATGT CCTCAGTTCT TACTTCTTCA CTGGTAAAGA
20951 CCGCAGGCAA GGTGGATACA AGCTTAGAAA CAGTGACCAG TTCACCTCAA
21051 AGATATAGAG ACAACGCATC CTTCCATAAA CACAGTAGTT ACCAATGTGG
21101 GGACCACCGG TTCAGCATTT GAATCACATT CTACTGTCTC AGCTTACCCA
21151 GAGCCATCTA AAGTCACATC TCCAAATGTT ACCACCTCCA CCATGGAAGA
21201 CACCACAATT TCCAGATCAA TACCTAAATC CTCTAAGACT ACAAGAACTG
21251 AGACTGAGAC AACTTCCTCC CTGACTCCTA AACTGAGGGA GACCAGCGTC
21301 TCCCAGGAGA TCACCTCGTC CACAGAGACA AGCACTGTTC CTTACAAAGA

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)	
21351	GCTCACTGGT GCCACTACCG AGGTATCCAG GACAGATGTC ACTTCCTCTA
21401	GCAGTACATC CTTCCCTGGC CCTGATCAGT CCACAGTGTC ACTAGACATC
21451	TCCACAGAAA CCAACACCAG GCTGTCTACC TCCCCAATAA TGACAGAATC
21501	TGCAGAAATA ACCATCACCA CCCAAACAGG TCCTCATGGG GCTACATCAC
21551	AGGATACTTT TACCATGGAC CCATCAAATA CAACCCCCCA GGCAGGGATC
21601	CACTCAGCTA TGACTCATGG ATTTTCACAA TTGGATGTGA CCACTCTTAT
21651	GAGCAGAATT CCACAGGATG TATCATGGAC AAGTCCTCCC TCTGTGGATA
21701	AAACCAGCTC CCCCTCTTCC TTTCTGCCCT CACCTGCAAT GACCACACCT
21751	TCCCTGATTT CTTCTACCTT ACCAGAGGAT AAGCTCTCCT CTCCTATGAC
21801	TTCACTTCTC ACCTCTGGCC TAGTGAAGAT TACAGACATA TTACGTACAC
21851	GCTTGGAACC TGTGACCAGC TCACTTCCAA ATTTCAGCAG CACCTCAGAT
21901	AAGATACTGG CCACTTCTAA AGACAGTAAA GACACAAAGG AAATTTTTCC
21951	TTCTATAAAC ACAGAAGAGA CCAATGTGAA AGCCAACAAC TCTGGACATG
22001	AATCCCATTC CCCTGCACTG GCTGACTCAG AGACACCCAA AGCCACAACT
22051	CAAATGGTTA TCACCACCAC TGTGGGAGAT CCAGCTCCTT CCACATCAAT
22101	GCCAGTGCAT GGTTCCTCTG AGACTACAAA CATTAAGAGA GAGCCAACAT
22151	ATTTCTTGAC TCCTAGACTG AGAGAGACCA GTACCTCTCA GGAGTCCAGC
22201	TTTCCCACGG ACACAAGTTT TCTACTTTCC AAAGTCCCCA CTGGTACTAT
22251	TACTGAGGTC TCCAGTACAG GGGTCATCTC TTCTAGCAAA ATTTCCACCC
22301	CAGACCATGA TAAGTCCACA GTGCCACCTG ACACCTTCAC AGGAGAGATC
22351	CCCAGGGTCT TCACCTCCTC TATTAAGACA AAATCTGCAG AAATGACGAT
22401	CACCACCCAA GCAAGTCCTC CTGAGTCTGC ATCGCACAGT ACCCTTCCCT
22451	TGGACACATC AACCACACTT TCCCAGGGAG GGACTCATTC AACTGTGACT
22501	CAGGGATTCC CATACTCAGA GGTGACCACT CTCATGGGCA TGGGTCCTGG
22551	GAATGTGTCA TGGATGACAA CTCCCCCTGT GGAAGAAACC AGCTCTGTGT
22601	CTTCCCTGAT GTCTTCACCT GCCATGACAT CCCCTTCTCC TGTTTCCTCC
22651	ACATCACCAC AGAGCATCCC CTCCTCTCCT CTTCCTGTGA CTGCACTTCC
22701	TACTTCTGTT CTGGTGACAA CCACAGATGT GTTGGGCACA ACAAGCCCAG
22751	AGTCTGTAAC CAGTTCACCT CCAAATTTGA GCAGCATCAC TCATGAGAGA
22801	CCGGCCACTT ACAAAGACAC TGCACACACA GAAGCCGCCA TGCATCATTC
22851	CACAAACACC GCAGTGACCA ATGTAGGGAC TTCCGGGTCT GGACATAAAT
22901	CACAATCCTC TGTCCTAGCT GACTCAGAGA CATCGAAAGC CACACCTCTG
22951	ATGAGTACCA CCTCCACCCT GGGGGACACA AGTGTTTCCA CATCAACTCC
23001	TAATATCTCT CAGACTAACC AAATTCAAAC AGAGCCAACA GCATCCCTGA
23051	GCCCTAGACT GAGGGAGAGC AGCACGTCTG AGAAGACCAG CTCAACAACA
23101	GAGACAAATA CTGCCTTTTC TTATGTGCCC ACAGGTGCTA TTACTCAGGC
23151	CTCCAGAACA GAAATCTCCT CTAGCAGAAC ATCCATCTCA GACCTTGATC

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)
23201 GGTCCACAAT AGCACCCGAC ATCTCCACAG GAATGATCAC CAGGCTCTTC
23251 ACCTCCCCCA TCATGACAAA ATCTGCAGAA ATGACCGTCA CCACTCAAAC
23301 AACTACTCCT GGGGCTACAT CACAGGGTAT CCTTCCCTGG GACACATCAA
23351 CCACACTTTT CCAGGGAGGG ACTCATTCAA CCGTGTCTCA GGGATTCCCA
23401 CACTCAGAGA TAACCACTCT TCGGAGCAGA ACCCCTGGAG ATGTGTCATG
23451 GATGACAACT CCCCCTGTGG AAGAAACCAG CTCTGGGTTT TCCCTGATGT
23501 CACCTTCCAT GACATCCCCT TCTCCTGTTT CCTCCACATC ACCAGAGAGC
23551 ATCCCCTCCT CTCCTCTCCC TGTGACTGCA CTTCTTACTT CTGTTCTGGT
23601 GACAACCACA AATGTATTGG GCACAACAAG CCCAGAGCCC GTAACGAGTT
23651 CACCTCCAAA TTTAAGCAGC CCCACACAGG AGAGACTGAC CACTTACAAA
23701 GACACTGCGC ACACAGAAGC CATGCATGCT TCCATGCATA CAAACACTGC
23751 AGTGGCCAAC GTGGGGACCT CCATTTCTGG ACATGAATCA CAATCTTCTG
23801 TCCCAGCTGA TTCAGACACA TCCAAAGCCA CATCTCCAAT GGGTACCACC
23851 TTCGCCATGG GGGATACAAG TGTTTCTACA TCAACTCCTG CCTTCTTTGA
23901 GACTAGAATT CAGACTGAAT CAACATCCTC TTTGATTCCT GGATTAAGGG
23951 ACACCAGGAC GTCTGAGGAG ATCAACACTG TGACAGAGAC CAGCACTGTC
24001 CTTTCAGAAG TGCCCACTAC TACTACTACT GAGGTCTCCA GGACAGAAGT
24051 TATCACTTCC AGCAGAACAA CCATCTCAGG GCCTGATCAT TCCAAAATGT
24101 CACCCTACAT CTCCACAGAA ACCATCACCA GGCTCTCCAC TTTTCCTTTT
24151 GTAACAGGAT CCACAGAAAT GGCCATCACC AACCAAACAG GTCCTATAGG
24201 GACTATCTCA CAGGCTACCC TTACCCTGGA CACATCAAGC ACAGCTTCCT
24251 GGGAAGGGAC TCACTCACCT GTGACTCAGA GATTTCCACA CTCAGAGGAG
24301 ACCACTACTA TGAGCAGAAG TACTAAGGGC GTGTCATGGC AAAGCCCTCC
24351 CTCTGTGGAA GAAACCAGTT CTCCTTCTTC CCCAGTGCCT TTACCTGCAA
24401 TAACCTCACA TTCATCTCTT TATTCCGCAG TATCAGGAAG TAGCCCCACT
24451 TCTGCTCTCC CTGTGACTTC CCTTCTCACC TCTGGCAGGA GGAAGACCAT
24501 AGACATGTTG GACACACACT CAGAACTTGT GACCAGCTCC TTACCAAGTG
24551 CAAGTAGCTT CTCAGGTGAG ATACTCACTT CTGAAGCCTC CACAAATACA
24601 GAGACAATTC ACTTTTCAGA GAACACAGCA GAAACCAATA TGGGGACCAC
24651 CAATTCTATG CATAAACTAC ATTCCTCTGT CTCAATCCAC TCCCAGCCAT
24701 CCGGACACAC ACCTCCAAAG GTTACTGGAT CTATGATGGA GGACGCTATT
24751 GTTTCCACAT CAACACCTGG TTCTCCTGAG ACTAAAAATG TTGACAGAGA
24801 CTCAACATCC CCTCTGACTC CTGAACTGAA AGAGGACAGC ACCGCCCTGG
24851 TGATGAACTC AACTACAGAG TCAAACACTG TTTTCTCCAG TGTGTCCCTG
24901 GATGCTGCTA CTGAGGTCTC CAGGGCAGAA GTCACCTACT ATGATCCTAC
24951 ATTCATGCCA GCTTCTGCTC AGTCAACAAA GTCCCCAGAC ATTTCACCTG

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)	
25001	AAGCCAGCAG CAGTCATTCT AACTCTCCTC CCTTGACAAT ATCTACACAC
25051	AAGACCATCG CCACACAAAC AGGTCCTTCT GGGGTGACAT CTCTTGGCCA
25101	ACTGACCCTG GACACATCAA CCATAGCCAC CTCAGCAGGA ACTCCATCAG
25151	CCAGAACTCA GGATTTTGTA GATTCAGAAA CAACCAGTGT CATGAACAAT
25201	GATCTCAATG ATGTGTTGAA GACAAGCCCT TTCTCTGCAG AAGAAGCCAA
25251	CTCTCTCTCT TCTCAGGCAC CTCTCCTTGT GACAACCTCA CCTTCTCCTG
25301	TAACTTCCAC ATTGCAAGAG CACAGTACCT CCTCTCTTGT TTCTGTGACC
25351	TCAGTACCCA CCCCTACACT GGCGAAGATC ACAGACATGG ACACAAACTT
25401	AGAACCTGTG ACTCGTTCAC CTCAAAATTT AAGGAACACC TTGGCCACTT
25451	CAGAAGCCAC CACAGATACA CACACAATGC ATCCTTCTAT AAACACAGCA
25501	GTGGCCAATG TGGGGACCAC CAGTTCACCA AATGAATTCT ATTTTACTGT
25551	CTCACCTGAC TCAGACCCAT ATAAAGCCAC ATCCGCAGTA GTTATCACTT
25601	CCACCTCGGG GGACTCAATA GTTTCCACAT CAATGCCTAG ATCCTCTGCG
25651	ATGAAAAAGA TTGAGTCTGA GACAACTTTC TCCCTGATAT TTAGACTGAG
25701	GGAGACTAGC ACCTCCCAGA AAATTGGCTC ATCCTCAGAC ACAAGCACGG
25751	TCTTTGACAA AGCATTCACT GCTGCTACTA CTGAGGTCTC CAGAACAGAA
25801	CTCACCTCCT CTAGCAGAAC ATCCATCCAA GGCACTGAAA AGCCCACAAT
25851	GTCACCGGAC ACCTCCACAA GATCTGTCAC CATGCTTTCT ACTTTTGCTG
25901	GCCTGACAAA ATCCGAAGAA AGGACCATTG CCACCCAAAC AGGTCCTCAT
25951	AGGGCGACAT CACAGGGTAC CCTTACCTGG GACACATCAA TCACAACCTC
26001	ACAGGCAGGG ACCCACTCAG CTATGACTCA TGGATTTTCA CAATTAGATT
26051	TGTCCACTCT TACGAGTAGA GTTCCTGAGT ACATATCAGG GACAAGCCCA
26101	CCCTCTGTGG AAAAAACCAG CTCTTCCTCT TCCCTTCTGT CTTTACCAGC
26151	AATAACCTCA CCGTCCCCTG TACCTACTAC ATTACCAGAA AGTAGGCCGT
26201	CTTCTCCTGT TCATCTGACT TCACTCCCCA CCTCTGGCCT AGTGAAGACC
26251	ACAGATATGC TGGCATCTGT GGCCAGTTTA CCTCCAAACT TGGGCAGCAC
26301	CTCACATAAG ATACCGACTA CTTCAGAAGA CATTAAAGAT ACAGAGAAAA
26351	TGTATCCTTC CACAAACATA GCAGTAACCA ATGTGGGGAC CACCACTTCT
26401	GAAAAGGAAT CTTATTCGTC TGTCCCAGCC TACTCAGAAC CACCCAAAGT
26451	CACCTCTCCA ATGGTTACCT CTTTCAACAT AAGGGACACC ATTGTTTCCA
26501	CATCCATGCC TGGCTCCTCT GAGATTACAA GGATTGAGAT GGAGTCAACA
26551	TTCTCCCTGG CTCATGGGCT GAAGGGAACC AGCACCTCCC AGGACCCCAT
26601	CGTATCCACA GAGAAAAGTG CTGTCCTTCA CAAGTTGACC ACTGGTGCTA
26651	CTGAGACCTC TAGGACAGAA GTTGCCTCTT CTAGAAGAAC ATCCATTCCA
26701	GGCCCTGATC ATTCCACAGA GTCACCAGAC ATCTCCACTG AAGTGATCCC
26751	CAGCCTGCCT ATCTCCCTTG GCATTACAGA ATCTTCAAAT ATGACCATCA
26801	TCACTCGAAC AGGTCCTCCT CTTGGCTCTA CATCACAGGG CACATTTACC

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)
26851 TTGGACACAC CAACTACATC CTCCAGGGCA GGAACACACT CGATGGCGAC
26901 TCAGGAATTT CCACACTCAG AAATGACCAC TGTCATGAAC AAGGACCCTG
26951 AGATTCTATC ATGGACAATC CCTCCTTCTA TAGAGAAAAC CAGCTTCTCC
27001 TCTTCCCTGA TGCCTTCACC AGCCATGACT TCACCTCCTG TTTCCTCAAC
27051 ATTACCAAAG ACCATTCACA CCACTCCTTC TCCTATGACC TCACTGCTCA
27101 CCCCTAGCCT AGTGATGACC ACAGACACAT TGGGCACAAG CCCAGAACCT
27151 ACAACCAGTT CACCTCCAAA TTTGAGCAGT ACCTCACATG AGATACTGAC
27201 AACAGATGAA GACACCACAG CTATAGAAGC CATGCATCCT TCCACAAGCA
27251 CAGCAGCGAC TAATGTGGAA ACCACCAGTT CTGGACATGG GTCACAATCC
27301 TCTGTCCTAG CTGACTCAGA AAAAACCAAG GCCACAGCTC CAATGGATAC
27351 CACCTCCACC ATGGGGCATA CAACTGTTTC CACATCAATG TCTGTTTCCT
27401 CTGAGACTAC AAAAATTAAG AGAGAGTCAA CATATTCCTT GACTCCTGGA
27451 CTGAGAGAGA CCAGCATTTC CCAAAATGCC AGCTTTTCCA CTGACACAAG
27501 TATTGTTCTT TCAGAAGTCC CCACTGGTAC TACTGCTGAG GTCTCCAGGA
27551 CAGAAGTCAC CTCCTCTGGT AGAACATCCA TCCCTGGCCC TTCTCAGTCC
27601 ACAGTTTTGC CAGAAATATC CACAAGAACA ATGACAAGGC TCTTTGCCTC
27651 GCCCACCATG ACAGAATCAG CAGAAATGAC CATCCCCACT CAAACAGGTC
27701 CTTCTGGGTC TACCTCACAG GATACCCTTA CCTTGGACAC ATCCACCACA
27751 AAGTCCCAGG CAAAGACTCA TTCAACTTTG ACTCAGAGAT TTCCACACTC
27801 AGAGATGACC ACTCTCATGA GCAGAGGTCC TGGAGATATG TCATGGCAAA
27851 GCTCTCCCTC TCTGGAAAAT CCCAGCTCTC TCCCTTCCCT GCTGTCTTTA
27901 CCTGCCACAA CCTCACCTCC TCCCATTTCC TCCACATTAC CAGTGACTAT
27951 CTCCTCCTCT CCTCTTCCTG TGACTTCACT TCTCACCTCT AGCCCGGTAA
28001 CGACCACAGA CATGTTACAC ACAAGCCCAG AACTTGTAAC CAGTTCACCT
28051 CCAAAGCTGA GCCACACTTC AGATGAGAGA CTGACCACTG GCAAGGACAC
28101 CACAAATACA GAAGCTGTGC ATCCTTCCAC AAACACAGCA GCGTCCAATG
28151 TGGAGATTCC CAGCTCTGGA CATGAATCCC CTTCCTCTGC CTTAGCTGAC
28201 TCAGAGACAT CCAAAGCCAC ATCACCAATG TTTATTACCT CCACCCAGGA
28251 GGATACAACT GTTGCCATAT CAACCCCTCA CTTCTTGGAG ACTAGCAGAA
28301 TTCAGAAAGA GTCAATTTCC TCCCTGAGCC CTAAATTGAG GGAGACAGGC
28351 AGTTCTGTGG AGACAAGCTC AGCCATAGAG ACAAGTGCTG TCCTTTCTGA
28401 AGTGTCCGTT GGTGCTACTA CTGAGATCTC CAGGACAGAA GTCACCTCCT
28451 CTAGCAGAAC ATCCATCTCT GGTTCTGCTG AGTCCACAAT GTTGCCAGAA
28501 ATATCCACCA CAAGAAAAAT CATTAAGTTC CCTACTTCCC CCATCCTGGC
28551 AGAATCATCA GAAATGACCA TCAAGACCCA AACAAGTCCT CCTGGGTCTA
28601 CATCAGAGAG TACCTTTACA TTAGACACAT CAACCACTCC CTCCTTGGTA

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)	
28651	ATAACCCATT CGACTATGAC TCAGAGATTG CCACACTCAG AGATAACCAC
28701	TCTTGTGAGT AGAGGTGCTG GGGATGTGCC ACGGCCCAGC TCTCTCCCTG
28751	TGGAAGAAAC AAGCCCTCCA TCTTCCCAGC TGTCTTTATC TGCCATGATC
28801	TCACCTTCTC CTGTTTCTTC CACATTACCA GCAAGTAGCC ACTCCTCTTC
28851	TGCTTCTGTG ACTTCACTTC TCACACCAGG CCAAGTGAAG ACTACTGAGG
28901	TGTTGGACGC AAGTGCAGAA CCTGAAACCA GTTCACCTCC AAGTTTGAGC
28951	AGCACCTCAG TTGAAATACT GGCCACCTCT GAAGTCACCA CAGATACGGA
29001	GAAAATTCAT CCTTTCTCAA ACACGGCAGT AACCAAAGTT GGAACTTCCA
29051	GTTCTGGACA TGAATCCCCT TCCTCTGTCC TACCTGACTC AGAGACAACC
29101	AAAGCCACAT CGGCAATGGG TACCATCTCC ATTATGGGGG ATACAAGTGT
29151	TTCTACATTA ACTCCTGCCT TATCTAACAC TAGGAAAATT CAGTCAGAGC
29201	CAGCTTCCTC ACTGACCACC AGATTGAGGG AGACCAGCAC CTCTGAAGAG
29251	ACCAGCTTAG CCACAGAAGC AAACACTGTT CTTTCTAAAG TGTCCACTGG
29301	TGCTACTACT GAGGTCTCCA GGACAGAAGC CATCTCCTTT AGCAGAACAT
29351	CCATGTCAGG CCCTGAGCAG TCCACAATGT CACAAGACAT CTCCATAGGA
29401	ACCATCCCCA GGATTTCTGC CTCCTCTGTC CTGACAGAAT CTGCAAAAAT
29451	GACCATCACA ACCCAAACAG GTCCTTCGGA GTCTACACTA GAAAGTACCC
29501	TTAATTTGAA CACAGCAACC ACACCCTCTT GGGTGGAAAC CCACTCTATA
29551	GTAATTCAGG GATTTCCACA CCCAGAGATG ACCACTTCCA TGGGCAGAGG
29601	TCCTGGAGGT GTGTCATGGC CTAGCCCTCC CTTTGTGAAA GAAACCAGCC
29651	CTCCATCCTC CCCGCTGTCT TTACCTGCCG TGACCTCACC TCATCCTGTT
29701	TCCACCACAT TCCTAGCACA TATCCCCCCC TCTCCCCTTC CTGTGACTTC
29751	ACTTCTCACC TCTGGCCCGG CGACAACCAC AGATATCTTG GGTACAAGCA
29801	CAGAACCTGG AACCAGTTCA TCTTCAAGTT TGAGCACCAC CTCCCATGAG
29851	AGACTGACCA CTTACAAAGA CACTGCACAT ACAGAAGCCG TGCATCCTTC
29901	CACAAACACA GGAGGGACCA ATGTGGCAAC CACCAGCTCT GGATATAAAT
29951	CACAGTCCTC TGTCCTAGCT GACTCATCTC CAATGTGTAC CACCTCCACC
30001	ATGGGGGATA CAAGTGTTCT CACATCAACT CCTGCCTTCC TTGAGACTAG
30051	GAGGATTCAG ACAGAGCTAG CTTCCTCCCT GACCCCTGGA TTGAGGGAGT
30101	CCAGTGGCTC TGAAGGGACC AGCTCAGGCA CCAAGATGAG CACTGTCCTC
30151	TCTAAAGTGC CCACTGGTGC TACTACTGAG ATCTCCAAGG AAGACGTCAC
30201	CTCCATCCCA GGTCCCGCTC AATCCACAAT ATCACCAGAC ATCTCCACAA
30251	GAACCGTCAG CTGGTTCTCT ACATCCCCTG TCATGACAGA ATCAGCAGAA
30301	ATAACCATGA ACACCCATAC AAGTCCTTTA GGGGCCACAA CACAAGGCAC
30351	CAGTACTTTG GCCACGTCAA GCACAACCTC TTTGACAATG ACACACTCAA
30401	CTATATCTCA AGGATTTTCA CACTCACAGA TGAGCACTCT TATGAGGAGG
30451	GGTCCTGAGG ATGTATCATG GATGAGCCCT CCCCTTCTGG AAAAAACTAG

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)
30501 ACCTTCCTTT TCTCTGATGT CTTCACCAGC CACAACTTCA CCTTCTCCTG
30551 TTTCCTCCAC ATTACCAGAG AGCATCTCTT CCTCTCCTCT TCCTGTGACT
30601 TCACTCCTCA CGTCTGGCTT GGCAAAAACT ACAGATATGT TGCACAAAAG
30651 CTCAGAACCT GTAACCAACT CACCTGCAAA TTTGAGCAGC ACCTCAGTTG
30701 AAATACTGGC CACCTCTGAA GTCACCACAG ATACAGAGAA AACTCATCCT
30751 TCTTCAAACA GAACAGTGAC CGATGTGGGG ACCTCCAGTT CTGGACATGA
30801 ATCCACTTCC TTTGTCCTAG CTGACTCACA GACATCCAAA GTCACATCTC
30851 CAATGGTTAT TACCTCCACC ATGGAGGATA CGAGTGTCTC CACATCAACT
30901 CCTGGCTTTT TTGAGACTAG CAGAATTCAG ACAGAACCAA CATCCTCCCT
30951 GACCCTTGGA CTGAGAAAGA CCAGCAGCTC TGAGGGGACC AGCTTAGCCA
31001 CAGAGATGAG CACTGTCCTT TCTGGAGTGC CCACTGGTGC CACTGCTGAA
31051 GTCTCCAGGA CAGAAGTCAC CTCCTCTAGC AGAACATCCA TCTCAGGCTT
31101 TGCTCAGCTC ACAGTGTCAC CAGAGACTTC CACAGAAACC ATCACCAGAC
31151 TCCCTACCTC CAGCATAATG ACAGAATCAG CAGAAATGAT GATCAAGACA
31201 CAAACAGATC CTCCTGGGTC TACACCAGAG AGTACTCATA CTGTGGACAT
31251 ATCAACAACA CCCAACTGGG TAGAAACCCA CTCGACTGTG ACTCAGAGAT
31301 TTTCACACTC AGAGATGACC ACTCTTGTGA GCAGAAGCCC TGGTGATATG
31351 TTATGGCCTA GTCAATCCTC TGTGGAAGAA ACCAGCTCTG CCTCTTCCCT
31401 GCTGTCTCTG CCTGCCACGA CCTCACCTTC TCCTGTTTCC TCTACATTAG
31451 TAGAGGATTT CCCTTCCGCT TCTCTTCCTG TGACTTCTCT TCTCACCCCT
31501 GGCCTGGTGA TAACCACAGA CAGGATGGGC ATAAGCAGAG AACCTGGAAC
31551 CAGTTCCACT TCAAATTTGA GCAGCACCTC CCATGAGAGA CTGACCACTT
31601 TGGAAGACAC TGTAGATACA GAAGACATGC AGCCTTCCAC ACACACAGCA
31651 GTGACCAACG TGAGGACCTC CATTTCTGGA CATGAATCAC AATCTTCTGT
31701 CCTATCTGAC TCAGAGACAC CCAAAGCCAC ATCTCCAATG GGTACCACCT
31751 ACACCATGGG GGAAACGAGT GTTTCCATAT CCACTTCTGA CTTCTTTGAG
31801 ACCAGCAGAA TTCAGATAGA ACCAACATCC TCCCTGACTT CTGGATTGAG
31851 GGAGACCAGC AGCTCTGAGA GGATCAGCTC AGCCACAGAG GGAAGCACTG
31901 TCCTTTCTGA AGTGCCCAGT GGTGCTACCA CTGAGGTCTC CAGGACAGAA
31951 GTGATATCCT CTAGGGGAAC ATCCATGTCA GGGCCTGATC AGTTCACCAT
32001 ATCACCAGAC ATCTCTACTG AAGCGATCAC CAGGCTTTCT ACTTCCCCCA
32051 TTATGACAGA ATCAGCAGAA AGTGCCATCA CTATTGAGAC AGGTTCTCCT
32101 GGGGCTACAT CAGAGGGTAC CCTCACCTTG GACACCTCAA CAACAACCTT
32151 TTGGTCAGGG ACCCACTCAA CTGCATCTCC AGGATTTTCA CACTCAGAGA
32201 TGACCACTCT TATGAGTAGA ACTCCTGGAG ATGTGCCATG GCCGAGCCTT
32251 CCCTCTGTGG AAGAAGCCAG CTCTGTCTCT TCCTCACTGT CTTCACCTGC

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)	
32301	CATGACCTCA ACTTCTTTTT TCTCCACATT ACCAGAGAGC ATCTCCTCCT
32351	CTCCTCATCC TGTGACTGCA CTTCTCACCC TTGGCCCAGT GAAGACCACA
32401	GACATGTTGC GCACAAGCTC AGAACCTGAA ACCAGTTCAC CTCCAAATTT
32451	GAGCAGCACC TCAGCTGAAA TATTAGCCAC GTCTGAAGTC ACCAAAGATA
32501	GAGAGAAAAT TCATCCCTCC TCAAACACAC CTGTAGTCAA TGTAGGGACT
32551	GTGATTTATA AACATCTATC CCCTTCCTCT GTTTTGGCTG ACTTAGTGAC
32601	AACAAAACCC ACATCTCCAA TGGCTACCAC CTCCACTCTG GGGAATACAA
32651	GTGTTTCCAC ATCAACTCCT GCCTTCCCAG AAACTATGAT GACACAGCCA
32701	ACTTCCTCCC TGACTTCTGG ATTAAGGGAG ATCAGTACCT CTCAAGAGAC
32751	CAGCTCAGCA ACAGAGAGAA GTGCTTCTCT TTCTGGAATG CCCACTGGTG
32801	CTACTACTAA GGTCTCCAGA ACAGAAGCCC TCTCCTTAGG CAGAACATCC
32851	ACCCCAGGTC CTGCTCAATC CACAATATCA CCAGAAATCT CCACGGAAAC
32901	CATCACTAGA ATTTCTACTC CCCTCACCAC GACAGGATCA GCAGAAATGA
32951	CCATCACCCC CAAAACAGGT CATTCTGGGG CATCCTCACA AGGTACCTTT
33001	ACCTTGGACA CATCAAGCAG AGCCTCCTGG CCAGGAACTC ACTCAGCTGC
33051	AACTCACAGA TCTCCACACT CAGGGATGAC CACTCCTATG AGCAGAGGTC
33101	CTGAGGATGT GTCATGGCCA AGCCGCCCAT CAGTGGAAAA AACTAGCCCT
33151	CCATCTTCCC TGGTGTCTTT ATCTGCAGTA ACCTCACCTT CGCCACTTTA
33201	TTCCACACCA TCTGAGAGTA GCCACTCATC TCCTCTCCGG GTGACTTCTC
33251	TTTTCACCCC TGTCATGATG AAGACCACAG ACATGTTGGA CACAAGCTTG
33301	GAACCTGTGA CCACTTCACC TCCCAGTATG AATATCACCT CAGATGAGAG
33351	TCTGGCCACT TCTAAAGCCA CCATGGAGAC AGAGGCAATT CAGCTTTCAG
33401	AAAACACAGC TGTGACTCAG ATGGGCACCA TCAGCGCTAG ACAAGAATTC
33451	TATTCCTCTT ATCCAGGCCT CCCAGAGCCA TCCAAAGTGA CATCTCCAGT
33501	GGTCACCTCT TCCACCATAA AAGACATTGT TTCTACAACC ATACCTGCTT
33551	CCTCTGAGAT AACAAGAATT GAGATGGAGT CAACATCCAC CCTGACCCCC
33601	ACACCAAGGG AGACCAGCAC CTCCCAGGAG ATCCACTCAG CCACAAAGCC
33651	AAGCACTGTT CCTTACAAGG CACTCACTAG TGCCACGATT GAGGACTCCA
33701	TGACACAAGT CATGTCCTCT AGCAGAGGAC CTAGCCCTGA TCAGTCCACA
33751	ATGTCACAAG ACATATCCAG TGAAGTGATC ACCAGGCTCT CTACCTCCCC
33801	CATCAAGGCA GAATCTACAG AAATGACCAT TACCACCCAA ACAGGTTCTC
33851	CTGGGGCTAC ATCAAGGGGT ACCCTTACCT TGGACACTTC AACAACTTTT
33901	ATGTCAGGGA CCCACTCAAC TGCATCTCAA GGATTTTCAC ACTCACAGAT
33951	GACCGCTCTT ATGAGTAGAA CTCCTGGAGA TGTGCCATGG CTAAGCCATC
34001	CCTCTGTGGA AGAAGCCAGC TCTGCCTCTT TCTCACTGTC TTCACCTGTC
34051	ATGACCTCAT CTTCTCCCGT TTCTTCCACA TTACCAGACA GCATCCACTC
34101	TTCTTCGCTT CCTGTGACAT CACTTCTCAC CTCAGGGCTG GTGAAGACCA

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)
34151 CAGAGCTGTT GGGCACAAGC TCAGAACCTG AAACCAGTTC ACCCCCAAAT
34201 TTGAGCAGCA CCTCAGCTGA AATACTGGCC ACCACTGAAG TCACTACAGA
34251 TACAGAGAAA CTGGAGATGA CCAATGTGGT AACCTCAGGT TATACACATG
34301 AATCTCCTTC CTCTGTCCTA GCTGACTCAG TGACAACAAA GGCCACATCT
34351 TCAATGGGTA TCACCTACCC CACAGGAGAT ACAAATGTTC TCACATCAAC
34401 CCCTGCCTTC TCTGACACCN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
34451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
34501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNCGGAAA CCAAGTTTCT
Exon 4
34551 AACCAACCCC TCCTTTTTGA CCCCAGTAGG ATTCAAACAA AGTCAAAGCT
34601 CTCACTGACT CCTGGGTTGA TGGAGACCAG CATCTCTGAA GAGACCAGCT
34651 CTGCCACAGA AAAAAGCACT GTCCTTTCTA GTGTGCCCAC TGGTGCTACT
34701 ACTGAGGTCT CCAGGACAGA AGCCATCTCT TCTAGCAGAA CATCCATCCC
34751 AGGCCCTGCT CAATCCACAA TGTCATCAGA CACCTCCATG GAAACCATCA
34801 CTAGAATTTC TACCCCCCTC ACAAGGAAAG AATCAACAGA CATGGCCATC
34851 ACCCCCAAAA CAGGTCCTTC TGGGGCTACC TCGCAGGGTA CCTTTACCTT
34901 GGACTCATCA AGCACAGCCT CCTGGCCAGG AACTCACTCA GCTACAACTC
34951 AGAGATTTCC ACAGTCAGTG GTGACAACTC CTATGAGCAG AGGTCCTGAG
35001 GATGTGTCAT GGCCAAGCCC GCTGTCTGTG GAAAAAAACA GCCCTCCATC
35051 TTCCCTGGTA TCTTCATCTT CAGTAACCTC ACCTTCGCCA CTTTATTCCA
35101 CACCATCTGG GAGTAGCCAC TCCTCTCCTG TCCCTGTCAC TTCTCTTTTC
35151 ACCTCTATCA TGATGAAGGC CACAGACATG TTGGATGCAA GTTTGGAACC
35201 TGAGACCACT TCAGCTCCCA ATATGAATAT CACCTCAGAT GAGAGTCTGG
35251 CCACTTCTAA AGCCACCACG GAGACAGAGG CAATTCACGT TTTTGAAAAT
35301 ACAGCAGCGT CCCATGTGGA AACCACCAGT GCTACAGAGG AACTCTATTC
35351 CTCTTCCCCA GGCTTCTCAG AGCCAACAAA AGTGATATCT CCAGTGGTCA
35401 CCTCTTCCTC TATAAGAGAC AACATGGTTT CCACAACAAT GCCTGGCTCC
35451 TCTGGCATTA CAAGGATTGA GATAGAGTCA ATGTCATCTC TGACCCCTGG
35501 ACTGAGGGAG ACCAGAACCT CCCAGGACAT CACCTCATCC ACAGAGACAA
35551 GCACTGTCCT TTACAAGATG TCCTCTGGTG CCACTCCTGA GGTCTCCAGG
35601 ACAGAAGTTA TGCCCTCTAG CAGAACATCC ATTCCTGGCC CTGCTCAGTC
35651 CACAATGTCA CTAGACATCT CCGATGAAGT TGTCACCAGG CTGTCTACCT
35701 CTCCCATCAT GACAGAATCT GCAGAAATAA CCATCACCAC CCAAACAGGT
35751 TATTCTCTGG CTACATCCCA GGTTACCCTT CCCTTGGGCA CCTCAATGAC
35801 CTTTTTGTCA GGGACCCACT CAACTATGTC TCAAGGACTT TCACACTCAG
35851 AGATGACCAA TCTTATGAGC AGGGGTCCTG AAAGTCTGTC ATGGACGAGC

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)	
35901	CCTCGCTTTG TGGAAACAAC TAGATCTTCC TCTTCTCTGA CATCATTACC
35951	TCTCACGACC TCACTTTCTC CTGTGTCCTC CACATTACTA GACAGTAGCC
36001	CCTCCTCTCC TCTTCCTGTG ACTTCACTTA TCCTCCCAGG CCTGGTGAAG
36051	ACTACAGAAG TGTTGGATAC AAGCTCAGAG CCTAAAACCA GTTCATCTCC
36101	AAATTTGAGC AGCACCTCAG TTGAAATACC GGCCACCTCT GAAATCATGA
36151	CAGATACAGA GAAAATTCAT CCTTCCTCAA ACACAGCGGT GGCCAAAGTG
36201	AGGACCTCCA GTTCTGTTCA TGAATCTCAT TCCTCTGTCC TAGCTGACTC
36251	AGAAACAACC ATAACCATAC CTTCAATGGG TATCACCTCC GCTGTGGACG
36301	ATACCACTGT TTTCACATCA AATCCTGCCT TCTCTGAGAC TAGGAGGATT
36351	CCGACAGAGC CAACATTCTC ATTGACTCCT GGATTCAGGG AGACTAGCAC
36401	CTCTGAAGAG ACCACCTCAA TCACAGAAAC AAGTGCAGTC CTTTATGGAG
36451	TGCCCACTAG TGCTACTACT GAAGTCTCCA TGACAGAAAT CATGTCCTCT
36501	AATAGAACAC ACATCCCTGA CTCTGATCAG TCCACGATGT CTCCAGACAT
36551	CATCACTGAA GTGATCACCA GGCTCTCTTC CTCATCCATG ATGTCAGAAT
36601	CAACACAAAT GACCATCACC ACCCAAAAAA GTTCTCCTGG GGCTACAGCA
36651	CAGAGTACTC TTACCTTGGC CACAACAACA GCCCCCTTGG CAAGGACCCA
36701	CTCAACTGTT CCTCCTAGAT TTTTACACTC AGAGATGACA ACTCTTATGA
36751	GTAGGAGTCC TGAAAATCCA TCATGGAAGA GCTCTCCCTT TGTGGAAAAA
36801	ACTAGCTCTT CATCTTCTCT GTTGTCCTTA CCTGTCACGA CCTCACCTTC
36851	TGTTTCTTCC ACATTACCGC AGAGTATCCC TTCCTCCTCT TTTTCTGTGA
36901	CTTCACTCCT CACCCCAGGC ATGGTGAAGA CTACAGACAC AAGCACAGAA
36951	CCTGGAACCA GTTTATCTCC AAATCTGAGT GGCACCTCAG TTGAAATACT
37001	GGCTGCCTCT GAAGTCACCA CAGATACAGA GAAAATTCAT CCTTCTTCAA
37051	GCATGGCAGT GACCAATGTG GGAACCACCA GTTCTGGACA TGAACTATAT
37101	TCCTCTGTTT CAATCCACTC GGAGCCATCC AAGGCTACAT ACCCAGTGGG
37151	TACTCCCTCT TCCATGGCTG AAACCTCTAT TTCCACATCA ATGCCTGCTA
37201	ATTTTGAGAC CACAGGATTT GAGGCTGAGC CATTTTCTCA TTTGACTTCT
37251	GGATTTAGGA AGACAAACAT GTCCCTGGAC ACCAGCTCAG TCACACCAAC
37301	AAATACACCT TCTTCTCCTG GGTCCACTCA CCTTTTACAG AGTTCCAAGA
37351	CTGATTTCAC CTCTTCTGCA AAAACATCAT CCCCAGACTG GCCTCCAGCC
37401	TCACAGTATA CTGAAATTCC AGTGGACATA ATCACCCCCT TTAATGCTTC
37451	TCCATCTATT ACGGAGTCCA CTGGGATAAC CTCCTTCCCA GAATCCAGGT
37501	TTACTATGTC TGTAACAGAA AGTACTCATC ATCTGAGTAC AGATTTGCTG
37551	CCTTCAGCTG AGACTATTTC CACTGGCACA GTGATGCCTT CTCTATCAGA
37601	GGCCATGACT TCATTTGCCA CCACTGGAGT TCCACGAGCC ATCTCAGGTT
37651	CAGGTAGTCC ATTCTCTAGG ACAGAGTCAG GCCCTGGGGA TGCTACTCTG
37701	TCCACCATTG CAGAGAGCCT GCCTTCATCC ACTCCTGTGC CATTCTCCTC

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)
37751 TTCAACCTTC ACTACCACTG ATTCTTCAAC CATCCCAGCC CTCCATGAGA
37801 TAACTTCCTC TTCAGCTACC CCATATAGAG TGGACACCAG TCTTGGGACA
37851 GAGAGCAGCA CTACTGAAGG ACGCTTGGTT ATGGTCAGTA CTTTGGACAC
37901 TTCAAGCCAA CCAGGCAGGA CATCTTCAAC ACCCATTTTG GATACCAGAA
37951 TGACAGAGAG CGTTGAGCTG GGAACAGTGA CAAGTGCTTA TCAAGTTCCT
38001 TCACTCTCAA CACGGTTGAC AAGAGAATGC GCATGGCGAG AAGGGAGAAG
38051 TGTAGTTGGA TGGATAAAAG GAAGAATGGA GAGAAGAGTG AATGGAAGGA
38101 AGCAAAGATG AAGCGGAGGA AGGATAGATG CACAGAAGGA AGGATGAAAA
38151 GAAAGAAAGA TGATGGAAGA CAGGATTGAA GGGGATATAG ATTGAAGGAA
38201 AGAAAGGTAG AAGGATGAAA TGAAGTAAAG ATTGAAGAAA AGATGGATGG
38251 AAAGAAGAAA GGAGGGTGCA CAAAAAATCT CACACTTCAC CACATATGAT
38301 TCATCCATAT AAGAAAAAAC CACTTGTACC CTCAAAGCTA TTGAAATACA
38351 AACTTTTAAA TTAAAATTTT AAAAAGCAAG AGAAAGGAAA GAAGGGAGGA
38401 AAGACAAAAG GAAGAATGGG TGATAGAAGG AAAGAATAAA AGGAAGAAAA
38451 AATGGAAGAA TAGATGATCA GATCTAGGGA TGAATGAAAG GAAGGATGGA
38501 CAAATCTATA GGTAGGTGGA TGGATCTATG GACAGGTGTG GCCACTTATG
38551 GCACATAGTC CCAGCTCCAG TTCATACTGA TGGACTTGAG GAGTGTTTGT
38601 GGCCAATGAA GTGGATCCAT TTAGACAGTG CTCTTCTTCT GAATGAGATG
Exon 5
38651 AGTTACCCCA GTTTTTCTCC CCACCTTCAT CTTCAGGAAC TGATGGCATT
38701 ATGGAACACA TCACAAAAAT ACCCAATGAA GCAGCACACA GAGGTACCAT
38751 AAGACCAGTC AAAGGCCCTC AGACATCCAC TTCGCCTGCC AGTCCTAAAG
38801 GTAGGTTTAA CTTTGCTTAC CTCCCAGTAA TGCCACTCGT GACCATATTT
38851 CCTCCTCCAG AGAGACAAAA TGTTTGTATT CTTTAGAGAG AGAATTGTGT
38901 GTGGTTGTCA TAGGTTTCCC TGTCTGAACT GAGTCTTTAT CTAATGGTTA
38951 CCAGGCAGAT GTTACCACTG TCTCTTTCTC CTCATGGCAT GCTGAGTGAG
39001 TTTTGTCCAA CATCAAATAT TCACAAATTT GTCCATATTA ACCAAATTTT
39051 AAAAATGCTC ATTAAAAACT TACTATGAGC TGGGCGCAGT GGCTCATGCC
39101 TGTAATCCCA ATACTTTGGG AGGCTGAGCT GGGTGGATCA CCAGAGGTCA
39151 AAAATTCGAG ACCAGTCTGA CCAAAATGGT GAAACTCCAT CTCTACTGAA
39201 AATATAAAAA TTAGCCGGGC ATGGTGGCAC ACACCGTAAT CACAGCTACT
39251 CAGGAGGCTG AGGCAAGAGA GTCACTTGAA CCACAGGAGG TAGAGGCTGC
39301 AGTGAGCTGA GCATTGTGCC AATGCACTCC AGCCTGGGTG GCAGAGCAAG
39351 ACTCCAGCTC AGAAATAAAT AATATATTAT ATATATATAT ATATGTTTTA
39401 TTTAGATGGA ATATACTATA TATATATGTA TATATATATG TATGTATATA
39451 TATATATGTA TGTATATATA TATATATATA TATATATATA TATATAGAGA

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)					
39501	GAGAGAGAGA	GAGAGAGAGA	GAGAGAGACA	GAGTATGTCT	GAGAATGCAT
39551	CCCGATAGTT	CTAGCAAGGT	AGGAAAAGGA	AGTATCATAA	CAGCCTTGAA
39601	GTAGCCTGTT	GAAACAGACA	GACTCTCTTG	TAAGAGAACT	CACAAAATCT
39651	AGGATTATAT	CTCCCATGAT	GAAAAATTTG	GAACTGTACA	TTTTTGTTTA
39701	ACTGTCACTT	AAATNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
39751	NNNNNNNNNN	NNNNNNNNNN	NCCAGGAGGC	ACTGTGCTTG	GCGCCTTTTT
39801	ACCAACACTT	TGAGATGGCC	ATTGTACTTA	TCCCCACTTT	ATAGACGGGA
39851	AAATGGAGGT	CCAGCAATAT	TTTTTAACTT	AAAGAGCCAC	CCATCTCTTT
39901	AGAGAAAGAG	CCAGAATCCC	AGGCAGGGGC	TATCTTATTC	CAGAGCCCAA
39951	GCTCTCAAAC	ACATGATACA	CAATACTTAA	TCTCTCTCAA	GTCAGAGGAG
40001	ATCCACTTAA	GTATACATCC	ATCCACATAT	TCATTCATTC	AATCATTCAA
40051	CAAATATTAG	TTGAGCACTT	ACCGTATGCC	AAACAGTCAA	ACGTGAATAG
40101	CTGTTACAAA	TGAGACTGTG	AAGGATGGTA	CAACGCAGAT	TCAGACAGTG
40151	TGATAAGGAA	ATATTGAGAA	GCAAAGATGA	GTTCTGGAGT	GAATTTGTAA
40201	AGGTGGATGT	GGGCTTGGAT	TTCAATAATG	GCAGAACTTA	AGGAATCTGA
40251	TGAGAAGTGG	GCACTTCAGG	CAGAGAGAAG	AGCTTGAACA	AGGCTCAGAG
40301	GCTGACAGTG	CAGGAAACAC	ATGGGAAGAG	GGAATAGAGT	AGCGGTCAAG
40351	AATTCACAGA	GGAGTTATAG	GTGAAGATGC	AACCAAGTTA	CAGACCAAGG
40401	TAAGATAGGG	GAATACCAAT	CACAATCTCT	TTTCCCATTC	CAGAAGCATC
40451	CCAGACACAT	CCTAGTAACC	GAGAGACATT	TCTCTCCCTT	TCCTCCTGTG
40501	GAGAATAAAT	AAGCTATTGC	AAGTCCAGTA	AGTGTAATCA	TTTTGTTCAA
Exon 6					
40551	ATTGTGTGCC	CATTCCCCAA	TTTACAGGAC	TACACACAGG	AGGGACAAAA
40601	AGAATGGAGA	CCACAACCAC	AGCTCTGAAG	ACCACCACCA	CAGCTCTGAA
40651	GACCACTTCC	AGAGCCACCT	TGACCACCAG	TGTCTATACT	CCCACTTTGG
40701	GAACACTGAC	TCCCCTCAAT	GCATCAATGC	AAATGGCCAG	CACAATCCCC
40751	ACAGAAATGA	TGATCACAAC	CCCATATGTT	TTCCCTGATG	TTCCAGAAAC
40801	GACATCCTCA	TTGGCTACCA	GCCTGGGAGC	AGAAACCAGC	ACAGCTCTTC
40851	CCAGGACAAC	CCCATCTGTT	TTCAATAGAG	AATCAGAGAC	CACAGCCTCA
40901	CTGGTCTCTC	GTTCTGGGGC	AGAGAGAAGT	CCGGTTATTC	AAACTCTAGA
40951	TGTTTCTTCT	AGTGAGCCAG	ATACAACAGC	TTCATGGGTT	ATCCATCCTG
41001	CAGAGACCAT	CCCAACTGTT	TCCAAGACAA	CCCCCAATTT	TTTCCACAGT
41051	GAATTAGACA	CTGTATCTTC	CACAGCCACC	AGTCATGGGG	CAGACGTCAG
41101	CTCAGCCATT	CCAACAAATA	TCTCACCTAG	TGAACTAGAT	GCACTGACCC
41151	CACTGGTCAC	TATTTCGGGG	ACAGATACTA	GTACAACATT	CCCAACACTG
41201	ACTAAGTCCC	CACATGAAAC	AGAGACAAGA	ACCACATGGC	TCACTCATCC
41251	TGCAGAGACC	AGCTCAACTA	TTCCCAGAAC	AATCCCCAAT	TTTTCTCATC

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)
41301 ATGAATCAGA TGCCACACCT TCAATAGCCA CCAGTCCTGG GGCAGAAACC
41351 AGTTCAGCTA TTCCAATTAT GACTGTCTCA CCTGGTGCAG AAGATCTGGT
41401 GACCTCACAG GTCACTAGTT CTGGGACAGA CAGAAATATG ACTATTCCAA
41451 CTTTGACTCT TTCTCCTGGT GAACCAAAGA CGATAGCCTC ATTAGTCACC
41501 CATCCTGAAG CACAGACAAG TTCGGCCATT CCAACTTCAA CTATCTCGCC
41551 TGCTGTATCA CGGTTGGTGA CCTCAATGGT CACCAGTTTG GCGGCAAAGA
41601 CAAGTACAAC TAATCGAGCT CTGACAAACT CCCCTGGTGA ACCAGCTACA
41651 ACAGTTTCAT TGGTCACGCA TCCTGCACAG ACCAGCCCAA CAGTTCCCTG
41701 GACAACTTCC ATTTTTTTCC ATAGTAAATC AGACACCACA CCTTCAATGA
41751 CCACCAGTCA TGGGGCAGAA TCCAGTTCAG CTGTTCCAAC TCCAACTGTT
41801 TCAACTGAGG TACCAGGAGT AGTGACCCCT TTGGTCACCA GTTCTAGGGC
41851 AGTGATCAGT ACAACTATTC CAATTCTGAC TCTTTCTCCT GGTGAACCAG
41901 AGACCACACC TTCAATGGCC ACCAGTCATG GGGAAGAAGC CAGTTCTGCT
41951 ATTCCAACTC CAACTGTTTC ACCTGGGGTA CCAGGAGTGG TGACCTCTCT
42001 GGTCACTAGT TCTAGGGCAG TGACTAGTAC AACTATTCCA ATTCTGACTT
42051 TTTCTCTTGG TGAACCAGAG ACCACACCTT CAATGGCCAC CAGTCATGGG
42101 ACAGAAGCTG GCTCAGCTGT TCCAACTGTT TTACCTGAGG TACCAGGAAT
42151 GGTGACCTCT CTGGTTGCTA GTTCTAGGGC AGTAACCAGT ACAACTCTTC
42201 CAACTCTGAC TCTTTCTCCT GGTGAACCAG AGACCACACC TTCAATGGCC
42251 ACCAGTCATG GGGCAGAAGC CAGCTCAACT GTTCCAACTG TTTCACCTGA
42301 GGTACCAGGA GTGGTGACCT CTCTGGTCAC TAGTTCTAGT GGAGTAAACA
42351 GTACAAGTAT TCCAACTCTG ATTCTTTCTC CTGGTGAACT AGAAACCACA
42401 CCTTCAATGG CCACCAGTCA TGGGGCAGAA GCCAGCTCAG CTGTTCCAAC
42451 TCCAACTGTT TCACCTGGGG TATCAGGAGT GGTGACCCCT CTGGTCACTA
42501 GTTCCAGGGC AGTGACCAGT ACAACTATTC CAATTCTAAC TCTTTCTTCT
42551 AGTGAGCCAG AGACCACACC TTCAATGGCC ACCAGTCATG GGGTAGAAGC
42601 CAGCTCAGCT GTTCTAACTG TTTCACCTGA GGTACCAGGA ATGGTGACCT
42651 CTCTGGTCAC TAGTTCTAGA GCAGTAACCA GTACAACTAT TCCAACTCTG
42701 ACTATTTCTT CTGATGAACC AGAGACCACA ACTTCATTGG TCACCCATTC
42751 TGAGGCAAAG ATGATTTCAG CCATTCCAAC TTTAGCTGTC TCCCCTACTG
42801 TACAAGGGCT GGTGACTTCA CTGGTCACTA GTTCTGGGTC AGAGACCAGT
42851 GCGTTTTCAA ATCTAACTGT TGCCTCAAGT CAACCAGAGA CCATAGACTC
42901 ATGGGTCGCT CATCCTGGGA CAGAAGCAAG TTCTGTTGTT CCAACTTTGA
42951 CTGTCTCCAC TGGTGAGCCG TTTACAAATA TCTCATTGGT CACCCATCCT
43001 GCAGAGAGTA GCTCAACTCT TCCCAGGACA ACCTCAAGGT TTTCCCACAG
43051 TGAATTAGAC ACTATGCCTT CTACAGTCAC CAGTCCTGAG GCAGAATCCA

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)	
43101	GCTCAGCCAT TTCAACAACT ATTTCACCTG GTATACCAGG TGTGCTGACA
43151	TCACTGGTCA CTAGCTCTGG GAGAGACATC AGTGCAACTT TTCCAACAGT
43201	GCCTGAGTCC CCACATGAAT CAGAGGCAAC AGCCTCATGG GTTACTCATC
43251	CTGCAGTCAC CAGCACAACA GTTCCCAGGA CAACCCCTAA TTATTCTCAT
43301	AGTGAACCAG ACACCACACC ATCAATAGCC ACCAGTCCTG GGGCAGAAGC
43351	CACTTCAGAT TTTCCAACAA TAACTGTCTC ACCTGATGTA CCAGATATGG
43401	TAACCTCACA GGTCACTAGT TCTGGGACAG ACACCAGTAT AACTATTCCA
43451	ACTCTGACTC TTTCTTCTGG TGAGCCAGAG ACCACAACCT CATTTATCAC
43501	CTATTCTGAG ACACACACAA GTTCAGCCAT TCCAACTCTC CCTGTCTCCC
43551	CTGGTGCATC AAAGATGCTG ACCTCACTGG TCATCAGTTC TGGGACAGAC
43601	AGCACTACAA CTTTCCCAAC ACTGACGGAG ACCCCATATG AACCAGAGAC
43651	AACAGCCATA CAGCTCATTC ATCCTGCAGA GACCAACACA ATGGTTCCCA
43701	GGACAACTCC CAAGTTTTCC CATAGTAAGT CAGACACCAC ACTCCCAGTA
43751	GCCATCACCA GTCCTGGGCC AGAAGCCAGT TCAGCTGTTT CAACGACAAC
43801	TATCTCACCT GATATGTCAG ATCTGGTGAC CTCACTGGTC CCTAGTTCTG
43851	GGACAGACAC CAGTACAACC TTCCCAACAT TGAGTGAGAC CCCATATGAA
43901	CCAGAGACTA CAGCCACGTG GCTCACTCAT CCTGCAGAAA CCAGCACAAC
43951	GGTTTCTGGG ACAATTCCCA ACTTTTCCCA TAGGGGATCA GACACTGCAC
44001	CCTCAATGGT CACCAGTCCT GGAGTAGACA CGAGGTCAGG TGTTCCAACT
44051	ACAACCATCC CACCCAGTAT ACCAGGGGTA GTGACCTCAC AGGTCACTAG
44101	TTCTGCAACA GACACTAGTA CAGCTATTCC AACTTTGACT CCTTCTCCTG
44151	GTGAACCAGA GACCACAGCC TCATCAGCTA CCCATCCTGG GACACAGACT
44201	GGCTTCACTG TTCCAATTCG GACTGTTCCC TCTAGTGAGC CAGATACAAT
44251	GGCTTCCTGG GTCACTCATC CTCCACAGAC CAGCACACCT GTTTCCAGAA
44301	CAACCTCCAG TTTTTCCCAT AGTAGTCCAG ATGCCACACC TGTAATGGCC
44351	ACCAGTCCTA GGACAGAAGC CAGTTCAGCT GTACTGACAA CAATCTCACC
44401	TGGTGCACCA GAGATGGTGA CTTCACAGAT CACTAGTTCT GGGGCAGCAA
44451	CCAGTACAAC TGTTCCAACT TTGACTCATT CTCCTGGTAT GCCAGAGACC
44501	ACAGCCTTAT TGAGCACCCA TCCCAGAACA GAGACAAGTA AAACATTTCC
44551	TGCTTCAACT GTGTTTCCTC AAGTATCAGA GACCACAGCC TCACTCACCA
44601	TTAGACCTGG TGCAGAGACT AGCACAGCTC TCCCAACTCA GACAACATCC
44651	TCTCTCTTCA CCCTACTTGT AACTGGAACC AGCAGAGTTG ATCTAAGTCC
44701	AACTGCTTCA CCTGGTGTTT CTGCAAAAAC AGCCCCACTT TCCACCCATC
44751	CAGGGACAGA AACCAGCACA ATGATTCCAA CTTCAACTCT TTCCCTTGGT
44801	TTACTAGAGA CTACAGGCTT ACTGGCCACC AGCTCTTCAG CAGAGACCAG
44851	CACGAGTACT CTAACTCTGA CTGTTTCCCC TGCTGTCTCT GGGCTTTCCA
44901	GTGCCTCTAT AACAACTGAT AAGCCCCAAA CTGTGACCTC CTGGAACACA

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)
44951 GAAACCTCAC CATCTGTAAC TTCAGTTGGA CCCCCAGAAT TTTCCAGGAC
45001 TGTCACAGGC ACCACTATGA CCTTGATACC ATCAGAGATG CCAACACCAC
45051 CTAAAACCAG TCATGGAGAA GGAGTGAGTC CAACCACTAT CTTGAGAACT
45101 ACAATGGTTG AAGCCACTAA TTTAGCTACC ACAGGTTCCA GTCCCACTGT
45151 GGCCAAGACA ACAACCACCT TCAATACACT GGCTGGAAGC CTCTTTACTC
45201 CTCTGACCAC ACCTGGGATG TCCACCTTGG CCTCTGAGAG TGTGACCTCA
45251 AGAACAAGTA AGAATAACTT TTTTATTGTG GTAAAATATA AATACTATAA
45301 AAATTGCCAT TCTAAACATT TTAATTGTAC AACTCAGCAG TACTAATACA
45351 TTCACATTGT TGTGCAACCC TCACCACTAT CTGTTTTCAA AACTTTTTTT
45401 ATCACCCCAA ACAGGACTGA AGGAATAATT TCCCATTCCC CATTCTCCCT
45451 AGTGCAGTGG TGCAATCTCG GCTCACCACA ACCTCTGAAC CTCTGTCTCC
45501 TGGGTTCAAG CAATTCTCCT GCATCAGCCT CCTGAGTAGT TGGGACTACA
45551 GGTGCACGCC ACCGTGCCTG GCTAATTTTT GTATTTTTAG TACAGACAGG
45601 GTTTTACCAT GTTGGTCAGG CTGGTCTCAA ACTCCTGACC TCAGGTGGTC
45651 CACACGCCTT GGCCTCCCAA AGTGCTGGGA TTACAAGTGT GAGACACTGT
45701 GCCCGGCCAT ATCTGTTAGA TCTTACTAAT CCTGTCAAGA GGATTCAGTG
45751 TCCTTTTTTT TTTTTCTTTC TTTTTTTTGA TAGAGTCTCC CTCTGGCACC
45801 CAGGCTGGAG TGCAGTGGTA CGGTCTTGGC TCACTGCAGC CTCCACCTCC
45851 CAGACTGAAG CGATTCTCCT GCCTCAGCCT CCCGAATAGC TGGGACTACA
45901 GGCGCGTGCC ACCACGCCCA GCTAATTTTT GCATTTTTAG TAGAGATGGG
45951 ATTTCACTAT GTTGGCCAGG CTGGTCTCAA ACTCCTGATC TCAAGTGATC
46001 CGCCCAAGGG CCTCCCAAAG TACTGGGATT ACAGGTAGGA GCCACCTCAC
46051 CTGGCCCTAT TTTCGGAATG GATTTTTTTT TAATGTTTAA AATGTCACCT
46101 AAGATTATTG TGAAGATCAA ATAAGATAAA ATCCTAATAA CCCAAGTAAA
46151 CCACAGGGCT CCACTTGGAC CAGTCTCAGA AGTTTCAAGA AAATCAGTCA
46201 GACCATCAAA TGTAAAATAA GTCTAAATTT TCTTTGCACT ATTCACAGAG
46251 TGCCAAAGAG GATCTAATTC ATGTTTCAGA ACATACCCTA CTTACTAAAA
46301 TCCCCTTTTC CTCATTTCTT CTCATTCTGC AACTTTATCA TCTCCTGCGG
46351 ACCCCCTAGC CTCTCCCCTC CCCATAGTCA GTCTCTCTCT CTCTCTTTCC
46401 CTCCCCTCTT ATTATCTCAA TTTCACACGA AAGAATTCCA GAAACTATAC
46451 TGCCAAAAGT CTTTCCTGTC TTTGAAAAGT TGGGAAAGAG GAGAAACTCA
46501 GACAGCAATG ACAAAATTAT ACGTAATGGA TGAAGGAAAC ACAAATAAGG
46551 CTGGAAACAG AAAATTTTGT CCCCATCATT TATTTAATGA AGGTGGCAGT
46601 ATTCCAGCCA CATAGTGAAC CCCCACAATA AGAAGGGGCC TCTGGCGATT
46651 GATTATTGTC ATTGTTGTTA ATGATAATGA GGGTGAGGAT ATCATGAGCA
46701 TCAGTGTAGG AGGCAGTTAA CTAATAAGAC CAAGCTGTTG GCTGGGCGTG

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)
46751 CTGGTTCACA CCTGCAGTCC CAGCACTTTG GGAGGCCAAA GTGGGTGGAT
46801 CACTTGAGGT CAGGAGTTCA AGACTAGCCT GGCCAACATG GTGAAACCTG
46851 GTCTCTACCA AAAATACAAA AATTAGTCAG GTGTGGTGGC GTGTGCCTGT
46901 AATGACAACT ACTTGGGAGG CTGAGGCAGG AGAATCACTT GAACCTGGGA
46951 GGCGGAGGCT GCAGTGAGAT GAGCTTGAAC CACTGCACTC CAGCCCGGGC
47001 AACAGAGAGA GACTCTTGTC TCAAAAAACA AAACAAACAA ACAAAAACTA
47051 AACCAAACAA AAAAAGACTA GCTGTTATTC ATTTATTTAT TTATTTATTT
47101 AGAGACGGAG TCTCGCTCTG TCACCCAGGC TGGAGTGCAG CGGCACAATC
47151 TTGGCTCACT GCAACCTCTG CCTCCCAGGT TCATGTGATT CTCCCGCCTC
47201 AGCCTCCCCA GCTGTTGTTA TTCATGAATG AACCTCAGAG AAAGCACACA
47251 GGAGGGTTGG TGCACCTGTG TTTTGAGTTC TACCCCTCCT TCCTCTCTTA
47301 ACTTCCTCCT GTCTTCTCAC TCTGATTCGT TCTTCCTTCC TCTCCCTCTC
Exon 7
47351 TCTCTGCAGG TTATAACCAT CGGTCCTGGA TCTCCACCAC CAGCAGTGAG
47401 TAAACATGGC CCTGAAGTCC CTATGCCCTG GGAATTCTTC CTCCCTAAGC
47451 CTGCCTTCCA GGAGGAAAGT ATCCCCCATT CCCTAGGTTC TCATCCCCAC
47501 AGAAACTCCA GAATAGCAAA AGTCTCAGGC TGAGCCAAGG CACAGATGCC
47551 AGTGCTCACC AAGAGTCCTA TTCTCCCCTC GCTAAATGAT AGGACCCAAC
47601 AAACCCGATT CACGCTGCGT TTTCTTTCAG CTCCGATGAC CTCCATGTTC
47651 TCTCCAAGGC CTCTCGTATC TGTGAGCCCC ACCCCCAGCG CTACAGGTAG
47701 GAATCTGGCT TCCAGCTCCC ATGAAACGTC GGCTGCCATT CAGTGGCTGA
47751 TTAATTGCTG TGTGGTCTGA GTCCTGATGC CCACCAAGTC TCAGCGTGTT
47801 CCCCTCTGTC CAATCTCATC CAACAATTTA AGCTAATGCT TGTTTAATGA
47851 TGTCCTCACT ATACCACCTT GGACACTTTC TTTTTGCCTG GATTTAAAGC
47901 TTCCATTTCT TTCCTTCCTT CCTTCTTTTC TTCCTTCCTT CCTTCCTTCC
47951 TTCCTTCCTT CCTTCCTTCC TTCCTTCCTT CCTTCCTTCC TCCTTCCTTC
48001 CTTCCTTTCT TCCTTTCTTC CTGTCTTTTT CTTTCTTTCC TTCTTTTGGC
48051 AGAGTCTCAC TCTGTCGCCC AGGCTGGAGT GCAATGGTGC AATCTCGGTT
48101 CACTGCAACC TCTGCCTCCC AGGTTCAAGC GATTCTCATG CCACATGCCA
48151 CTATGCCTGG CTAATTTTTG TTTTTTTGTT TTTTGGGGGG TTTTTTGAGA
48201 CAGAGTCTCA GTCTGTTGCC CAAGCTGGAG TGCAGTGGCA TGATCTCGGG
48251 TCACTGCAAC CTCCTTCTCC CAGGTTCAAG CGATTTTCCT GCCTCAGCCT
48301 CCTGAGTAGC TGGAACTACA GGCACGCACC ATCACACCGG CTAATTTTTT
48351 GTGTTTTTAG TAGAGACGAC GGTTTTGCAA TGTGGGCCAG GCTTGTCTCG
48401 AACTCCTGAC CTCAAGTGAT CCTCCAGCCT CGGCCTCTCA AAGTGCTGGG
48451 ATTACAAGTG TGAGCCACTG CACCAGGCCA AAAACTTGTA TTTCAATAGT
48501 CATTGAGGCT GGGTGCAGTG GCTCACGCCT GTAATCCCAG CACTTTGGGA

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)
48551 GGCTGAGGCC AGTGGATCAT GAGGTCAGGA GATCAAGACC ACCCTGGCTA
48601 ACACAGTGAA ACCCCATCTC TACTAAAAAT ACACACAAAA ATTAGCCGGG
48651 CATGGTGGCA AGATGCCTGT AGTCCCAGCT ACTCAGGAGG CTGAGGCAGG
48701 AGAATGGCGT GAACCTGGGA GGCAGAGCTT GCAGTGAGCG GAGATCGCAC
48751 CGCTGCACTC CAGCCTGGGC AACAGAGAGC GACTCTGTCT CAAAAAAAAA
48801 AATATATATA TATATATATA TATATTCATT GAGACCGACT CTGACTTAAA
48851 AGCAGTAATG AATGGTGTAG GTTTTGGTAA ATTACAGGTC TTGCTTTAAG
48901 TCCTGGTCCT CTCTTTTGCT CACTGTGTGG CCCCGGAAGA GCCATGTAAC
48951 CTCTCCAGGC TTCAGTGTCC ATTTTTAGAA CGGAGTAAGT GAATAAGCTG
49001 TGTCCAATCA TCTCTGGCCA TATCAGCTTC ATTTTTTTTT TCCTCCAGGG
49051 TCCAAACATC CCTCCACCCT CAGAGTCTTT GCACCTGGTG TTCTTGTCCT
49101 TCAAATCTCA GCTTGGATCA CCCTTTATAA AGTAGCATTT CCCCCGTATA
49151 CGCATCTTGC ACACAGCCAA TCTCTATTCT ACCTCTATGC TCACTTCCTT
49201 CCTGGCAATT ATTACTACAG CTGGGCCCTT GAACAGCATG AGGGTTCAGG
49251 GTGCTGACCC CTATGCATTC AAAAATCCAC ATATAACTTT TTTTTTTTTG
49301 AGATGGAGTT TCACACTTGT TGCCCAGGCT GGAGTGCAGT GGCGCCATCT
49351 TGGCTCACTG CAAACTCTGC CTCCTGGGTT CAAGTGATTC TCCTGCCTCA
49401 GCCTCCTGAG TAGCTGGGAT TACAGGCATG TGCCACCATG CCCAGCTAAT
49451 TTTGTATTTT TAGTAGAGAT GAGGTTTCTC CATGTTCGCC AGGCTGCTCT
49501 TGAACTCCTG ACTTCAGGTG ATCCGCCTGC CTTGGCCTCC CAAAGTGCTG
49551 GGATTACAGG CATGAGCCAT GATGCCCGGC CATTTGCTAA TGGCATCTAG
49601 TAAGTAGAGG CCAGAGATGT TGCAAAACAT CCAACAATGC ACAAAGCAGC
49651 CTCCTATCAA AACACATTAT CCAGACCAAA ATGTCAATAG GGCTGAGGTT
49701 GAGCATCTGC TGTACACAGA TTCCAAGTTC TGGTACAAAT CTCGTAGTTC
49751 TCTGAGGGCT CATCTTTCAA TGCCTAGCAC ATCAAAGGAG GCCAATTTCC
49801 TCTTCCCTTT CACCTCCTGG TATGAAATGT TTCCTCCTCC ACCTTGATCC
49851 TGTAAGAGCC CAGCTGGAGT TTGCAGACGA CGGGGAAAGA AATGGGTGAG
49901 GGAGGGTCCT ATGGTTGAGT CTCCGCAGTG GGCCCTGGGT GCCCAGTTCA
49951 CCCTCCTCCC CTTCATTTTC TCCATCATGA CAACTCAAGG CAAATTCTCA
50001 GTTTCCATGG GCCAGTGGAA TCCACTGACT TCATGAAATA ACCCCACCCT
50051 GAGCAAATAC CCCTCAAATA ATAACTGTTT ACACAACATC AGTGGCAACA
50101 ATGACCCAAG CAGCAATGCC ACCACCAGAA TAGCAACCAT AACAGCAGCT
50151 CATTTTCATC AAAAGGAAAC TGTAGGGCCA GGCACAGTGG CTCACACCTA
50201 TATTCCCAGC ATTTTGGGAG GCTGAGGCAG GCAGATCACC TGAGGTCAGG
50251 AGTTCAAGAC CAGCCCAGCC AACATGGTGA AACCCCATCT CTACTAAAAA
50301 TACAAAAACT AGCCAGGCTT GGTGGCATGT GCCTGTAATC CTAGCTACTC

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)
50351 GGGAGGCTGA GGCAGGAGAA TTGCTTGAAC CTGGGAGGCA GAGGTTGCAG
50401 TGAGCTGAGA TTGTGCCACT GCACTCCAGC CTGGGCGACA GAGCAAGACT
50451 CCGTCTGAAA AAAAAAAAAA AAGGAATTGT GCCAGGAATT GTGATGAGAA
50501 CTTTATATGC ATTATCTCCT ATTAATATTA CCCAAACCTC CGTGAGTTAG
50551 TATACTCATT TCTACAGAGA GCATTTATGC ATCCAGGGAG GAAGTAATTA
50601 GCCCAGAATT ACTCAGTTAT GACACAGGAC AGTATGAAAA CTCCAACCGA
50651 AGATTGGAGA CTCATGAAAA CTCCAGGCTC CTAACTACAA GACATCACTG
50701 TGGATCGTCC AAATAGAGCA AGCCCCAATC TCAGGACAGG AATGAGGCAT
50751 GAATGGCCTC TATGCTAATG ATCTAACCTA ATGCTGAATT TGTTACTTCC
50801 CTTCTGAATC CACTTGGAGA TTTCCTTTAT ATCTGACTTG AAATAGAGGA
50851 TATATACTCC TCTATCCTTG ACATAGGAGA TAATACACAG AAAGTATTTC
50901 ATTGTAGTAT CAAGTACACA TCCTGTTCTG TGTCCATAGG ATTATGACTA
50951 ATTTAGGGCA TGGCTTAACA GTGTGGTACT ATTGAATGAC AGACAGATGT
51001 CTGTTTTGTT GGATGCAGGA CAAGCCATGT AACCTCCCCA GACTTTAGTG
51051 TCCCCTCTGT GGAATGGAAT AAAAATACTA CGTGGGATTG TTCTGATAAT
51101 CAAATGAGAT AATTCAGGAA CAACCCAGAT AAATAACAGG GCTGCCCTGG
51151 GTTCTGTCTT TCCTTGTATC TCTCACAGAG CCTCAAAGGA GATGCAATCC
51201 ATGACCTAGA GAAACACTCA GGACAAATTC TCTTTTCCCC AGTTCCTTTC
51251 TTGCTCCAAT GGCAACACCA CCCCTCTCAT CCTGAAGTCT CTTGTTTTTA
51301 CCACCACACC TATTTTGCCA AATTTTCTCC AATATTCCAA ACCATATGAA
51351 ACCTTTCTTT CTTTCTTTTC TTTCCTTCCT TTCCTTCTTT CTTTCTTTTT
51401 TCTCTTCTTT TCTTTTCTTT TTGAGACATG GTCTCACTCT GTTGCACAGG
51451 CTGGAGTGCA ATGGCACGAT CTTTGCTCAC TGCAACCTCC GCCTCCCAGG
51501 TTCAAGAGAT TCTCTTGCCT CAGCCTCCTG AGTAGCTGGG ATTACAGGCG
51551 CCCACCGCCA CGCCACGCTA ATTTTTGTGT TCTTAGTGGA GACGGGGTTT
51601 CGCCATGTTG GCCAGGCTGG TCTTGAACTC CTGACCTCAA GTGATTTGCC
51651 CATCTCGGTC TCCCAAAGTG CTAGGATTAC AGGCGTGAGC CACCAAGCCC
51701 GGCCCCATAT GAACCGTTTC TATCCCTCAT TTCTCTGTAC TTTTACCTAA
51751 AAACACCACT CCCTTCACCC ATCACATTTT TGTCAATTCT ACATCACACA
51801 CACACACACA CACACACACA CACACACAGA GAAAGTAAGT TGGAAAAAAA
51851 TTATACTATC ATGAAATTTT GTGAAAGGAG GTAAGCTGAG AGAGTAAGAA
51901 TCAAACTAAA TTATCTTTAT GGGTAGAAAG CACACTCATC CATACATGTG
51951 TCTTTCCACC CTTGTAATGT ATTTATTATT ATTGTTTGTA TATACTAGAT
52001 TCCCAATAAA TAGGGACAGC TATTATGGTA TTTTTATTTC AGGAATAATA
52051 ATAGTGATGA TTTCCACCAT TATTGTCAAA GGACAAAGCA CAAAATATGT
52101 ACCAAATAAA ATATAGCCAT TATCCTTTAT TCACAAAAGA TCTTGGCCCC
52151 ACCTCTTCTC AATGAAATGT CCATGACTTG TTCAACTTTG GCCACTCTGG

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)
52201 GCTGAGAGAT GGAGGTTCCC TTGCGAGCTG AAGTCACACA TCGAAGGTGG
52251 AAGCCCCTCC CCTCCCTCTG GCTGGCTGAG GGATAGCCCA GATGGGCTCA
52301 TCATGAAAGT TTCCCATTAT TTCCATTTCT GGATCTACCA TCTTCCCCTC
52351 CCCTACCTCT CACCCATCAT AATTGTCCTT CTTTACTCTT TCCTCCCTAT
Exon 8
52401 CTGCAGGTTA TAACCGTCGG TACTGGACCC CTGCCACCAG CAGTGAGTAT
52451 TCAAACCTGT GATATTCCAA TGCCCTTGGG ACCCTTCCTC CCCAAGGTGC
52501 ATTCCTCAGA AGAGAAACTG ATCATTCTCC CTCCCTACGT GCCCAGCCAC
52551 AGCCTCAGAG CAGCCCCTAA CCCGTCAAGG TCTTGGTGTG AGTCAAGATA
52601 GAAGTCCAAA TTCCAATGAG CAGTTCCTGT CCCATATTCC TTTAGGAAGA
Exon 9
52651 CACCCAATCA TTTCTCCATG TTCTTTTTTT CTCAGCTCCA GTGACTTCTA
52701 CATTCTCCCC AGGGATTTCC ACATCCTCCA TCCCCAGCTC CACAGGTAGG
52751 AAGCTCCTCT CTGGCATCTA TGAAATTTAA CACTGCATGG TCTGTTCCCT
52801 GCTGACCACC CAGACTCAGC CTGTTCCACT CGCCCTCTCA CTCTCTCTCT
52851 CTCTCTTTTT TTTTTTTTTT TTTTTTTTTT TTTACGGAGT CTTGCTCTGT
52901 CACCCAGGCT GGAGTGGAAT GGTGTGATCT CGGCTCACTG CAACCTTCGC
52951 CTCCCAGGTT CACGTGATTC TCCTGCCTCA GCCTCCGGAG TAGCTGGGAT
53001 TACAGGTGCA CACCACCATG CCTGGCTAAT TTTTTGTATT TTTAGTAGAG
53051 ACGGGGTTTC ACCATGTTGG CCAGGCTGGT CTTGAACTCC TGACCTCAAG
53101 TGATCTACCC ACCTTGGCCT CCCAAAGTGC TGGGATTATA GGCATGAGCC
53151 ACCACGCCAG GCCCACTCTC TAAATTTTGA CCACCCTGCC TTGAGTGGTC
53201 TTCTAGCACC CTAACCTCTG TCTAACCTCG AGAGCTTTGC ACTAGCGATT
53251 CCTGGGGACC AGCTATGGTT GGTATCTTCT CAACTTTCTA ATTTTTTTAA
53301 AATTATTATT ATTATTATTA TTATTTTAAA TGGAGTCTCG CTCTGTCACC
53351 CAGGCTGGAG TGCAGTGGCA CCATCTCGGC TCATTGCAAC CTCTACCTCC
53401 CGGGTTCATG CAATTTTCCT GCCTCAGCCA GAAATTTTCT CAGTGGTCGA
53451 GATTGTGCCA CTGCACTCCA GCCTGGGCAA TGGAGCTAGG CTCCATCTCA
53501 AAAAAAAAAA AAAAAAGACG GAGGTCGGGC ATTCCTAACC CTTAACCCTG
53551 CCTTGTGATT CTGGAGTTAT GAGATAGAAC CTGGTGTCCC GTAATTAAAA
53601 TTCCGCCTTC AGGCCTTATG TTTTGTGAGT CACAACACTG CAAACTTTTT
53651 ACATGCTGTA GACAGGATGT TCACTCTCCA CTTCCTCACT GCTCTGCTCT
53701 AATCAATTCA ACCATTTATG TGACATGCCT AACCCCTCTG GGCTTGTACG
53751 TATGTAACAT GTATTACAAA GCAAGTCATT CCATGATCAA TGCTGTCACT
53801 TTTTCTAGGT GCTTTCAAAA TTTGTTCTTC ATCATTGATT TTCAGTAGTT
53851 TGATTACGAT GTGTCTGGGC ATGGTTTTCT TTGAGTTTAT CCTGCTTAAA

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)
53901 GTGTTCTCAG CTTCTTGAGT CTCAAAGTGT TTATTTTCTG CTCTGATTCT
53951 TTCTCCCCTT CGGACCTCCA ATGAAATGAT GTTGCCCGAA GAGACCCTGA
54001 GGTTCTGTTC ATTTTGTTAT TTATCAATCT TTTTTCCTCT CCGAATTTCA
54051 GGTTTAATAA TTTTTTTTTT TTTTTTGAGA CGGAGTCTCG CTCTGTCGCC
54101 CAGGCTGGAG TGCAGTGGCG CGATCTCGGC TCACCGCAAG CTCCGCCCCC
54151 TGGGTTCACG CCATTCTCCT GCCTCAGCCT CCGGAGTAGC TGGGATTACA
54201 GGCACCCGCC ACCATGCCCG GCTAATTTTT TGTATTTTTT AGTAGAGACG
54251 GGGTTTCACC GTATTAGCCA GGATGGTCTC AATCTCCTGA CCTCGTGATC
54301 CGCCCGCCTC AGCCTCCTAA AGAGCTGGGA TTACAGGCGT GAGCCACTGC
54351 GCCCGGCCCA GGTTTAATAA TTTTTATAGA ATATTTTCAC AATCACCAAG
54401 CCTTTTCTCT ACCAGCTCCA TTCTGCCCAT CCATTGAATT CTTTTTATCT
54451 CAGTTACTTT ATGTTTCAGT TCGAAAGTTT CTACTTGGTT AGATAGATAG
54501 ATGTTATATC ATATATTATA TGTTATATAA AAATATATTT ATGGTTATAC
54551 ATATAACATA TATGTTATAT ATAGTTATTT ATATAGCCAT AACTATATAT
54601 AGCCATATAT ATAGTTATAT ATAACCATAT ATATAGTTAC CATATAGTAA
54651 CCACATATAT AAAACATATA TATATAGTGT CTCTCTATAT ATAGTTATAT
54701 ATATAGTTTC TATATCTGTA ACTATATATA GTTATATATG TATGTTTCTC
54751 TGTATATAAA TATATATATT TCTATATATA TAGTTATACA CATTATATAT
54801 ATAACTGGGA GATGTTGGTA AAGGATGGCG TGAGGAAACC TGGAGCAGTC
54851 ATGGTAATCC TCGCTCTGCT CCGAACTCCT CAAGAGCAGG AGAAGGGTCC
54901 TCCTCATTCT CCAGCCATGT TGACTTTGAG CAATTTACTC ATCCTCTCAG
54951 TACCTCAGTT TCCTCACCTG CCAATTGAGG ATAATAATAT TTCATAAATT
55001 GTTTGCAAAT GTTATATGCA ACTCTACGTA AGAACACCTA GCACAGGGGC
55051 TACCAGGGAA TTTGGTTTAA CAAATATTTA TCAGGCACCT ATTCTGGGCT
55101 GGGCAGGGGG GATAAGATGT TGACTAAGTC AAATGCAGTC CCTCCCCTCA
55151 CCAAGTTTAC AGTGTATTGG GCAAGACTGA AATGGAACAA GCAATTACAA
55201 TTGACAATAA AAGACAACCA AGTTATTGAG CACTTACTAT ATGGCATGCC
55251 ATATGCTATG TATTTTTTTT ATTTTTAACT TTTCATTTTG AAATAAATAA
55301 TAAATATAAA GTAAATAATA ATATAAATAA ATAATAAATA ACTTTTCATT
55351 TTGAAATAAA TAATAAATAA ATTCAGGAGA TGTTGCGAAA ATAGTGTAGC
55401 ATTCCCCTGT ATCCTTCACC CAGTTTCTCC CCAATGGCTA CATCTTACAT
55451 AACTCTAATA CAATATCAAA AGCAGGAAAC TGACATTGTT AAAATCCATT
55501 TTACTGGTTT TACACGCGTG TGTGCATATG TGAGCTTGTG TATGTGCGTG
55551 TGTGTGCAGG CATGTGTGTG CATGCACGCC TGTGTGTGCA TATGTGCATG
55601 TGTGCATGCG TGTGTGCATG TGTGCATGTG TGTGTGCATG CGTGCGTGCG
55651 TGCGTGCATC TGTGTGCATG TATGCACATG TGTGTGTGTC TGTGCACGTG
55701 TGTGCATGCA TGTGTGTGTG CGTGTGTGTT GGTAGCCCTA TGCAATTTTT

TABLE 1-continued

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)					
55751	ATCACATGGG	CATAGCCCTA	TAATCACCAC	CACCATCAAG	ATTCAGAACT
55801	GTTCCATTCC	CCCAAAGATT	CCCCTCATGC	TAGCCTTCGT	AATCATGCCC
55851	ACTGAGCCCA	ACACTATTGC	ATAGAATAGC	TATTCTACTC	TCCATCTCCA
55901	TCTCTGTCTC	TACAATTTTC	TTTTGAAGAT	GTTATATAAA	TGGAAATGTA
55951	CAACATGTCA	CCTTTGAAAT	TGGCTTCTTT	TCCACTCAGT	GTAATGCCCT
56001	GGAGATGTGC	TCTTTTTAAC	AGTCATGTAA	CCTTCCTAAT	TTCCCTCCAA
56051	AATATCATTA	TGCCCCTCGC	CGCCTTTTTT	TTTTTTTTTT	TTTTTTGAGA
56101	CAGAGTCTCG	CTCTGTTGCC	CAGGCTGGAG	TGCAGTGGTA	TAATCTCAGC
56151	TCACTGCAGC	CTCCGTCTCC	CGGGTTCAAG	GGATTCCCCT	GCCTCAGCCT
56201	CCCAAGTAGC	CAGGATTACA	AGTGCATGCC	ACCACGCCTG	GCTAATTTTT
56251	GTATTTTTAG	TCGAGACGGG	GTTTCATTGT	GTTGGCCAGG	CTGGTCTCGA
56301	ATTCCTGACC	TCAAGTGATC	TGCCCGCCTT	GGCCTCCCAA	AGTGCTGGGA
56351	TTACAGGTGT	GAGCCACCGC	GCCCGACCCA	TATTGCCCAT	TGTATTACAG
56401	CGGAAGAAAC	TGAGGTATGG	ACAGGTAACA	TGTCCATGGT	CACTTGGCTG
56451	GTGAGGGGCA	GAGAGGAGAT	TTGAAACCAA	ATCTGACTCA	CTAGTGTGGC
56501	CGTAACCATG	GTAACTATGT	CTCTCTACCA	TGTGGTCTCC	TCTTTATTAA
56551	AGGAAGGGCA	AGTTCTGGGA	GTTTTGGGAG	TTTTGGGCTT	GAGTGGGGAA
56601	GGGTAGCCAA	GTAAAGCAGG	TGAGAGAAGG	TCTGCTTTAA	GGACTGCTGT
56651	TTGATTTTTA	TTGTTGTTGT	TCAGTGTTCA	ATGGGATTGA	GTTGACTCTT
56701	TTTTCCCTTC	TTGTTCCCCA	AAGCATGAGA	CTGTTCCGGT	CCTTTTCCCT
56751	TTTAACTTCT	CAGCTAGAGT	TTGTTAGGGC	GGGTATGGGC	ACCTGGCAGA
56801	GTCTGAGACC	TCAGCTTCCA	GTAGGCACAC	GTTCTGACCC	AATACACCTA
56851	CCCTGGTCCC	CTAACCTGCT	TCTGGTCCCC	TAACCTGCTT	CTGGGCCCAG
56901	GTAATGCATT	TTAGGAACAT	CCCACTTTTC	TCCTTACCTG	GCTTTCCATT
56951	ATCCGTCCAA	ACTAAAGCAC	CCACCTGTCT	GCTTCAGACT	CTTGCTTCAA
57001	GCACTCCGTC	TGGGTCCTCA	GAAATTGACT	TACAGTCAGT	TCAGATCTGA
57051	CTCAGGCGTG	GCCTTCTTTT	CTCCTTCCTT	GC	

TABLE 2

Genomic Repeats (SEQ ID NO: 2)					
	ExonR1				
1	AGCAGCCACA	GTCCCATTCA	TGGTGCCATT	CACCCTCAAC	TTCACCATCA
51	CCAACCTGCA	GTACGAGGAG	GACATGCGGC	ACCCTGGTTC	CAGGAAGTTC
101	AACGCCACAG	AGAGAGAACT	GCAGGGTCTG	GTGAGAGCCC	CGCCCACCGT
151	ACTCCTCCCT	CGCCCACTTA	GACAAACCAG	CCCACCTCAC	ACTGCCTCGC

TABLE 2-continued

Genomic Repeats (SEQ ID NO: 2)					
201	CCACTGATGC	CAGCCACGCC	CACCTCATCC	AACCCCAGAC	ACCTTTCCCT
251	GCCCCACCCA	CTGATTTTAG	CCAAGCCCAC	CTCACCCCAC	CCAGCCTACT
301	GATGCCAGCC	ACGCCCACCT	TTCCCTGCCC	CGCCCACTGA	TTTCAGCCAC
351	GCCCACCTCA	CCCTGGTCCA	CCCCTCCAAT	GCCCCACTCT	TCCTGGCTTC
Exon R2					
401	CCGCAGCTGT	TGTTTCTCAC	CTCCCCTCTC	CTTCCTTGCA	GCTCAAACCC
451	TTGTTCAGGA	ATAGCAGTCT	GGAATACCTC	TATTCAGGCT	GCAGACTAGC
501	CTCACTCAGG	TGAGACGCTC	CTTAAGAAAA	ACACAGCCCA	ACAGGTGAAT
551	ATGACCCTAG	TCTCTGGGCT	CCCTGACTCT	GTTCATACTT	GGAACAACTA
601	TTGCCCATGG	ATACTAAGCA	TCACCACCAG	CAGCAGCAGA	TAACTATTCC
651	TAAGACCCAA	GGCACTGCAT	TATGTACTTT	ATATTTAATG	CCTCATCAGT
701	GCTTGCAACA	GCCTCATGAA	GCAGGAGCAG	AAGGGGAAAC	TGAGGCCCAG
751	ATTAAGTGGC	TTGTGCCAGG	ACACACAAAG	CAACTGCAGC	ACTTCAGGTT
801	CTATATCCAA	ACTCCTATCC	CTTAGGTGGC	ACTTCCTCCT	CTGCCCCCAT
851	TATGAACTTG	CAGCATGTGG	AAAACCCCAA	TCTGACTTCC	CTCTAAGGGA
901	ACTTGCCCAG	AGAATCTAAG	AGGGGAGGAA	AGGAAGGCGT	TCAGCCCTTA
951	CAGGCAGGAG	GTCAGCTCCT	GAGTGGCTCA	GATGCAGCCA	CAGAGGGCCT
1001	GGCCGGTCTG	AGGGTGACTG	AGAGGCACCG	AGGGCACTGT	CCCTGAGTGC
1051	TGGAAAGGGC	AGGTCTTTTA	GGGTAGACAG	CGGTTGATAT	CATTTCCTGC
1101	CTGGCATTCT	CACCTTCCAC	ACCTCTCTCA	CAGAATCTCC	AAGTGTGGCT
1151	CTCCCAAGAG	AGAGTGTCAG	TCATCTACCT	CCAGCTTCCT	TTCCTTCCCA
1201	GGGGGAAGAG	GGGACAGGGG	GGCCCTAGTG	GCTAAGAGCA	TTGGTGAACT
1251	CAGGCAGACC	TCAGTTCTGA	ACCAACCCAG	CTCTGCCATT	TACTATCTGT
1301	GACTCTGAGC	AAGTGCCTGA	AGCCTTCTGT	GCCCTATTTC	CTGACATATT
1351	ATATATATAA	AATACATATA	TTATATATAG	ACATATTTTA	TATACATATT
1401	GAGGCATATT	TTATAAACAT	GTTTATAGAC	ACATTTTTAT	ATGCATATGT
1451	TATATACGTA	TATAACATAT	GTTATATATA	ATGTATATAT	TATACATATT
1501	GTTATATTGT	ATACATGTTA	TATATGTTAT	AGCATATATA	GTACAAGTTA
1551	TATATAACAC	ATACATTATG	TTACATATAA	TGTATATGTT	ATATATGATA
1601	TATTATATAT	AATTATATAT	TATATAAAAC	TGTTATATAT	AATTATATAT
1651	AATATATAGT	TGTTATATAT	AATTATATAA	TTGTTATATA	TTATATACAA
1701	CATATAACAT	ACATTATATA	TTGTTATATA	TAATATAATA	TATACATATA
1751	TAACATATGT	ATAACTTTTA	TGTTATACAT	AATGTATATA	ACATATATGT
1801	GTATGTGTGA	TGTACATAAC	ATATCTGACA	TTAACATATA	ACATATGATA
1851	TAACAATATT	ATATGTTATA	ACATAATATA	TGTTATAATA	TAACAATATT
1901	ATATGTTATA	ACTTATACTG	TCATATGTAA	CATATACATA	ATATTTTATA
1951	AATCAGTTTA	ATATACATTA	TGTTACATAT	AATGTATGTT	ATATATGATA

TABLE 2-continued

Genomic Repeats (SEQ ID NO: 2)				
2001	TATTATATAT	AATTATATTA	TACATAATTG	TTATATATAA	TGCATACATT
2051	GTATTTGTTA	CGTATTATAT	GCAACATATG	GGGATCCTCT	AGAGTCGGAC
2101	CAGCGGCAGC	AGCTGCCTGC	CTTTTNNNNN	NNNNNNNNNN	NNNNNNNNNN
2151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
2201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
2251	ATATACATAC	ATAACATATG	TATAACTTAT	ATGTTATATA	TAAGTATATA
2301	ACATATATGT	GTATGTGATG	TATATAACAT	ATCTGACATT	AACATATAAC
2351	ATATGTTATA	ATATGACATA	TTATATATAT	TACATATAAC	GTATATCATG
2401	TATAATATAA	TGTGTATATA	TAATATATTA	AAGTATATAA	GTATAAATAC
2451	ATGTAATATT	TAAATATATA	TTATATATAG	TATACATGTG	GATACATACA
2501	ACTTCTACAT	ATACCTAGTA	TATATTCTAT	ATATAAACAG	TCCATGAATT
2551	ACAATGATTC	AACTTATGAT	TTTTCAAACT	TTGTGATAAT	GCCATAGCAA
2601	TATGCATTCA	GTAGAAAGCA	TACCTTCAAC	ACCCATGCAA	CCATTCTGTC
2651	ATTCACTTTC	AGTACAATAT	TCAATAAATT	ATATGAGATA	TTCAACAGTT
2701	TATTATAAAA	TAGGCTTTGT	GTTAGGTGAT	TTTGCCCACA	TGTAGGCTAA
2751	TGTAAGGGTT	CAGAGCATGT	TTAAGGTAGG	ATAGGCTAAC	CTATCATGTT
2801	CTGTAGGTTA	GGTATAGTCG	ATTTTTATTT	TTATTTTTAT	TTTTGAGACA
2851	GAGTCTTGCT	CTGTCACCCA	GACTGGAATG	CACTGGTGCG	ATCATAGCTC
2901	ACTGCAGCCT	TGAACTCCTG	GGCTCAAGTG	ATCCTCCTAC	CTCAGCCTCC
2951	TGAGTAGCTG	GGACTACAGG	TGTGTGCCAC	CACACCTGGC	TATTTTTTTT
3001	TTAATTTTTT	TTTTTTTGTG	GAGAGGAGGG	TCTTGCCATG	TTGCCCAGGT
3051	GGCCTTGAAC	TCCTGGGCTC	AAGGAATCCT	CCCACCTTGG	CCTCCCAAAA
3101	TCCTGGGATT	ACAGGTGTGA	GCCATCACGC	CCGGCTACAG	GGCATTTTTG
3151	ACTTATGACA	TTTTCAGTTC	ACAATGGATT	TGTCAGGGCT	GGGCATGATG
3201	GCTCACACCT	GTCATCCCAG	CACTTTGGGA	GGCTGAGGCA	GGTGGATCAC
3251	TTGAGGCCAG	GAGTTTGAGA	CCAGGCTGTC	CAAATGGCAA	AATCTTGTCT
3301	CTACTAAAAA	TACAAAAATT	AGCCAGGCGT	GGTGTGACAA	CTGTAGTTCC
3351	AGCTACTCGG	GAGACTGAAG	CGTGAGAATC	ACTTGAACTT	AGGAGATGGA
3401	AGTTACAGTG	AGTCAAGATC	ACACCACCGC	ACTCCAGCCT	GGATGACAGA
3451	GCAAGACTCT	TGTCTCCAAA	AAACAAAAAA	CAGGCTGGGT	GCATGGCTCA
3501	TGCCTGTAAT	CCCAGCAGTT	TGGGAAGCTG	AGGCAGGTTT	ATCACCTGAG
3551	GTCAGTAGTT	CACGATCAGC	TTGGCAAACA	TGGAGAAAAC	CCATCTCTAC
3601	TAAAAATACA	AAAATTAGCT	GGATGTGGTG	GTGGGTACCT	GTAGTCCCAG
3651	CTACTCGGGA	GGCTGAGGCA	GGAGAATGGA	TTGAACCTGG	GAGGCAGAGG
3701	TTGCAGTGAG	CCAAGATCAC	ACCATTGAAC	TCCAGCCTGG	GCAACAGAGT
3751	GAGACTCCAT	CTCCAAAAAC	AAAAGAAAGC	AAAAACAAAA	AAATAAAATA

TABLE 2-continued

Genomic Repeats (SEQ ID NO: 2)					
3801	AAAAACCTGT	GTTTATCAGG	ACATAATACC	ATCATGAGTC	AAGAAGCATC
3851	TAAATGTACA	TGGTAGTTAT	ATAAAAATAG	TTATATAGTT	ATATACAATA
3901	GTTATATATA	AACCAGTTTA	ATATATGTTA	AGTAGAGGTA	TATGGTAGTT
3951	ATATAAAAAA	TAGTTATATA	ATAGTTATAG	AGTTATATAA	TTATATAAAA
4001	TAGTTATATA	TAAACCAGTT	TAATATATGT	TAGGTAGAGG	TATAATAATA
4051	TATATTGTAT	ATACTATATA	ATATAGTAAT	GTATAAAATG	CAAAACGATA
4101	TCATATATTT	CTATATTAAG	TTTATATTTA	CAGATCTACA	TTTTATATAT
4151	TTTATGTTAT	ATACAATTGT	GTTATACATA	ATATAATTAG	TATAGTACTG
4201	ACTTGGGGAA	TTGAGCAGTA	CCAACCCATA	GGGATGTTTG	AGGATGAAAA
4251	TATGTGATTA	TGAATACAAA	ATGCTGGGCC	TGCTGCATAG	GAAGTATTTA
4301	ATAAATGGTA	GTTGTTACTA	TAAAGTCGTT	CCTACTATAG	AGCTACTCAC
4351	AACCTGGGAC	ATAGGGAAAG	AGCCCGTTTC	CCTCTAATCA	CTCAATAGTG
4401	GGTGGCTAGG	TAGGTGAGTC	CACATCCTGT	GGCCGGGAAC	AGGTGCTGAG
4451	ACATGAAGAC	CTTCTGACTG	CATGTTGGAC	CAGCCACAGT	TTCAGACGGA
4501	CCAGCCAAAA	AGGGCATTTT	CCCCAAGCCA	TTTAGCTCCC	TTGAGTCTCA
4551	TAACAAATCT	CCTAGACCCT	GCTGGTCCAT	AGGATCTAGA	GAGGATGACT
4601	TGAACCTTCT	GATCCCACCA	TTTGAAAACG	CCATGCCATG	GGCACCAGTA
4651	GGAGGGCCAC	TGCTACGTGC	ACCAGTACAA	GGGCCACTGC	CATGGATTAC
4701	AGATTAACCC	TAAGTATAGC	TGTCGCACAC	CTAGTACTTC	AGGAGGCTTA
4751	TTCGGGGCCA	TGCAGATCCC	TGGCATTATT	ATCCTAGGAT	CCTACACCAA
4801	GCAAAGCAGG	AGCTGCCCCT	CCTCATAAAC	CCATAAGCCC	TCCTCTTGAG
4851	CAAAGCAGCT	GGGAAGGCCA	GAAGTTATTC	AAGCTCCCCT	CTGCCCCGGT
4901	TCCAAAGACA	GACAGCTCAA	GCCTACATGC	AGCAAACCCT	ATAAAAGTGT
4951	CACCTCTTGG	CATTTCTGCC	ATGGTAATGC	TTTCTGCTTC	CACTAATAAT
5001	CCTAGTAATT	TGTTTATGGT	GGGCATCTCT	CTGATGAGAA	CCACATTCTT
5051	TTTTTTTTTT	TTTTTTTTTT	TTGAGATAGA	GTCTCACTCT	GTTGCCCAGA
5101	CTGGAGTGCA	GTGGCGCGAT	CTCGGCTCAC	TGTAACCTTT	GGCTCCTAGG
5151	TTCAAGCAAT	TCTCCTGCCT	CAGCCTCCCA	AGTAGCTGGG	ACTGCAGGCA
5201	CGTACCACCA	TGCCCAGCTA	ATTTTTGTAT	TTTTAGTTGA	GACGGGGTTT
5251	CACCATGTTA	GCCAGGATGG	TCTCAATCTC	TTGACCTCAT	GATCCACCTG
5301	CCTTGGCCTC	CCAAAGTGTT	GGGATTACAG	GCATGAGCCA	CCATGCCTAG
5351	CCTGAGAGCC	ACATTCTTGT	TAACCACAAT	TTTCTCAGAG	TCTGCATTAG
5401	GGGTTGACAA	AGAGTGGAAA	GGAAGGACAA	AAGGATGGAG	AGGTGGATGG
Exon R3					
5451	ACTAAGCATA	TGTAGGTTCT	TACCCAGGCC	AGAGAAGGAT	AGCTCAGCCA
5501	CGGCAGTGGA	TGCCATCTGC	ACACATCGCC	CTGACCCTGA	AGACCTCGGA
5551	CTGGACAGAG	AGCGACTGTA	CTGGGAGCTG	AGCAATCTGA	CAAATGGCAT

TABLE 2-continued

Genomic Repeats (SEQ ID NO: 2)					
5601	CCAGGAGCTG	GGCCCCTACA	CCCTGGACCG	GAACAGTCTC	TATGTCAATG
5651	GTGAGCAGCT	GTGATGTGGT	TGGAGGCTCT	TCCTCCTTGC	TGAGCAGCCT
5701	GTAATCACTG	GCTTGAGGTC	ACACTCACTG	TCAGGCAATT	GAAAATTTGG
5751	TCCTGTGCTC	TACATGGGAT	GACTAATTTC	CGGACTTCAT	GGTATCTTTT
5801	TTTTTTTTTT	TTTTTTTTTG	AGATGGAGTC	TCGCTCTGTC	ACCAGGCTGA
5851	GGTGCAGTGG	CATGATCTCA	GCTCACTGCA	ACCTCCGCCT	CCCGGATTCA
5901	AGCAATTCTC	CTGCCTCAGC	CTCCTGAGTA	GCTGGGACTA	CAGGTGCATG
5951	CCACCACACC	CAGCTAATTT	TTGTATTTTT	AGTAGAGACA	GGGTTTCACC
6001	ATGTTGGTCA	GGATGGTCTC	AATCTCTTGA	CCTTCTACTC	CACCTTGCCT
6051	TGGCCTCCCA	AAGTACTGGG	ATTACAGGCT	TGAGCCACCA	CACCTGGCCA
6101	GGACTTCATG	GTTTCTTCAT	CATCATGGAA	TGAATTCCAT	CAGGGCATTC
6151	TTCCCTGATG	TGAGGGCACT	GATAGGAAAT	CTTTAATGGT	CCCTGCTGCA
6201	TGAAACTGCT	TCCATTGCAC	CAGGGTAGCC	CTGACCCCTA	TTTGGTCCCC
6251	CACATCTCCT	TGTAACTTAC	CCACACTCCT	CCCTCCTTCT	CTGTGCAGGT
Exon R4					
6301	TTCACCCATC	GAAGCTCTAT	GCCCACCACC	AGCAGTGAGT	ATTCAACTCA
6351	TGTCCACATG	CCCATGATCC	TACACCAAGC	AAAGCAGGAG	CTGCCCCTCC
6401	TCATAAACCC	ATAAGTCCTC	CTCTTGAGCA	AAGTAGCTGG	GAAGGCAGAA
6451	GTTATTCAAG	CTCCCCTCTG	CCCCAGTTTC	AAAGACAGAC	TCAGCTCAAG
6501	CCCACATGCA	GCAAACCCTA	TAAAAGTCTC	ACCTCTTGGC	ATTTCTGCCA
6551	TGGTAATGCT	TTCTGCTCTC	ACTAATGAGG	ACTTCTCCTC	AGCTCCTGGG
Exon R5					
6601	ACCTCCACAG	TGGATGTGGG	AACCTCAGGG	ACTCCATCCT	CCAGCCCCAG
6651	CCCCACGAGT	AAGTACCAGT	CAATGGCATC	TCTATTAGAG	CATGCTATCT
6701	CTGTCATTTT	TACTCAGATG	AAGATGGAAA	ATCATAGCAA	ATCTACTGAT
6751	AGTGAGTGGA	CCAACGAAAT	TTGTTGGCCA	CCTAGTGTGT	ACCAGATCCT
6801	AGAGATACAG	GAGGGAAAAC	AAAACCAATA	CAAAATTTCT	GCTCTCAGTG
6851	AGCTTGTATT	CTTGTCATGA	TGATGATGTT	GGTGGTGGTG	CTGTTGATGA
6901	CGATGATGAT	GATGATGATG	ATGATGATGC	TGGTGATACT	GTTGATGGTG
6951	ATAGTGATGT	TGATGACAAT	GATGATGATG	ATGATGTTGA	AGAAAATGAT
7001	GCTGGTGATG	GTGGTGGGGG	TTATTATGGT	AATAATGATA	TGTTGAGTGT
7051	GACGATGATG	GTGGTGGTGT	TGATGATGAT	GATGATTATT	ATGCTAGTGA
7101	CATTGATGAT	GGTAATGGTG	ATATCAACGA	CAGTGACAAT	GATGGTGATG
7151	AGGATGATGT	CGGTGATGGT	GGTGGGGTTA	TGATGGTAAT	GATATGTTGA
7201	ATGTGATGAT	GGTGATGATG	ATATTTGTGG	TTCATGATGG	GGATTGTCAT
7251	GGTGGTGCTG	GTGGTACTTG	TGATGACAAT	AATGATAATA	ATGATGACAA

TABLE 2-continued

Genomic Repeats (SEQ ID NO: 2)					
7301	TGATAGTGAT	GATGGTGATG	GTGATAATAA	AGATAACAGA	TATCACCTTA
7351	CAATATTGAG	CACTAAATAT	GTACCAAGAG	CTATGCTCAG	TATCTAACTA
7401	CTATTATATA	ATCTACTTTA	GAAAATGAAT	TGTATCATAG	ATAAGAAAGG
7451	CGTGGAAAAT	ATTTATTATG	TCACTCAATT	TAATTGCTGC	ATATGGTTAT
7501	TACAAAGTGC	TATTCTCTCT	ACTTTGAACA	TAATGTTTAT	TTCACACTCC
Exon R1					
7551	CACTATAGCT	GCTGGCCCTC	TCCTGATGCC	GTTCACCCTC	AACTTCACCA
7601	TCACCAACCT	GCAGTACGAG	GAGGACATGC	GTCGCACTGG	CTCCAGGAAG
7651	TTCAACACCA	TGGAGAGTGT	CCTGCAGGGT	CTGGTTAGTG	TCCTGCCCTC
7701	CACACTCTGC	CCTGCTCATG	ATACCCAGTC	CCTCTTACAT	CATCCATGCC
7751	AGGGCAATGG	AAGAATATCA	AACCCAACTC	ACTTTTGCCC	CAAGAGATGC
7801	AAGCCTCAGC	CAGGAGCGGT	GGCTCACGCC	TGTAATACCA	GCATTTGGGA
7851	GGCCAAGGCG	GGTGGATCAC	CTGAGGTCAG	GAGTTTGTGA	CCAGCCTGGC
7901	CAACATAGTG	AAACCTCATC	CCTACTAAAA	TACAAAAATT	AGCCAAGCAT
7951	GGTGGTGCAT	GCCTGTAATC	CCAGCTACTT	GGGAGGGTGA	GGCAAGAGAA
8001	TCACTTGAAT	CAAGGAGGCA	GAGGTTGCAG	TGAGTCAAGA	TCATGCCACT
8051	TTACTCCAGC	CTAGGCAAAA	AAGCGAAACT	CCATCTCACA	AAAAAAAGAA
8101	AAAAAGAGAG	AGATGCAAGC	CTCCCCCACC	AAGGCCAGCC	CTGCCCACCT
8151	CACTTCTGCC	TGGCTCTTAC	ATAAAACTTA	GCCCTCCTAC	TCACTGCCCT
Exon R2					
8201	CTCCCTCCTC	CACAGCTCAA	GCCCTTGTTC	AAGAACACCA	GTGTTGGCCC
8251	TCTGTACTCT	GGCTGCAGAT	TGACCTTGCT	CAGGTGAGAA	CTTAGAATTT
8301	CCAGCCTGGC	TGCCCCACTT	GTACTCACTC	CAAAAGACTT	TGCACTGCTT
8351	CCTTGCTGCA	CTTCCTAGGG	ATATCCTCAC	CAAAGGTGGA	ATTCAGGAGT
8401	CACAGGCTTC	AGGATCAGTG	TGTTTCCTGA	CAGTAACACC	CCTACACTCC
8451	ACCTCAACAG	AGAGAATCTG	CATGGCCCAT	CATCAGGATT	GAGCCTCTCC
8501	CTTTATCATC	CCTCTGAATT	CCCTCCATTC	CCTGTGCCTC	CCTTTCCTTT
8551	ACATGTTAAA	TTCTGTCCCC	AGGATTTCTT	TCAGGACAAT	CATGCCTTAT
8601	CCACGTGATT	TCATCCTCAT	TTCGAGCTCT	TCACTGGGCT	CAAGTCCGGC
8651	TCCCCGTCCC	GTCCATGAAA	GTGTCAGTTT	CATCTTGTCA	CTGTATCCGT
8701	GACTCCACTC	ACAGTCCTCA	GCAAGCCAAT	AGTCCATGCA	CTAAGAGTCG
8751	ATGTGGCTTC	TCACCTCTTT	CCCAGGTTTC	TCATTTCTCT	GGTCCTTGCT
8801	GTCCTTCCCT	CAGCAATCGC	AAGACCCTTC	CTAGATAAAC	TTTTCATTGT
Exon R3					
8851	GATTTTTCCC	ACTGACCCTC	CCCAGGCCCG	AGAAAGATGG	GGCAGCCACT
8901	GGAGTGGATG	CCATCTGCAC	CCACCGCCTT	GACCCCAAAA	GCCCTGGACT
8951	CAACAGGGAG	CAGCTGTACT	GGGAGCTAAG	CAAACTGACC	AATGACATTG

TABLE 2-continued

Genomic Repeats (SEQ ID NO: 2)
9001 AAGAGCTGGG CCCCTACACC CTGGACAGGA ACAGTCTCTA TGTCAATGGT
9051 GAGTGGCTGT GATGTGGTTG AAATCTCTTC CCCCTTGCTG GGCAGCCTCT
9101 AATCTCTAAC TAGAGATCAC ACTCCCTGCC TGGCCTTTGA AAATTCTGTC
9151 ATGTGCTCTA CATGGGATGA CTAAGGTCTG GACTTCATGG TTTCCTTACC
9201 ATCATGGACT GTGTTCCCTC AGGGCATTCT TTCCTGATGT GAGGATGCTG
9251 ATAGAAAATC TTCAATTGTC CCTGTACCAT GAAACTCGGT TCATTGCACC
9301 AGGGTAGCAT TGACCTCCAT TTGGTCCCCC ACCTCTCCTT GTCTCTTACC
Exon R4
9351 CACTCTCCTC CCTCCTTCTC TATGCAGGTT TCACCCATCA GAGCTCTGTG
9401 TCCACCACCA GCAGTGAGTA TTCAACTCAT ATCCACATGC CTCGGTTCCT
9451 ACACCAAGAG GAGCAGGAGC TGGCCCCTCC TCATAAACCC ATTAAGTCCT
9501 CTTCATAAGC AAAGGATTTA GGAGGGCAGA AGTTATTTAA GTGTCCCTCT
9551 GCCCAGCTCA AGAGACCGAC CCAGCTCAAG CTACACATGC AACAAACCCC
9601 ATAAATAGTC TCCCCTCTTG CCATTTCTGC CAAGAGAGTG CTTTATGCTT
Exon R5
9651 TCACTGATGA GAACTTTTCC TCAGCTCCTG GGACCTCCAC AGTGGATCTC
9701 AGAACCTCAG GGACTCCATC CTCCCTCTCC AGCCCCACAA GTAAGTATCA
9751 GTCAATGACA TCTCTATGAG AGCATACCTG ATTAGTGTAA ACATCTCTGT
9801 CATTTTCACT CAAATAAAGA TGGAAAATCA TAGTAAATCT AGTGATACTG
9851 AGTGGACAAA TTTGTTTGTT TGTTTTTTCT CATCCTTTTC ACTTTTTTTA
9901 TTATACTTTA AGTTTTAGGG TACATGTGCA CAATGTGCAG TTTAGTTACA
9951 CATGTATACA TGTGCCATGC TGGTGTGCTG CACCCATTTG CTCGTCATTT
10001 AGCATTAAGT ATATGTCCTA TGCGATCCAA GCCCACGCGC CGCACCACGT
10051 GCAACAGTTT CACAGATTGG ATGGTCCGAT ANNNNNNNNN NNNNNNNNNN
10101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
10151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
Exon R1
10201 CTTCACCATC ACCAACCTGC AGTATGAGGA GGACATGCAT CGCCCTGGAT
10251 CTAGGAAGTT CAACACCACA GAGAGGGTCC TGCAGGGTCT GGTTAGCACC
10301 CTGCCCTCTT CACTCTCCCC CGCCCTGGAT GCCGAGCCCC TCATACAACA
10351 TTCATGCCAG GGCAATGGAA GAATATCGCA CCAACCTTGC CCTCATCCCC
10401 AGAGATGCAA GCCTCACCCA CTGAGGCCAG CCACTCTCAT GGGTGTCTGC
10451 CCCACCCACC TCACTTTTGT CCCCACACAG GGACCTTAGC CCTCCTACTT
Exon R2
10501 ACCTCTCTCT CCCTCCCCCA CAGCTTAGTC CCATATTCAA GAACACCAGT
10551 GTTGGCCCTC TGTACTCTGG CTGCAGACTG ACCTCTCTCA GGTGAGACCT

TABLE 2-continued

Genomic Repeats (SEQ ID NO: 2)
10601 TAGAAGATCC AGCCTGGCTG CCCCAGTTGT TCCCACTCCA GTAGATTTTG
10651 CTCTGCTTCC TTGCTGCACC TCCTAGGGAT ATCCTCACCA AAAGGGGAAT
10701 TCAGGAGTCA CTGGCTTCTG GACCAATGTG TTTCCTGATA GTAACACTCC
10751 CACACCTCAC CTCAACAGGG AGAATCTGCA TGGTCCATCA TCAGGATTGA
10801 GCCTCTATCC TGATCATCCC TCAGAATTCC CTGCCCCTCC CTTTCATTTA
10851 GGTGTTAAAT TCTGTCCCCA GAATTTCTCT CAAGACAATC ATGCCTCATC
10901 CAAGTGCTTT CATCCCTGTT TCTAGCTCTT CACTGGTCTC AAGTCTGGGC
10951 TCTCCTGTCC CCATGCTATG AGAATGCAGG TTTCACCTTG CACTTTTATA
11001 AGCATGGTTG TATCTGTGAC TCTGTGCACA GTCCCAAGCA AGCCAGTAGT
11051 CCATGCACTC AGAGAATCTA AGTGTAGCTT CTCACCTCTT TCCCAGGTTT
11101 CTCATTTCCT CTGGTTCTTT ACTGTCTTTC CATCAGCAGT CTCAGGACAC
Exon R3
11151 AACCTAAGTA ATCTTTTCAT AGTCATTCTC CCCACCTACC TTCCCCAGGT
11201 CTGAGAAGGA TGGAGCAGCC ACTGGAGTGG ATGCCATCTG CATCCATCAT
11251 CTTGACCCCA AAAGCCCTGG ACTCAACAGA GAGCGGCTGT ACTGGGAGCT
11301 GAGCCGACTG ACCAATGGCA TCAAAGAGCT GGGCCCCTAC ACCCTGGACA
11351 GGAACAGTCT CTATGTCAAT GGTGAGCAGC TGTGATGTGG TTGGAGTCTT
11401 TTCCTTCTAG AGTCTGGAAA GAATCTAATC TGTGGCTTGA AGTCACACTC
11451 CCTGCCTGGC CATTGAATAT TCTGTCATGT GGTGTAGATG GGATGACAAA
11501 GTTCTGGACT TCACAGTTTC TTCATTGTCG TGAACTGTGT TCCCTCAGGG
11551 CACTCTTCCC TGTTGTGAGG ATACTGATAG GAATTCTTTA ATGGCCCCAG
11601 TCCCATGAAA CTCATTGTCC CATGAAACTC ATTTAATTGC ATTGGGATTG
11651 CCATGACCTT ATTGTGTCCC TCGTATCTCC TTAACGCTTA CCAAGTCTCC
Exon R4
11701 TCCCTCCTTC TCTATGCAGG TTTCACCCAT CGGACCTCTG TGCCCACCAC
11751 CAGCAGTGAG TATTCAACTC ATGTCCACAT GCCCCTGATC CTACATTAAG
11801 TGGAGCAGGA GCTGGCCCCT CCTCTTAAAC CCATAAGTCC TCCTCTTGAG
11851 CAAAGGAGCT GGGAAGGCAG AAGTTATTGA AGCTCCCTTC CACCTAGCTC
11901 CAAAGACAGG CCCAGCTCAT GCCCGTATGC AGCAGACCTC ATAATAGTCT
11951 ACCTTCTTGC CATTTCTGCC ATGAGATTAT TTTCTGCTTT CACTGATGAG
Exon R5
12001 CACTTTTTCT CAGCTCCTGG GACCTCCACA GTGGACNNNN NNNNNNNNNN
12051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
12101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
Exon R1
12151 ATTTTCAATT CCCACTACAG CTGCTGGCCC TCTCCTGGTG CTGTTCACCC
12201 TCAACTTCAC CATCACCAAC CTGAAGTATG AGGAGGACAT GCATCGCCCT

TABLE 2-continued

Genomic Repeats (SEQ ID NO: 2)
12251 GGCTCCAGGA AGTTCAACAC CACTGAGAGG GTCCTGCAGA CTCTGGTTAG
12301 TGCCCTTCCC TCCTCACTCT GCCCAGCCCC AGATATCCAG TCCCTTCTAC
12351 ATCATCCATG CCAGGGTGAT GAAAGAAGAT AGCAACAACT TCCCCCCTTC
12401 CCCCCAAGAG ATGCAAGCCC CACCCACAGA GACCAGTCCT GCTTATTGGT
12451 GCCTGCTCCA CCCACCTCAC ATCTGCCCCG ACACACACAC ACCTTAGCCC
Exon R2
12501 CACTACTCAC CTCCCTCTCC CTCCTCTACA GCTTGGTCCTATGTTCAAGA
12551 ACACCAGTGT TGGCCTTCTG TACTCTGGCT GCAGACTGAC CTTGCTCAGG
12601 TGAGACTTTA GAAGAGCCAG CCTGGGTGCC CAAACTTGTT CCCACTCTAA
12651 AAGACTTTGC ACTGCTTCCT TGCTGCACTT CCTAGGTATA TCTTCACCAC
12701 AAGGGGAATT CAGGAGTCAT TGGCTTGAGA ACCAGTTGTT TCCTGATAGT
12751 AACACCCCCA TGCCCCAACT CAACATGCAA AATCTTCATG GTTCATCATC
12801 AGGATTGAGA CACTACCCTG ATTACCCATC TGAATTCCCT CCTTTCCCTG
12851 ACCCCTCCCT TTCATTTAGG TGTTAAATTC TGTCCCCAGG ATTTCTCTCA
12901 AGATAACCAT GCCTCATCCA CATACATGCA TCCGCCTTTC AAGCTCATCA
12951 CTAGTCTGAA GCTCTGGGTT CTCCTGTTCC CATGCCATGA GAATGCAGGT
13001 TTCACCTTGC ACTTTTATAA AAATTATTAT ATCCATGACT CTGCTTGCAG
13051 TCCCAGACCA AGATAGTGGT CTATGTACTC AGATAATCTA AGTGCAGATT
13101 CTCACCTCTT TCCCAGATTT CTCATTTCCT CTGGTTCCTT GATATGTTTC
13151 CCTCAGCAAT CTCAAGACAA GTCCTAGGCA ATCTTTTCAT TGTCATTCCC
Exon R3
13201 CCTCCTACCT TCCTCAGGTC CGAGAAGGAT GGAGCAGCCA CTGGAGTGGA
13251 TGCCATCTGC ACCCACCGTC TTGACCCCAA AAGCCCTGGA GTGGACAGGG
13301 AGCAGCTATA CTGGGAGCTG AGCCAGCTGA CCAATGGCAT CAAAGAGCTG
13351 GGCCCCTACA CCCTGGACAG GAACAGTCTC TATGTCAATG GTGAGCAGCT
13401 GTGATATGGT AGGGGTCTCT TCCTCCTGGC TGTGCAACCA TCTAATCTCT
13451 GGCTTGGGGG CACACTCCCT GCCTGGCCAT TGAAAATTCT GTCACGTGCT
13501 CTACATGGGA TGACTAAGTT CTGGACTTCA TGGTTTCTTT GTTATCATGA
13551 GAGGCATTCC CTCTGGGCAC TCTTCCCTGT TGTGAGGATG CTGATAGGAA
13601 ATCTTTAATG ACCCCTGTCC CATGAAACTC ATTTAATTGC ACCAGGGTAG
13651 TCCTGAACTC TATCGCGTCC CCCACATCTC CTTAACCCTT ACCCAGTCTC
Exon R4
13701 CTCCCTCCTT CTCTATGCAG GTTTCACCCA TTGGATCCCT GTGCCCACCA
13751 GCAGCAGTGA GTATTCAACT CATGTCCATG ATGCCCCTGA TCCTACATCA
13801 AGTGGAGCAA GAGCTGGCCC CTCCTCTTTA ACCCATAAGT CCTCCTCTTG
13851 AGCAAATGAG CTGGGAAGGC AGAAGTTACT CAAGCTCCCC TCTGCCCCAG

TABLE 2-continued

Genomic Repeats (SEQ ID NO: 2)				
13901	CTCCAAAGAC	AGACCCAGCT	CAAGCCCACA	TGCAGCAGAC	CTCATAATAG
13951	TCTATCTTCT	TGCCATTTCT	GCCATGAGAG	TGCTTTCTGC	TTTCACTGAT
Exon R5					
14001	GAGGACTTTT	TTCAGCTCCT	GGGACCTCCA	CAGTGGACCT	TGGGTCAGGG
14051	ACTCCATCCT	CCCTCCCCAG	CCCCACAAGT	AAGTACCAGC	CAATGGTATC
14101	TGTATTAGAT	CATGCCTGAT	GAATGCAAAC	ATCTGTGCCA	TTTTCAGTCA
14151	AATGAAAATG	GAAAATCATA	ATAAATCTAG	TGATACTGAG	TGAACCAAAA
14201	AAAATGTATT	GGCCACCTAC	AGTGTACCAG	ACCCTAGGGA	TATAGCAAGG
14251	AAAATAGAAC	CAATAAAAAC	ATCTCTGCCC	TCAGTGAGCT	TGTGTTCATG
14301	TGATGATATG	ATGGTGGTGG	TGGTGGTAAT	AGTAATAATG	ACATATTCAG
14351	TTTGATGATA	ATTTATGATT	ATGGTGTTGC	TGTTGATGAT	GGTGGTGGTG
14401	ATGTTACTGA	CAATGATGGT	GACGGATCTT	TGAGGATATT	GTCCGTGATG
14451	GTCGTGAAGA	TTATGATGAT	AATGATGATG	TGTTAAGTGT	GATGATGATG
14501	ATGATCTGTG	GTGATGCTGT	TTAGGATGCT	GTTCCGTGGT	ACCGATGATA
14551	TTGATGTTGG	TCGTGGTTAT	GTTGTATGAC	AATGACAATG	ATGGTGATGA
14601	GGATAATCGC	CAGTGATGGT	GTGGGTTTAT	GATGATGATG	ATGTGTTGAA
14651	TGTGGTGATG	ATAATGTTCG	TGGTGGTCGT	GATGGGCATT	ACTATGGCAG
14701	TGATGGTCAT	AATAATGATG	GTGATGGTGA	CAATGATAGC	AAGGATGATG
14751	ATGGCAATAA	AGATAGTACA	TAACATCAGA	CAATATTGAG	CTCTGAATAT
14801	GCACCACGAG	GAGTGCTCAG	CATCTAAATA	CTATTATATA	ATATATTTTT
14851	GTAAAAATAA	ATTGTATTGT	TTTAGGCAAG	GGAAGCATGG	TAAATATTTT
14901	GTCACTCAAT	TTAAATTCTG	CATATGTTTA	AAGATAAGTC	TATTGCAAAC
14951	TCCTATTTTC	TCTACTTTGG	ACATAGTGTT	TGTTTCCCAC	CTCCACTACA
Exon R1					
15001	GCTGCTGGCC	CTCTCCTGGT	GCCATTCACC	CTCAACTTCA	CCATCACCAA
15051	CCTGCAGTAC	GAGGAGGACA	TGCATCACCC	AGGCTCCAGG	AAGTTCAACA
15101	CCACGGAGCG	GGTCCTGCAG	GGTCTGGTTA	GTGCTCCACC	CTCCTCACTC
15151	CGCCCCACCC	CAGAGAGTCA	GTACCTCCTA	CATCATCCAT	GCCAGGTGAT
15201	GGAACAAGAT	CATACCCACC	TCACCCTTGC	CCCAAGAGAT	GCAAGCCATG
15251	CCCATTGAAA	CCAGCCCCAC	TCACTGATGC	CTGTTACTGC	CCCACCTGAC
15301	TTCTGCCCTA	CACACCCACA	CACGCAACTT	AGCCCTCCTA	CTCATCTCCT
Exon R2					
15351	TCTCCCTCCT	CCACAGCTTG	GTCCCATGTT	CAAGAACACC	AGTGTCGGCC
15401	TTCTGTACTC	TGGCTGCAGA	CTGACCTTGC	TCAGGTGAGA	CCTTAGAAGA
15451	TCAAGCTTGG	CTGCCCCACT	TGTTNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN

TABLE 2-continued

Genomic Repeats (SEQ ID NO: 2)
Exon R1
15601 NGTGTTAGTC TACTTTTGAA CACTGTTTAT TTCCCATCTT CACTATAGCC
15651 GCCAGCCCTC TCCTGGTGCT ATTCACAATT AACTTCACCA TCACTAACCT
15701 GCGGTATGAG GAGAACATGC ATCAGCCTGG CTCTAGAAAG TTTAACACCA
15751 CGGAGAGAGT CCTTCAGGGT CTGGTAAGAG CCCCACATAC CTCATTCTAC
15801 CGCCACTCAC CATGTTTAGT CCTGCCCACC TCACCTATTG CAGAGCATGG
15851 AAGATCTCAT CTACCTCATC TTGCCCCCAG ATATGCATAC CCCAACCACT
15901 GATGCCAGCC CCACCAACTG TTGCCAGCCC TGCCCACCTC CCTTCTACCA
15951 CACCCCTATG ACTTCAGTCC TCCCACTCAC CTCCCTCTCC CTCCTCCACA
Exon R2
16001 GCTCAGGCCT GTGTTCAAGA ACACCAGTGT TGGCCCTCTG TACTCTGGCT
16051 GCAGACTGAC CTTGCTCAGG TGAGAACTGA GAACAGCCAG TCTGACTGAT
16101 CTGAGCAGTT TGACCTGCTT CCCTTCTGCA CTCCCTGGAG ATGTCCGCAG
16151 CCAGGTGGAA TCCAGGAGGC AGTGGCTCTA AGACCAATGT GCTTCCTGTT
16201 CCCACCACCT CCCACCTCAA CTGAGAGATG CAGAGCCCAT CAGCAGGACT
16251 GAGCTTCTAC CTTGGTCATC CCTCTGAATT CCCTCCTTTC CCCTACCTGC
16301 CTTTCCACAA GTGGTTCAAT TCTGTTCCCA GGATTTCTCC CAAGAAAAAC
16351 ATGCCTCGTC CACTTGCTTT CATCCCCAAA CCTAGCTCTT CACCTGTCTC
16401 AAGTATGAGT TCTCCTTACC CCATGCTACA AGAATGCAGT TTCCACTTTG
16451 CAATTTTATA AAAATCCTTG CATCCATGAT TCTGCTCATA GTTGCTAAGA
16501 GTCAGTGCAC TCAGAGAATG GAAGTATGGC TTCTCACTTC TCTACCAGGC
16551 TTCTCATTTC CTCTGGCCCC CTCCTGTCCT GCCCTGTGGG ATCTCAGAAC
16601 CCCTCCCTAG GCAATCCGTG TATTGTCTTT CCCCAATCTT GCCCTCCCCA
Exon R3
16651 GGCCCAAGAA GGATGGGGCA GCCACCAAAG TGGATGCCAT CTGCACTTAC
16701 CGCCCTGATC CCAAAAGCCC TGGACTGGAC AGAGAGCAGC TATACTGGGA
16751 GCTGAGCCAG CTGACCCACA GCATCACTGA GCTGGGCCCC TACACACTGG
16801 ACAGGGACAG TCTCTATGTC AATGGTGAGT AGTTGTGATG TGGTTGGAGT
16851 CTCTTCCTCC TTGCTGGGCA GCCTCTACTC TCTGCCTTGA GGTCACGCTC
16901 CCTGCCTGGC TATTGAATGC TCATCCATGT TGTCTGTATG TGATGGCTGA
16951 GGTTGGAACT TCATGGTTTC TATTTCATCT TGGACTGAGT TCATCCTCAG
17001 GATCTGCTTT CTGGATCTGA GGGTGCTGAT AGAGAATCTT CAATGGTTCG
17051 TGTTCTGGGA AATTCCTTCC ATTGCACCAG GGTACCCTGA CCCCTATATA
17101 GTTCCCCACC ACTCCCTTAA CCCTTACCCA CCCTCTTCCC TCCCTCTCTA

TABLE 2-continued

Genomic Repeats (SEQ ID NO: 2)					
Exon R4					
17151	TGCAGGTTTC	ACACAGCGGA	GCTCTGTGCC	CACCACTAGC	AGTGAGTATC
17201	CACTGATTTC	CAGTGCTCCT	GATCCTACAT	CATGCAGGGC	AAGAACTGAC
17251	CCCTCCTCAC	ATGCCCCTAT	GTCCTCTATG	AGCAAAGGAG	CTGGGACAGC
17301	ACAAGTTACT	CCCTTTCCCT	TCTGGCCCAA	GTCTCTTCAG	AGAGAGACCC
17351	AGCTCAAGCC	CCACATGCAG	CAAGGTCCAT	AAATACTCCT	ACCTGCTGGC
17401	ATTTCTGCCA	TGAGAGGGTT	CAACACTTTC	ACTAATGAGG	CCTTCTCCTC
Exon R5					
17451	AGTTCCTGGG	ACCCCCACAG	TGGACCTGGG	AACATCTGGG	ACTCCAGTTT
17501	CTAAACCTGG	TCCCTCGGGT	AAGTACAAAT	CAATCGCATC	TCTGTTAGAG
17551	CATGCCTGAT	GACTGTCAAC	ATCTCTGCCA	TTTTCACTTA	AATAAAGATA
17601	AAAAATCCTA	GTGAATCTAC	GGATGAGGAG	TCATCCAGCA	AACTTAATTG
17651	AGTGCCTAGT	TTCTGCAGGG	CTCTAGGGAT	AAGAAAGGGG	ACACAAAACA
17701	GTTAAAAATA	TCTGCTGCAA	GAAAGCTTAT	TTTATTGTGA	GGGTGATGGG
17751	AGTTGGTGGT	GGTGAAGTTA	CTGGAGATGA	TGACAATAAG	AATGGTGATG
17801	CTAGTGATGA	TGATGGTGAT	AAGGATGATA	ATTATGAAGA	TGGTGGTGGT
17851	GATGATGATG	ATGGTNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
Exon R1					
18501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NGCTGCCAGC	CCTCTCCTGG
18551	TGCTATTCAC	TCTCAACTTC	ACCATCACCA	ACCTGCGGTA	TGAGGAGAAC
18601	ATGCAGCACC	CTGGCTCCAG	GAAGTTCAAC	ACCACGGAGA	GGGTCCTTCA
18651	GGGCCTGNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN

TABLE 2-continued

Genomic Repeats (SEQ ID NO: 2)
Exon R2
18851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNCTC AGGTCCCTGT
18901 TCAAGAGCAC CAGTGTTGGC CCTCTGTACT CTGGCTGCAG ACTGACTTTG
18951 CTCAGGNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNAGAAT
19001 TCAGTCGACC TACCGGCTTT GATGATTGCT CAGTTGAACT TAGAAATGCA
19051 CTGTCTGCCC AATGGTCCAG TCTCATGAGT GTGACTCTTT TCTGCCTCTC
19101 TTGGGTATCT GATCAAGATG GACTCAGGAA AAGTGCTCCA GATAACTGTC
19151 TCCAATATAA CACTGCCCCT GCCATCACAC CCAAATGACT GGAAGTTTCA
19201 CAGGGTCATC AGCAGGGATT GGACTTCCAC CCCGGCCATC CCTCTGAATT
19251 TTCCCTCTTT TCTCCCCACC TCCCTTGCCC TTAGGTGTTA AAATTCTCTA
19301 ACTAAGATTT CTCTCAAGAC AAATGTGCCT CATTCACTTG TTTAATTCCC
19351 AATTCCAGCT TGTCACCTGT CTCAAGTCTA GGCTGTCCTG TCCCCATGCC
19401 ATGAGAATGC AAGAACCACA CTGAAATGTT AGAAAAATTC TTTTATCCAC
19451 AAGTATGCTC ACCGTCCCAA GCTGGACAGT AGTCAGTGCA CTCAGAGAAT
19501 CTAAGTGTGG CTTCTCATCT GTGTACCAGG CTTCTCATTT CCTGTGGGCC
19551 CTTCTTGTCC TTCCCTCCGC AATCTTGGGA CTCCTCCCTA GACAAAACTT
Exon R3
19601 TATTATTATT CCCCTCACCT GCCCTCTCCA GGCCTGAAAA GGATGGGACA
19651 GCCACTGGAG TGGATGCCAT CTGCACCCAC CACCCTGACC CCAAAAGCCC
19701 TAGGCTGGAC AGAGAGCAGC TGTATTGGGA GCTGAGCCAG CTGACCCACA
19751 ATATCACTGA GCTGGGCCCC TATGCCCTGG ACAACGACAG CCTCTTTGTC
19801 AATGGTGAGC AATTGTGATG TGGTTGGAGT TTCTTCTTCC TTGCTGAGCA
19851 GGCCTCTACT CTCTGTCTTG AGGTCACTCT CCCTGCCTGG CCACTGGTCT
19901 TGGCCATGTT GTCTGTATTT GATGATTGAT ATGAACTTCA CCGTTTCTTC
19951 TTCATCTTGT ACTGGAGACC TTCATCCTCA GGACCTTCTT CCCTGATCTG
20001 AGTGTACTTG TATAGAATCC TCAAAGCCCA TGTTCCCTGA AACTCCTTCA
20051 ATTGCACCAT GGTAGCACTG ACCCCTTTTG GTCCCCCACC TTNNNNNNNN
Exon R4
20101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN TTCACTCATC
20151 GGAGCTCTGT GTCCACCACC AGCACTNNNN NNNNNNNNNN NNNNNNNNNN
20201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
20251 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
20301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
Exon R5
20351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNCCTG GGACCCCCAC
20401 AGTGTATCTG GGAGCATCTA AGACTCCAGC CTCGATATTT GGCCCTTCAN

TABLE 2-continued

Genomic Repeats (SEQ ID NO: 2)
20451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNGACTCCA GCCTCGATAT
20501 TTGGCCCTTC AGGTAAGTAC CAGTCAATGG CACCTCTATT AGAGTATGCA
20551 TGATGAGTGT CAACATCTCT GTCCTTTTCA CTCAAATAAG ATTAAAAATC
20601 ATAGCAAATT GTACGTGATG ATGAGTCACC CAACAAACTT CTTTGAGTAC
20651 CCACTCTCTG CCAGGCCCTA GAGATAAGGC AGGGAACACA AAAGAGGTAA
20701 AAATCTCTGC CCTCAGAGAG CTTCTTTTAT TTTGAGGATG ATGTGGGATA
20751 GTGGTGATGA TGATGTTGCT GGAGATGATT ACAATAATGA TGGTGATGCT
20801 TATGACCATG ATGTGATGAT GATGGTGATT ATGAAGATGA TGATGATGAT
20851 ATTGATGATG GTAGTGGTTT TGACAGTAAT GATGATGTGA TGATGATGAT
20901 GATAGTGGTG GTGGTGATTA TGGGAAGGAT GACAGTGGTG GTGGTGATGG
20951 TGGTGGTTGT GGTGGTGATT GACAATGTGG TGGTGATATT GACAATGAGG
21001 ATGATGATGA TAGTGGTGGT GGTTATGATG GTTAAGGATG ATGTGATGAT
21051 GGTGTTGGTG ATCACGGTAC TAGTGGTGGT GATGTGGACC GTCATGGTTG
21101 TGGTTGTGGT GGTGATGGTG GTGATCATGA TGATAATGAG GATGATGGTG
21151 GTGATTGTCA TGATGGTAAG GATGAAACAG TGATGGTGTT GGTGACCATG
21201 TTCCTGGTGG TGATGGTGCA GGTGATGATG TGGATGATGA TGGTGATGGT
21251 GGTGGAGATG ATAGGGATTA TGAATATGGT TCGGGTCTCT GACTGGTGGT
21301 GGTGATGACA ATAATGAAAA TGATGGTCAC AGTGTTGGTG ATGATGATGG
21351 TGGTGATAAC AAAGGTAATA GATAGTGTCT AGTATTATGG AACACAGAAC
21401 ATCACCAAAG GTTATGCTCA GCATCTAACT ATTATTATTT AGCATGCTCT
21451 ATGAAAAACT TTGATCGTTA TAGTCAAGGG AGGCATGAAA ACCTTCTATT
21501 TTATCACTCT CTTTAAATCT GGTTGCATAT GTTTAGAAAT AAATCTATTA
21551 CAAACTCTTA AATGTTCTCT ACTTTTGAAC ATAGTGTTTA TTTCCCACCT
Exon R1
21601 CCACTACAGC TGCCAGCCAT CTCCTGATAC TATTCACCCT CAACTTCACC
21651 ATCACTAACC TGCGGTATGA GGAGAACATG TGGCCTGGCT CCAGGAAGTT
21701 CAACACTACA GAGAGGGTCC TTCAGGGCCT GGTGAGAGCC CTGCCCACCT
21751 CACTCTGCCC TGCCCACCTT GTCTTGTTCC ACCTACGTCA CCCATTCCAA
21801 GGCATGGAAG AAGATCTCAC CCACCTCCCC TCACCTGAGA GATAGCCCCG
21851 CCCCCTGATT ACAGCCCCTT CCACCTTACA TCTTCCTCAC TTCTATGTCC
Exon R2
21901 TCAGCCATCT TACTCACCTC CCTCTTCCTC CTCCACAGGC TAAGGCCCTT
21951 GTTCAAGAAC ACCAGTGTTG GCCCTCTGTA CTCTGGCTGC AGGCTGACCT
22001 TGCTCAGGTG AGAACTGAGA ATAACCAGTC TGGCTACCCC AAGTGTTCCC
22051 AGGCCCAAGG AGTTTCATCA GCTTTCTTCC TTCCCTCCCT ATGGAAGTCC
22101 TCAGCACAAG TGGAATTCAG GCGTTGGTGG CTCCAGGATG AACATATCTG
22151 CTGATCCTAC CACCTCCCCC ATCAATCGAG AGAATTTGCA GGGCCCATCA

TABLE 2-continued

Genomic Repeats (SEQ ID NO: 2)
22201 GCCAGATCAG GCTTCTACTT TGGTCATCCT TCTGAATTTC TTACTTCTCC
22251 CTACCTCCCT CTCCTTCAGG TGTTAAATTC TCTTCCAAGG TTTCTCTCAA
22301 GATAAACATC CCCCATCCAC TTGCTTTCAT CCCCAATTCC AGCTCTTAAT
22351 ATTTCTCAAG TCTGGGCTCT CCTGTCCCCA TACCATGAGA ATGCAATTTT
22401 ATAAAATTCT TGTATTCCTG ACTCTACTCA CATTCCCAGG CTGCCTGGAA
22451 GTTGGTGCAT TCAGAGAATC TTAGTATGGC TTCTCACCTG TCTACCAGGA
22501 TTCTCATTTC CTCTGTCCCC TTCCTGTCCT GCCCCCAGGA ATCTCAGGAT
22551 GCCTCCCCAT AGGCAATCTA TTTAATGTCA TCCCCCTTAT CTGCCCTCCC
Exon R3
22601 TAGGCCAGAG AAAGATGGGG AAGCCACCGG AGTGGATGCC ATCTGCACCC
22651 ACCGCCCTGA CCCCACAGGC CCTGGGCTGG ACAGAGAGCA GCTGTATTTG
22701 GAGCTGAGCC AGCTGACCCA CAGCATCACT GAGCTGGGCC CCTACACACT
22751 GGACAGGGAC AGTCTCTATG TCAATGGTGA GCGGCTGTGA TGTGGTTGGA
22801 GATTCTTCCT CTTTGCTGGA CAGCTTCTTA CTCTCTGACT TGAGGTCACA
22851 CTCCCTGACT GGCCATTGAC GTCTTGGCTA TGTTGTCTGT ATGTGATGAC
22901 TGATGTCTGA ACTTCATAGT TTCTTCATCT TGGACTGAGT TCATCCTCAG
22951 TACCTTCTTC CCTGATCTGA GGGTACTGAT AGAGAATCTT CAAAGGCCCC
23001 TGTTCCTTGA AACTTCTTCC ATTCCACTAG GGTATCTGTG ACCCCTATTT
23051 GATTCCCCAC CTCTCCCTTA ACCCTTACCC ACTCTCCTCC CTCCTTCTCT
Exon R4
23101 GTGCAGGTTT CACCCATCGG AGCTCTGTAC CCACCACCAG CAGTGAGTAT
23151 TCAACCGATG CTCCAGTAGC CCCAATTATA CACCAAGCAG GGCAGGAGCT
23201 GTCCTGTCTT CCTATGCCCC TATGTCCTCT TCATAAAGGA AGGGGCTGGG
23251 AGGGCACAAG TTATTCCCTT TCCCTTCTGG CCAGCTCCAG AGAGAGACCC
23301 AGCTCAGGCC CGATATGCAG CAAGGCCTGT AAATAGTTTT ATTTGCTGAC
23351 CTTTCTGCCA TGAGAGGCTT GGATGCTTCC CCTGAAGAGG GTTTCTCTGT
23401 AGCTCTTGGG ACTACCACAG TGGACCTGGG AAACTCTGGG GATCCACCCC
23451 TTCTACTGGT CCCTTGAATA AGTACCAGCC AATGGCACCT CTGTTAGAGC
23501 ATGGCTGATG AGTGTAAACA TCTCTTCCAT TATTCAGTCA AATAAAGATG
23551 GAAATTCTTT ATAAATCTAG TGATGATGAG CCAACCAACA AACTTTATTG
23601 AGCATTGTGA CAAGCCCTGG GGCTCTGCCA AATCCTGGGG ATATGGCATG
23651 GATCATGAAA CAATTAATAA TCTCTCCTCT CAGAGAGCTA TTTTTATGAT
23701 GATACTGATG GTGGCAATGA TGATGATGTT GATGGTGATT ATGACCATGA
23751 TGACAATGGT GATGGTGGTG GTGATGATGG TAATGATGAT GATGGTGATG
23801 TTGGTAATGA TGGTGGTGAT TATGACAATA ATGATGGTGA TGGTGACAGG
23851 GATGGTGATG ATTATGATGG TGGTGGTGAT AACAAAGTTA ATGGATAATA

TABLE 2-continued

Genomic Repeats (SEQ ID NO: 2)					
23901	TATGAACTTA	TTGGCTACTG	AATATGCACC	AAAGTGCTAT	GCTCAGTGTT
23951	TAACTAGTAC	TATTTAATAT	GATTTCTAAA	AAAAATCTTG	AATTATTATA
24001	GGCAGAAGAA	TCATGGGAAC	CTTTTATTTT	GTCACTCACT	TTAAGTCCTA
24051	TTGCATATTT	TTTAAGTCAA	TTGCAAACAC	AGTTTCTCTG	CTTTGAACAT
24101	TGTGTTTATA	TCCAGTCACC	CCAATAGTGC	ATAAACCTGC	TGATTGGAGC
24151	AACTGTGTCT	TACTCCCTTG	TGCTTCCCTA	GTATCTGCTT	CAGGACCTTG
24201	TACATGGTAG	ATCGACAGAT	TTAGATCTAC	AGGAAAATAT	GGATTTTCCC
24251	AGGGAAGGAA	GGAATGAAGT	ATGCTTTCTT	ATAATGTATG	GAAACTTTCC
24301	TCTTCTGCCT	TGGTTCAACT	TTAGTGTCTG	CCAGAGTTTA	CACTGGAAAA
24351	CTATATGGCA	TCTGCTCCAC	TCCCTCATCC	ATGACAGACA	TCATTAATTG
24401	ATTGCAGCAT	TCATGGCAGA	CATCACCAAT	TGATAATAGC	ATTCATTTTC
24451	TCTCAGTTCA	AAACAGCTTC	AGAATGGTTA	CCAAAAAAAA	AAAATTCAGT
24501	CGCTACCAAT	TCAATTGGAG	CTGACTCAGG	ATTATGGGAC	AGAATTCAAG
24551	AGAGTTAGGT	TCCTTGATGA	TGTGTAGTGG	CTATTTGTTT	TCCGGTCCAG
24601	GCTAATNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
24651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
24701	CTTTGTGCGG	CAAAGTTCAG	GGGCCCCAAA	AATTTCTGTG	CCCCAATCAT
24751	GGCGGACCTA	GGTTTAGGCA	CAAATTCCAG	GGATTAAGTC	CCTGGAGATG
24801	TTATGGCTTT	TGGTTTTCCT	AGAAAGGCTC	AGCTCAGGCT	CAGCTTGGTC
24851	ATGCTGATAT	CCTTTCTTCC	ACTTGGTCGA	TTTGGCTGTT	GATACTTATG
24901	TATGCTTCAC	GAAGTTTTTG	TGCTGTGTTT	TTCAGCTCCA	TCGGTTGGTT
24951	TATGTTCCTC	TCTAAACTGG	TTATTCTAGT	TAGCAATTCC	TTTAACCTTT
25001	CATCAAGGTG	CTTAGCTTTG	CATTGCATTA	GAACATGCTC	CTTTAGCTCA
25051	TCGTACTTTT	TTATTGCCCA	TCTTCTGAAG	CCTACTTCTG	TCAATTCATC
25101	CATCTGATCC	TCCATCCAGT	TCTGCACCCT	TAATGGAGAG	ATGTTGCGGT
25151	CATTTGGAGG	AAAAGAGGCA	CTCTGGCCTT	TTGGGTTTTC	AGCATTTTTT
25201	TGTTGATTAT	TTCCCATCTT	CAGGAGTTTT	AGTTTCAGGC	TTTGAGGCTG
25251	CTGATCCTTG	GATGGGGTTT	TTATGGGGGT	CTTTTGGTTG	TTGTTGTTGA
25301	TGATGATGAT	GTTATTGTCA	CTTTCTGCTT	GTTTTTCTTT	CAATAGTCAG
25351	GTCCCTCTTC	TGTAGGGCTG	CTGCAGTTTG	CTAGGGGTTC	ACTTCAGGCC
25401	CTATTCATCT	GATTCGCTCC	CATGTCTGGA	GGTGTCACTC	AAGGAGGCTT
25451	GGAGAGCAGC	GAACATAGGT	GCCTGCTTCT	TCTGGGACCT	CTGACCTCGA
25501	GGGACACCAA	CCTGATGCCA	GTAGGATCGC	TCCTGTGTAG	GGTGTCTGAC
25551	AACTATTGTT	GGAGGGTTTC	GCCCAGTTGA	CTGGCATGGA	GAGCAGGACC
25601	CATTTAATGA	AGCACTTTGT	CCCCTGGTGG	AGAGGGGGTT	CTTCACTGGG
25651	GGGAAACCAC	ATGTCTGGGC	TGCTTGGATT	CCTCAGAACT	ACCAGAGGAG
25701	AGGCTAAGTC	TGCTGGTCCA	CAGAGACTAC	AGCCATCCCT	CCCACTAGGG

TABLE 2-continued

Genomic Repeats (SEQ ID NO: 2)
25751 GCCCAAGCCC AGGGAGTCCA AATTCTGTCT CTGAGCCTCT GGCTGGAGTC
25801 TTTGGAGATC CTGCAAGGAA GCTCTGCCCA CTGAGGAAGG ATGGGTCAGG
25851 GTTAGCCCTG AAGAGGCACT CTGGCTGCAG ACTGCCACAG CCGGTGTGTT
25901 GGGCTGTGGG GACAAGTCTT GGGACCAAGC CGTCCAGCCT ACCCGGCTCT
25951 AGCAGGGGAA AAGTACAGCC TGGAGCTATT GAAAGGGGTG CCGCCCTTCC
26001 CCCGCCCAGG GAGCTTAGCG TGTTAGGCAG TTGTGAGTCC AGTGCTGGCT
26051 GTCGCCCCTT CCCCAAGGAA CAAAAAAGAC TTAGCAGGCA GCCGCAGCCA
26101 GTGCTGGTCG CCCCTCCCCC GGGGAGTTCC GTAGGCTTAG GCAGATTCCA
26151 GCTGTAAGAA TCTGCGTGTT CTGGGGTTGG GACACTAGGT CCCAGTGGCA
26201 TGGGTTCGCG AGTGAGATCT TCCAATCTGT GAGTTGCACA GTTCCGTGGA
26251 AAAAGCACAG TTTCCCCCTC TTGGGTAGCC CGCTCACTCA CCACCTCCCT
26301 TGGCTGGAAG GAGGGGGTTC CCCTTCCCCG TGTGTCTCTC AGGTGGGCCA
26351 CCACACCACA CTGCTCTTCC TTCTCTCTGT GGGTCACTGC CAGCCTTCTA
26401 GTCAATTTTG ATGAGGGAAC CTGGACATTT TGGTTGCCAG GAAGGATCAC
26451 ACACTTATTA CAGTTTTTTT CAATGTGAGC CTCTGAGCGC TGCTGCTTAT
26501 AGTCGACCAT CTTGGCCCCC AGAGTCACAC ATCTGTTATT TTTTGATGTT
26551 TTGATTGTGG CAATTCTTGC AGAAGTAAGG TGGTATCACC TTATGGTTTT
26601 GATTTCCCTG GTCATTAGTG ATGTTGAACA TTTTTTTCAT ATGTTCATTA
26651 GCCATTTGTA TATATTCTTT CAACAACTGT CTATTTATGT CCTTAGCCCA
26701 CTTTTTGATG GGATTGTTTT TTTCTTGCCA ATTTGTTTGA GTTCGTTGTA
26751 GATTCTAGAT ATTAGTCCTT TGTTGGATAT ATAGATTGTG AAGATTTTCT
26801 CCCACTCTGT GGGTTGTCTG TTTACTCTAC TGACTGTGAA GGAAAAGTCA
26851 ATTTCTTATA CGAATTTGTC TCACTCCTAC TTCCAAATGA GATCCTGGGG
26901 TTTTTTTTTT CTGTTAATCC TTCACAATAC TTCTCCCACT TTTTTGAACT
26951 CATTTGTTTA TATTCTGTTG TCTGCTTCTC TTTTATAGGA ATGTGACTTC
27001 TTATGGGCTT TCTCTATTAT ACCACATATG GGTTTTTGTT TTGTTTTGTT
27051 TTGTTTTGTT TTGTTTTTGT CCTCGGATCC ATTCTCCAAC CTCCTCCAGC
27101 CTTCCCGTGC TCTGTGGGAT AGACGTCTGA CTCATGAAAA CTACATTTCC
27151 CAGGCTCCCA TGCTAACTAG CTTCCTGTTA GGTTCAGCCA ATAGGAGGCA
27201 TTGGTGGGAC AATGGTGGGC GGGGCTATGG AAGGGCCAGA GTATTTCTGT
27251 ACCCCGCCCC CCTGCTCCCC TTCCAATGTT CCTGGAGCGG TGTAGGACCA
27301 ATACTGTATA TATGGAAGGA AGGCAAGGTG GATAGATTGG AAGGAAGAAG
27351 TGACAGATGG AAAGAAGAAG TGATAAATGG CAAGCGAGGC AAGGGAGCAG
27401 AGGATGGATG AGTGGATTGC AAGAAAGAAA AAAATGGATG AAATATAAAA
27451 GGAGCAGGAC AGATGGATAA GTAGATGGAA GTAAGAAAAG ACTGGTGTAA
27501 GAAAGGAACG ATTGATGATG GATGATGAAT GGATCAGTGG TGATTGGGTG

TABLE 2-continued

Genomic Repeats (SEQ ID NO: 2)					
27551	AAGGGATGAA	TGGATGGATG	GACAGATGGA	TGAACAGATG	GGTGGGTGGA
27601	TAGATGGATG	GATGGATAAA	ATGGGTAGGT	GGATGGATGG	ATGGATGGAC
27651	AGATGGGTGG	GTAGGTGGAT	GGATGGATAG	ATGGATGGAT	AAGTGAATGG
27701	ATGGATGGAT	GGATGGATGG	ATAAATGGAT	GGATGGGTGA	AAGGAAGGAA
27751	AGAAGTGAGA	GAAGGAAGAG	GAAGGATAGA	CAGATGTTAG	AAGGTACAAA
27801	TGAAAGGAAG	GAAGCCAGCA	AGAAAGAAAG	GATGCATTAA	TAGAATGAAA
27851	GATGGAAGGG	AAGAAGAAAG	GATGGAAAGA	GAGAAGGAAG	AATGAACAGA
27901	AGGAAGTTCA	AGAGTGGTGA	AAAGAAGAAA	GGCAGGGAGA	GAAGGAGAAG
27951	TAAACTTTTC	TTCTAGAGAT	TTGTCTTAAA	CCTTAGCTTG	GCTGGACACT
28001	GTGGTTCACG	CCTGTAATCC	CAGCACTTTG	GGAGGCCGAG	GCGGGTGGAT
28051	CATGAGGTCA	GGAGATCAAG	ACCATCCTGG	CTAACACGGT	GAAACCCTGT
28101	CTCTACTAAA	AATACAAAAA	AAATTTAGTC	AGGTGTGGTG	GTGCATGCCT
28151	GTGGTCCCAG	CTACTCAGGA	GGCTGAGGCA	GGAGAATGGC	ATAAAACCTG
28201	GGAGGCAGAG	CTTGCAGTGA	GCCAAGATCA	CACCACTGCA	CTCTAGCCTG
28251	GGCGACAAAG	TGAGACTCTG	TCTCAAACAA	AAACAAAACA	AAAAAACAAA
28301	AACAAAAAAC	AAAACCAAAC	CAAAACAAAA	AAAAAAACCT	TAACTCATAC
28351	TTTCATAAAG	TTCCACACAC	AGGGAGTGAT	TAGAAAGCAT	TTGCTGATAT
28401	ATTTTATATA	ATAAACATGT	ACACCATATT	GACCTGTGTG	CCCAGCAGTG
28451	CTTACATGAT	TTACAATGAT	TAACTTGTTT	AAGCTTCATA	ACAACGGTTG
28501	AGGCAGGAAA	CATCATTGTG	AACCATTGTC	ATCTCATTTT	ACAGATGAGT
28551	AAACTGAAGT	GCTGAGAGGT	TGGTTATGGC	TGCAAAGATT	GTTGGCCATG
28601	TTAACCAATG	CATAGAAGAT	TAGCATACCT	GGTTGTGAGT	GCAGGAGAGA
28651	GAGAGAAATG	GGAGAAAGGC	AGAGAAGGAT	CGATGGGGAG	AGAGGAAGAG
28701	AGAGAGAGAG	AATAAATTTT	TTAAAAATGT	CTAGAGTCAT	GACTTCCGCA
28751	TCAGTGTGGT	AATATGCAGC	CTTTACCCTG	GGAAAGATCA	GAACCATTGG
28801	TACTTTTTAC	AGAATCTTCC	CTTCCTGCAT	TTGGGTAGAA	GGACCCCATC
28851	TGGACATCCC	AAATCATTAA	GCACACCCTT	ACTGGCTGCT	GGAGTTGTCT
28901	CCATTAAAAG	TCACCGTTGG	GTTTATTAAG	AGGCGGACAC	AGGGTCCTTA
28951	GAACACACTG	CCCCCACCTG	TCCCACACCA	CCCCCCACCC	ACCCATCATC
Exon R1					
29001	CTCCCCAAGA	GCTTCATCTC	TCTCTCTCTT	CCCCCTGCCC	TAGCCGGGGT
29051	GGTCAGCGAG	GAGCCATTCA	CACTGAACTT	CACCATCAAC	AACCTGCGCT
29101	ACATGGCGGA	CATGGGCCAA	CCCGGCTCCC	TCAAGTTCAA	CATCACAGAC
29151	AACGTCATGC	AGCACCTGGT	GAGAGGCCTG	CCTCCCGCTG	CAGCCCTGCC
29201	ATGCCCATCC	TAGGGCTGTT	GCCTGCCTGC	CTCTGACCAA	CCCAAGCTCC

TABLE 2-continued

Genomic Repeats (SEQ ID NO: 2)
Exon R2
29251 CTTCTCCCTC TGCAGCTCAG TCCTTTGTTC CAGAGGAGCA GCCTGGGTGC
29301 ACGGTACACA GGCTGCAGGG TCATCGCACT AAGGTGAGAA ACTCCCCCAC
29351 CCACAGCGCA CCACCAAGAA CTTAGAGTTC TGACTGGGAG GTCCCTCTTG
29401 GGTTGGGGTG GGCTACATAT TTTTTTAAAT CTTTTTATCT TTCCTTTTTT
29451 TTTTTTTGAG ATGAAGTTTC GCTCTCGTTG CCCAGGCTAG AGTGCAATGG
29501 CACGATCTTG GCTCACTGCA ACCTCTGCCT CCCGGGTTCA AGTGATTATC
29551 CTGCCTCAGC CTCCCCAGTA GCTGGGATTA CAGGCAGGCA CCACCATGCC
29601 TGGCTAATTG TTTTGTATTT TTAGTAGAGA TGGGGTGTCT CCATGTTGAT
29651 CAGGCTGGTC TTGAACTCCT GACTTCAGGT GATCCACCCT CCTCAGCCTC
29701 CCAAAGTGCT GGGATTACAG GCGTGAGCCA CCATATCTGG CCCCATTCTT
29751 TTTTTTTAAA TGAATTTAAG GAGTGCAAAT GCAGTTTTTG TTACATGCAT
29801 ATATTCCATA GTGAAGTCTG CAGACAGTAG ACTTCCAGAC AGTAGCTTCT
29851 GGTGTATCAC CCGAATAGTG TACATTGTAC TTATTAAGTG AGGTTCCCCA
29901 CCCTTCTCCC ACTCTCCCAC CTTTCTGAGT ATCCAGTGTC TATTATTCCA
29951 CACTCCAGGT CCATGCTCTC ACGTATAAGT GAGAACGTAT GGTATTCCAC
30001 CATGAGCTAA TGGACATGGA GTCCATTGGC TCCCACTTAT AAGTGAGAGC
30051 ATGCGGTATT TGACTATTTC TGAGTTTCAC TTAAGATAAT GGACTCCCAT
30101 TCCATCCATG TTGCTGCAAA ATACATGATT TCACTCTTTT TATGGCTGAA
30151 TAGTATTTCG TGGTATATAT ATATACCACA TTTTCTTTAT CCAGTCTTCT
30201 ACTGATGGAC ACTTAGGTTG GGTCCATACC TTTGCTGTTG AAATAGTGCT
30251 GCAATAAACA TACACGTGCA GGTGTCTTTC TTATATAAAT GATTTCTTTT
30301 TTTCTTTCCT TTTTTTTGAT ATAACGAATT TCTTTTATTT GGGTTAAATC
30351 CCCCAATAGT GGGATTGNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
30401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
30451 TGACCTGTCC GTATTGATAT ATAAAATGCT GCATTTAAAG TGTACAACTT
30501 GATATTTTGG TATACATTGT TAAATCATGG CCACATTTCA GCTAATTAAT
30551 ATATCTATTA TCTCTACATA GTTATCATGT TTGTACCCTT TGACCAGCAT
30601 CACCCCATTT GCTCCTCCTC CCAGCCCCTG GCAACCACCA TCCTACTCTC
30651 TGCTTCTATG AGTCTGACAA TTTTAGATTC CACCTATAAG TTAGATTATG
30701 CGGTATTTGT CTTTCTGTGC CTGGCTTATT TCACTTAGCC TAATGTCCTC
30751 CAGCTCCATC TATGTTATCC CAAGTGGCAG GATTTTCATC TTTCTTATAT
30801 ATTTCATTGT ATATGTGTAT GCCACATTTT CTTTACCCAT TCATCCATTG
30851 AAGGTCATTT AGCTTGTTTC CATATCTTGG CTATTTTGAA TAGTGCTGCA
30901 ATGAACATAG GAGTGCAGAT ATCTCTTTAA GATACTGGTT TCATTTCTTT
30951 CTTTCTTCTC TTTTTTTTTT TTCTGAGACA GAGTCTGACT CTGTCGCTCA
31001 AGCTGGAGTA CAGTGGTGCA ATCTTGGCTC ACTGCAAACT CTGCCTCCTG

TABLE 2-continued

Genomic Repeats (SEQ ID NO: 2)
31051 AGTTCAAGCG ATTCTCGTGC CTCAACCTCC CAGGGAGTTT TGCTCTTGCT
31101 GCCCAGGCTG AAGTGCAGTG GTGCAATCTT CACTCACCAC AACCTGTGCC
31151 TCCCGGGTTC AAGCGATTCT CGTGCCTCAG CCTCCCAGGT AGCAAGGATT
31201 ACAGGCGCCC AACACCACAC CAGGCTAAAT TTTTTTGCAT TTTTAGTAGA
31251 GACGGGGTTT TGCCATGTTG GCCAGGCTGG TCTCAAATTC CTGGCCTCAA
31301 GTGATCCACC TGCCTCAGCC TCCTGAAGTG CTGGGATTTT ACAGGCATGA
31351 ACCACCACAC ATGGCCTCAT TTCTTTTAGA TATATATGGG TTGAGCTATT
31401 CTCAGAGGGT CCTTTTCTGC ATCTATTTAA GATCACATTT TTTTTATATT
31451 GTGGCAAAAA TACATGTAAC ATAAAATCTG CCATTTTAAC CATTTTTAAA
31501 TGTACAATTC AGTGACATTG ATTATATTCA CAATGTCATA CAGCCATCAC
31551 CACTATTTAT TTCTAATACT TTTCCATTGG GTAGATCCCC AACAGTGGGA
31601 TTGCTGGGTC AAATGGTAGT TCTGATTTTT TTTTTTTGTT TTTTGAGAAA
31651 TCTCCATACT GTTTTTCATT TGAGGTTGTA CTAATTTACA TTCCCACCAA
31701 CAGTGTATAA GAGTTTCCTA GGCCGGGCAT GGTGGCTTAT GCCTGTAATC
31751 CCAGCACTTT GCGAGGCCCA GGTGGGTGGA TCATGAGGTC AGGAGATCGA
31801 GACCACCCTG GCTAACATGG TGAAACCCCG TCTCTACTAA AAATGCAAAA
31851 AATTAGCCGG GCGTGGTGGC GGGTGCCTGT AGTCCCAGCT ACTGGAGAGG
31901 CTGAGGCAGG AGAATGGCAT GAACCCTGAA GGCGGGGCTT GCAGTGAGCT
31951 GAGATCGCAC CACTGCACAC TTCAACCTAG GCGACAGAGC GAGACTCCAT
32001 CTCAAAAAAA AAAAAAAAAA AAAAGGTTTC CTTTCAGTGC ATCCTTGCCA
32051 ACTTGAGTTT TCTGGGTTGG TTTGCACTCT CATGGTATTT ACTAGATACT
32101 TCTCCATTTA TATTTTTACT CAACCCATGC CCATAACACC ACTCCTCTAC
32151 CATTCCCACC AACCATGTAT AAGAGTTCCT TTTCTTGCAT CCTTGCCAAC
32201 TTGACTTCTT TGGGTCAGTT TGCACTCTCT TGGTATTTAC TATTTACTTC
32251 TCCATTTATA TTTTTAGTCA ACTGATGCCC ATGGCACCGC TCCTCTGAGG
32301 CAGGTGCTGG GTACTAGAGT GATAAGACAG ATGCTGTCCC TGCCCTCACC
32351 CAGTGGAGAA GAACAGATGC TAAACAGGAA CATAAATATC TAAGTAAAAT
32401 GGCTTCAAAT GGAGTAAAGT GATATGAAAC ATAAATAAAT AGCAAGTGAT
32451 GGGTAGAGCA ACTTTACCCA GGATGAATCT TGGGCTGTGT CCCAAATGGC
32501 CATGAAAACT GTTCCAGGCA GGGAGAACAG CATGAGAAAA GGTCTTGAGG
32551 TGCAAATGAG CTTGGCATGT TCTATGAACA GCAAAGAGGC CAGTGTGGCT
32601 GGAGCAGAGA GAGAGCAAGA AGAAAAGAGA GAAAGGATGA GACTCAAGAC
32651 ATCAGCAAGT TTGAAGGGCC TTGGAGGACT TGGATTTTTT TTTTTAAGAC
32701 AGCTTTGTTC TTGTTGCCCA GGCATGATCT CGGCTCACCA CAACCTCCGC
32751 CTCCTGGGTT CAAACGATTC CTCTGCCTCA GCCTCCCGAG TAGCTGGGGG
32801 TAACAGGCAT GTGCCCACCA CACCTGGCTA ATTTTGTATT TTTAGTAGAA

TABLE 2-continued

Genomic Repeats (SEQ ID NO: 2)					
32851	ATGGGGCTTC	TCCATGGTTG	GTCAGGCTGG	TCTCGAACTC	CCGACCTCAG
32901	GTGATCCGAC	CGCCTCGGCC	TCCCAAAGTG	CTGGGATTAT	AGGTGTGAGC
32951	CACTGCACCT	GGCTTGGATT	TTTTTTGTTC	TATATTGTGG	TAACATACAC
33001	ATCACATTAA	ATTGATCATT	TTAGCTATAT	TTCCCGTTCA	GTGGCATCAA
33051	GCACATTCAC	ATTATTGTGC	AACCATCACC	ACTATCATCC	ATCTCCAGAA
33101	CTTTCTCATC	TTCCCAAACT	GAAACTCCAT	CCCCATGAAA	CACTCATTCC
33151	TCATCCCCCT	CCTCAAGCCT	CTGGCACCCA	CCATTCTACT	TTCTGTCTCT
33201	GTGAATCTGA	TGATTCTGAG	GACCTCCTAT	GAATGGAGGA	ATCATATGGT
33251	ATATGTCCTG	GTTTATACTG	TATGGCTGGC	TTATTTCACC	AAGCATAATG
33301	TCCTCAAAGT	TCATCCATGT	TGTAGCATGT	GTCAGAATTC	CCTTCCTTTT
33351	CCACTTGTAT	GTAAATGCTG	TATTGTGTTT	CTCCATTCAT	TAGGACTTTG
33401	ATTTTTGCAG	GGAGTTGTCA	AGGGGTGCTG	GGTTCTGGGG	CTTCAATATA
33451	ATAAGAGTAA	GCTAAACTGG	TTCATTTCCT	CCTTCGTGGA	GACCATGTTC
33501	TGGTAGGAAC	AGGAACAAAT	AATTTATGAT	TACATAGAGG	GTGACCAGGG
33551	CAGTGACAGG	GGAAGAGTGG	AGGATTGTGG	GACCCAGAGG	AGGCTCCTGA
33601	CCTTGCCTAG	GAAGATAGGA	GGAGGAAGAG	GAGGAGGAAG	AGGAGGAGGA
33651	AGAGGAGGAG	GAGGAGGAGG	AGGGAGTCCT	CTAAGCTGAG	ACCTGGAGGA
33701	TGACCAGGAA	GTTATCCAGG	TAAGGAGAAA	TGGGGAGAAG	CTTCCAGACA
33751	AAAGTAACAG	CAATTGCAAA	GATCCTGAGA	TGATAGATAA	GGTCAGGTGG
33801	AGAAAGTGCA	AACTGTCAAT	GAGACCAAAA	TATGGACTGT	GAGTTGTGCA
33851	GTGACCACAA	GTGGAGAGGT	GCTAGGTGGC	CTTCATCCCC	CAAAGCTGCA
Exon R3					
33901	CCTCTCCCTC	CTCAGGTCTG	TGAAGAACGG	TGCTGAGACA	CGGGTGGACC
33951	TCCTCTGCAC	CTACCTGCAG	CCCCTCAGCG	GCCCAGGTCT	GCCTATCAAG
34001	CAGGTGTTCC	ATGAGCTGAG	CCAGCAGACC	CATGGCATCA	CCCGGCTGGG
34051	CCCCTACTCT	CTGGACAAAG	ACAGCCTCTA	CCTTAACGGT	GAGCAGCTAT
34101	CAGCCCCATC	TCCCTGCCCC	ACCCCCCAGC	CCCCACTGCA	GTCCAGGAGG
34151	GTGTCTGTTT	GCCGGTTCTC	TAGGGAAAGA	CTTGGGGTTC	AAGTCTTGGC
34201	ATTACCACTG	GCCCTCCCAT	AACCACAATG	CAAGGTTGGA	CTTTGATTAA
34251	TCCCATTTTA	CAGATGAAGA	AACTGAGGCT	TAGACAGGCT	AAGCAATTTA
34301	CCTTGACAGT	GGTGGAACCA	GGATATGAAC	TCCACTTGTC	AGCATTCGGT
34351	GCTATGATCC	ACTCCACATG	TTTAACTCAC	AGAAGAGTCT	TCCTGGTGGG
34401	GGCACTTGGG	GGACAAAAAA	CACATTTCCG	GCTGTGAGCA	GTGGCTCACA
34451	CCTGTAATCC	CAGCACTTTG	GGAGGCCAAG	GCGGGCGGAT	CACAAGGTCA
34501	AGAGATTGAG	ACCACCCTGG	ACAACATAGT	GAAACCCTGT	CTCTACTAAA
34551	AATACAAAAA	TTAGCTGGGT	GTGGTGGCGC	ACGCCTGTAG	TCCCACCTAC
34601	TCGGGAGGCT	GAGGCAGGAG	AATCGCTTGA	ACTCGGGAGG	CAGAGGTTGC

TABLE 2-continued

Genomic Repeats (SEQ ID NO: 2)
34651 AGTGAGCCAA GATTGCGCCA TTGCACTCCA GTCTGGGTGA CAAGAGTGAA
34701 ACTCTGTCTC AAAAAAAAAA AAAACAATTT CCCCTCCCTG CTTTCTTCTC
34751 ACCATTGACG AGGGATGGGC TTCTCTCCTA CCTGAGGCCC CCTATACCAG
34801 GAAGATCTAT GGGATCTAAT CTTCAGCGCA CACTGGGCCT CAGCATTGGT
34851 CTAGAACTCA GGATAAGATA GCATTTAAGA AGGCATCCCC TAAATGGGGT
34901 TCTGAGAGGC AAAGCATGAC CGTGGAGAAT TGACAAAATA GCTCGCCTTT
34951 CATCCCCTCC ACCGCCAACC CAAGAACAGT GCTTATCATC ATGACCCCAT
35001 GAGGTGGGCA CCCCATATCA CTTATATGAG GTACCTTTAG GTAGGTACCG
35051 GGATGTGGAG AGACATCCTG GGCTTTCATT ACTCTTATTT TAGCAAAGAG
35101 GGAATCTGAG GCACAGAGAA GGGAAGGGAC TTGCCCATGC CCACAGCGAG
35151 TTTTTGGCTA GTATGGGTCT TGATGTTCTT TCTGGGTCCG TNNNNNNNNN
35201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
35251 NNNNNNNNNT TCCTGCGTGG GAGATGTGTG GATTTGATTT GTATCTGGAA
35301 AGATGATTTT TTATTGGTGA CAAAGCAGTT AAAGTTAATC TTCACAGTTG
35351 TGCGGAGAGT GACCACGCGA GTTAGTCTTA TCCTTATTTT TTTGATCATC
35401 CCGCTACACA AGACAAAGCG AACCGCACAG GCAACATCAG CAGGCCCCAT
35451 TGGTGTGTTC CCCTCTATGG GTCCATGTGT TCTCATCATT AGCTCCCACG
35501 TATAAAGTGA GAAGATGGCA GTATTGGTTT TCTGTTCCTG CATTAGTTTG
35551 GTAAGGATAA TGACCTCCAG CTCCAACCAT GTTCCTGCAA CGGACATGAT
35601 CTCATTCTTT TTTATAGCTG CATAGTATTC CATGGTGTAT ATGTTCCTCA
35651 TGTTCTTTAT CCAGTCTATC CTTGATGGGC ATTTAAGTAG ATTCCATGTC
35701 TTTGCTATTG TGAATAGTGC TTCAGTGAAC AGGTGTCTTT ATGATAGAAA
35751 AATTTATATG CCTTTGGGCA TATATGCAGT GATGAGATTG CTGGGTCAGA
35801 CGGTAGTTCT GTTTTTAGCT CTTTGAGGAA TCATCCTGCT GCTTTCTACA
35851 GTGGATGAAC TAATTTACAC TCCCACCAAC AGTGTATAAA CACTCCTTTT
35901 TATCTGCAAC CTCAGCAGCA TGGTTTTATT TCTCTTTATG GCTGAATAGT
35951 GTTCCATTGT GCATATATAC CACACTTTCT TTATGGATTC ATCTGCTGAT
36001 GGACATATAG GTTGATTCCA CATCTCTGCT ATTGTGAATA GTGCTGTGAT
36051 AAACACACAG GTGCGGGTTG GGTCTTGATG ATCTCAGTTA ACATCCAGTC
36101 CCTTCAACTT GGCTATTGCA GGGAGCTGTT CCCCCTTGTA AACTGCACAG
36151 CTTATGTGCT TCATTTTGTT CCTTCATTTA GATTTACCAA GCAGCTACTA
36201 TTAACCAGGC CACAATGTGC CTCGCCCCCA GGAACAGAGA TAGGTTACAT
36251 GTGCATCCTG TCCTAATGTA ATCTCCAGGG GGGCGGAGAC TGTTTTGTTC
36301 TACCCTATAT TCCCCAAATG TAAAGGGAGC CTTGCACATA CTAAGCCCTT
36351 AATAAACATT CATTGGGTGG AGGAATAGAT TGGAGGAGGC CTGGAAGGGG
36401 AGGCGGGGGT TATGGATGGA TAGGAGGATA GACTTGTGAA CACAAAGGTA

TABLE 2-continued

Genomic Repeats (SEQ ID NO: 2)
36451 GTGAGAGCCT CTCATTGGAG GCATGCTGGA GACGTGAGTA GGGAAGGGTC
36501 AGTGCTAATT GAAATATCAG GAAATTCTTT CTAGTGGTGA ACACATTTAA
36551 GTCAAATATT AGATGATACA TAAATGTATC CATAATCTCT AGATACACAA
36601 AGGGAAAGGC ATCCAGGCAG GGGCCCCATA TGGACAAAGG CATGGAGTAT
36651 CTGGGACGGT TCCACCACCT CCTCTTACGT GTGACTTCTT TGTTTCAAGG
Exon R4
36701 TTACAATGAA CCTGGTCTAG ATGAGCCTCC TACAAGTACG TGTCTTTGAA
36751 TCTAGTGCCC ATTTCAATCT CCATGGGTCT TGGTTCAAGC TTTTCTCCTC
36801 ATTCATGAAG GAAGGTTGCC CCAAATTCGG GCTGGTCCCC TAGGTGGTGA
36851 GGGGCATTGT CTCAGTGGGA GGAAGAATGC TGAGTCCTTG GCCCTGTTTT
36901 TAGACCTGCA GCCATAGTCT TGGCTTTGTG AATTTTCCAT GTCCCTCTGG
36951 GTTGGAGGAA GAAGTTTGAA CAAGCATTCC CTACACGGGA TAGAGGTTGA
37001 GGTCAGATGA TGACCTCTGT TAGTCTGTAC CCTCCTTGAT AAGAAAATCT
37051 CCTCCAAGTG CCCCAGCAGA GGCTTCATGG TCAAGCTGCA GACTCTGCTG
37101 GCTACTGGTT TTGGCTAAAT TTGCCCATTG CCTCATCCAG TGATCCACTC
37151 GTCTATCTTT CCAGCCATCC ATTTTTCTAT CCTTCCAGTC ATCTCTCAGA
37201 CACCACCTGT CCTTCCATCC ATCCATCCGT CCATCCATTT ACCCATCCAT
37251 CCATCCACCC CATTTTCCTG ACCATTTACC TCCTCGTCCT TCCTTCCATC
37301 TGTCCTTTTA TCCATCTATT CATCCATCAC CCATCCTCCT GCCCATTCAC
37351 CTGCTTGTCC CTCCTTTCTT CTGTCCTTCT ATACATCCAT CCATCCATCC
37401 ATCCATCCAT CCACCCATCC ACTCATCCAC CACCCACCCA TCCTTCTGCC
37451 CACTCACTCG CTAGCCCCTC CTTCCTTCTG TCCTTCCATC CATCCATCCA
37501 CCCATCTTCC TGCCCATTCA CCTGCTTGTC CTTCCTTCTA TCTGTCTTTT
37551 ATCCATCTCT CCATCCATTC TCACCATCCA TCCATCCATC CTTCTCCCTA
37601 TTCACTGGTT TGTCTTTCCT TCTGTCCTTC CAACCATCCA CCCATCTCTC
37651 CATTCATTCT CCTCTTCATT CACCATGTTT CCTTATTTCT GTCTCTTCCA
37701 TCCATCCATC TATCCAGACA GACATCTCCT CCCCCCATTC TCCTCCCCAT
37751 TCACTCAATT GTCCTTCCTT CCATCTGTCC TTTTATCCAT CCATCCACCC
37801 ATCCATCCAT CCATCTATCC TTCTCCCCAT TCACCTGTTT GTCCTTCTTT
37851 CTGTCCTTCC AACCATCCAT CCATCCATCA TCCATCCATC TATCCTTTTC
37901 CCCATTCACC TGTTTTGTCC TTCCTTCTGT CCTTCCAACA TCCCTCCATC
37951 TCTCCATCCA TCCTCCTGCC TATTCATCTG CTTGTCTTTC CTTCCTTCTG
38001 TCCTTCCATC CATTCATCCA TCTGCCCATC CACCCACTCA TCCTCTTGCC
38051 CATTCACCTG CTTGTCCTTC CTTCCACCTG TCCTTTTATC CATCCATCCA
38101 TCCATCCATC TTGCTCACTC CTCCACTCAC ACAATCACTC CTTCCCTCAG
38151 TCTCATTTAT GGCCCACCTG TGAATGGTTG TCCTGGCTTG GACCACTGAT
38201 GAAGCCCAGG GGAGCTTCTC CCACTAGTGG TGGGCTTTTG TCCTCTCTGA

TABLE 2-continued

Genomic Repeats (SEQ ID NO: 2)
Exon R5
38251 TGGACTGTTC CTTCCACAGC TCCCAAGCCA GCCACCACAT TCCTGCCTCC
38301 TCTGTCAGAA GCCACAACAG GTATTTGGGG CCATTTTTCC TCCTCGAAGA
38351 TTAGAATAGC ATTTCAATCA GACACCTGCC CTCGTGGAGT CCCAGATTTT
38401 ATGAAATAAA TAGACCATCA TAATGTCAGA TGTTTTGGGG TGAGATACCT
38451 GGCATAGTTG GGAAGGAGGA GGGCTTTCTG GAGAAAGTTT CACCTGAACT
38501 GAGTCTTTAA GGATGACTAA GAGTGATTCA GGCAAATAGG GCATGAATAG
38551 TATAACTGAA AGAGGGGAAT CTGTGAGCAA AGCCTCAGTG GCCAGAAACA
38601 GCATAGAGTA TAGGGAGAAG TGAGAGAAAT TTGGTTTGCA TGAAACATAA
38651 AGCTTAACCC AGAGTGGATG GATAAGTGAG ACTGAAAGGT CAGCAGGAGC
38701 CAGATTGGGA AGGGCCTTGA ATGCCAAGTC AAGAAATTTG AACTTAACAC
38751 TGAAGGCCAT AGGGAGCTGT GGATGGTACT AGAGCAGGGG CAGCCATAGT
38801 GAGATTGTCA TTTCAGAAAG ATTCTTCTTG TGTTCAGTAT AGAGAATGTC
38851 CTTTAGACAG GGCATCCAGT GAGTCTGCCA GGTGCTAATC AGGGTGAGAG
38901 AAAATAAGAC CTGAACTGGG ATAGGGGGAG GAGAGAGAGG ATATATGTGA
38951 TGAATATTCA GTAAAGAGAA TTGGTGTTAC TTGGAGGGGA GAAGACACAT
39001 AGCTTCTGAC TTGCGATGGC CACACTCAGT TTAATAATGA GCGCAGTCTG
39051 ATCTAGTCTC AGACCAGCCC TCAGTTGCAG ACGTCTCTCC TCCCCTCCTG
Exon R1
39101 CAGCATGGGG TACCACCTGA AGACCCTCAC ACTCAACTTC ACCATCTCCA
39151 ATCTCCAGTA TTCACCAGAT ATGGGCAAGG GCTCAGCTAC ATTCAACTCC
39201 ACCGAGGGGG TCCTTCAGCA CCTGGTGAGA CCCTGGTCCC AGCAGCTCCT
39251 GGTGGGATAA ATCCTACCCC CAACCTCTGT TCCTCGGCTT ACCCTCTTCC
Exon R2
39301 TCCTTCCTCT CAAGCTCAGA CCCTTGTTCC AGAAGAGCAG CATGGGCCCC
39351 TTCTACTTGG GTTGCCAACT GATCTCCCTC AGGTGAGACC ACTTCCTGGC
39401 CATTTGCCAG TAACAACCAC CCCTTTTGTG ACCACCCCTT CCTCAGCTTT
39451 CCCCTGCTCC TCCCTCCACT GCTCTTTACC TGCAGAGGTC TCGGGACCTC
Exon R3
39501 TCTAGAGTCC TCAAATGCCT CTCTCCCCAG GCCTGAGAAG GATGGGGCAG
39551 CCACTGGTGT GGACACCACC TGCACCTACC ACCCTGACCC TGTGGGCCCC
39601 GGGCTGGACA TACAGCAGCT TTACTGGGAG CTGAGTCAGC TGACCCATGG
39651 TGTCACCCAA CTGGGCTTCT ATGTCCTGGA CAGGGATAGC CTCTTCATCA
39701 ATGGTGAGTG TCAGGCTGAA CTTGGATTTA CAGTGACTTT TGGGGAGTTG
39751 GTTTCTTTGT TTTTGAGATG GAGTCTCACT CTATCACCCA GGCTGGAGTG
39801 CAATGGTGCA ATCTTGGCTC TGCAACAGTG ATTCTCCTGC CTCAGCCTCC

TABLE 2-continued

Genomic Repeats (SEQ ID NO: 2)					
39851	CAAGTAGCTG	GGATTTACAG	GTGCATGCCA	CCACGCTCAG	CTAATTTTTG
39901	TATTTTTAGT	AGAGATGGGG	TTTCACCATG	TTGCCCAGGC	TGGTCTCGAA
39951	CTCCTGACCT	CAGGTGATCC	ACCTGCCTTG	GCCTCCCAAA	GTGCCAGGAT
40001	TACAGGCATG	AGCCACCATG	CCCGGCCCAC	CATGACTATT	ATTTGTCCCT
40051	GTTGTATGCC	CTTTCCTCTC	TAAAAAAAAT	AGCCCAAGGC	CTGGCTGGGG
40101	GACACCCTTC	CCCAAACCAC	CAAGGGGAGG	GTCTTTCCCA	TTATTTTGAG
40151	TAAATAGCAT	GAAATTCTTT	GACCAAATTA	ATGTCATAAA	TTGTTTGTCT
40201	CTTTCTCCTT	CACTTTTGTT	TCCAACTTGG	TTGCGGTATA	ACTATCAAAT
40251	ACAATTGTAT	GTATTTAAGA	TGTATAATGC	AGTGATTTAA	TATATGTGTA
40301	GCTTATGAAA	TGATTACCAT	GATCAAATTA	GTTAACACTG	CTTTCATGTC
40351	ACATAGTTAC	CGTGTGTCTG	TGTGCGTCTG	TGTGAGTTAG	AGAGAAAGAG
40401	AACATTTAAG	GTCTACCCTC	ATAGAAAATT	TCAGGTTTAC	AATACAGTAT
40451	TATTAACTAT	AATCATCAAG	CTTTATACTC	GATCCCCAGA	ACTTATTCAT
40501	CTTGTAACTA	AAAGTTTGTA	TTTTGTGACC	AACATCTCCC	CATTTTCTCT
40551	ATCACCACCC	CCATGCCCCC	AGCCCCTGAT	AACCATCATG	CTACTCTCTG
40601	CTTCTGTAAG	TTTGACTTCT	GATCCCACAT	ATAAGTGAGA	TCATGCAGTA
40651	TTTGTTTCTC	TCTATCTGGT	ATATTTCACT	TAGCATAATG	AACCCCCCCC
40701	AGGTACATCC	ATAATGAATT	TCAATTCAAA	ACCCAAGTGG	CTGAGTCGTG
40751	GCATCCTTTG	GGACAGGATA	GCAGGTCCCT	TCTATATAAG	GATCCTCTGT
40801	GTCAGTGGTT	ATTACCAGGG	GACAATTCTG	CACTTCTGCC	CCACCCCACC
40851	CCCCAACTGG	GAGACTCTAG	GCAATATCCG	AAATCATTTT	TGGGTATCAC
40901	AACTCAGGGA	GGGAAGGAGG	GTGCAACTGG	CACCTAGTGG	GTCGGTAGCC
40951	CATTTTCCAG	TGCACAGGAG	ACAACCACCC	CAGGGAATGA	TCCAGCCCCA
41001	AATGCCAATA	ATTTCAAGGG	TGAGAAATCC	TGTTGTACAT	GGTCTCAAAG
41051	TTCTTAGGTG	GGCACAAGGC	TGACATTTAT	CACACTTTAC	TGTAATTACT
41101	TGTTAAATTT	ATCTGATTCC	CCCTTACCCT	GTGAACTCAA	CAAAATTACG
41151	GTCTATTATG	AGTGCCACTG	TACCCTCGGT	TCGCAGTACA	TCAGCACATC
41201	ATAGTATGGA	AAGAATCATT	GAATGAGTGA	GCAAATTAAA	GATTTGTGTC
41251	TCTGCTGTAA	CTCACATTCA	TTAATTCATT	CATTCAGCAA	ACATATATGG
41301	GTGGCTGTTC	TGCCCCAAGC	CTTGTACTGG	GTCTGGAGAT	AGAAGACACA
41351	TTTTTCTGTC	TCTGAAAAAC	TCATACTCAA	GTTAACAACA	AATTACGGGC
41401	ACAACAAAGA	CCCCACTGCT	GTTATTAACA	GGGTACTATG	GGAGCTGAGA
41451	GGAGGAGTAA	ATTAAGGAGG	GCTTCCTGGA	GGAGGGTGTT	ATATACCCGG
41501	CCCTGTGCCG	GGACACATAA	TGATAAGACA	GACTTGGGCC	TCTGCTGTCC
41551	TGGAGCTCCC	TCTCACTGGG	CTCTTGAAGC	GTGAGCAGGA	GTTTTGCAGG
41601	AAATGAAAAG	GATGCATTCC	TAGAAGTGGG	AACTGCATAG	CACATGCAGG
41651	AAAGCTCAGC	TCAGAAGAAT	CTGTGTAATA	TTCCATTTTT	CCCTCTCTTT

TABLE 2-continued

Genomic Repeats (SEQ ID NO: 2)				
41701	GGGGCAACTT	TCTGTCTAAG	AGCTCCTGCA	ATGCCCAGCG	TGTGGACCTG
41751	AAATTGATTC	TGACAGTAGG	CAGGGGACTG	CTGGGCAACT	TTGGCTCTGC
41801	ATTTTGTGAT	CAACATTTCC	CCACCATATG	TTGCCTTTTC	TTCTTCTCTG
Exon R4					
41851	TGGCTCCAGG	CTATGCACCC	CAGAATTTAT	CAATCCGGGG	CGAGTACCAG
41901	ATAAATTTCC	ACATTGTCAA	CTGGAACCTC	AGTAATCCAG	ACCCCACATC
41951	CTCAGAGTAC	ATCACCCTGC	TGAGGGACAT	CCAGGACAAG	GTGGGGCATC
42001	TCTCACCCCT	CCCGTCTTCT	CTGTCCTGTG	TGCTTCTCTC	CCTCTTCTAC
42051	CTGATTTCTC	TGTTAAGTGA	TCACTTTAAA	TGCTTCACTT	CACTATGTAT
42101	TCTGGGTTCT	CTCTCAGTTT	CCAAAAGTAC	TCTCTTGACT	ACCATTCCCA
42151	TTTCACAGAT	GGGCAAACTG	AGGCTCAGAA	AGGGGCGTGG	TGTGCCTAGG
42201	GTCATACAGT	GCTTTAGGAA	CAGAGTTAGG	ATTTGAACTC	TGGTCCCCTT
42251	TGCTCCAAGT	CCTGTGTTTT	TTTCCACTGG	CATCAGCGGC	CCCTCCACCC
42301	CCAAGAGGCC	TCCATCTCAC	CCACTCTCCC	TACCCATCTT	TCTAGGTC

TABLE 3

Genomic Carboxy Terminal (SEQ ID NO: 3)					
Exon C1					
1	ACCACACTCT	ACAAAGGCAG	TCAACTACAT	GACACATTCC	GCTTCTGCCT
51	GGTCACCAAC	TTGACGTAAG	TTCTGAAGGT	CATAAGCAGT	GACCAAGCTT
101	GTGGCTGTGT	CTCTGAGCAC	CCTTGAGCTA	GACGTCCCCA	GTGGGGTACC
151	CATTCTCCCC	TACATCCCTG	TCTAGCTAAT	CCTACCATCT	CCTCCCATAA
201	ATCCTCAAGG	TAGGGAGTGA	GGATTAACCT	CATGGGGCCA	CCAACTCCCA
251	GCATACACCT	TCTTTTTTTT	CTGGACACTT	GGGAAAATAT	AACTTTTTGA
301	TGTAGAACTC	AAAATATTAG	CCCAATAATA	ATATTTAACA	TCAACCAGCC
351	TCCTCTCATT	TAATTCTCAC	AACAGAATCT	ATGAGTTGAG	TGCAAAAATC
401	ATCCCTATTG	TGCAGATGGG	AAAACTGAGG	GTCAGAAAAG	TGAACTTCCC
451	AAGAACTGTC	AAAGTTGGGA	TTTGAACCCA	GGTCTCTGAT	GACTGGATGA
501	AGGAATGAAG	ATACCTATAC	TTGGGAATGA	GGAGGGTCGA	CAGGACACGA
551	GGGCTGACTT	TGTATATTTC	TAAACTTCAA	AGATTTTCTG	TATTTCAGCT
601	GGGAATATGG	TAGAAGGTTA	ATTGGAACAA	AAAAATGCAA	AGCAATGAAT
651	AAGACCTCAG	TATTTGCTAT	GCACAACAGG	GTGACTGTAG	TCCCACAAAT
701	AACTTCACTG	TACATTGTTA	AAATATAACT	AAAGGTGTAT	GCTTGGATTG
751	TTTGCAACAC	AAAGGATATA	TGCTTGAGGG	GATGGATACC	CCATTTACCC
801	TGATGATTAT	TATGCATTAC	ATGCTTGTAT	CAAAACATCT	CATATACCCC

TABLE 3-continued

Genomic Carboxy Terminal (SEQ ID NO: 3)	
851	ATAAATATAA AAACACCTAC TATGTACCCC AAAAAATTAA AAACAAATAA
1051	AGGCATGGTG GCACACACCT GTAGTCCCAG CCACTCAGGA AGCTGAGGTG
1101	GGAGGATCGC CTGAGCCTAG GAGGCTGTAC TCCAGCCTGG GTGACAGAGC
1151	GAGACTCTAT CTCAAAAAAT AAAATAAAAT AATAAAAAGT AGAAATCAAG
1201	AGGGAAAATG TGGGAGAAAT TGGGATAATT TTAACAATAC CTTCCACCAG
1251	AGTGATGATG AAGAATGCAT AAGTCACTTC TTAGTGGTCT TGATCTATAA
1301	AAAGTGTTCA ATAAATATCG ATTATTGTTA CTGTTATTGC TTCTAGACGT
1351	AATTCCTGGA AGCATTTTTT TTTTTTTTTT TTTTGAGATG GAGTCATGCT
1401	CTGTTGCTCA GGCTGGAGTG CAGTGGTATG ATCTCGGCTC ACTACAACTG
1451	CCTCCTGGGT TCAAGCAATT CTCCTGCCTC AGCCCCCCAT GTAGCAGGGA
1501	CTACAGGCAT GCGCCACCAC ACCCGGTGAA GTTTTGTATT TTTATTAGAG
1551	ACAGGGTTTT GCCATGTTGG TCAGGCTGGT CTCGAACTCC TGACCTCAGG
1601	CAATTTGCCT GCCTCGGCCT CCCAAAGTGC TGAGATTACA GGCTTGGGCC
1651	ACTGCATCCA GCCGAAGGCC TCCCATTTTG ATCAGAACCC TTCTCTAGAC
1701	TGAGGGTGGG TGCCTCTAGA TCTTTTGCTC TTTAAAGACA GCAACCGATG
1751	ACCCTGCTGA TGCTGAGTAC TGGCTGAATT CCTGTGGTCT CTGTCCCTAG
Exon C2	
1801	GATGGACTCC GTGTTGGTCA CTGTCAAGGC ATTGTTCTCC TCCAATTTGG
1851	ACCCCAGCCT GGTGGAGCAA GTCTTTCTAG ATAAGACCCT GAATGCCTCA
1901	TTCCATTGGC TGGGCTCCAC CTACCAGTTG GTGGACATCC ATGTGACAGG
1951	TACAAGGTGG GGTGGCTGGT TTCCTAACTG GAAGAGGTGG GGTTATGAGG
2001	AAAGATGGGG CTTCTCGGTA CCAGTGGAAT TGGTGGAGGC TCTAGAGAGG
2051	GAAAGGGAGG CTTTCTGGAG ACCCATGTAG GTGACCTCTG GCAGTAGATC
2101	ATCCAACGAG GCAGGAACAG AACACCAGCC ATTGCATCTA AGAGAATAGC
2151	TATTTTTACA TGTAAAAAGA ATTGTGTTGA ATGAATGAAT CAATAGATCA
2201	TTTATTTTGA ATCAATTTAT TGATTCATTC ATTTAATTAA TGAATAATAA
2251	ATGATTCAGT ACATAATTGA TTAATTGATG TAATTGAGAA TTGATTTAAT
2301	TGATTAATTG ATCAATTAAA ATGATCAATT AAATGAATGA ATCAGTAAAT
2351	GAATAATTCA TTCATTCAAT AAACAATGGA AGTAGGCCGG GCATGGTGGC
2401	TCACGCCTGT AATACCAGTA CTTTGGGAGG CCCAGGCAGG CAGATCACGA
2451	GGTCAGGAGA TTGAGACCAT CCTGGCTAAC ACGGTGAAAC CCTGTCTCTA
2501	CTAAAAATAC AAAAAAAATT AGCCAGGCAT GGTGGTGGCC ACCTGTAGTC
2551	GCAGCTACTC GGGAGGCTGA GGCAGGAGAA TGGCGTGAAC CCGGGAGGCA
2601	GAGCTTGCAG TGAGCCGAGA TCGCGCCACT GCACTCCAGC CTGGGCGACA
2651	GATGGAGACT CTGTCTCAAA AATAAATAAA TAAATAAAAA TAAAAAATAA
2701	ATAAACAATG GAAGTAAACA CGTACTGATA ACACAGTGTG ATCATTGCTA
2751	TGATAAGGGA ATTTCAGGGG CCTGTGGGAG CCCCAAGGAG GAACACACAA

TABLE 3-continued

Genomic Carboxy Terminal (SEQ ID NO: 3)					
2801	CCTTGTCTTG	GAAAGTTTTA	TGTAGGAAGG	GGTGAAGAAG	CTGAGATCTG
2851	ACAGAGAATG	GGACCTAGCC	AGGGGTAATA	GATGGAGAAT	TGTGCTCCAT
2901	GCATCTATAA	CCTAGAAGAT	AGAAAGAATA	TGGCATCTGG	CCGGGTGCGG
2951	TGGCTCACGC	CTGTAGTCCC	AGCACTTTCA	GAGGCTGAGA	TGGGTGGATC
3001	ACCTGAGGTC	AGGAGTTCAA	GACCAGCCTG	ACCAATATGA	TGAAACCCCA
3051	TCTCTGCTAA	AAATACAAAA	ATTAGCCAGG	CATGGTGGTG	CGTGCCTGTA
3101	ATCCCAGCCA	CTTGGGAGGC	TGAGAGAGGA	GAACTGCTTG	AACTCGGGAG
3151	GCGGAGGTTG	CAGTGAGCCG	AGATTGTGCC	ATTGCACTCA	AGCCTGGGCA
3201	AAAAGAGCAA	AACTGCATTT	CAAAAAAAAA	AAAAGTGGCA	TTTTGGGGCA
3251	AGTTTAAGAA	GATTGGTGTA	GCTGGAGCAT	CCACTTTGAT	ACTGGAGAGG
3301	TGACAGTTGA	AGCCAAAGAT	GTGGGCAGAG	ACTTTGTTGG	GCACTGGAAT
3351	GGCTTGGGGA	GGAACATGAC	ACACTCATGA	GTTCTGCTTT	AGAAAGAAAA
3401	TGAAATGAAT	TCTGCTCATC	CTCTGGGTGC	TGTGTGCAGA	ATGGAGGGTG
3451	GGGGGAGAGA	AGAGCAAAGG	CAAGAAGACC	CTTTAGGAAC	AATGATCATT
3501	AGTTAGAAGA	CTCTGGGTTT	CTCAGCACCT	GCAATTGCTG	ACTACACCCC
3551	CAGAGAAACC	CAGTCTCTTT	TCCCCCATGT	TGTAGAGAAT	TCTTACAATG
3601	CTTGGTAGAA	AGAGAATTGA	ACAGGTAGAT	GGGTGGATGG	ATACAAGCTG
3651	GACAGATGGA	TGGAGGAAGA	TCCTCCATCC	AATATAGAGC	TGTTACCTAA
3701	AACCCTCCAT	CCCACCTTTA	AAATCCTAGC	TCAGCCAGGC	GCGGTGGCTC
3751	ACACCTGTAA	TCCCAGCACT	TTGGGAGGCC	AAGGCGGGTG	GATCACTTGA
3801	GGTCGGGGGT	TCGAGACCAG	TCTGACCAAC	ATGGTGAAAC	CCCCTTCTCC
3851	ACTAAAAATA	CAAAAAAAAA	AAAAAGTTAG	CCAGGCAGGG	TGGCGCATGC
3901	CTGTAATCCC	GCTACTCGGG	AGGCTGAGGC	AGGAGAATGG	CTTGCACCCA
3951	GGAGGTGGAG	GTTGTGGTGA	GCCAAGATCA	CGCCATTACA	CTCCAGCCTG
4001	GGCAAAGAGA	GTGAAACTGT	CTCAAAAAAC	AAAACAAATG	ACCCCCCTGC
4051	CAAAAAAAAA	AAAAAAAAAA	AAGAAAAGAA	AAAAAGAAAA	GCCTAGCTCA
4101	GCTCACACTG	TCAGGAATAA	GTAAGCTAGC	TGGAATCATC	TCTTTCTTAA
Exon C3					
4151	AACCCTGCCT	TGATAGTGGA	TTTTTACATA	CTTTTTTTTT	AATTCTAGAA
4201	ATGGAGTCAT	CAGTTTATCA	ACCAACAAGC	AGCTCCAGCA	CCCAGCACTT
4251	CTACCTGAAT	TTCACCATCA	CCAACCTACC	ATATTCCCAG	GACAAAGCCC
4301	AGCCAGGCAC	CACCAATTAC	CAGAGGAACA	AAAGGAATAT	TGAGGATGCG
4351	GTGAGAAGGG	GGTGGTATGT	CCACTCTGTT	GCCATGCAGA	AACTGACTTA
4401	TGCATACTGG	GTAGCCACAG	GGTGACTTTT	TATAACAATC	CACAAAGACA
4451	GGTTCTTATT	CCCATTTAAT	ACACAAGCAC	AGAGAGGTTC	AGTAGCTGAC
4501	CCAAGGTCAC	ACAGCTAAGT	CATACCCTAG	AAGAGCATGT	CCTTTGATAT

TABLE 3-continued

Genomic Carboxy Terminal (SEQ ID NO: 3)					
4551	ACATACCTGG	GCAAGTGGTT	GTCATGACAA	GAAGCAAAAT	AGACGGAGAA
4601	GTGTGCTCAG	TGGCTGAAAA	TTCTCTGATG	CTACTGGGGC	CAGGATTCTG
Exon C4					
4651	ACCTAAGAAA	CATCGCCCTG	TCTTTCAGCT	CAACCAACTC	TTCCGAAACA
4701	GCAGCATCAA	GAGTTATTTT	TCTGACTGTC	AAGTTTCAAC	ATTCAGGTAA
4751	GTTCTAACTC	AGGACCTAAT	GACTCTAGGA	ACTTCTGCTG	TCCTTTAAAT
4801	AGAAGTGTCC	CCAAGCCATA	GCTTTGATGG	AAGAGAGCCC	TAGAAATAGA
4851	GAGCTGTTAA	CTAAAAACTA	GCTTTTTCCT	AAAGCTGGAG	CCCAACTGGC
4901	TTCAACACTC	AAGAGAGCTG	GTGTAAATCT	CAGCAGACAT	AAAGGTACCT
4951	GGTGCTGAGG	CCATGGAGTC	TAGAGTGTAG	AATCTACTAC	ATTAAGACAT
5001	CAGCTACTGA	AATCAGGACC	CATGGAAGAC	GGGGGAAGGA	GGGGACTAAA
5051	ACCAGATTAC	TTAGAATCTA	GCAGCCTAAC	TGTGCTTTTC	AATGAGAGGT
5101	ATCATTTCCA	ATGGTGGGGG	GTACCAATGA	TTTTTTTTTT	TTGACAACTG
5151	CCTTGAGAAC	AGGCTTTCCT	CACTAAACAA	ATTCTGAATC	AGAACAAATA
5201	AAGATAAGCC	CTGAGAATAG	GGCTTTTTCA	AGGAGCTGCC	AAACAGATCA
5251	AATAGTGACT	ATGTTCTGCA	GATTGATGTC	TGGAGAACTC	TACAGCTATT
5301	TTGACTGCTA	GGCAGCTGGT	TTTCACAGAT	ATCATGATTC	TGAGGCTGCC
5351	AGTTTTCAAA	GTTACCGAGG	ATCTTGCTGG	ATGCAGTGGC	TTGCGACTGT
5401	AATCCCAGCC	CTTTGGGAGG	CCAAGGTGGG	TAGATCGCTT	GAGCTCAGGA
5451	GTTTGAGACC	AGCCTGGGCA	ATATGGTGAA	AACCCATCTC	TACAAAAAAT
5501	ACAAAAATCA	GCTGAGCATA	GTGGCATGTG	CTGTAGTCCC	AGTTACTTAG
5551	GAGGCTGAGG	TGGGAGGATG	GCTTGAGCCC	AGGAGGCAGA	GGTTGCAGTG
5601	AGCTGACATT	GTGCCATGCA	CTCTAGCCTG	GGCAACAGAG	CCAAAGCCTG
5651	TCTCAAAAAA	AAAAAAACAA	ATAATAATAA	TAATAAAATA	CTGAGGATCT
5701	TGAAAGAGCA	CTGTGGAAAT	AATGCAAGTT	AAAATGCCAC	AAAGCTTGCT
5751	CTTTTTACTG	AGATTTAACA	CTTTCCTTAA	CTAAACACCC	CTCGAATTTT
5801	TGCAAGCCTT	TGGTTCACTT	CTAGACTTCT	GGAAAAATTG	ATTTGGACTA
5851	TTTTGGCCAA	TGTTCTCATT	GATTTTATGG	GTATTCAGAA	GTTGTTACCC
5901	CAACATTCCA	GAAATGTTCT	CCCTGTGGCT	ATTACTTTAT	TTATTTATTT
5951	ATTTATTTAT	TTATTTATTT	ATTTGAGACG	GAGTCTCCCT	CTGTTGCCCA
6001	GGCTGGAGTG	CAGTGGCGCA	ATCTCAGCTC	ACTGCAACCT	CCGCTTCCCA
6051	GGTTCAAGCG	ATTCTCCTGC	CTCAGCCTCC	CAAGTAGCTG	GGATTATGGA
6101	TGTGCACCAC	CACACCGGCT	AATTTTTGTG	TTTTTAGTAG	AGATGGGGTT
6151	TCACTGTGTT	GGCCAGGCTG	GTCTCGAACT	CCTGATCTCA	AGTGATCCAC
6201	CCGCCTTGGC	CTCCCAAAGT	GCTGGGATAA	CAGGCATGAG	CCACTGTGCC
6251	TGACCTCCCT	GTGGCTATTT	TTAAATGAAT	TAAGTGGAAT	AAAATTAGAA
6301	ATTCAGTTCT	TCTCCCACGC	TAGCTGCATT	TTAAGCATTT	AATAACAACA

TABLE 3-continued

Genomic Carboxy Terminal (SEQ ID NO: 3)					
6351	TGAAGCTACT	AATGGCTGCA	TTGTGTAGTG	CAGATGTAGA	ATTTTTTTTT
6401	TGTTTTTTGT	TTTGTTTTTG	AGATGGAGTC	TCGCTCTGTC	ACCAGGCTAG
6451	AGTGCAGTGG	CGTGATCTCG	TCTCACTGCA	ATCTCTACTC	CCCGATTCAA
6501	GTGATTCTCC	TGCCTCAGCC	TCCCAAGTAG	CTGGGATTAC	AGGCACGTGC
6551	CACCACACCC	AGCTAATATT	TGTATGGATG	GTCTCAATCT	CCTGACCTCG
6601	TGATTTGTAT	GGATGGTCTC	GATCTGACCT	CATGATCCGC	CTGCCTGGGC
6651	CTCCCAAAGT	GCTGGGATTA	CAGGCGTGAG	CCACTGTGCC	CGGCCGACAT
6701	AGAATGTTTA	CATCATTGCA	GAAAGTTTCT	GCAGGAAGAG	CCTAGAAGGA
6751	GAAAGCCTAG	AATCATGATA	AAATTGCAGA	TATCTTTGCT	TATCCCTGTC
Exon C5					
6801	CCCTTCCAGG	TCTGTCCCCA	ACAGGCACCA	CACCGGGGTG	GACTCCCTGT
6851	GTAACTTCTC	GCCACTGGCT	CGGAGAGTAG	ACAGAGTTGC	CATCTATGAG
6901	GAATTTCTGC	GGATGACCCG	GAATGGTACC	CAGCTGCAGA	ACTTCACCCT
6951	GGACAGGAGC	AGTGTCCTTG	TGGATGGTAA	AGCTCCCTGG	GTCATTGGGA
7001	CTGAGGTGGA	AGCTCCCACT	TCCTCACCTG	GGTCCTTCCC	TGGGAATCTG
7051	AAGGCTTGGG	GTTGATTCGT	CATCGAGCTT	TCTCAGACTG	GGAGAAAGTG
7101	GCTTAGTTCT	CCTAAGCTTT	ACCCATCATT	GAAGGAAAGA	AAAGGACGCC
7151	CGAGGGATAT	GGGAGGCATT	TGCCCTCTTC	TGGCCAGCTC	TGTGACCTCA
7201	GGCTAGTCAC	ATCTCCTTTC	TGGACTTCTT	ATCTCTCTGT	ACTTAGCAAG
7251	CCACTTGGTT	TTTGGTTCCC	ATCTTGCCTG	CCCTAGATGG	TATTGCTCCT
7301	CCACCCCCAG	GCAGCTGCAG	TGTTAAACAA	TTACCCTGAT	TAGTTATTGT
7351	TGTTGTGTTG	TTTGTTTGTT	TTTGAGACAG	GGTCTCACTC	TGTCACCTAG
7401	GCTGGAGTGC	AGTGACATGA	TCTCAGCTCA	CTGCAACCTC	AACCCCTGGA
7451	CTCAAGCAAT	CCACCCACTT	CAGCCTCCCA	AGTAACTGGG	ACTACAGCCA
7501	TGCGCCACCA	CACCCGGATA	ATTTTTGTAT	TTTTTCTAGA	GATGGGGTTT
7551	TGCAACATTG	CCCAGGCTGG	TCTTGAACTC	CTGAGCTCAA	GCATGCCACC
7601	TGCTTCAGCC	TCCCAAAGTG	CTGGGATTAC	AGGCAGGCAG	GCACCACTGC
7651	AGCTGGTTCT	GGTTTTTTGT	GTTTGTTTTT	TTCTTTTAGA	GGCAGGGTCT
7701	CGCTCTGTTA	ACCAGAATGG	AGTACAGTGG	TGCAATCATA	GCTCACTGCA
7751	GTCTTGAACT	CCTGGGCTCA	AGCGATCCTC	CCACCTCAGC	CTCCTGAGTA
7801	CCTGGAACTA	CAGGCACGTG	TCACCACGCC	TTGCTAATTT	CTAAATTTTT
7851	TGTAGAGACA	GGGTCTCACT	ATGTTGCCCA	GACTGGTCTC	TAATTCCTGG
7901	CCACAAGTGA	TCCTCCTGCC	TCAGCAGGTC	AATGAGGGCT	TCCAGTTTCA
7951	AGTTGTATGT	GATTCATCCT	CAACAAATGT	GGTAGGATGG	ACCTATTTTC
8001	CAACTCCAGA	GATGGCTTCA	AGGTGGCTCA	ACTTTGCATA	TCCAATTTTA
8051	CCCATTCAAA	GAATAGTTAT	ATACATTGTA	CCATGTATCA	GGAATATAAC

TABLE 3-continued

Genomic Carboxy Terminal (SEQ ID NO: 3)					
8101	AGAGAGTAAC	TGTTTGCTCT	TTCACCACTA	TATTCCAAGA	ACCCCATATT
8151	CTGCCTGGCA	CATAATAAAC	ACTCAAGTCA	TATTTGCAGA	AGGAATAACT
8201	AGATTTCATA	CAAGGTTCTT	TTCAAGTCAA	ATGCGAATAA	CGTTTTAGAC
8251	GGGACCTTCC	AATGCCTGTG	TGCACTGTCC	TTGATTCCGA	ATTATTGTTG
8301	TGCAAGAGAG	CACTGTTGAT	CCTTCAGAAT	CAACAAGCCT	TTCACATGCC
8351	TGTCACAGGT	TTTTCTTTTT	CTTGTTTTAC	CAATTTTGTT	TGTTGTTTGT
8401	TTGTTGTTAT	TGTTTTGTTT	TGTTTTTGTT	TTTTATTTGT	TTTTATTTTT
8451	TCTTTTTTTT	TGAGACAGAG	TCTCGCTCTG	TCACCCAGGC	TGGAGTGCAG
8501	TGGCACGATC	TCCGCCCACT	GCAAGCTCCG	CCTCCTGGGT	TCATGCCATT
8551	TTCCTGCCTC	AGCCTCCTGA	GTAGCTGGGA	CTACAGGCGC	CTGCCACCAT
8601	GTCTGGCTAA	TTTTTTTTGT	ATTTTTAGTA	GAAACAGGGT	TTCACCATGT
8651	TGACCAGGAT	GGTCTCGATC	TCCTGACCTC	GTGATCTGCC	CACCTGGGCC
8701	TCCCAAAGTG	CTGGGATTAC	AGGCGTGAGC	CACCACACCC	AGCCCCAATT
8751	TTTTTTTTAA	TTAAAATTGT	TGTCAGCTCA	CAAGCTTTCT	AAAAACAGGC
8801	CATGGACCCA	GCATCGCTGT	AGTTTGCCAA	ACCCTTGCCT	TGAATCAGTA
8851	CCATCCAATA	GAACTTTCTG	CAGTGATAGA	AAATGTTTCT	ATCTGTGCTA
8901	TTCAGCACAA	AGCCATGTGT	GATTACTAAG	CTTGAAGTGT	GGTTAATGTA
8951	ACTGAGATAC	CGAAGTTTTA	ATTTTATTTA	ATTTTAATTT	AAAAAGCCAC
9001	TTGTGGCTGC	TCCATATTGC	ACACTACTTT	TTAAAATTAT	TATTTGTATA
9051	TATTTAAGGG	GCACAAGTAC	AATTTTGTTG	CATGGATTTA	TAGCCCAGTG
9101	GGGAAGTCTG	GGCTTTTAGG	GTATCTATTA	CCTGAATAAT	GTACATTGTA
9151	CCCATTGAGT	AATTTCTCAT	CATCCACTCT	CCTCCACTCC	CCAACCCTTC
9201	CAAGTTTCCA	CTGTCTATTA	TTCCACTCTC	TATGTCCATG	CCTATGCATT
9251	ATTTAGCATT	GACATGTCTA	TGCATTATTT	AGTCAAATAC	ATGTGCTATT
9301	TGACTTCCTG	TATCTGAGTT	GTTTGACTTA	AGATAATGAC	CTTCACTTGC
9351	ATCCATGTTG	CTGCAAAAGA	CATGATTTCA	TTCTTTTTTA	TGCCTGGGTG
9401	GTATTGCATT	GTGTGTGTGT	GTGTGTGTGT	GTGTGTAGAG	AGAGAGAGAG
9451	ATCACATTTT	CTTTATACAG	TCCTCCATTG	ATGGGCACTT	AGGTTGATTC
9501	CATATCTTTG	CTATTGTGAA	TAGTTTTGTG	ATAAACACAC	AGGTTCAGGT
9551	GTCTTTTTGA	CAAAATTATT	TATTTTCCTT	TGTGTAGATA	CCCAGTCGTG
9601	GGATTCCTGG	ATCAAATGGT	AGTTTCATTT	TTAGTTATTT	GAGAAATCTC
9651	CACGTTTTTC	ATAGAGATTA	TACTAAATTA	CATTCCCACC	AACAGTGTGT
9701	AACGGTTCAC	TTTTCTTGCA	TCCTTTTTAA	CATCTGTTAT	TTTTGTCTTT
9751	TTAGTAACAG	CCATTCTGAC	TGGCGTAAGG	TGGTATCTCA	TCATGGTTTT
9801	AATCTGTATT	TCTCTGATTA	TTAGTAATGT	CGAGCATTTT	TTCATATGCT
9851	TGTTAGCCAT	TGGTATGTCT	TCTACATCTT	TAAGAAGCTG	GCTATGGGCT
9901	GGGCGCAGTG	GCTCACACCT	GTAATCCCAG	CACTTTGGGA	GGCCGAGGCA

TABLE 3-continued

Genomic Carboxy Terminal (SEQ ID NO: 3)
9951 GGCGGATCAC GAGGTCAGGA GTTAAAAACC AGCCTGGCCA ACATGGTAAA
10001 ACCCTGCCTC TACTAAAAAT ACAAAAAATT ACCCAGGCAT GGTGGTGCGC
10051 CTGTAATCCC AGCTACTCAG GAAGCTGAGG CAGGAGAATC ACTTGAACCC
10101 AGGAGGCGGA GGTTGCAGTG AGACGAGATC ACATCATTGC ACTCCAGCCT
10151 GGGTGACAGA GTGAGACTCT ATCTTGAGAA AAAAAAAAAG TTGGCTATAA
10201 CAGGGTTGTA GAAGTAGAGG AACCAGTAAC CCTTCTCGCC ATGCCTGATG
10251 ATGGCTTTAC ATCCCTGTCT TCATGGAGTT TATGCTGTCG TGAGGAATAA
10301 CAAGAACAGG CAGTTGTCAA TTATAAATTA TTTGATGTGA ACCTATTCAT
10351 ACATGGGTGT GGTCATCAGG GAAGGCTTCC TGGAGGAAAT GACATTGAAG
10401 GTGAATTCTA AAAGATGACG ATAAACCACC AAGTGAAGGA GAGCTTAAAT
10451 GTGTTTTTAG GCAGAAGAAA AACCTTTTGG GTGAAAATTT TAAAACTTAG
10501 AGAGGTCCCA TCAGTTTCCA ACTGCGATGA TCCATTCTCT CCACCACTGC
10551 CCTTGGGCCC AGCCCAATTT AGGTCCACCA TGCCCAGAGG CATGAATTTA
10601 ACTTATGACA CTCTTGTGGT GGAATAATGG CTTTGGGCTT ATGTAGCCAT
10651 GTGTCATTTT TTTAGAGATA CAAATTGAAA TATTTGGGGT GAGATGTCAT
10701 GGTGTCTACT GGCCTCTAAA ACTTCAGTGA AAACATTTAC TTTCACTGAA
10751 ATGTCAATAA ATCATAAATT GGATGTATAT GTTTTAGTTG GAGGAAATAT
10801 AAACCACTAA ATCTAGGTGA TGCATATTTA TTATACTCTT CTCTCTGCTT
10851 TTTTGTACGC TTGTAAAATT GTATTTAAAA GAATAAGACA CACTTGGCCG
10901 GGCGCGGTGG CTCACGCCTG TAATCCCAGC ACTTTGGGAG ACCGAGGTGG
10951 GTGGATCATG AGGTCAGGAG TTCAAGACCA GCCTGGCCAA CATGGTAAAA
11001 CTCCATCACT ACATACAAAA ATTAGCCAGG CATTTTGGCG GGCACCTGTA
11051 ATCTCAGCTA CTTGGGAGGC TGAAGCAGGA GAATTGCTTG AACCCGGGAA
11101 GCAGAGGTTG CAGTGAGCCA AGATCACGCC ACTGCACTCT AGCCTGGGCA
11151 ACAGAGCAAG ACTCCATCTC CAGAAAAAAA AAAAAAAAAA GACACACTCA
Exon C6
11201 CATGCACCCT CCATTTCTTT CATTTCTAGG GTATTCTCCC AACAGAAATG
11251 AGCCCTTAAC TGGGAATTCT GGTAAGTCTC AAAGAAGCCC CAGCCCAGGG
11301 TAGGGAGGGG GTAGCCTGAT GGTGCTTTGC CTTGTCCAAG AGCACCAGGC
11351 ACACAGAGTC TTGGATGAGG ATCAAAATTG CCAACCCATG GCAAAGACTA
11401 TTGAGGCATA GTAAAGGGAT AGCAGGGATC CTGGCTTTCT GGGGGCCCAG
11451 TTTTTGGGGG CATCAGAGGC ATGAGGTGTT GAGCCACTAA GCTCTCTTCC
11501 CCAGGGGCTG TGCCCATCCT CAGGCCACAT AGGGTCCAAG AAGGAGCCCT
Exon C7
11551 GGGACGTGGC AGGAGGTGGC TCACCCCAGC CCTTGTCTCC CCAGACCTTC
11601 CCTTCTGGGC TGTCATCCTC ATCGGCTTGG CAGGACTCCT GGGAGTCATC

TABLE 3-continued

Genomic Carboxy Terminal (SEQ ID NO: 3)					
11651	ACATGCCTGA	TCTGCGGTGT	CCTGGTGAGC	AAGGAAGGGT	TGCTTGTCTT
11701	CTTAACAATT	GGGTTGTAAG	AGTTCTTAAT	ATATTATAAA	ACCATACTAT
11751	ACTATACACA	AGTCCTTTGC	TGGATATATG	TTTTGCAAAT	ATTTTCTCCC
11801	AGTTCACGGA	GTGGCTTTCC	TATTTTCTTT	TTATAATTTT	ATTTTTAATT
11851	AATTGACAAA	TAATGAATGC	ATATATTTAG	GGGATACAAT	GTGATGCTTT
11901	GGTATATGTA	CAATTATGGA	ATGACTCAAT	CAAGCTAATT	AATATGTCCC
11951	TCACCTCTCA	TACTTATTAT	TTCTTTGTGG	TGTGAACATT	GGCAACCTAT
12001	ACTCTTAGCA	ATTTTGAAAT	CTACATTATT	ATTAACTATA	GTTACTATGT
12051	TATGCAGATC	TCAAAAACTT	CACAACCTAT	ATGCTGATTA	CAAGATATTG
12101	AGAGAAAAAG	TGATTGCAAA	GAGTGTAAAT	AAAATAATGT	AAGAGGGAAA
12151	AATGTAACAA	AATTAGTCGT	TAGGGAAATG	TACACGGAAG	TCACAATGAG
12201	AGGCCACTTT	TCACAAGAAT	GGATAAAATT	GAAAAGATTG	ACTATAACAA
12251	GTGTTGGTGA	AAATGTGACA	GAACTGGAAC	TCTCATAAAG	TGAAAGTGGA
12301	AAATAGCTTG	GCCATTTCTT	TGAAAATTAC	ACACACCTAC	CGTAAGACCT
12351	ACCATCCCAC	TACTAGTAAT	TTATCTAAGA	GAAATAAAAA	CATATGTCTA
12401	TATGAAGACT	TGTACACAAG	TAAATGTTCA	TAACAGCTTT	GTTTGTAATA
12451	GCCAAACTCT	GAAAACAAGC	CCCTAATGTC	CATTAACAAA	TATATCCTGA
12501	CAATGGAATA	TTATTCAGCA	ACAAAAAGGA	ATTATTAATA	CATTAATAAA
12551	TTATACAGCA	ACATGTATAA	ATTGCAAAAT	AGTTATGCCT	AGTGAAAGAA
12601	TCCAGATGAA	GAAAAGAGTA	CATGCCATAT	GATTCCCTTA	ATAGACAAAT
12651	TCTAGAAAAT	ACAAACTAAT	CTGTAAGGAC	AGGAATCAGA	TCAGCGGTTG
12701	CCTGGGAATG	AAAATGTGTT	TGCAGTGGCA	GGGAAAAAGG	AATTGTAAAA
12751	GAGCAGGAAG	AAAGTTTTTT	TGTTGTTTTT	TTTTTGTTTT	TTCTTGAGAC
12801	AGAGTCTTAG	TCTATCGCCC	AAGCTGGAGT	GCAATGGCAC	GATCTCAGCT
12851	CATTGCAACC	TCTGCCTCTC	GGGTTCAAGC	GTTTTTCCTG	CCCCAGCCTC
12901	CCAAGTAGCT	GGGATTACAC	ATGCGCACCA	CCACACTCAG	CTAATTTTTG
12951	TATTTTTAGT	AGAGACGGGG	TTTTACCATG	TTGGCCAGGC	TGGTCTCGAA
13001	CTCCTGACCT	CAGGTGATCC	ACCCGCCTTG	GCCTCCCAAA	GTGCTGGGAT
13051	TACAGGAGTG	AGCCACCATG	CCTGGCCAGG	ACGAAAGTTT	TGGGGATGAT
13101	GGATGGATGT	TCCTTATGTT	GATTGTGGTG	ACGATTCAAT	AAGTTATGAT
13151	CAGAACTTAT	CAAAACATTC	ACTTTAAATG	TGTGCAGTTT	ATTTTATGTC
13201	AGTTATGCCT	CAGTTAAGCT	GGACAGATGT	AGAGGAGGAA	GGGAGGGAGA
13251	GAGGGGGCTG	AGATCAGGAC	CAAAAGCCAG	AGAGAAAGAG	ACTGAGAATG
13301	AGATGAGAGA	GAAATGGTAT	TTAGACAGAA	GACAGGCGAT	AGATGATTGA
13351	TAGTTGACAG	ATGATTGGTG	GATANNNNNN	NNNNNNNNNN	NNNNNNNNNN
13401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
13451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN

TABLE 3-continued

Genomic Carboxy Terminal (SEQ ID NO: 3)				
13501	AGGAGGTTTA	AACAAAACGC	AATTATGTTG	AAATGACAAT	GATTGTGGAT
13551	ATAAAGGTAG	ATAGAAATAG	ATATTTGTGA	AGATAATGGT	TAGATAAAAA
13601	TGATAGGTAA	CAGATATTGA	TAGATCTTGA	TAAGTAGATG	ATAAATACAT
13651	GATTGATGGA	TGACAGGTGA	TTGATAGATG	ATTTGATGGA	TTATAAATAG
13701	GAGATGATTG	AGAGGTGAGA	GATAATTGAT	GGTTATTTGA	TTGGTAGATA
13751	ATTGATTGAC	AGGTTGATAA	ATATTGATAG	CTAGATGATA	GATAAATAGA
13801	TCATTGGTAG	ATATGTGATA	TATTGATAAA	GAAATTCAGA	GGCAAAAGGA
13851	GAGAGAAATG	AAGGGGATAT	CGGAGGGGGA	AAAATTTTTT	TAAACCGAGA
13901	GTGAAACAAG	GAGACAGAAG	AAAAGAAAGT	GGTGAAAAGA	GGAAAAGAAC
13951	TGAGGGAGAA	ATTAAATGAA	ACAATGAAGG	GAGACAGAGG	AAGCATAAGG
Exon C8					
14001	CCTCTGGCTT	TGGCCATATT	CTCACCCCTG	TGGTCTCCTC	TCCCTGGACG
14051	GCTGACCAGT	CCATTCTCAC	GCCTCCTCCT	CACCCTCATA	GGTGACCACC
14101	CGCCGGCGGA	AGAAGGAAGG	AGAATACAAC	GTCCAGCAAC	AGTGCCCAGG
14151	CTACTACCAG	TCACACCTAG	ACCTGGAGGA	TCTGCAATGA	CTGGAACTTG
14201	CCGGTGCCTG	GGGTGCCTTT	CCCCCAGCCA	GGGTCCAAAG	AAGCTTGGCT
14251	GGGGCAGAAA	TAAACCATAT	TGGTCGG		

TABLE 4

Human cDNA of CA125 (SEQ ID NO: 4)					
1	AAGCGTTGCA	CAATTCCCCC	AACCTCCATA	CATACGGCAG	CTCTTCTAGA
51	CACAGGTTTT	CCCAGGTCAA	ATGCGGGGAC	CCCAGCCATA	TCTCCCACCC
101	TGAGAAATTT	TGGAGTTTCA	GGGAGCTCAG	AAGCTCTGCA	GAGGCCACCC
151	TCTCTGAGGG	GATTCTTCTT	AGACCTCCAT	CCAGAGGCAA	ATGTTGACCT
201	GTCCATGCTG	AAACCCTCAG	GCCTTCCTGG	GTCATCTTCT	CCCACCCGCT
251	CCTTGATGAC	AGGGAGCAGG	AGCACTAAAG	CCACACCAGA	AATGGATTCA
301	GGACTGACAG	GAGCCACCTT	GTCACCTAAG	ACATCTACAG	GTGCAATCGT
351	GGTGACAGAA	CATACTCTGC	CCTTTACTTC	CCCAGATAAG	ACCTTGGCCA
401	GTCCTACATC	TTCGGTTGTG	GGAAGAACCA	CCCAGTCTTT	GGGGGTGATG
451	TCCTCTGCTC	TCCCTGAGTC	AACCTCTAGA	GGAATGACAC	ACTCCGAGCA
501	AAGAACCAGC	CCATCGCTGA	GTCCCCAGGT	CAATGGAACT	CCCTCTAGGA
551	ACTACCCTGC	TACAAGCATG	GTTTCAGGAT	TGAGTTCCCC	AAGGACCAGG
601	ACCAGTTCCA	CAGAAGGAAA	TTTTACCAAA	GAAGCATCTA	CATACACACT
651	CACTGTAGAG	ACCACAAGTG	GCCCAGTCAC	TGAGAAGTAC	ACAGTCCCCA
701	CTGAGACCTC	AACAACTGAA	GGTGACAGCA	CAGAGACCCC	CTGGGACACA

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)	
751	AGATATATTC CTGTAAAAAT CACATCTCCA ATGAAAACAT TTGCAGATTC
801	AACTGCATCC AAGGAAAATG CCCCAGTGTC TATGACTCCA GCTGAGACCA
851	CAGTTACTGA CTCACATACT CCAGGAAGGA CAAACCCATC ATTTGGGACA
901	CTTTATTCTT CCTTCCTTGA CCTATCACCT AAAGGGACCC CAAATTCCAG
951	AGGTGAAACA AGCCTGGAAC TGATTCTATC AACCACTGGA TATCCCTTCT
1001	CCTCTCCTGA ACCTGGCTCT GCAGGACACA GCAGAATAAG TACCAGTGCG
1051	CCTTTGTCAT CATCTGCTTC AGTTCTCGAT AATAAAATAT CAGAGACCAG
1101	CATATTCTCA GGCCAGAGTC TCACCTCCCC TCTGTCTCCT GGGGTGCCCG
1151	AGGCCAGAGC CAGCACAATG CCCAACTCAG CTATCCCTTT TTCCATGACA
1201	CTAAGCAATG CAGAAACAAG TGCCGAAAGG GTCAGAAGCA CAATTTCCTC
1251	TCTGGGGACT CCATCAATAT CCACAAAGCA GACAGCAGAG ACTATCCTTA
1301	CCTTCCATGC CTTCGCTGAG ACCATGGATA TACCCAGCAC CCACATAGCC
1351	AAGACTTTGG CTTCAGAATG GTTGGGAAGT CCAGGTACCC TTGGTGGCAC
1401	CAGCACTTCA GCGCTGACAA CCACATCTCC ATCTACCACT TTAGTCTCAG
1451	AGGAGACCAA CACCCATCAC TCCACGAGTG GAAAGGAAAC AGAAGGAACT
1501	TTGAATACAT CTATGACTCC ACTTGAGACC TCTGCTCCTG GAGAAGAGTC
1551	CGAAATGACT GCCACCTTGG TCCCCACTCT AGGTTTTACA ACTCTTGACA
1601	GCAAGATCAG AAGTCCATCT CAGGTCTCTT CATCCCACCC AACAAGAGAG
1651	CTCAGAACCA CAGGCAGCAC CTCTGGGAGG CAGAGTTCCA GCACAGCTGC
1701	CCACGGGAGC TCTGACATCC TGAGGGCAAC CACTTCCAGC ACCTCAAAAG
1751	CATCATCATG GACCAGTGAA AGCACAGCTC AGCAATTTAG TGAACCCCAG
1801	CACACACAGT GGGTGGAGAC AAGTCCTAGC ATGAAAACAG AGAGACCCCC
1851	AGCATCAACC AGTGTGGCAG CCCCTATCAC CACTTCTGTT CCCTCAGTGG
1901	TCTCTGGCTT CACCACCCTG AAGACCAGCT CCACAAAAGG GATTTGGCTT
1951	GAAGAAACAT CTGCAGACAC ACTCATCGGA GAATCCACAG CTGGCCCAAC
2001	CACCCATCAG TTTGCTGTTC CCACTGGGAT TTCAATGACA GGAGGCAGCA
2051	GCACCAGGGG AAGCCAGGGC ACAACCCACC TACTCACCAG AGCCACAGCA
2101	TCATCTGAGA CATCCGCAGA TTTGACTCTG GCCACGAACG GTGTCCCAGT
2151	CTCCGTGTCT CCAGCAGTGA GCAAGACGGC TGCTGGCTCA AGTCCTCCAG
2201	GAGGGACAAA GCCATCATAT ACAATGGTTT CTTCTGTCAT CCCTGAGACA
2251	TCATCTCTAC AGTCCTCAGC TTTCAGGGAA GGAACCAGCC TGGGACTGAC
2301	TCCATTAAAC ACTAGACATC CCTTCTCTTC CCCTGAACCA GACTCTGCAG
2351	GACACACCAA GATAAGCACC AGCATTCCTC TGTTGTCATC TGCTTCAGTT
2401	CTTGAGGATA AAGTGTCAGC GACCAGCACA TTCTCACACC ACAAAGCCAC
2451	CTCATCTATT ACCACAGGGA CTCCTGAAAT CTCAACAAAG ACAAAGCCCA
2501	GCTCAGCCGT TCTTTCCTCC ATGACCCTAA GCAATGCAGC AACAAGTCCT
2551	GAAAGAGTCA GAAATGCAAC TTCCCCTCTG ACTCATCCAT CTCCATCAGG

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)
2601 GGAAGAGACA GCAGGGAGTG TCCTCACTCT CAGCACCTCT GCTGAGACTA
2651 CAGACTCACC TAACATCCAC CCAACTGGGA CACTGACTTC AGAATCGTCA
2701 GAGAGTCCTA GCACTCTCAG CCTCCCAAGT GTCTCTGGAG TCAAAACCAC
2751 ATTTTCTTCA TCTACTCCTT CCACTCATCT ATTTACTAGT GGAGAAGAAA
2801 CAGAGGAAAC TTCGAATCCA TCTGTGTCTC AACCTGAGAC TTCTGTTTCC
2851 AGAGTAAGGA CCACCTTGGC CAGCACCTCT GTCCCTACCC CAGTATTCCC
2901 CACCATGGAC ACCTGGCCTA CACGTTCAGC TCAGTTCTCT TCATCCCACC
2951 TAGTGAGTGA GCTCAGAGCT ACGAGCAGTA CCTCAGTTAC AAACTCAACT
3001 GGTTCAGCTC TTCCTAAAAT ATCTCACCTC ACTGGGACGG CAACAATGTC
3051 ACAGACCAAT AGAGACACGT TTAATGACTC TGCTGCACCC CAAAGCACAA
3101 CTTGGCCAGA GACTAGTCCC AGATTCAAGA CAGGGTTACC TTCAGCAACA
3151 ACCACTGTTT CAACCTCTGC CACTTCTCTC TCTGCTACTG TAATGGTCTC
3201 TAAATTCACT TCTCCAGCAA CTAGTTCCAT GGAAGCAACT TCTATCAGGG
3251 AACCATCAAC AACCATCCTC ACAACAGAGA CCACGAATGG CCCAGGCTCT
3301 ATGGCTGTGG CTTCTACCAA CATCCCAATT GGAAAGGGCT ACATTACTGA
3351 AGGAAGATTG GACACAAGCC ATCTGCCCAT TGGAACCACA GCTTCCTCTG
3401 AGACATCTAT GGATTTTACC ATGGCCAAAG AAAGTGTCTC AATGTCAGTA
3451 TCTCCATCTC AGTCCATGGA TGCTGCTGGC TCAAGCACTC CAGGAAGGAC
3501 AAGCCAATTC GTTGACACAT TTTCTGATGA TGTCTATCAT TTAACATCCA
3551 GAGAAATTAC AATACCTAGA GATGGAACAA GCTCAGCTCT GACTCCACAA
3601 ATGACTGCAA CTCACCCTCC ATCTCCTGAT CCTGGCTCTG CTAGAAGCAC
3651 CTGGCTTGGC ATCTTGTCCT CATCTCCTTC TTCTCCTACT CCCAAAGTCA
3701 CAATGAGCTC CACATTTTCA ACTCAGAGAG TCACCACAAG CATGATAATG
3751 GACACAGTTG AAACTAGTCG GTGGAACATG CCCAACTTAC CTTCCACGAC
3801 TTCCCTGACA CCAAGTAATA TTCCAACAAG TGGTGCCATA GGAAAAAGCA
3851 CCCTGGTTCC CTTGGACACT CCATCTCCAG CCACATCATT GGAGGCATCA
3901 GAAGGGGGAC TTCCAACCCT CAGCACCTAC CCTGAATCAA CAAACACACC
3951 CAGCATCCAC CTCGGAGCAC ACGCTAGTTC AGAAAGTCCA AGCACCATCA
4001 AACTTACCAT GGCTTCAGTA GTAAAACCTG GCTCTTACAC ACCTCTCACC
4051 TTCCCCTCAA TAGAGACCCA CATTCATGTA TCAACAGCCA GAATGGCTTA
4101 CTCTTCTGGG TCTTCACCTG AGATGACAGC TCCTGGAGAG ACTAACACTG
4151 GTAGTACCTG GGACCCCACC ACCTACATCA CCACTACGGA TCCTAAGGAT
4201 ACAAGTTCAG CTCAGGTCTC TACACCCCAC TCAGTGAGGA CACTCAGAAC
4251 CACAGAAAAC CATCCAAAGA CAGAGTCCGC CACCCCAGCT GCTTACTCTG
4301 GAAGTCCTAA AATCTCAAGT TCACCCAATC TCACCAGTCC GGCCACAAAA
4351 GCATGGACCA TCACAGACAC AACTGAACAC TCCACTCAAT TACATTACAC

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)					
4401	AAAATTGGCA	GAAAAATCAT	CTGGATTTGA	GACACAGTCA	GCTCCAGGAC
4451	CTGTCTCTGT	AGTAATCCCT	ACCTCCCCTA	CCATTGGAAG	CAGCACATTG
4501	GAACTAACTT	CTGATGTCCC	AGGGGAACCC	CTGGTCCTTG	CTCCCAGTGA
4551	GCAGACCACA	ATCACTCTCC	CCATGGCAAC	ATGGCTGAGT	ACCAGTTTGA
4601	CAGAGGAAAT	GGCTTCAACA	GACCTTGATA	TTTCAAGTCC	AAGTTCACCC
4651	ATGAGTACAT	TTGCTATTTT	TCCACCTATG	TCCACACCTT	CTCATGAACT
4701	TTCAAAGTCA	GAGGCAGATA	CCAGTGCCAT	TAGAAATACA	GATTCAACAA
4751	CGTTGGATCA	GCACCTAGGA	ATCAGGAGTT	TGGGCAGAAC	TGGGGACTTA
4801	ACAACTGTTC	CTATCACCCC	ACTGACAACC	ACGTGGACCA	GTGTGATTGA
4851	ACACTCAACA	CAAGCACAGG	ACACCCTTTC	TGCAACGATG	AGTCCTACTC
4901	ACGTGACACA	GTCACTCAAA	GATCAAACAT	CTATACCAGC	CTCAGCATCC
4951	CCTTCCCATC	TTACTGAAGT	CTACCCTGAG	CTCGGGACAC	AAGGGAGAAG
5001	CTCCTCTGAG	GCAACCACTT	TTTGGAAACC	ATCTACAGAC	ACACTGTCCA
5051	GAGAGATTGA	GACTGGCCCA	ACAAACATTC	AATCCACTCC	ACCCATGGAC
5101	AACACAACAA	CAGGGAGCAG	TAGTAGTGGA	GTCACCCTGG	GCATAGCCCA
5151	CCTTCCCATA	GGAACATCCT	CCCCAGCTGA	GACATCCACA	AACATGGCAC
5201	TGGAAAGAAG	AAGTTCTACA	GCCACTGTCT	CTATGGCTGG	GACAATGGGA
5251	CTCCTTGTTA	CTAGTGCTCC	AGGAAGAAGC	ATCAGCCAGT	CATTAGGAAG
5301	AGTTTCCTCT	GTCCTTTCTG	AGTCAACTAC	TGAAGGAGTC	ACAGATTCTA
5351	GTAAGGGAAG	CAGCCCAAGG	CTGAACACAC	AGGGAAATAC	AGCTCTCTCC
5401	TCCTCTCTTG	AACCCAGCTA	TGCTGAAGGA	AGCCAGATGA	GCACAAGCAT
5451	CCCTCTAACC	TCATCTCCTA	CAACTCCTGA	TGTGGAATTC	ATAGGGGGCA
5501	GCACATTTTG	GACCAAGGAG	GTCACCACAG	TTATGACCTC	AGACATCTCC
5551	AAGTCTTCAG	CAAGGACAGA	GTCCAGCTCA	GCTACCCTTA	TGTCCACAGC
5601	TTTGGGAAGC	ACTGAAAATA	CAGGAAAAGA	AAAACTCAGA	ACTGCCTCTA
5651	TGGATCTTCC	ATCTCCAACT	CCATCAATGG	AGGTGACACC	ATGGATTTCT
5701	CTCACTCTCA	GTAATGCCCC	CAATACCACA	GATTCACTTG	ACCTCAGCCA
5751	TGGGGTGCAC	ACCAGCTCTG	CAGGGACTTT	GGCCACTGAC	AGGTCATTGA
5801	ATACTGGTGT	CACTAGAGCC	TCCAGATTGG	AAAACGGCTC	TGATACCTCT
5851	TCTAAGTCCC	TGTCTATGGG	AAACAGCACT	CACACTTCCA	TGACTGACAC
5901	AGAGAAGAGT	GAAGTGTCTT	CTTCAATCCA	TCCCCGACCT	GAGACCTCAG
5951	CTCCTGGAGC	AGAGACCACT	TTGACTTCCA	CTCCTGGAAA	CAGGGCCATA
6001	AGCTTAACAT	TGCCTTTTTC	ATCCATTCCA	GTGGAAGAAG	TCATTTCTAC
6051	AGGCATAACC	TCAGGACCAG	ACATCAACTC	AGCACCCATG	ACACATTCTC
6101	CCATCACCCC	ACCAACAATT	GTATGGACCA	GTACAGGCAC	AATTGAACAG
6151	TCCACTCAAC	CACTACATGC	AGTTTCTTCA	GAAAAAGTTT	CTGTGCAGAC
6201	ACAGTCAACT	CCATATGTCA	ACTCTGTGGC	AGTGTCTGCT	TCCCCTACCC

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)
6251 ATGAGAATTC AGTCTCTTCT GGAAGCAGCA CATCCTCTCC ATATTCCTCA
6301 GCCTCACTTG AATCCTTGGA TTCCACAATC AGTAGGAGGA ATGCAATCAC
6351 TTCCTGGCTA TGGGACCTCA CTACATCTCT CCCCACTACA ACTTGGCCAA
6401 GTACTAGTTT ATCTGAGGCA CTGTCCTCAG GCCATTCTGG GGTTTCAAAC
6451 CCAAGTTCAA CTACGACTGA ATTTCCACTC TTTTCAGCTG CATCCACATC
6501 TGCTGCTAAG CAAAGAAATC CAGAAACAGA GACCCATGGT CCCCAGAATA
6551 CAGCCGCGAG TACTTTGAAC ACTGATGCAT CCTCGGTCAC AGGTCTTTCT
6601 GAGACTCCTG TGGGGGCAAG TATCAGCTCT GAAGTCCCTC TTCCAATGGC
6651 CATAACTTCT AGATCAGATG TTTCTGGCCT TACATCTGAG AGTACTGCTA
6701 ACCCGAGTTT AGGCACAGCC TCTTCAGCAG GGACCAAATT AACTAGGACA
6751 ATATCCCTGC CCACTTCAGA GTCTTTGGTT TCCTTTAGAA TGAACAAGGA
6801 TCCATGGACA GTGTCAATCC CTTTGGGGTC CCATCCAACT ACTAATACAG
6851 AAACAAGCAT CCCAGTAAAC AGCGCAGGTC CACCTGGCTT GTCCACAGTA
6901 GCATCAGATG TAATTGACAC ACCTTCAGAT GGGGCTGAGA GTATTCCCAC
6951 TGTCTCCTTT TCCCCCTCCC CTGATACTGA AGTGACAACT ATCTCACATT
7001 TCCCAGAAAA GACAACTCAT TCATTTAGAA CCATTTCATC TCTCACTCAT
7051 GAGTTGACTT CAAGAGTGAC ACCTATTCCT GGGGATTGGA TGAGTTCAGC
7101 TATGTCTACA AAGCCCACAG GAGCCAGTCC CTCCATTACA CTGGGAGAGA
7151 GAAGGACAAT CACCTCTGCT GCTCCAACCA CTTCCCCCAT AGTTCTCACT
7201 GCTAGTTTCA CAGAGACCAG CACAGTTTCA CTGGATAATG AAACTACAGT
7251 AAAAACCTCA GATATCCTTG ACGCACGGAA AACAAATGAG CTCCCCTCAG
7301 ATAGCAGTTC TTCTTCTGAT CTGATCAACA CCTCCATAGC TTCTTCAACT
7351 ATGGATGTCA CTAAAACAGC CTCCATCAGT CCCACTAGCA TCTCAGGAAT
7401 GACAGCAAGT TCCTCCCCAT CTCTCTTCTC TTCAGATAGA CCCCAGGTTC
7451 CCACATCTAC AACAGAGACA AATACAGCCA CCTCTCCATC TGTTTCCAGT
7501 AACACCTATT CTCTTGATGG GGGCTCCAAT GTGGGTGGCA CTCCATCCAC
7551 TTTACCACCC TTTACAATCA CCCACCCTGT CGAGACAAGC TCGGCCCTAT
7601 TAGCCTGGTC TAGACCAGTA AGAACTTTCA GCACCATGGT CAGCACTGAC
7651 ACTGCCTCCG GAGAAAATCC TACCTCTAGC AATTCTGTGG TGACTTCTGT
7701 TCCAGCACCA GGTACATGGG CCAGTGTAGG CAGTACTACT GACTTACCTG
7751 CCATGGGCTT TCTCAAGACA AGTCCTGCAG GAGAGGCACA CTCACTTCTA
7801 GCATCAACTA TTGAACCAGC CACTGCCTTC ACTCCCCATC TCTCAGCAGC
7851 AGTGGTCACT GGATCCAGTG CTACATCAGA AGCCAGTCTT CTCACTACGA
7901 GTGAAAGCAA AGCCATTCAT TCTTCACCAC AGACCCCAAC TACACCCACC
7951 TCTGGAGCAA ACTGGGAAAC TTCAGCTACT CCTGAGAGCC TTTTGGTAGT
8001 CACTGAGACT TCAGACACAA CACTTACCTC AAAGATTTTG GTCACAGATA

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)					
8051	CCATCTTGTT	TTCAACTGTG	TCCACGCCAC	CTTCTAAATT	TCCAAGTACG
8101	GGGACTCTGT	CTGGAGCTTC	CTTCCCTACT	TTACTCCCGG	ACACTCCAGC
8151	CATCCCTCTC	ACTGCCACTG	AGCCAACAAG	TTCATTAGCT	ACATCCTTTG
8201	ATTCCACCCC	ACTGGTGACT	ATAGCTTCGG	ATAGTCTTGG	CACAGTCCCA
8251	GAGACTACCC	TGACCATGTC	AGAGACCTCA	AATGGTGATG	CACTGGTTCT
8301	TAAGACAGTA	AGTAACCCAG	ATAGGAGCAT	CCCTGGAATC	ACTATCCAAG
8351	GAGTAACAGA	AAGTCCACTC	CATCCTTCTT	CCACTTCCCC	CTCTAAGATT
8401	GTTGCTCCAC	GGAATACAAC	CTATGAAGGT	TCGATCACAG	TGGCACTTTC
8451	TACTTTGCCT	GCGGGAACTA	CTGGTTCCCT	TGTATTCAGT	CAGAGTTCTG
8501	AAAACTCAGA	GACAACGGCT	TTGGTAGACT	CATCAGCTGG	GCTTGAGAGG
8551	GCATCTGTGA	TGCCACTAAC	CACAGGAAGC	CAGGGTATGG	CTAGCTCTGG
8601	AGGAATCAGA	AGTGGGTCCA	CTCACTCAAC	TGGAACCAAA	ACATTTTCTT
8651	CTCTCCCTCT	GACCATGAAC	CCAGGTGAGG	TTACAGCCAT	GTCTGAAATC
8701	ACCACGAACA	GACTGACAGC	TACTCAATCA	ACAGCACCCA	AAGGGATACC
8751	TGTGAAGCCC	ACCAGTGCTG	AGTCAGGCCT	CCTAACACCT	GTCTCTGCCT
8801	CCTCAAGCCC	ATCAAAGGCC	TTTGCCTCAC	TGACTACAGC	TCCCCCATCA
8851	ACTTGGGGGA	TCCCACAGTC	TACCTTGACA	TTTGAGTTTT	CTGAGGTCCC
8901	AAGTTTGGAT	ACTAAGTCCG	CTTCTTTACC	AACTCCTGGA	CAGTCCCTGA
8951	ACACCATTCC	AGACTCAGAT	GCAAGCACAG	CATCTTCCTC	ACTGTCCAAG
9001	TCTCCAGAAA	AAAACCCAAG	GGCAAGGATG	ATGACTTCCA	CAAAGGCCAT
9051	AAGTGCAAGC	TCATTTCAAT	CAACAGGTTT	TACTGAAACC	CCTGAGGGAT
9101	CTGCCTCCCC	TTCTATGGCA	GGGCATGAAC	CCAGAGTCCC	CACTTCAGGA
9151	ACAGGGGACC	CTAGATATGC	CTCAGAGAGC	ATGTCTTATC	CAGACCCAAG
9201	CAAGGCATCA	TCAGCTATGA	CATCGACCTC	TCTTGCATCA	AAACTCACAA
9251	CTCTCTTCAG	CACAGGTCAA	GCAGCAAGGT	CTGGTTCTAG	TTCCTCTCCC
9301	ATAAGCCTAT	CCACTGAGAA	AGAAACAAGC	TTCCTTTCCC	CCACTGCATC
9351	CACCTCCAGA	AAGACTTCAC	TATTTCTTGG	GCCTTCCATG	GCAAGGCAGC
9401	CCAACATATT	GGTGCATCTT	CAGACTTCAG	CTCTGACACT	TTCTCCAACA
9451	TCCACTCTAA	ATATGTCCCA	GGAGGAGCCT	CCTGAGTTAA	CCTCAAGCCA
9501	GACCATTGCA	GAAGAAGAGG	GAACAACAGC	TGAAACACAG	ACGTTAACCT
9551	TCACACCATC	TGAGACCCCA	ACATCCTTGT	TACCTGTCTC	TTCTCCCACA
9601	GAACCCACAG	CCAGAAGAAA	GAGTTCTCCA	GAAACATGGG	CAAGCTCTAT
9651	TTCAGTTCCT	GCCAAGACCT	CCTTGGTTGA	AACAACTGAT	GGAACGCTAG
9701	TGACCACCAT	AAAGATGTCA	AGCCAGGCAG	CACAAGGAAA	TTCCACGTGG
9751	CCTGCCCCAG	CAGAGGAGAC	GGGGACCAGT	CCAGCAGGCA	CATCCCCAGG
9801	AAGCCCAGAA	GTGTCTACCA	CTCTCAAAAT	CATGAGCTCC	AAGGAACCCA
9851	GCATCAGCCC	AGAGATCAGG	TCCACTGTGC	GAAATTCTCC	TTGGAAGACT

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)
9901 CCAGAAACAA CTGTTCCCAT GGAGACCACA GTGGAACCAG TCACCCTTCA
9951 GTCCACAGCC CTAGGAAGTG GCAGCACCAG CATCTCTCAC CTGCCCACAG
10001 GAACCACATC ACCAACCAAG TCACCAACAG AAAATATGTT GGCTACAGAA
10051 AGGGTCTCCC TCTCCCCATC CCCACCTGAG GCTTGGACCA ACCTTTATTC
10101 TGGAACTCCA GGAGGGACCA GGCAGTCACT GGCCACAATG TCCTCTGTCT
10151 CCCTAGAGTC ACCAACTGCT AGAAGCATCA CAGGGACTGG TCAGCAAAGC
10201 AGTCCAGAAC TGGTTTCAAA GACAACTGGA ATGGAATTCT CTATGTGGCA
10251 TGGCTCTACT GGAGGGACCA CAGGGGACAC ACATGTCTCT CTGAGCACAT
10301 CTTCCAATAT CCTTGAAGAC CCTGTAACCA GCCCAAACTC TGTGAGCTCA
10351 TTGACAGATA AATCCAAACA TAAAACCGAG ACATGGGTAA GCACCACAGC
10401 CATTCCCTCC ACTGTCCTGA ATAATAAGAT AATGGCAGCT GAACAACAGA
10451 CAAGTCGATC TGTGGATGAG GCTTATTCAT CAACTAGTTC TTGGTCAGAT
10501 CAGACATCTG GGAGTGACAT CACCCTTGGT GCATCTCCTG ATGTCACAAA
10551 CACATTATAC ATCACCTCCA CAGCACAAAC CACCTCACTA GTGTCTCTGC
10601 CCTCTGGAGA CCAAGGCATT ACAAGCCTCA CCAATCCCTC AGGAGGAAAA
10651 ACAAGCTCTG CGTCATCTGT CACATCTCCT TCAATAGGGC TTGAGACTCT
10701 GAGGGCCAAT GTAAGTGCAG TGAAAAGTGA CATTGCCCCT ACTGCTGGGC
10751 ATCTATCTCA GACTTCATCT CCTGCGGAAG TGAGCATCCT GGACGTAACC
10801 ACAGCTCCTA CTCCAGGTAT CTCCACCACC ATCACCACCA TGGGAACCAA
10851 CTCAATCTCA ACTACCACAC CCAACCCAGA AGTGGGTATG AGTACCATGG
10901 ACAGCACCCC GGCCACAGAG AGGCGCACAA CTTCTACAGA ACACCCTTCC
10951 ACCTGGTCTT CCACAGCTGC ATCAGATTCC TGGACTGTCA CAGACATGAC
11001 TTCAAACTTG AAAGTTGCAA GATCTCCTGG AACAATTTCC ACAATGCATA
11051 CAACTTCATT CTTAGCCTCA AGCACTGAAT TAGACTCCAT GTCTACTCCC
11101 CATGGCCGTA TAACTGTCAT TGGAACCAGC CTGGTCACTC CATCCTCTGA
11151 TGCTTCAGCT GTAAAGACAG AGACCAGTAC AAGTGAAAGA ACATTGAGTC
11201 CTTCAGACAC AACTGCATCT ACTCCCATCT CAACTTTTTC TCGTGTCCAG
11251 AGGATGAGCA TCTCAGTTCC TGACATTTTA AGTACAAGTT GGACTCCCAG
11301 TAGTACAGAA GCAGAAGATG TGCCTGTTTC AATGGTTTCT ACAGATCATG
11351 CTAGTACAAA GACTGACCCA AATACGCCCC TGTCCACTTT TCTGTTTGAT
11401 TCTCTGTCCA CTCTTGACTG GGACACTGGG AGATCTCTGT CATCAGCCAC
11451 AGCCACTACC TCAGCTCCTC AGGGGGCCAC AACTCCCCAG GAACTCACTT
11501 TGGAAACCAT GATCAGCCCA GCTACCTCAC AGTTGCCCTT CTCTATAGGG
11551 CACATTACAA GTGCAGTCAC ACCAGCTGCA ATGGCAAGGA GCTCTGGAGT
11601 TACTTTTTCA AGACCAGATC CCACAAGCAA AAAGGCAGAG CAGACTTCCA
11651 CTCAGCTTCC CACCACCACT TCTGCACATC CAGGGCAGGT GCCCAGATCA

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)
11701 GCAGCAACAA CTCTGGATGT GATCCCACAC ACAGCAAAAA CTCCAGATGC
11751 AACTTTTCAG AGACAAGGGC AGACAGCTCT TACAACAGAG GCAAGAGCTA
11801 CATCTGACTC CTGGAATGAG AAAGAAAAAT CAACCCCAAG TGCACCTTGG
11851 ATCACTGAGA TGATGAATTC TGTCTCAGAA GATACCATCA AGGAGGTTAC
11901 CAGCTCCTCC AGTGTATTAA AGGACCCTGA ATACGCTGGA CATAAACTTG
11951 GAATCTGGGA CGACTTCATC CCCAAGTTTG GAAAAGCAGC CCATATGAGA
12001 GAGTTGCCCC TTCTGAGTCC ACCACAGGAC AAAGAGGCAA TTCACCCTTC
12051 TACAAACACA GTAGAGACCA CAGGCTGGGT CACAAGTTCC GAACATGCTT
12101 CTCATTCCAC TATCCCAGCC CACTCAGCGT CATCCAAACT CACATCTCCA
12151 GTGGTTACAA CCTCCACCAG GGAACAAGCA ATAGTTTCTA TGTCAACAAC
12201 CACATGGCCA GAGTCTACAA GGGCTAGAAC AGAGCCTAAT TCCTTCTTGA
12251 CTATTGAACT GAGGGACGTC AGCCCTTACA TGGACACCAG CTCAACCACA
12301 CAAACAAGTA TTATCTCTTC CCCAGGTTCC ACTGCGATCA CCAAGGGGCC
12351 TAGAACAGAA ATTACCTCCT CTAAGAGAAT ATCCAGCTCA TTCCTTGCCC
12401 AGTCTATGAG GTCGTCAGAC AGCCCCTCAG AAGCCATCAC CAGGCTGTCT
12451 AACTTTCCTG CCATGACAGA ATCTGGAGGA ATGATCCTTG CTATGCAAAC
12501 AAGTCCACCT GGCGCTACAT CACTAAGTGC ACCTACTTTG GATACATCAG
12551 CCACAGCCTC CTGGACAGGG ACTCCACTGG CTACGACTCA GAGATTTACA
12601 TACTCAGAGA AGACCACTCT CTTTAGCAAA GGTCCTGAGG ATACATCACA
12651 GCCAAGCCCT CCCTCTGTGG AAGAAACCAG CTCTTCCTCT TCCCTGGTAC
12701 CTATCCATGC TACAACCTCG CCTTCCAATA TTTTGTTGAC ATCACAAGGG
12751 CACAGTCCCT CCTCTACTCC ACCTGTGACC TCAGTTTTCT TGTCTGAGAC
12801 CTCTGGCCTG GGGAAGACCA CAGACATGTC GAGGATAAGC TTGGAACCTG
12851 GCACAAGTTT ACCTCCCAAT TTGAGCAGTA CAGCAGGTGA GGCGTTATCC
12901 ACTTATGAAG CCTCCAGAGA TACAAAGGCA ATTCATCATT CTGCAGACAC
12951 AGCAGTGACG AATATGGAGG CAACCAGTTC TGAATATTCT CCTATCCCAG
13001 GCCATACAAA GCCATCCAAA GCCACATCTC CATTGGTTAC CTCCCACATC
13051 ATGGGGGACA TCACTTCTTC CACATCAGTA TTTGGCTCCT CCGAGACCAC
13101 AGAGATTGAG ACAGTGTCCT CTGTGAACCA GGGACTTCAG GAGAGAAGCA
13151 CATCCCAGGT GGCCAGCTCT GCTACAGAGA CAAGCACTGT CATTACCCAT
13201 GTGTCTAGTG GTGATGCTAC TACTCATGTC ACCAAGACAC AAGCCACTTT
13251 CTCTAGCGGA ACATCCATCT CAAGCCCTCA TCAGTTTATA ACTTCTACCA
13301 ACACATTTAC AGATGTGAGC ACCAACCCCT CCACCTCTCT GATAATGACA
13351 GAATCTTCAG GAGTGACCAT CACCACCCAA ACAGGTCCTA CTGGAGCTGC
13401 AACACAGGGT CCATATCTCT TGGACACATC AACCATGCCT TACTTGACAG
13451 AGACTCCATT AGCTGTGACT CCAGATTTTA TGCAATCAGA GAAGACCACT
13501 CTCATAAGCA AAGGTCCCAA GGATGTGACC TGGACAAGCC CTCCCTCTGT

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)
13551 GGCAGAAACC AGCTATCCCT CTTCCCTGAC ACCTTTCTTG GTCACAACCA
13601 TACCTCCTGC CACTTCCACG TTACAAGGGC AACATACATC CTCTCCTGTT
13651 TCTGCGACTT CAGTTCTTAC CTCTGGACTG GTGAAGACCA CAGATATGTT
13701 GAACACAAGC ATGGAACCTG TGACCAATTC ACCTCAAAAT TTGAACAATC
13751 CATCAAATGA GATACTGGCC ACTTTGGCAG CCACCACAGA TATAGAGACT
13801 ATTCATCCTT CCATAAACAA AGCAGTGACC AATATGGGGA CTGCCAGTTC
13851 AGCACATGTA CTGCATTCCA CTCTCCCAGT CAGCTCAGAA CCATCTACAG
13901 CCACATCTCC AATGGTTCCT GCCTCCAGCA TGGGGGACGC TCTTGCTTCT
13951 ATATCAATAC CTGGTTCTGA GACCACAGAC ATTGAGGGAG AGCCAACATC
14001 CTCCCTGACT GCTGGACGAA AAGAGAACAG CACCCTCCAG GAGATGAACT
14051 CAACTACAGA GTCAAACATC ATCCTCTCCA ATGTGTCTGT GGGGGCTATT
14101 ACTGAAGCCA CAAAAATGGA AGTCCCCTCT TTTGATGCAA CATTCATACC
14151 AACTCCTGCT CAGTCAACAA AGTTCCCAGA TATTTTCTCA GTAGCCAGCA
14201 GTAGACTTTC AAACTCTCCT CCCATGACAA TATCTACCCA CATGACCACC
14251 ACCCAGACAG GGTCTTCTGG AGCTACATCA AAGATTCCAC TTGCCTTAGA
14301 CACATCAACC TTGGAAACCT CAGCAGGGAC TCCATCAGTG GTGACTGAGG
14351 GGTTTGCCCA CTCAAAAATA ACCACTGCAA TGAACAATGA TGTCAAGGAC
14401 GTGTCACAGA CAAACCCTCC CTTTCAGGAT GAAGCCAGCT CTCCCTCTTC
14451 TCAAGCACCT GTCCTTGTCA CAACCTTACC TTCTTCTGTT GCTTTCACAC
14501 CGCAATGGCA CAGTACCTCC TCTCCTGTTT CTATGTCCTC AGTTCTTACT
14551 TCTTCACTGG TAAAGACCGC AGGCAAGGTG GATACAAGCT TAGAAACAGT
14601 GACCAGTTCA CCTCAAAGTA TGAGCAACAC TTTGGATGAC ATATCGGTCA
14651 CTTCAGCAGC CACCACAGAT ATAGAGACAA CGCATCCTTC CATAAACACA
14701 GTAGTTACCA ATGTGGGGAC CACCGGTTCA GCATTTGAAT CACATTCTAC
14751 TGTCTCAGCT TACCCAGAGC CATCTAAAGT CACATCTCCA AATGTTACCA
14801 CCTCCACCAT GGAAGACACC ACAATTTCCC GATCAATACC TAAATCCTCT
14851 AAGACTACAA GAACTGAGAC TGAGACAACT TCCTCCCTGA CTCCTAAACT
14901 GAGGGAGACC AGCATCTCCC AGGAGATCAC CTCGTCCACA GAGACAAGCA
14951 CTGTTCCTTA CAAAGAGCTC ACTGGTGCCA CTACCGAGGT ATCCAGGACA
15001 GATGTCACTT CCTCTAGCAG TACATCCTTC CCTGGCCCTG ATCAGTCCAC
15051 AGTGTCACTA GACATCTCCA CAGAAACCAA CACCAGGCTG TCTACCTCCC
15101 CAATAATGAC AGAATCTGCA GAAATAACCA TCACCACCCA AACAGGTCCT
15151 CATGGGGCTA CATCACAGGA TACTTTTACC ATGGACCCAT CAAATACAAC
15201 CCCCCAGGCA GGGATCCACT CAGCTATGAC TCATGGATTT TCACAATTGG
15251 ATGTGACCAC TCTTATGAGC AGAATTCCAC AGGATGTATC ATGGACAAGT
15301 CCTCCCTCTG TGGATAAAAC CAGCTCCCCC TCTTCCTTTC TGTCCTCACC

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)
15351 TGCAATGACC ACACCTTCCC TGATTTCTTC TACCTTACCA GAGGATAAGC
15401 TCTCCTCTCC TATGACTTCA CTTCTCACCT CTGGCCTAGT GAAGATTACA
15451 GACATATTAC GTACACGCTT GGAACCTGTG ACCAGCTCAC TTCCAAATTT
15501 CAGCAGCACC TCAGATAAGA TACTGGCCAC TTCTAAAGAC AGTAAAGACA
15551 CAAAGGAAAT TTTTCCTTCT ATAAACACAG AAGAGACCAA TGTGAAAGCC
15601 AACAACTCTG GACATGAATC CCATTCCCCT GCACTGGCTG ACTCAGAGAC
15651 ACCCAAAGCC ACAACTCAAA TGGTTATCAC CACCACTGTG GGAGATCCAG
15701 CTCCTTCCAC ATCAATGCCA GTGCATGGTT CCTCTGAGAC TACAAACATT
15751 AAGAGAGAGC CAACATATTT CTTGACTCCT AGACTGAGAG AGACCAGTAC
15801 CTCTCAGGAG TCCAGCTTTC CCACGGACAC AAGTTTTCTA CTTTCCAAAG
15851 TCCCCACTGG TACTATTACT GAGGTCTCCA GTACAGGGGT CAACTCTTCT
15901 AGCAAAATTT CCACCCCAGA CCATGATAAG TCCACAGTGC CACCTGACAC
15951 CTTCACAGGA GAGATCCCCA GGGTCTTCAC CTCCTCTATT AAGACAAAAT
16001 CTGCAGAAAT GACGATCACC ACCCAAGCAA GTCCTCCTGA GTCTGCATCG
16051 CACAGTACCC TTCCCTTGGA CACATCAACC ACACTTTCCC AGGGAGGGAC
16101 TCATTCAACT GTGACTCAGG GATTCCCATA CTCAGAGGTG ACCACTCTCA
16151 TGGGCATGGG TCCTGGGAAT GTGTCATGGA TGACAACTCC CCCTGTGGAA
16201 GAAACCAGCT CTGTGTCTTC CCTGATGTCT TCACCTGCCA TGACATCCCC
16251 TTCTCCTGTT TCCTCCACAT CACCACAGAG CATCCCCTCC TCTCCTCTTC
16301 CTGTGACTGC ACTTCCTACT TCTGTTCTGG TGACAACCAC AGATGTGTTG
16351 GGCACAACAA GCCCAGAGTC TGTAACCAGT TCACCTCCAA ATTTGAGCAG
16401 CATCACTCAT GAGAGACCGG CCACTTACAA AGACACTGCA CACACAGAAG
16451 CCGCCATGCA TCATTCCACA AACACCGCAG TGACCAATGT AGGGACTTCC
16501 GGGTCTGGAC ATAAATCACA ATCCTCTGTC CTAGCTGACT CAGAGACATC
16551 GAAAGCCACA CCTCTGATGA GTACCACCTC CACCCTGGGG GACACAAGTG
16601 TTTCCACATC AACTCCTAAT ATCTCTCAGA CTAACCAAAT TCAAACAGAG
16651 CCAACAGCAT CCCTGAGCCC TAGACTGAGG GAGAGCAGCA CGTCTGAGAA
16701 GACCAGCTCA ACAACAGAGA CAAATACTGC CTTTTCTTAT GTGCCCACAG
16751 GTGCTATTAC TCAGGCCTCC AGAACAGAAA TCTCCTCTAG CAGAACATCC
16801 ATCTCAGACC TTGATCGGCC CACAATAGCA CCCGACATCT CCACAGGAAT
16851 GATCACCAGG CTCTTCACCT CCCCCATCAT GACAAAATCT GCAGAAATGA
16901 CCGTCACCAC TCAAACAACT ACTCCTGGGG CTACATCACA GGGTATCCTT
16951 CCTTGGGACA CATCAACCAC ACTTTTCCAG GGAGGGACTC ATTCAACCGT
17001 GTCTCAGGGA TTCCCACACT CAGAGATAAC CACTCTTCGG AGCAGAACCC
17051 CTGGAGATGT GTCATGGATG ACAACTCCCC CTGTGGAAGA AACCAGCTCT
17101 GGGTTTTCCC TGATGTCACC TTCCATGACA TCCCCTTCTC CTGTTTCCTC
17151 CACATCACCA GAGAGCATCC CCTCCTCTCC TCTCCCTGTG ACTGCACTTC

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)
17201 TTACTTCTGT TCTGGTGACA ACCACCAATG TATTGGGCAC AACAAGCCCA
17251 GAGACCGTAA CGAGTTCACC TCCAAATTTA AGCAGCCCCA CACAGGAGAG
17301 ACTGACCACT TACAAAGACA CTGCGCACAC AGAAGCCATG CATGCTTCCA
17351 TGCATACAAA CACTGCAGTG GCCAACGTCG GGACCTCCAT TTCTGGACAT
17401 GAATCACAAT CTTCTGTCCC AGCTGATTCA CACACATCCA AAGCCACATC
17451 TCCAATGGGT ATCACCTTCG CCATGGGGGA TACAAGTGTT TCTACATCAA
17501 CTCCTGCCTT CTTTGAGACT AGAATTCAGA CTGAATCAAC ATCCTCTTTG
17551 ATTCCTGGAT TAAGGGACAC CAGGACGTCT GAGGAGATCA ACACTGTGAC
17601 AGAGACCAGC ACTGTCCTTT CAGAAGTGCC CACTACTACT ACTACTGAGG
17651 TCTCCAGGAC AGAAGTTATC ACTTCCAGCA GAACAACCAT CTCAGGGCCT
17701 GATCATTCCA AAATGTCACC CTACATCTCC ACAGAAACCA TCACCAGGCT
17751 CTCCACTTTT CCTTTTGTAA CAGGATCCAC AGAAATGGCC ATCACCAACC
17801 AAACAGGTCC TATAGGGACT ATCTCACAGG CTACCCTTAC CCTGGACACA
17851 TCAAGCACAG CTTCCTGGGA AGGGACTCAC TCACCTGTGA CTCAGAGATT
17901 TCCACACTCA GAGGAGACCA CTACTATGAG CAGAAGTACT AAGGGCGTGT
17951 CATGGCAAAG CCCTCCCTCT GTGGAAGAAA CCAGTTCTCC TTCTTCCCCA
18001 GTGCCTTTAC CTGCAATAAC CTCACATTCA TCTCTTTATT CCGCAGTATC
18051 AGGAAGTAGC CCCACTTCTG CTCTCCCTGT GACTTCCCTT CTCACCTCTG
18101 GCAGGAGGAA GACCATAGAC ATGTTGGACA CACACTCAGA ACTTGTGACC
18151 AGCTCCTTAC CAAGTGCAAG TAGCTTCTCA GGTGAGATAC TCACTTCTGA
18201 AGCCTCCACA AATACAGAGA CAATTCACTT TTCAGAGAAC ACAGCAGAAA
18251 CCAATATGGG GACCACCAAT TCTATGCATA AACTACATTC CTCTGTCTCA
18301 ATCCACTCCC AGCCATCCGG ACACACACCT CCAAAGGTTA CTGGATCTAT
18351 GATGGAGGAC GCTATTGTTT CCACATCAAC ACCTGGTTCT CCTGAGACTA
18401 AAAATGTTGA CAGAGACTCA ACATCCCCTC TGACTCCTGA ACTGAAAGAG
18451 GACAGCACCG CCCTGGTGAT GAACTCAACT ACAGAGTCAA ACACTGTTTT
18501 CTCCAGTGTG TCCCTGGATG CTGCTACTGA GGTCTCCAGG GCAGAAGTCA
18551 CCTACTATGA TCCTACATTC ATGCCAGCTT CTGCTCAGTC AACAAAGTCC
18601 CCAGACATTT CACCTGAAGC CAGCAGCAGT CATTCTAACT CTCCTCCCTT
18651 GACAATATCT ACACACAAGA CCATCGCCAC ACAAACAGGT CCTTCTGGGG
18701 TGACATCTCT TGGCCAACTG ACCCTGGACA CATCAACCAT AGCCACCTCA
18751 GCAGGAACTC CATCAGCCAG AACTCAGGAT TTTGTAGATT CAGAAACAAC
18801 CAGTGTCATG AACAATGATC TCAATGATGT GTTGAAGACA AGCCCTTTCT
18851 CTGCAGAAGA AGCCAACTCT CTCTCTTCTC AGGCACCTCT CCTTGTGACA
18901 ACCTCACCTT CTCCTGTAAC TTCCACATTG CAAGAGCACA GTACCTCCTC
18951 TCTTGTTTCT GTGACCTCAG TACCCACCCC TACACTGGCG AAGATCACAG

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)
19001 ACATGGACAC AAACTTAGAA CCTGTGACTC GTTCACCTCA AAATTTAAGG
19051 AACACCTTGG CCACTTCAGA AGCCACCACA GATACACACA CAATGCATCC
19101 TTCTATAAAC ACAGCAATGG CCAATGTGGG GACCACCAGT TCACCAAATG
19151 AATTCTATTT TACTGTCTCA CCTGACTCAG ACCCATATAA AGCCACATCC
19201 GCAGTAGTTA TCACTTCCAC CTCGGGGGAC TCAATAGTTT CCACATCAAT
19251 GCCTAGATCC TCTGCGATGA AAAAGATTGA GTCTGAGACA ACTTTCTCCC
19301 TGATATTTAG ACTGAGGGAG ACTAGCACCT CCCAGAAAAT TGGCTCATCC
19351 TCAGACACAA GCACGGTCTT TGACAAAGCA TTCACTGCTG CTACTACTGA
19401 GGTCTCCAGA ACAGAACTCA CCTCCTCTAG CAGAACATCC ATCCAAGGCA
19451 CTGAAAAGCC CACAATGTCA CCGGACACCT CCACAAGATC TGTCACCATG
19501 CTTTCTACTT TTGCTGGCCT GACAAAATCC GAAGAAAGGA CCATTGCCAC
19551 CCAAACAGGT CCTCATAGGG CGACATCACA GGGTACCCTT ACCTGGGACA
19601 CATCAATCAC AACCTCACAG GCAGGGACCC ACTCAGCTAT GACTCATGGA
19651 TTTTCACAAT TAGATTTGTC CACTCTTACG AGTAGAGTTC CTGAGTACAT
19701 ATCAGGGACA AGCCCACCCT CTGTGGAAAA AACCAGCTCT TCCTCTTCCC
19751 TTCTGTCTTT ACCAGCAATA ACCTCACCGT CCCCTGTACC TACTACATTA
19801 CCAGAAAGTA GGCCGTCTTC TCCTGTTCAT CTGACTTCAC TCCCCACCTC
19851 TGGCCTAGTG AAGACCACAG ATATGCTGGC ATCTGTGGCC AGTTTACCTC
19901 CAAACTTGGG CAGCACCTCA CATAAGATAC CGACTACTTC AGAAGACATT
19951 AAAGATACAG AGAAAATGTA TCCTTCCACA AACATAGCAG TAACCAATGT
20001 GGGGACCACC ACTTCTGAAA AGGAATCTTA TTCGTCTGTC CCAGCCTACT
20051 CAGAACCACC CAAAGTCACC TCTCCAATGG TTACCTCTTT CAACATAAGG
20101 GACACCATTG TTTCCACATC CATGCCTGGC TCCTCTGAGA TTACAAGGAT
20151 TGAGATGGAG TCAACATTCT CCGTGGCTCA TGGGCTGAAG GGAACCAGCA
20201 CCTCCCAGGA CCCCATCGTA TCCACAGAGA AAAGTGCTGT CCTTCACAAG
20251 TTGACCACTG GTGCTACTGA GACCTCTAGG ACAGAAGTTG CCTCTTCTAG
20301 AAGAACATCC ATTCCAGGCC CTGATCATTC CACAGAGTCA CCAGACATCT
20351 CCACTGAAGT GATCCCCAGC CTGCCTATCT CCCTTGGCAT TACAGAATCT
20401 TCAAATATGA CCATCATCAC TCGAACAGGT CCTCCTCTTG GCTCTACATC
20451 ACAGGGCACA TTTACCTTGG ACACACCAAC TACATCCTCC AGGGCAGGAA
20501 CACACTCGAT GGCGACTCAG GAATTTCCAC ACTCAGAAAT GACCACTGTC
20551 ATGAACAAGG ACCCTGAGAT TCTATCATGG ACAATCCCTC CTTCTATAGA
20601 GAAAACCAGC TTCTCCTCTT CCCTGATGCC TTCACCAGCC ATGACTTCAC
20651 CTCCTGTTTC CTCAACATTA CCAAAGACCA TTCACACCAC TCCTTCTCCT
20701 ATGACCTCAC TGCTCACCCC TAGCCTAGTG ATGACCACAG ACACATTGGG
20751 CACAAGCCCA GAACCTACAA CCAGTTCACC TCCAAATTTG AGCAGTACCT
20801 CACATGTGAT ACTGACAACA GATGAAGACA CCACAGCTAT AGAAGCCATG

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)
20851 CATCCTTCCA CAAGCACAGC AGCGACTAAT GTGGAAACCA CCTGTTCTGG
20901 ACATGGGTCA CAATCCTCTG TCCTAACTGA CTCAGAAAAA ACCAAGGCCA
20951 CAGCTCCAAT GGATACCACC TCCACCATGG GGCATACAAC TGTTTCCACA
21001 TCAATGTCTG TTTCCTCTGA GACTACAAAA ATTAAGAGAG AGTCAACATA
21051 TTCCTTGACT CCTGGACTGA GAGAGACCAG CATTTCCCAA AATGCCAGCT
21101 TTTCCACTGA CACAAGTATT GTTCTTTCAG AAGTCCCCAC TGGTACTACT
21151 GCTGAGGTCT CCAGGACAGA AGTCACCTCC TCTGGTAGAA CATCCATCCC
21201 TGGCCCTTCT CAGTCCACAG TTTTGCCAGA AATATCCACA AGAACAATGA
21251 CAAGGCTCTT TGCCTCGCCC ACCATGACAG AATCAGCAGA AATGACCATC
21301 CCCACTCAAA CAGGTCCTTC TGGGTCTACC TCACAGGATA CCCTTACCTT
21351 GGACACATCC ACCACAAAGT CCCAGGCAAA GACTCATTCA ACTTTGACTC
21401 AGAGATTTCC ACACTCAGAG ATGACCACTC TCATGAGCAG AGGTCCTGGA
21451 GATATGTCAT GGCAAAGCTC TCCCTCTCTG GAAAATCCCA GCTCTCTCCC
21501 TTCCCTGCTG TCTTTACCTG CCACAACCTC ACCTCCTCCC ATTTCCTCCA
21551 CATTACCAGT GACTATCTCC TCCTCTCCTC TTCCTGTGAC TTCACTTCTC
21601 ACCTCTAGCC CGGTAACGAC CACAGACATG TTACACACAA GCCCAGAACT
21651 TGTAACCAGT TCACCTCCAA AGCTGAGCCA CACTTCAGAT GAGAGACTGA
21701 CCACTGGCAA GGACACCACA AATACAGAAG CTGTGCATCC TTCCACAAAC
21751 ACAGCAGCGT CCAATGTGGA GATTCCCAGC TTTGGACATG AATCCCCTTC
21801 CTCTGCCTTA GCTGACTCAG AGACATCCAA AGCCACATCA CCAATGTTTA
21851 TTACCTCCAC CCAGGAGGAT ACAACTGTTG CCATATCAAC CCCTCACTTC
21901 TTGGAGACTA GCAGAATTCA GAAAGAGTCA ATTTCCTCCC TGAGCCCTAA
21951 ATTGAGGGAG ACAGGCAGTT CTGTGGAGAC AAGCTCAGCC ATAGAGACAA
22001 GTGCTGTCCT TTCTGAAGTG TCCATTGGTG CTACTACTGA GATCTCCAGG
22051 ACAGAAGTCA CCTCCTCTAG CAGAACATCC ATCTCTGGTT CTGCTGAGTC
22101 CACAATGTTG CCAGAAATAT CCACCACAAG AAAAATCATT AAGTTCCCTA
22151 CTTCCCCCAT CCTGGCAGAA TCATCAGAAA TGACCATCAA GACCCAAACA
22201 AGTCCTCCTG GGTCTACATC AGAGAGTACC TTTACATTAG ACACATCAAC
22251 CACTCCCTCC TTGGTAATAA CCCATTCGAC TATGACTCAG AGATTGCCAC
22301 ACTCAGAGAT AACCACTCTT GTGAGTAGAG GTGCTGGGGA TGTGCCACGG
22351 CCCAGCTCTC TCCCTGTGGA AGAAACAAGC CCTCCATCTT CCCAGCTGTC
22401 TTTATCTGCC ATGATCTCAC CTTCTCCTGT TTCTTCCACA TTACCAGCAA
22451 GTAGCCACTC CTCTTCTGCT TCTGTGACTT CACCTCTCAC ACCAGGCCAA
22501 GTGAAGACTA CTGAGGTGTT GGACGCAAGT GCAGAACCTG AAACCAGTTC
22551 ACCTCCAAGT TTGAGCAGCA CCTCAGTTGA AATACTGGCC ACCTCTGAAG
22601 TCACCACAGA TACGGAGAAA ATTCATCCTT TCCCAAACAC GGCAGTAACC

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)
22651 AAAGTTGGAA CTTCCAGTTC TGGACATGAA TCCCCTTCCT CTGTCCTACC
22701 TGACTCAGAG ACAACCAAAG CCACATCGGC AATGGGTACC ATCTCCATTA
22751 TGGGGGATAC AAGTGTTTCT ACATTAACTC CTGCCTTATC TAACACTAGG
22801 AAAATTCAGT CAGAGCCAGC TTCCTCACTG ACCACCAGAT TGAGGGAGAC
22851 CAGCACCTCT GAAGAGACCA GCTTAGCCAC AGAAGCAAAC ACTGTTCTTT
22901 CTAAAGTGTC CACTGGTGCT ACTACTGAGG TCTCCAGGAC AGAAGCCATC
22951 TCCTTTAGCA GAACATCCAT GTCAGGCCCT GAGCAGTCCA CAATGTCACA
23001 AGACATCTCC ATAGGAACCA TCCCCAGGAT TTCTGCCTCC TCTGTCCTGA
23051 CAGAATCTGC AAAAATGACC ATCACAACCC AAACAGGTCC TTCGGAGTCT
23101 ACACTAGAAA GTACCCTTAA TTTGAACACA GCAACCACAC CCTCTTGGGT
23151 GGAAACCCAC TCTATAGTAA TTCAGGGATT TCCACACCCA GAGATGACCA
23201 CTTCCATGGG CAGAGGTCCT GGAGGTGTGT CATGGCCTAG CCCTCCCTTT
23251 GTGAAAGAAA CCAGCCCTCC ATCCTCCCCG CTGTCTTTAC CTGCCGTGAC
23301 CTCACCTCAT CCTGTTTCCA CCACATTCCT AGCACATATC CCCCCCTCTC
23351 CCCTTCCTGT GACTTCACTT CTCACCTCTG GCCCGGCGAC AACCACAGAT
23401 ATCTTGGGTA CAAGCACAGA ACCTGGAACC AGTTCATCTT CAAGTTTGAG
23451 CACCACCTCC CATGAGAGAC TGACCACTTA CAAAGACACT GCACATACAG
23501 AAGCCGTGCA TCCTTCCACA AACACAGGAG GGACCAATGT GGCAACCACC
23551 AGCTCTGGAT ATAAATCACA GTCCTCTGTC CTAGCTGACT CATCTCCAAT
23601 GTGTACCACC TCCACCATGG GGGATACAAG TGTTCTCACA TCAACTCCTG
23651 CCTTCCTTGA GACTAGGAGG ATTCAGACAG AGCTAGCTTC CTCCCTGACC
23701 CCTGGATTGA GGGAGTCCAG TGGCTCTGAA GGGACCAGCT CAGGCACCAA
23751 GATGAGCACT GTCCTCTCTA AAGTGCCCAC TGGTGCTACT ACTGAGATCT
23801 CCAAGGAAGA CGTCACCTCC ATCCCAGGTC CCGCTCAATC CACAATATCA
23851 CCAGACATCT CCACAAGAAC CGTCAGCTGG TTCTCTACAT CCCCTGTCAT
23901 GACAGAATCA GCAGAAATAA CCATGAACAC CCATACAAGT CCTTTAGGGG
23951 CCACAACACA AGGCACCAGT ACTTTGGCCA CGTCAAGCAC AACCTCTTTG
24001 ACAATGACAC ACTCAACTAT ATCTCAAGGA TTTTCACACT CACAGATGAG
24051 CACTCTTATG AGGAGGGGTC CTGAGGATGT ATCATGGATG AGCCCTCCCC
24101 TTCTGGAAAA AACTAGACCT TCCTTTTCTC TGATGTCTTC ACCAGCCACA
24151 ACTTCACCTT CTCCTGTTTC CTCCACATTA CCAGAGAGCA TCTCTTCCTC
24201 TCCTCTTCCT GTGACTTCAC TCCTCACGTC TGGCTTGGCA AAAACTACAG
24251 ATATGTTGCA CAAAAGCTCA GAACCTGTAA CCAACTCACC TGCAAATTTG
24301 AGCAGCACCT CAGTTGAAAT ACTGGCCACC TCTGAAGTCA CCACAGATAC
24351 AGAGAAAACT CATCCTTCTT CAAACAGAAC AGTGACCGAT GTGGGGACCT
24401 CCAGTTCTGG ACATGAATCC ACTTCCTTTG TCCTAGCTGA CTCACAGACA
24451 TCCAAAGTCA CATCTCCAAT GGTTATTACC TCCACCATGG AGGATACGAG

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)
24501 TGTCTCCACA TCAACTCCTG GCTTTTTTGA GACTAGCAGA ATTCAGACAG
24551 AACCAACATC CTCCCTGACC CTTGGACTGA GAAAGACCAG CAGCTCTGAG
24601 GGGACCAGCT TAGCCACAGA GATGAGCACT GTCCTTTCTG GAGTGCCCAC
24651 TGGTGCCACT GCTGAAGTCT CCAGGACAGA AGTCACCTCC TCTAGCAGAA
24701 CATCCATCTC AGGCTTTGCT CAGCTCACAG TGTCACCAGA GACTTCCACA
24751 GAAACCATCA CCAGACTCCC TACCTCCAGC ATAATGACAG AATCAGCAGA
24801 AATGATGATC AAGACACAAA CAGATCCTCC TGGGTCTACA CCAGAGAGTA
24851 CTCATACTGT GGACATATCA ACAACACCCA ACTGGGTAGA AACCCACTCG
24901 ACTGTGACTC AGAGATTTTC ACACTCAGAG ATGACCACTC TTGTGAGCAG
24951 AAGCCCTGGT GATATGTTAT GGCCTAGTCA ATCCTCTGTG GAAGAAACCA
25001 GCTCTGCCTC TTCCCTGCTG TCTCTGCCTG CCACGACCTC ACCTTCTCCT
25051 GTTTCCTCTA CATTAGTAGA GGATTTCCCT TCCGCTTCTC TTCCTGTGAC
25101 TTCTCTTCTC ACCCCTGGCC TGGTGATAAC CACAGACAGG ATGGGCATAA
25151 GCAGAGAACC TGGAACCAGT TCCACTTCAA ATTTGAGCAG CACCTCCCAT
25201 GAGAGACTGA CCACTTTGGA AGACACTGTA GATACAGAAG ACATGCAGCC
25251 TTCCACACAC ACAGCAGTGA CCAACGTGAG GACCTCCATT TCTGGACATG
25301 AATCACAATC TTCTGTCCTA TCTGACTCAG AGACACCCAA AGCCACATCT
25351 CCAATGGGTA CCACCTACAC CATGGGGGAA ACGAGTGTTT CCATATCCAC
25401 TTCTGACTTC TTTGAGACCA GCAGAATTCA GATAGAACCA ACATCCTCCC
25451 TGACTTCTGG ATTGAGGGAG ACCAGCAGCT CTGAGAGGAT CAGCTCAGCC
25501 ACAGAGGGAA GCACTGTCCT TTCTGAAGTG CCCAGTGGTG CTACCACTGA
25551 GGTCTCCAGG ACAGAAGTGA TATCCTCTAG GGGAACATCC ATGTCAGGGC
25601 CTGATCAGTT CACCATATCA CCAGACATCT CTACTGAAGC GATCACCAGG
25651 CTTTCTACTT CCCCCATTAT GACAGAATCA GCAGAAAGTG CCATCACTAT
25701 TGAGACAGGT TCTCCTGGGG CTACATCAGA GGGTACCCTC ACCTTGGACA
25751 CCTCAACAAC AACCTTTTGG TCAGGGACCC ACTCAACTGC ATCTCCAGGA
25801 TTTTCACACT CAGAGATGAC CACTCTTATG AGTAGAACTC CTGGAGATGT
25851 GCCATGGCCG AGCCTTCCCT CTGTGGAAGA AGCCAGCTCT GTCTCTTCCT
25901 CACTGTCTTC ACCTGCCATG ACCTCAACTT CTTTTTTCTC CGCATTACCA
25951 GAGAGCATCT CCTCCTCTCC TCATCCTGTG ACTGCACTTC TCACCCTTGG
26001 CCCAGTGAAG ACCACAGACA TGTTGCGCAC AAGCTCAGAA CCTGAAACCA
26051 GTTCACCTCC AAATTTGAGC AGCACCTCAG CTGAAATATT AGCCACGTCT
26101 GAAGTCACCA AAGATAGAGA GAAAATTCAT CCCTCCTCAA ACACACCTGT
26151 AGTCAATGTA GGGACTGTGA TTTATAAACA TCTATCCCCT TCCTCTGTTT
26201 TGGCTGACTT AGTGACAACA AAACCCACAT CTCCAATGGC TACCACCTCC
26251 ACTCTGGGGA ATACAAGTGT TTCCACATCA ACTCCTGCCT TCCCAGAAAC

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)				
26301	TATGATGACA	CAGCCAACTT	CCTCCCTGAC	TTCTGGATTA AGGGAGATCA
26351	GTACCTCTCA	AGAGACCAGC	TCAGCAACAG	AGAGAAGTGC TTCTCTTTCT
26401	GGAATGCCCA	CTGGTGCTAC	TACTAAGGTC	TCCAGAACAG AAGCCCTCTC
26451	CTTAGGCAGA	ACATCCACCC	CAGGTCCTGC	TCAATCCACA ATATCACCAG
26501	AAATCTCCAC	GGAAACCATC	ACTAGAATTT	CTACTCCCCT CACCACGACA
26551	GGATCAGCAG	AAATGACCAT	CACCCCCAAA	ACAGGTCATT CTGGGGCATC
26601	CTCACAAGGT	ACCTTTACCT	TGGACACATC	AAGCAGAGCC TCCTGGCCAG
26651	GAACTCACTC	AGCTGCAACT	CACAGATCTC	CACACTCAGG GATGACCACT
26701	CCTATGAGCA	GAGGTCCTGA	GGATGTGTCA	TGGCCAAGCC GCCCATCAGT
26751	GGAAAAAACT	AGCCCTCCAT	CTTCCCTGGT	GTCTTTATCT GCAGTAACCT
26801	CACCTTCGCC	ACTTTATTCC	ACACCATCTG	AGAGTAGCCA CTCATCTCCT
26851	CTCCGGGTGA	CTTCTCTTTT	CACCCCTGTC	ATGATGAAGA CCACAGACAT
26901	GTTGGACACA	AGCTTGGAAC	CTGTGACCAC	TTCACCTCCC AGTATGAATA
26951	TCACCTCAGA	TGAGAGTCTG	GCCACTTCTA	AAGCCACCAT GGAGACAGAG
27001	GCAATTCAGC	TTTCAGAAAA	CACAGCTGTG	ACTCAGATGG GCACCATCAG
27051	CGCTAGACAA	GAATTCTATT	CCTCTTATCC	AGGCCTCCCA GAGCCATCCA
27101	AAGTGACATC	TCCAGTGGTC	ACCTCTTCCA	CCATAAAAGA CATTGTTTCT
27151	ACAACCATAC	CTGCTTCCTC	TGAGATAACA	AGAATTGAGA TGGAGTCAAC
27201	ATCCACCCTG	ACCCCCACAC	CAAGGGAGAC	CAGCACCTCC CAGGAGATCC
27251	ACTCAGCCAC	AAAGCCAAGC	ACTGTTCCTT	ACAAGGCACT CACTAGTGCC
27301	ACGATTGAGG	ACTCCATGAC	ACAAGTCATG	TCCTCTAGCA GAGGACCTAG
27351	CCCTGATCAG	TCCACAATGT	CACAAGACAT	ATCCAGTGAA GTGATCACCA
27401	GGCTCTCTAC	CTCCCCCATC	AAGGCAGAAT	CTACAGAAAT GACCATTACC
27451	ACCCAAACAG	GTTCTCCTGG	GGCTACATCA	AGGGGTACCC TTACCTTGGA
27501	CACTTCAACA	ACTTTTATGT	CAGGGACCCA	CTCAACTGCA TCTCAAGGAT
27551	TTTCACACTC	ACAGATGACC	GCTCTTATGA	GTAGAACTCC TGGAGATGTG
27601	CCATGGCTAA	GCCATCCCTC	TGTGGAAGAA	GCCAGCTCTG CCTCTTTCTC
27651	ACTGTCTTCA	CCTGTCATGA	CCTCATCTTC	TCCCGTTTCT TCCACATTAC
27701	CAGACAGCAT	CCACTCTTCT	TCGCTTCCTG	TGACATCACT TCTCACCTCA
27751	GGGCTGGTGA	AGACCACAGA	GCTGTTGGGC	ACAAGCTCAG AACCTGAAAC
27801	CAGTTCACCC	CCAAATTTGA	GCAGCACCTC	AGCTGAAATA CTGGCCACCA
27851	CTGAAGTCAC	TACAGATACA	GAGAAACTGG	AGATGACCAA TGTGGTAACC
27901	TCAGGTTATA	CACATGAATC	TCCTTCCTCT	GTCCTAGCTG ACTCAGTGAC
27951	AACAAAGGCC	ACATCTTCAA	TGGGTATCAC	CTACCCCACA GGAGATACAA
28001	ATGTTCTCAC	ATCAACCCCT	GCCTTCTCTG	ACACCAGTAG GATTCAAACA
28051	AAGTCAAAGC	TCTCACTGAC	TCCTGGGTTG	ATGGAGACCA GCATCTCTGA
28101	AGAGACCAGC	TCTGCCACAG	AAAAAAGCAC	TGTCCTTTCT AGTGTGCCCA

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)
28151 CTGGTGCTAC TACTGAGGTC TCCAGGACAG AAGCCATCTC TTCTAGCAGA
28201 ACATCCATCC CAGGCCCTGC TCAATCCACA ATGTCATCAG ACACCTCCAT
28251 GGAAACCATC ACTAGAATTT CTACCCCCCT CACAAGGAAA GAATCAACAG
28301 ACATGGCCAT CACCCCCAAA ACAGGTCCTT CTGGGGCTAC CTCGCAGGGT
28351 ACCTTTACCT TGGACTCATC AAGCACAGCC TCCTGGCCAG GAACTCACTC
28401 AGCTACAACT CAGAGATTTC CACAGTCAGT GGTGACAACT CCTATGAGCA
28451 GAGGTCCTGA GGATGTGTCA TGGCCAAGCC CGCTGTCTGT GGAAAAAAAC
28501 AGCCCTCCAT CTTCCCTGGT ATCTTCATCT TCAGTAACCT CACCTTCGCC
28551 ACTTTATTCC ACACCATCTG GGAGTAGCCA CTCCTCTCCT GTCCCTGTCA
28601 CTTCTCTTTT CACCTCTATC ATGATGAAGG CCACAGACAT GTTGGATGCA
28651 AGTTTGGAAC CTGAGACCAC TTCAGCTCCC AATATGAATA TCACCTCAGA
28701 TGAGAGTCTG GCCACTTCTA AAGCCACCAC GGAGACAGAG GCAATTCACG
28751 TTTTTGAAAA TACAGCAGCG TCCCATGTGG AAACCACCAG TGCTACAGAG
28801 GAACTCTATT CCTCTTCCCC AGGCTTCTCA GAGCCAACAA AAGTGATATC
28851 TCCAGTGGTC ACCTCTTCCT CTATAAGAGA CAACATGGTT TCCACAACAA
28901 TGCCTGGCTC CTCTGGCATT ACAAGGATTG AGATAGAGTC AATGTCATCT
28951 CTGACCCCTG GACTGAGGGA GACCAGAACC TCCCAGGACA TCACCTCATC
29001 CACAGAGACA AGCACTGTCC TTTACAAGAT GTCCTCTGGT GCCACTCCTG
29051 AGGTCTCCAG GACAGAAGTT ATGCCCTCTA GCAGAACATC CATTCCTGGC
29101 CCTGCTCAGT CCACAATGTC ACTAGACATC TCCGATGAAG TTGTCACCAG
29151 GCTGTCTACC TCTCCCATCA TGACAGAATC TGCAGAAATA ACCATCACCA
29201 CCCAAACAGG TTATTCTCTG GCTACATCCC AGGTTACCCT TCCCTTGGGC
29251 ACCTCAATGA CCTTTTTGTC AGGGACCCAC TCAACTATGT CTCAAGGACT
29301 TTCACACTCA GAGATGACCA ATCTTATGAG CAGGGGTCCT GAAAGTCTGT
29351 CATGGACGAG CCCTCGCTTT GTGGAAACAA CTAGATCTTC CTCTTCTCTG
29401 ACATCATTAC CTCTCACGAC CTCACTTTCT CCTGTGTCCT CCACATTACT
29451 AGACAGTAGC CCCTCCTCTC CTCTTCCTGT GACTTCACTT ATCCTCCCAG
29501 GCCTGGTGAA GACTACAGAA GTGTTGGATA CAAGCTCAGA GCCTAAAACC
29551 AGTTCATCTC CAAATTTGAG CAGCACCTCA GTTGAAATAC CGGCCACCTC
29601 TGAAATCATG ACAGATACAG AGAAAATTCA TCCTTCCTCA AACACAGCGG
29651 TGGCCAAAGT GAGGACCTCC AGTTCTGTTC ATGAATCTCA TTCCTCTGTC
29701 CTAGCTGACT CAGAAACAAC CATAACCATA CCTTCAATGG GTATCACCTC
29751 CGCTGTGGAC GATACCACTG TTTTCACATC AAATCCTGCC TTCTCTGAGA
29801 CTAGGAGGAT TCCGACAGAG CCAACATTCT CATTGACTCC TGGATTCAGG
29851 GAGACTAGCA CCTCTGAAGA GACCACCTCA ATCACAGAAA CAAGTGCAGT
29901 CCTTTATGGA GTGCCCACTA GTGCTACTAC TGAAGTCTCC ATGACAGAAA

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)					
29951	TCATGTCCTC	TAATAGAACA	CACATCCCTG	ACTCTGATCA	GTCCACGATG
30001	TCTCCAGACA	TCATCACTGA	AGTGATCACC	AGGCTCTCTT	CCTCATCCAT
30051	GATGTCAGAA	TCAACACAAA	TGACCATCAC	CACCCAAAAA	AGTTCTCCTG
30101	GGGCTACAGC	ACAGAGTACT	CTTACCTTGG	CCACAACAAC	AGCCCCCTTG
30151	GCAAGGACCC	ACTCAACTGT	TCCTCCTAGA	TTTTTACACT	CAGAGATGAC
30201	AACTCTTATG	AGTAGGAGTC	CTGAAAATCC	ATCATGGAAG	AGCTCTCCCT
30251	TTGTGGAAAA	AACTAGCTCT	TCATCTTCTC	TGTTGTCCTT	ACCTGTCACG
30301	ACCTCACCTT	CTGTTTCTTC	CACATTACCG	CAGAGTATCC	CTTCCTCCTC
30351	TTTTTCTGTG	ACTTCACTCC	TCACCCCAGG	CATGGTGAAG	ACTACAGACA
30401	CAAGCACAGA	ACCTGGAACC	AGTTTATCTC	CAAATCTGAG	TGGCACCTCA
30451	GTTGAAATAC	TGGCTGCCTC	TGAAGTCACC	ACAGATACAG	AGAAAATTCA
30501	TCCTTCTTCA	AGCATGGCAG	TGACCAATGT	GGGAACCACC	AGTTCTGGAC
30551	ATGAACTATA	TTCCTCTGTT	TCAATCCACT	CGGAGCCATC	CAAGGCTACA
30601	TACCCAGTGG	GTACTCCCTC	TTCCATGGCT	GAAACCTCTA	TTTCCACATC
30651	AATGCCTGCT	AATTTTGAGA	CCACAGGATT	TGAGGCTGAG	CCATTTTCTC
30701	ATTTGACTTC	TGGATTTAGG	AAGACAAACA	TGTCCCTGGA	CACCAGCTCA
30751	GTCACACCAA	CAAATACACC	TTCTTCTCCT	GGGTCCACTC	ACCTTTTACA
30801	GAGTTCCAAG	ACTGATTTCA	CCTCTTCTGC	AAAAACATCA	TCCCCAGACT
30851	GGCCTCCAGC	CTCACAGTAT	ACTGAAATTC	CAGTGGACAT	AATCACCCCC
30901	TTTAATGCTT	CTCCATCTAT	TACGGAGTCC	ACTGGGATAA	CCTCCTTCCC
30951	AGAATCCAGG	TTTACTATGT	CTGTAACAGA	AAGTACTCAT	CATCTGAGTA
31001	CAGATTTGCT	GCCTTCAGCT	GAGACTATTT	CCACTGGCAC	AGTGATGCCT
31051	TCTCTATCAG	AGGCCATGAC	TTCATTTGCC	ACCACTGGAG	TTCCACGAGC
31101	CATCTCAGGT	TCAGGTAGTC	CATTCTCTAG	GACAGAGTCA	GGCCCTGGGG
31151	ATGCTACTCT	GTCCACCATT	GCAGAGAGCC	TGCCTTCATC	CACTCCTGTG
31201	CCATTCTCCT	CTTCAACCTT	CACTACCACT	GATTCTTCAA	CCATCCCAGC
31251	CCTCCATGAG	ATAACTTCCT	CTTCAGCTAC	CCCATATAGA	GTGGACACCA
31301	GTCTTGGGAC	AGAGAGCAGC	ACTACTGAAG	GACGCTTGGT	TATGGTCAGT
31351	ACTTTGGACA	CTTCAAGCCA	ACCAGGCAGG	ACATCTTCAA	CACCCATTTT
31401	GGATACCAGA	ATGACAGAGA	GCGTTGAGCT	GGGAACAGTG	ACAAGTGCTT
31451	ATCAAGTTCC	TTCACTCTCA	ACACGGTTGA	CAAGAACTGA	TGGCATTATG
31501	GAACACATCA	CAAAAATACC	CAATGAAGCA	GCACACAGAG	GTACCATAAG
31551	ACCAGTCAAA	GGCCCTCAGA	CATCCACTTC	GCCTGCCAGT	CCTAAAGGAC
31601	TACACACAGG	AGGGACAAAA	AGAATGGAGA	CCACCACCAC	AGCTTTGAAG
31651	ACCACCACCA	CAGCTTTGAA	GACCACTTCC	AGAGCCACCT	TGACCACCAG
31701	TGTCTATACT	CCCACTTTGG	GAACACTGAC	TCCCCTCAAT	GCATCAAGGC
31751	AAATGGCCAG	CACAATCCTC	ACAGAAATGA	TGATCACAAC	CCCATATGTT

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)
31801 TTCCCTGATG TTCCAGAAAC GACATCCTCA TTGGCTACCA GCCTGGGAGC
31851 AGAAACCAGC ACAGCTCTTC CCAGGACAAC CCCATCTGTT CTCAATAGAG
31901 AATCAGAGAC CACAGCCTCA CTGGTCTCTC GTTCTGGGGC AGAGAGAAGT
31951 CCGGTTATTC AAACTCTAGA TGTTTCTTCT AGTGAGCCAG ATACAACAGC
32001 TTCATGGGTT ATCCATCCTG CAGAGACCAT CCCAACTGTT TCCAAGACAA
32051 CCCCCAATTT TTTCCACAGT GAATTAGACA CTGTATCTTC CACAGCCACC
32101 AGTCATGGGG CAGACGTCAG CTCAGCCATT CCAACAAATA TCTCACCTAG
32151 TGAACTAGAT GCACTGACCC CACTGGTCAC TATTTCGGGG ACAGATACTA
32201 GTACAACATT CCCAACACTG ACTAAGTCCC CACATGAAAC AGAGACAAGA
32251 ACCACATGGC TCACTCATCC TGCAGAGACC AGCTCAACTA TTCCCAGAAC
32301 AATCCCCAAT TTTTCTCATC ATGAATCAGA TGCCACACCT TCAATAGCCA
32351 CCAGTCCTGG GGCAGAAACC AGTTCAGCTA TTCCAATTAT GACTGTCTCA
32401 CCTGGTGCAG AAGATCTGGT GACCTCACAG GTCACTAGTT CTGGGACAGA
32451 CAGAAATATG ACTATTCCAA CTTTGACTCT TTCTCCTGGT GAACCAAAGA
32501 CGATAGCCTC ATTAGTCACC CATCCTGAAG CACAGACAAG TTCGGCCATT
32551 CCAACTTCAA CTATCTCGCC TGCTGTATCA CGGTTGGTGA CCTCAATGGT
32601 CACCAGTTTG GCGGCAAAGA CAAGTACAAC TAATCGAGCT CTGACAAACT
32651 CCCCTGGTGA ACCAGCTACA ACAGTTTCAT TGGTCACGCA TCCTGCACAG
32701 ACCAGCCCAA CAGTTCCCTG GACAACTTCC ATTTTTTTCC ATAGTAAATC
32751 AGACACCACA CCTTCAATGA CCACCAGTCA TGGGGCAGAA TCCAGTTCAG
32801 CTGTTCCAAC TCCAACTGTT TCAACTGAGG TACCAGGAGT AGTGACCCCT
32851 TTGGTCACCA GTTCTAGGGC AGTGATCAGT ACAACTATTC CAATTCTGAC
32901 TCTTTCTCCT GGTGAACCAG AGACCACACC TTCAATGGCC ACCAGTCATG
32951 GGGAAGAAGC CAGTTCTGCT ATTCCAACTC CAACTGTTTC ACCTGGGGTA
33001 CCAGGAGTGG TGACCTCTCT GGTCACTAGT TCTAGGGCAG TGACTAGTAC
33051 AACTATTCCA ATTCTGACTT TTTCTCTTGG TGAACCAGAG ACCACACCTT
33101 CAATGGCCAC CAGTCATGGG ACAGAAGCTG GCTCAGCTGT TCCAACTGTT
33151 TTACCTGAGG TACCAGGAAT GGTGACCTCT CTGGTTGCTA GTTCTAGGGC
33201 AGTAACCAGT ACAACTCTTC CAACTCTGAC TCTTTCTCCT GGTGAACCAG
33251 AGACCACACC TTCAATGGCC ACCAGTCATG GGGCAGAAGC CAGCTCAACT
33301 GTTCCAACTG TTTCACCTGA GGTACCAGGA GTGGTGACCT CTCTGGTCAC
33351 TAGTTCTAGT GGAGTAAACA GTACAAGTAT TCCAACTCTG ATTCTTTCTC
33401 CTGGTGAACT AGAAACCACA CCTTCAATGG CCACCAGTCA TGGGGCAGAA
33451 GCCAGCTCAG CTGTTCCAAC TCCAACTGTT TCACCTGGGG TATCAGGAGT
33501 GGTGACCCCT CTGGTCACTA GTTCCAGGGC AGTGACCAGT ACAACTATTC
33551 CAATTCTAAC TCTTTCTTCT AGTGAGCCAG AGACCACACC TTCAATGGCC

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)
33601 ACCAGTCATG GGGTAGAAGC CAGCTCAGCT GTTCTAACTG TTTCACCTGA
33651 GGTACCAGGA ATGGTGACCT CTCTGGTCAC TAGTTCTAGA GCAGTAACCA
33701 GTACAACTAT TCCAACTCTG ACTATTTCTT CTGATGAACC AGAGACCACA
33751 ACTTCATTGG TCACCCATTC TGAGGCAAAG ATGATTTCAG CCATTCCAAC
33801 TTTAGCTGTC TCCCCTACTG TACAAGGGCT GGTGACTTCA CTGGTCACTA
33851 GTTCTGGGTC AGAGACCAGT GCGTTTTCAA ATCTAACTGT TGCCTCAAGT
33901 CAACCAGAGA CCATAGACTC ATGGGTCGCT CATCCTGGGA CAGAAGCAAG
33951 TTCTGTTGTT CCAACTTTGA CTGTCTCCAC TGGTGAGCCG TTTACAAATA
34001 TCTCATTGGT CACCCATCCT GCAGAGAGTA GCTCAACTCT TCCCAGGACA
34051 ACCTCAAGGT TTTCCCACAG TGAATTAGAC ACTATGCCTT CTACAGTCAC
34101 CAGTCCTGAG GCAGAATCCA GCTCAGCCAT TTCAACTACT ATTTCACCTG
34151 GTATACCAGG TGTGCTGACA TCACTGGTCA CTAGCTCTGG GAGAGACATC
34201 AGTGCAACTT TTCCAACAGT GCCTGAGTCC CCACATGAAT CAGAGGCAAC
34251 AGCCTCATGG GTTACTCATC CTGCAGTCAC CAGCACAACA GTTCCCAGGA
34301 CAACCCCTAA TTATTCTCAT AGTGAACCAG ACACCACACC ATCAATAGCC
34351 ACCAGTCCTG GGGCAGAAGC CACTTCAGAT TTTCCAACAA TAACTGTCTC
34401 ACCTGATGTA CCAGATATGG TAACCTCACA GGTCACTAGT TCTGGGACAG
34451 ACACCAGTAT AACTATTCCA ACTCTGACTC TTTCTTCTGG TGAGCCAGAG
34501 ACCACAACCT CATTTATCAC CTATTCTGAG ACACACACAA GTTCAGCCAT
34551 TCCAACTCTC CCTGTCTCCC CTGGTGCATC AAAGATGCTG ACCTCACTGG
34601 TCATCAGTTC TGGGACAGAC AGCACTACAA CTTTCCCAAC ACTGACGGAG
34651 ACCCCATATG AACCAGAGAC AACAGCCATA CAGCTCATTC ATCCTGCAGA
34701 GACCAACACA ATGGTTCCCA AGACAACTCC CAAGTTTTCC CATAGTAAGT
34751 CAGACACCAC ACTCCCAGTA GCCATCACCA GTCCTGGGCC AGAAGCCAGT
34801 TCAGCTGTTT CAACGACAAC TATCTCACCT GATATGTCAG ATCTGGTGAC
34851 CTCACTGGTC CCTAGTTCTG GGACAGACAC CAGTACAACC TTCCCAACAT
34901 TGAGTGAGAC CCCATATGAA CCAGAGACTA CAGTCACGTG GCTCACTCAT
34951 CCTGCAGAAA CCAGCACAAC GGTTTCTGGG ACAATTCCCA ACTTTTCCCA
35001 TAGGGGATCA GACACTGCAC CCTCAATGGT CACCAGTCCT GGAGTAGACA
35051 CGAGGTCAGG TGTTCCAACT ACAACCATCC CACCCAGTAT ACCAGGGGTA
35101 GTGACCTCAC AGGTCACTAG TTCTGCAACA GACACTAGTA CAGCTATTCC
35151 AACTTTGACT CCTTCTCCTG GTGAACCAGA GACCACAGCC TCATCAGCTA
35201 CCCATCCTGG GACACAGACT GGCTTCACTG TTCCAATTCG GACTGTTCCC
35251 TCTAGTGAGC CAGATACAAT GGCTTCCTGG GTCACTCATC CTCCACAGAC
35301 CAGCACACCT GTTTCCAGAA CAACCTCCAG TTTTTCCCAT AGTAGTCCAG
35351 ATGCCACACC TGTAATGGCC ACCAGTCCTA GGACAGAAGC CAGTTCAGCT
35401 GTACTGACAA CAATCTCACC TGGTGCACCA GAGATGGTGA CTTCACAGAT

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)
35451 CACTAGTTCT GGGGCAGCAA CCAGTACAAC TGTTCCAACT TTGACTCATT
35501 CTCCTGGTAT GCCAGAGACC ACAGCCTTAT TGAGCACCCA TCCCAGAACA
35551 GGGACAAGTA AAACATTTCC TGCTTCAACT GTGTTTCCTC AAGTATCAGA
35601 GACCACAGCC TCACTCACCA TTAGACCTGG TGCAGAGACT AGCACAGCTC
35651 TCCCAACTCA GACAACATCC TCTCTCTTCA CCCTACTTGT AACTGGAACC
35701 AGCAGAGTTG ATCTAAGTCC AACTGCTTCA CCTGGTGTTT CTGCAAAAAC
35751 AGCCCCACTT TCCACCCATC CAGGGACAGA GACCAGCACA ATGATTCCAA
35801 CTTCAACTCT TTCCCTTGGT TTACTAGAGA CTACAGGCTT ACTGGCCACC
35851 AGCTCTTCAG CAGAGACCAG CACGAGTACT CTAACTCTGA CTGTTTCCCC
35901 TGCTGTCTCT GGGCTTTCCA GTGCCTCTAT AACAACTGAT AAGCCCCAAA
35951 CTGTGACCTC CTGGAACACA GAAACCTCAC CATCTGTAAC TTCAGTTGGA
36001 CCCCCAGAAT TTTCCAGGAC TGTCACAGGC ACCACTATGA CCTTGATACC
36051 ATCAGAGATG CCAACACCAC CTAAAACCAG TCATGGAGAA GGAGTGAGTC
36101 CAACCACTAT CTTGAGAACT ACAATGGTTG AAGCCACTAA TTTAGCTACC
36151 ACAGGTTCCA GTCCCACTGT GGCCAAGACA ACAACCACCT TCAATACACT
36201 GGCTGGAAGC CTCTTTACTC CTCTGACCAC ACCTGGGATG TCCACCTTGG
36251 CCTCTGAGAG TGTGACCTCA AGAACAAGTT ATAACCATCG GTCCTGGATC
36301 TCCACCACCA GCAGTTATAA CCGTCGGTAC TGGACCCCTG CCACCAGCAC
36351 TCCAGTGACT TCTACATTCT CCCCAGGGAT TTCCACATCC TCCATCCCCA
36401 GCTCCACAGC AGCCACAGTC CCATTCATGG TGCCATTCAC CCTCAACTTC
36451 ACCATCACCA ACCTGCAGTA CGAGGAGGAC ATGCGGCACC CTGGTTCCAG
36501 GAAGTTCAAC GCCACAGAGA GAGAACTGCA GGGTCTGCTC AAACCCTTGT
36551 TCAGGAATAG CAGTCTGGAA TACCTCTATT CAGGCTGCAG ACTAGCCTCA
36601 CTCAGGCCAG AGAAGGATAG CTCAGCCATG GCAGTGGATG CCATCTGCAC
36651 ACATCGCCCT GACCCTGAAG ACCTCGGACT GGACAGAGAG CGACTGTACT
36701 GGGAGCTGAG CAATCTGACA AATGGCATCC AGGAGCTGGG CCCCTACACC
36751 CTGGACCGGA ACAGTCTCTA TGTCAATGGT TTCACCCATC GAAGCTCTAT
36801 GCCCACCACC AGCACTCCTG GGACCTCCAC AGTGGATGTG GGAACCTCAG
36851 GGACTCCATC CTCCAGCCCC AGCCCCACGG CTGCTGGCCC TCTCCTGATG
36901 CCGTTCACCC TCAACTTCAC CATCACCAAC CTGCAGTACG AGGAGGACAT
36951 GCGTCGCACT GGCTCCAGGA AGTTCAACAC CATGGAGAGT GTCCTGCAGG
37001 GTCTGCTCAA GCCCTTGTTC AAGAACACCA GTGTTGGCCC TCTGTACTCT
37051 GGCTGCAGAT TGACCTTGCT CAGGCCCGAG AAAGATGGGG CAGCCACTGG
37101 AGTGGATGCC ATCTGCACCC ACCGCCTTGA CCCCAAAAGC CCTGGACTCA
37151 ACAGGGAGCA GCTGTACTGG GAGCTAAGCA AACTGACCAA TGACATTGAA
37201 GAGCTGGGCC CCTACACCCT GGACAGGAAC AGTCTCTATG TCAATGGTTT

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)
37251 CACCCATCAG AGCTCTGTGT CCACCACCAG CACTCCTGGG ACCTCCACAG
37301 TGGATCTCAG AACCTCAGGG ACTCCATCCT CCCTCTCCAG CCCCACAATT
37351 ATGGCTGCTG GCCCTCTCCT GGTACCATTC ACCCTCAACT TCACCATCAC
37401 CAACCTGCAG TATGGGGAGG ACATGGGTCA CCCTGGCTCC AGGAAGTTCA
37451 ACACCACAGA GAGGGTCCTG CAGGGTCTGC TTGGTCCCAT ATTCAAGAAC
37501 ACCAGTGTTG GCCCTCTGTA CTCTGGCTGC AGACTGACCT CTCTCAGGTC
37551 TGAGAAGGAT GGAGCAGCCA CTGGAGTGGA TGCCATCTGC ATCCATCATC
37601 TTGACCCCAA AAGCCCTGGA CTCAACAGAG AGCGGCTGTA CTGGGAGCTG
37651 AGCCAACTGA CCAATGGCAT CAAAGAGCTG GGCCCCTACA CCCTGGACAG
37701 GAACAGTCTC TATGTCAATG GTTTCACCCA TCGGACCTCT GTGCCCACCA
37751 CCAGCACTCC TGGGACCTCC ACAGTGGACC TTGGAACCTC AGGGACTCCA
37801 TTCTCCCTCC CAAGCCCCGC AACTGCTGGC CCTCTCCTGG TGCTGTTCAC
37851 CCTCAACTTC ACCATCACCA ACCTGAAGTA TGAGGAGGAC ATGCATCGCC
37901 CTGGCTCCAG GAAGTTCAAC ACCACTGAGA GGGTCCTGCA GACTCTGCTT
37951 GGTCCTATGT TCAAGAACAC CAGTGTTGGC CTTCTGTACT CTGGCTGCAG
38001 ACTGACCTTG CTCAGGTCCG AGAAGGATGG AGCAGCCACT GGAGTGGATG
38051 CCATCTGCAC CCACCGTCTT GACCCCAAAA GCCCTGGACT GGACAGAGAG
38101 CAGCTATACT GGGAGCTGAG CCAGCTGACC AATGGCATCA AAGAGCTGGG
38151 CCCCTACACC CTGGACAGGA ACAGTCTCTA TGTCAATGGT TTCACCCATT
38201 GGATCCCTGT GCCCACCAGC AGCACTCCTG GGACCTCCAC AGTGGACCTT
38251 GGGTCAGGGA CTCCATCCTC CCTCCCCAGC CCCACAGCTG CTGGCCCTCT
38301 CCTGGTGCCA TTCACCCTCA ACTTCACCAT CACCAACCTG CAGTACGAGG
38351 AGGACATGCA TCACCCAGGC TCCAGGAAGT TCAACACCAC GGAGCGGGTC
38401 CTGCAGGGTC TGCTTGGTCC CATGTTCAAG AACACCAGTG TCGGCCTTCT
38451 GTACTCTGGC TGCAGACTGA CCTTGCTCAG GTCCGAGAAG GATGGAGCAG
38501 CCACTGGAGT GGATGCCATC TGCACCCACC GTCTTGACCC CAAAAGCCCT
38551 GGAGTGGACA GGGAGCAGCT ATACTGGGAG CTGAGCCAGC TGACCAATGG
38601 CATCAAAGAG CTGGGTCCCT ACACCCTGGA CAGAAACAGT CTCTATGTCA
38651 ATGGTTTCAC CCATCAGACC TCTGCGCCCA ACACCAGCAC TCCTGGGACC
38701 TCCACAGTGG ACCTTGGGAC CTCAGGGACT CCATCCTCCC TCCCCAGCCC
38751 TACATCNGCT GGCCCTCTCC TGGTNCCNTT CACCCTCAAC TTCACCATCA
38801 CCAACCTGCA GTACGAGGAG GACATGCGGC ACCCNGGNTC CAGGAAGTTC
38851 AACACCACNG AGAGGGTNCT GCAGGGTCTG CTNAAGCCCC TNTTCAAGAG
38901 CACCAGTGTT GGCCCTCTGT ACTCTGGCTG CAGACTGACC TTGCTCAGGT
38951 CCGAGAAGGA TGGAGCAGCC ACTGGAGTGG ATGCCATCTG CACCCACCGT
39001 CTTGACCCCA AAAGCCCTGG AGTGGACAGG GAGCAGCTAT ACTGGGAGCT
39051 GAGCCAGCTG ACCAATGGCA TCAAAGAGCT GGGTCCCTAC ACCCTGGACA

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)
39101 GAAACAGTCT CTATGTCAAT GGTTTCACCC ATCAGACCTC TGCGCCCAAC
39151 ACCAGCACTC CTGGGACCTC CACAGTGGAC CTTGGGACCT CAGGGACTCC
39201 ATCCTCCCTC CCCAGCCCTA CATCTGCTGG CCCTCTCCTG GTGCCATTCA
39251 CCCTCAACTT CACCATCACC AACCTGCAGT ACGAGGAGGA CATGCATCAC
39301 CCAGGCTCCA GGAAGTTCAA CACCACGGAG CGGGTCCTGC AGGGTCTGCT
39351 TGGTCCCATG TTCAAGAACA CCAGTGTCGG CCTTCTGTAC TCTGGCTGCA
39401 GACTGACCTT GCTCAGGCCT GAGAAGAATG GGGCAGCCAC TGGAATGGAT
39451 GCCATCTGCA GCCACCGTCT TGACCCCAAA AGCCCTGGAC TCAACAGAGA
39501 GCAGCTGTAC TGGGAGCTGA GCCAGCTGAC CCATGGCATC AAAGAGCTGG
39551 GCCCCTACAC CCTGGACAGG AACAGTCTCT ATGTCAATGG TTTCACCCAT
39601 CGGAGCTCTG TGGCCCCCAC CAGCACTCCT GGGACCTCCA CAGTGGACCT
39651 TGGGACCTCA GGGACTCCAT CCTCCCTCCC CAGCCCCACA ACAGCTGTTC
39701 CTCTCCTGGT GCCGTTCACC CTCAACTTTA CCATCACCAA TCTGCAGTAT
39751 GGGGAGGACA TGCGTCACCC TGGCTCCAGG AAGTTCAACA CCACAGAGAG
39801 GGTCCTGCAG GGTCTGCTTG GTCCCTTGTT CAAGAACTCC AGTGTCGGCC
39851 CTCTGTACTC TGGCTGCAGA CTGATCTCTC TCAGGTCTGA GAAGGATGGG
39901 GCAGCCACTG GAGTGGATGC CATCTGCACC CACCACCTTA ACCCTCAAAG
39951 CCCTGGACTG GACAGGGAGC AGCTGTACTG GCAGCTGAGC CAGATGACCA
40001 ATGGCATCAA AGAGCTGGGC CCCTACACCC TGGACCGGAA CAGTCTCTAC
40051 GTCAATGGTT TCACCCATCG GAGCTCTGGG CTCACCACCA GCACTCCTTG
40101 GACTTCCACA GTTGACCTTG GAACCTCAGG GACTCCATCC CCCGTCCCCA
40151 GCCCCACAAC TGCTGGCCCT CTCCTGGTGC CATTCACCCT CAACTTCACC
40201 ATCACCAACC TGCAGTATGA GGAGGACATG CATCGCCCTG GATCTAGGAA
40251 GTTCAACACC ACAGAGAGGG TCCTGCAGGG TCTGCTTAGT CCCATTTTCA
40301 AGAACTCCAG TGTTGGCCCT CTGTACTCTG GCTGCAGACT GACCTCTCTC
40351 AGGCCCGAGA AGGATGGGGC AGCAACTGGA ATGGATGCTG TCTGCCTCTA
40401 CCACCCTAAT CCCAAAAGAC CTGGACTGGA CAGAGAGCAG CTGTACTGGG
40451 AGCTAAGCCA GCTGACCCAC AACATCACTG AGCTGGGCCC CTACAGCCTG
40501 GACAGGGACA GTCTCTATGT CAATGGTTTC ACCCATCAGA ACTCTGTGCC
40551 CACCACCAGT ACTCCTGGGA CCTCCACAGT GTACTGGGCA ACCACTGGGA
40601 CTCCATCCTC CTTCCCCGGC CACACAGAGC CTGGCCCTCT CCTGATACCA
40651 TTCACTTTCA ACTTTACCAT CACCAACCTG CATTATGAGG AAAACATGCA
40701 ACACCCTGGT TCCAGGAAGT TCAACACCAC GGAGAGGGTT CTGCAGGGTC
40751 TGCTCAAGCC CTTGTTCAAG AACACCAGTG TTGGCCCTCT GTACTCTGGC
40801 TGCAGACTGA CCTCTCTCAG GCCCGAGAAG GATGGGGCAG CAACTGGAAT
40851 GGATGCTGTC TGCCTCTACC ACCCTAATCC CAAAAGACCT GGGCTGGACA

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)				
40901	GAGAGCAGCT	GTACTGGGAG	CTAAGCCAGC	TGACCCACAA	CATCACTGAG
40951	CTGGGCCCCT	ACAGCCTGGA	CAGGGACAGT	CTCTATGTCA	ATGGTTTCAC
41001	CCATCAGAAC	TCTGTGCCCA	CCACCAGTAC	TCCTGGGACC	TCCACAGTGT
41051	ACTGGGCAAC	CACTGGGACT	CCATCCTCCT	TCCCCGGCCA	CACAGAGCCT
41101	GGCCCTCTCC	TGATACCATT	CACTTTCAAC	TTTACCATCA	CCAACCTGCA
41151	TTATGAGGAA	AACATGCAAC	ACCCTGGTTC	CAGGAAGTTC	AACACCACGG
41201	AGAGGGTTCT	GCAGGGTCTG	CTCAAGCCCT	TGTTCAAGAA	CACCAGTGTT
41251	GGCCCTCTGT	ACTCTGGCTG	CAGACTGACC	TTGCTCAGAC	CTGAGAAGCA
41301	TGAGGCAGCC	ACTGGAGTGG	ACACCATCTG	TACCCACCGC	GTTGATCCCA
41351	TCGGACCTGG	ACTGGACAGG	GAGCGGCTAT	ACTGGGAGCT	GAGCCAGCTG
41401	ACCAACAGCA	TTACCGAACT	GGGACCCTAC	ACCCTGGACA	GGGACAGTCT
41451	CTATGTCAAT	GGCTTCAACC	CTCGGAGCTC	TGTGCCAACC	ACCAGCACTC
41501	CTGGGACCTC	CACAGTGCAC	CTGGCAACCT	CTGGGACTCC	ATCCTCCCTG
41551	CCTGGCCACA	CAGCCCCTGT	CCCTCTCTTG	ATACCATTCA	CCCTCAACTT
41601	TACCATCACC	AACCTGCATT	ATGAGGAAAA	CATGCAACAC	CCTGGTTCCA
41651	GGAAGTTCAA	CACCACGGAG	AGGGTTCTGC	AGGGTCTGCT	CAAGCCCTTG
41701	TTCAAGAACA	CCAGTGTTGG	CCCTCTGTAC	TCTGGCTGCA	GACTGACCTT
41751	GCTCAGACCT	GAGAAGCATG	AGGCAGCCAC	TGGAGTGGAC	ACCATCTGTA
41801	CCCACCGCGT	TGATCCCATC	GGACCTGGAC	TGNACAGNGA	GCNGCTNTAC
41851	TGGGAGCTNA	GCCANCTGAC	CAANNNCATC	NNNGAGCTGG	GNCCCTACAC
41901	CCTGGACAGG	NACAGTCTCT	ATGTCAATGG	TTTCACCCAT	CNGANCTCTG
41951	NGCCCACCAC	CAGCACTCCT	GGGACCTCCA	CAGTGNACNT	NGGNACCTCN
42001	GGGACTCCAT	CCTCCNTCCC	CNGCCNCACA	TCTGCTGGCC	CTCTCCTGGT
42051	GCCATTCACC	CTCAACTTCA	CCATCACCAA	CCTGCAGTAC	GAGGAGGACA
42101	TGCATCACCC	AGGCTCCAGG	AAGTTCAACA	CCACGGAGCG	GGTCCTGCAG
42151	GGTCTGCTTG	GTCCCATGTT	CAAGAACACC	AGTGTCGGCC	TTCTGTACTC
42201	TGGCTGCAGA	CTGACCTTGC	TCAGGCCTGA	GAAGAATGGG	GCAGCCACTG
42251	GAATGGATGC	CATCTGCAGC	CACCGTCTTG	ACCCCAAAAG	CCCTGGACTC
42301	GACAGAGAGC	AGCTGTACTG	GGAGCTGAGC	CAGCTGACCC	ATGGCATCAA
42351	AGAGCTGGGC	CCCTACACCC	TGGACAGGAA	CAGTCTCTAT	GTCAATGGTT
42401	TCACCCATCG	GAGCTCTGTG	GCCCCCACCA	GCACTCCTGG	GACCTCCACA
42451	GTGGACCTTG	GGACCTCAGG	GACTCCATCC	TCCCTCCCCA	GCCCCACAAC
42501	AGCTGTTCCT	CTCCTGGTGC	CGTTCACCCT	CAACTTTACC	ATCACCAATC
42551	TGCAGTATGG	GGAGGACATG	CGTCACCCTG	GCTCCAGGAA	GTTCAACACC
42601	ACAGAGAGGG	TCCTGCAGGG	TCTGCTTGGT	CCCTTGTTCA	AGAACTCCAG
42651	TGTCGGCCCT	CTGTACTCTG	GCTGCAGACT	GATCTCTCTC	AGGTCTGAGA
42701	AGGATGGGGC	AGCCACTGGA	GTGGATGCCA	TCTGCACCCA	CCACCTTAAC

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)
42751 CCTCAAAGCC CTGGACTGGA CAGGGAGCAG CTGTACTGGC AGCTGAGCCA
42801 GATGACCAAT GGCATCAAAG AGCTGGGCCC CTACACCCTG GACCGGAACA
42851 GTCTCTACGT CAATGGTTTC ACCCATCGGA GCTCTGGGCT CACCACCAGC
42901 ACTCCTTGGA CTTCCACAGT TGACCTTGGA ACCTCAGGGA CTCCATCCCC
42951 CGTCCCCAGC CCCACAACTG CTGGCCCTCT CCTGGTGCCA TTCACCCTAA
43001 ACTTCACCAT CACCAACCTG CAGTATGAGG AGGACATGCA TCGCCCTGGA
43051 TCTAGGAAGT TCAACGCCAC AGAGAGGGTC CTGCAGGGTC TGCTTAGTCC
43101 CATATTCAAG AACTCCAGTG TTGGCCCTCT GTACTCTGGC TGCAGACTGA
43151 CCTCTCTCAG GCCCGAGAAG GATGGGGCAG CAACTGGAAT GGATGCTGTC
43201 TGCCTCTACC ACCCTAATCC CAAAAGACCT GGACTGGACA GAGAGCAGCT
43251 GTACTGGGAG CTAAGCCAGC TGACCCACAA CATCACTGAG CTGGGCCCCT
43301 ACAGCCTGGA CAGGGACAGT CTCTATGTCA ATGGTTTCAC CCATCAGAGC
43351 TCTATGACGA CCACCAGAAC TCCTGATACC TCCACAATGC ACCTGGCAAC
43401 CTCGAGAACT CCAGCCTCCC TGTCTGGACC TACGACCGCC AGCCCTCTCC
43451 TGGTGCTATT CACAATCAAC TGCACCATCA CCAACCTGCA GTACGAGGAG
43501 GACATGCGTC GCACTGGCTC CAGGAAGTTC AACACCATGG AGAGTGTCCT
43551 GCAGGGTCTG CTCAAGCCCT TGTTCAAGAA CACCAGTGTT GGCCCTCTGT
43601 ACTCTGGCTG CAGATTGACC TTGCTCAGGC CCAAGAAAGA TGGGGCAGCC
43651 ACTGGAGTGG ATGCCATCTG CACCCACCGC CTTGACCCCA AAAGCCCTGG
43701 ACTCAACAGG GAGCAGCTGT ACTGGGAGCT AAGCAAACTG ACCAATGACA
43751 TTGAAGAGCT GGGCCCCTAC ACCCTGGACA GGAACAGTCT CTATGTCAAT
43801 GGTTTCACCC ATCAGAGCTC TGTGTCCACC ACCAGCACTC CTGGGACCTC
43851 CACAGTGGAT CTCAGAACCT CAGGGACTCC ATCCTCCCTC TCCAGCCCCA
43901 CAATTATGNC NNCTGNCCCT CTCCTGNTNC CNTTCACCNT CAACTTNACC
43951 ATCACCAACC TGCANTANGN GGANNACATG CNNCNCCCNG GNTCCAGGAA
44001 GTTCAACACC ACNGAGAGGG TCCTACAGGG TCTGCTCAGG CCCTTGTTCA
44051 AGAACACCAG TGTCAGCTCT CTGTACTCTG GTTGCAGACT GACCTTGCTC
44101 AGGCCTGAGA AGGATGGGGC AGCCACCAGA GTGGATGCTG CCTGCACCTA
44151 CCGCCCTGAT CCCAAAAGCC CTGGACTGGA CAGAGAGCAA CTATACTGGG
44201 AGCTGAGCCA GCTAACCCAC AGCATCACTG AGCTGGGACC CTACACCCTG
44251 GACAGGGTCA GTCTCTATGT CAATGGCTTC AACCCTCGGA GCTCTGTGCC
44301 AACCACCAGC ACTCCTGGGA CCTCCACAGT GCACCTGGCA ACCTCTGGGA
44351 CTCCATCCTC CCTGCCTGGC CACACANCNN CTGNCCCTCT CCTGNTNCCN
44401 TTCACCNTCA ACTTNACCAT CACCAACCTG CANTANGNGG ANNACATGCN
44451 NCNCCCNGGN TCCAGGAAGT TCAACACCAC NGAGAGGGTT CTGCAGGGTC
44501 TGCTCAAACC CTTGTTCAGG AATAGCAGTC TGGAATACCT CTATTCAGGC

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)
44551 TGCAGACTAG CCTCACTCAG GCCAGAGAAG GATAGCTCAG CCATGGCAGT
44601 GGATGCCATC TGCACACATC GCCCTGACCC TGAAGACCTC GGACTGGACA
44651 GAGAGCGACT GTACTGGGAG CTGAGCAATC TGACAAATGG CATCCAGGAG
44701 CTGGGCCCCT ACACCCTGGA CCGGAACAGT CTCTACGTCA ATGGTTTCAC
44751 CCATCGGAGC TCTGGGCTCA CCACCAGCAC TCCTTGGACT TCCACAGTTG
44801 ACCTTGGAAC CTCAGGGACT CCATCCCCCG TCCCCAGCCC CACAACTGCT
44851 GGCCCTCTCC TGGTGCCATT CACCCTCAAC TTCACCATCA CCAACCTGCA
44901 GTATGAGGAG GACATGCATC GCCCTGGTTC CAGGAGGTTC AACACCACGG
44951 AGAGGGTTCT GCAGGGTCTG CTCACGCCCT TGTTCAAGAA CACCAGTGTT
45001 GGCCCTCTGT ACTCTGGCTG CAGACTGACC TTGCTCAGAC CTGAGAAGCA
45051 AGAGGCAGCC ACTGGAGTGG ACACCATCTG TACCCACCGC GTTGATCCCA
45101 TCGGACCTGG ACTGGACAGA GAGCGGCTAT ACTGGGAGCT GAGCCAGCTG
45151 ACCAACAGCA TCACAGAGCT GGGACCCTAC ACCCTGGATA GGGACAGTCT
45201 CTATGTCAAT GGCTTCAACC CTTGGAGCTC TGTGCCAACC ACCAGCACTC
45251 CTGGGACCTC CACAGTGCAC CTGGCAACCT CTGGGACTCC ATCCTCCCTG
45301 CCTGGCCACA CAGCCCCTGT CCCTCTCTTG ATACCATTCA CCCTCAACTT
45351 TACCATCACC GACCTGCATT ATGAAGAAAA CATGCAACAC CCTGGTTCCA
45401 GGAAGTTCAA CACCACGGAG AGGGTTCTGC AGGGTCTGCT CAAGCCCTTG
45451 TTCAAGAGCA CCAGCGTTGG CCCTCTGTAC TCTGGCTGCA GACTGACCTT
45501 GCTCAGACCT GAGAAACATG GGGCAGCCAC TGGAGTGGAC GCCATCTGCA
45551 CCCTCCGCCT TGATCCCACT GGTCCTGGAC TGGACAGAGA GCGGCTATAC
45601 TGGGAGCTGA GCCAGCTGAC CAACAGCGTT ACAGAGCTGG GCCCCTACAC
45651 CCTGGACAGG GACAGTCTCT ATGTCAATGG CTTCACCCAT CGGAGCTCTG
45701 TGCCAACCAC CAGTATTCCT GGGACCTCTG CAGTGCACCT GGAAACCTCT
45751 GGGACTCCAG CCTCCCTCCC TGGCCACACA GCCCCTGGCC CTCTCCTGGT
45801 GCCATTCACC CTCAACTTCA CTATCACCAA CCTGCAGTAT GAGGAGGACA
45851 TGCGTCACCC TGGTTCCAGG AAGTTCAGCA CCACGGAGAG AGTCCTGCAG
45901 GGTCTGCTCA AGCCCTTGTT CAAGAACACC AGTGTCAGCT CTCTGTACTC
45951 TGGTTGCAGA CTGACCTTGC TCAGGCCTGA GAAGGATGGG GCAGCCACCA
46001 GAGTGGATGC TGTCTGCACC CATCGTCCTG ACCCCAAAAG CCCTGGACTG
46051 GACAGAGAGC GGCTGTACTG GAAGCTGAGC CAGCTGACCC ACGGCATCAC
46101 TGAGCTGGGC CCCTACACCC TGGACAGGCA CAGTCTCTAT GTCAATGGTT
46151 TCACCCATCA GAGCTCTATG ACGACCACCA GAACTCCTGA TACCTCCACA
46201 ATGCACCTGG CAACCTCGAG AACTCCAGCC TCCCTGTCTG GACCTACGAC
46251 CGCCAGCCCT CTCCTGGTGC TATTCACAAT TAACTTCACC ATCACTAACC
46301 TGCGGTATGA GGAGAACATG CATCACCCTG GCTCTAGAAA GTTTAACACC
46351 ACGGAGAGAG TCCTTCAGGG TCTGCTCAGG CCTGTGTTCA AGAACACCAG

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)
46401 TGTTGGCCCT CTGTACTCTG GCTGCAGACT GACCACGCTC AGGCCCAAGA
46451 AGGATGGGGC AGCCACCAAA GTGGATGCCA TCTGCACCTA CCGCCCTGAT
46501 CCCAAAAGCC CTGGACTGGA CAGAGAGCAG CTATACTGGG AGCTGAGCCA
46551 GCTAACCCAC AGCATCACTG AGCTGGGCCC CTACACCCAG GACAGGGACA
46601 GTCTCTATGT CAATGGCTTC ACCCATCGGA GCTCTGTGCC AACCACCAGT
46651 ATTCCTGGGA CCTCTGCAGT GCACCTGGAA ACCTCTGGGA CTCCAGCCTC
46701 CCTCCCTGGC CACACAGCCC CTGGCCCTCT CCTGGTGCCA TTCACCCTCA
46751 ACTTCACTAT CACCAACCTG CAGTATGAGG AGGACATGCG TCACCCTGGT
46801 TCCAGGAAGT TCAACACCAC GGAGAGAGTC CTGCAGGGTC TGCTCAAGCC
46851 CTTGTTCAAG AGCACCAGTG TTGGCCCTCT GTACTCTGGC TGCAGACTGA
46901 CCTTGCTCAG GCCTGAAAAA CGTGGGGCAG CCACCGGCGT GGACACCATC
46951 TGCACTCACC GCCTTGACCC TCTAAACCCA GGACTGGACA GAGAGCAGCT
47001 ATACTGGGAG CTGAGCAAAC TGACCCGTGG CATCATCGAG CTGGGCCCCT
47051 ACCTCCTGGA CAGAGGCAGT CTCTATGTCA ATGGTTTCAC CCATCGGACC
47101 TCTGTGCCCA CCACCAGCAC TCCTGGGACC TCCACAGTGG ACCTTGGAAC
47151 CTCAGGGACT CCATTCTCCC TCCCAAGCCC CGCANCNNCT GNCCCTCTCC
47201 TGNTNCCNTT CACCNTCAAC TTNACCATCA CCAACCTGCA NTANGNGGAN
47251 NACATGCNNC NCCCNGGNTC CAGGAAGTTC AACACCACNG AGAGGGTCCT
47301 GCAGACTCTG CTTGGTCCTA TGTTCAAGAA CACCAGTGTT GGCCTTCTGT
47351 ACTCTGGCTG CAGACTGACC TTGCTCAGGT CCGAGAAGGA TGGAGCAGCC
47401 ACTGGAGTGG ATGCCATCTG CACCCACCGT CTTGACCCCA AAAGCCCTGG
47451 AGTGGACAGG GAGCAACTAT ACTGGGAGCT GAGCCAGCTG ACCAATGGCA
47501 TTAAAGAACT GGGCCCCTAC ACCCTGGACA GGAACAGTCT CTATGTCAAT
47551 GGGTTCACCC ATTGGATCCC TGTGCCCACC AGCAGCACTC CTGGGACCTC
47601 CACAGTGGAC CTTGGGTCAG GGACTCCATC CTCCCTCCCC AGCCCCACAA
47651 CTGCTGGCCC TCTCCTGGTG CCGTTCACCC TCAACTTCAC CATCACCAAC
47701 CTGAAGTACG AGGAGGACAT GCATTGCCCT GGCTCCAGGA AGTTCAACAC
47751 CACAGAGAGA GTCCTGCAGA GTCTGCTTGG TCCCATGTTC AAGAACACCA
47801 GTGTTGGCCC TCTGTACTCT GGCTGCAGAC TGACCTTGCT CAGGTCCGAG
47851 AAGGATGGAG CAGCCACTGG AGTGGATGCC ATCTGCACCC ACCGTCTTGA
47901 CCCCAAAAGC CCTGGAGTGG ACAGGGAGCA GCTATACTGG GAGCTGAGCC
47951 AGCTGACCAA TGGCATCAAA GAGCTGGGTC CCTACACCCT GGACAGAAAC
48001 AGTCTCTATG TCAATGGTTT CACCCATCAG ACCTCTGCGC CCAACACCAG
48051 CACTCCTGGG ACCTCCACAG TGGACCTTGG GACCTCAGGG ACTCCATCCT
48101 CCCTCCCCAG CCCTACANCN NCTGNCCCTC TCCTGNTNCC NTTCACCNTC
48151 AACTTNACCA TCACCAACCT GCANTANGNG GANNACATGC NNCNCCCNGG

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)
48201 NTCCAGGAAG TTCAACACCA CNGAGNGNGT NCTGCAGGGT CTGCTNNNNC
48251 CCNTNTTCAA GAACNCCAGT GTNGGCCNTC TGTACTCTGG CTGCAGACTG
48301 ACCTNNCTCA GGNCNGAGAA GNATGGNGCA GCCACTGGAN TGGATGCCAT
48351 CTGCANCCAC CNNCNTNANC CCAAAAGNCC TGGACTGNAC AGNGAGCNGC
48401 TNTACTGGGA GCTNAGCCAN CTGACCAANN NCATCNNNGA GCTGGGNCCC
48451 TACACCCTGG ACAGGNACAG TCTCTATGTC AATGGTTTCA CCCATTGGAT
48501 CCCTGTGCCC ACCAGCAGCA CTCCTGGGAC CTCCACAGTG GACCTTGGGT
48551 CAGGGACTCC ATCCTCCCTC CCCAGCCCCA CAACTGCTGG CCCTCTCCTG
48601 GTGCCGTTCA CCCTCAACTT CACCATCACC AACCTGAAGT ACGAGGAGGA
48651 CATGCATTGC CCTGGCTCCA GGAAGTTCAA CACCACAGAG AGAGTCCTGC
48701 AGAGTCTGCT TGGTCCCATG TTCAAGAACA CCAGTGTTGG CCCTCTGTAC
48751 TCTGGCTGCA GACTGACCTC GCTCAGGTCC GAGAAGGATG GAGCAGCCAC
48801 TGGAGTGGAT GCCATCTGCA CCCACCGTGT TGACCCCAAA AGCCCTGGAG
48851 TGGACAGGGA GCAGCTATAC TGGGAGCTGA GCCAGCTGAC CAATGGCATC
48901 AAAGAGCTGG GTCCCTACAC CCTGGACAGA AACAGTCTCT ATGTCAATGG
48951 TTTCACCCAT CAGACCTCTG CGCCCAACAC CAGCACTCCT GGGACCTCCA
49001 CAGTGNACNT NGGNACCTCN GGGACTCCAT CCTCCNTCCC CNGCCNCACA
49051 TCTGCTGGCC CTCTCCTGGT GCCATTCACC CTCAACTTCA CCATCACCAA
49101 CCTGCAGTAC GAGGAGGACA TGCATCACCC AGGCTCCAGG AAGTTCAACA
49151 CCACGGAGCG GGTCCTGCAG GGTCTGCTTG GTCCCATGTT CAAGAACACC
49201 AGTGTCGGCC TTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGCCTGA
49251 GAAGAATGGG GCAACCACTG GAATGGATGC CATCTGCACC CACCGTCTTG
49301 ACCCCAAAAG CCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC
49351 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA
49401 CAGTCTCTAT GTCAATGGTT TCACCCATCN GANCTCTGNG CCCACCACCA
49451 GCACTCCTGG GACCTCCACA GTGNACNTNG GNACCTCNGG GACTCCATCC
49501 TCCNTCCCCN GCCNCACANC NNCTGNCCCT CTCCTGNTNC CNTTCACCNT
49551 CAACTTNACC ATCACCAACC TGCANTANGN GGANNACATG CNNCNCCCNG
49601 GNTCCAGGAA GTTCAACACC ACNGAGAGGG TTCTGCAGGG TCTGCTCAAA
49651 CCCTTGTTCA GGAATAGCAG TCTGGAATAC CTCTATTCAG GCTGCAGACT
49701 AGCCTCACTC AGGCCAGAGA AGGATAGCTC AGCCATGGCA GTGGATGCCA
49751 TCTGCACACA TCGCCCTGAC CCTGAAGACC TCGGACTGGA CAGAGAGCGA
49801 CTGTACTGGG AGCTGAGCAA TCTGACAAAT GGCATCCAGG AGCTGGGCCC
49851 CTACACCCTG GACCGGAACA GTCTCTATGT CAATGGTTTC ACCCATCGAA
49901 GCTCTATGCC CACCACCAGC ACTCCTGGGA CCTCCACAGT GGATGTGGGA
49951 ACCTCAGGGA CTCCATCCTC CAGCCCCAGC CCCACGACTG CTGGCCCTCT
50001 CCTGATACCA TTCACCCTCA ACTTCACCAT CACCAACCTG CAGTATGGGG

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)
50051 AGGACATGGG TCACCCTGGC TCCAGGAAGT TCAACACCAC AGAGAGGGTC
50101 CTGCAGGGTC TGCTTGGTCC CATATTCAAG AACACCAGTG TTGGCCCTCT
50151 GTACTCTGGC TGCAGACTGA CCTCTCTCAG GTCTGAGAAG GATGGAGCAG
50201 CCACTGGAGT GGATGCCATC TGCATCCATC ATCTTGACCC CAAAAGCCCT
50251 GGACTCAACA GAGAGCGGCT GTACTGGGAG CTGAGCCAAC TGACCAATGG
50301 CATCAAAGAG CTGGGCCCCT ACACCCTGGA CAGGAACAGT CTCTATGTCA
50351 ATGGTTTCAC CCATCGGACC TCTGTGCCCA CCACCAGCAC TCCTGGGACC
50401 TCCACAGTGG ACCTTGGAAC CTCAGGGACT CCATTCTCCC TCCCAAGCCC
50451 CGCAACTGCT GGCCCTCTCC TGGTGCTGTT CACCCTCAAC TTCACCATCA
50501 CCAACCTGAA GTATGAGGAG GACATGCATC GCCCTGGCTC CAGGAAGTTC
50551 AACACCACTG AGAGGGTCCT GCAGACTCTG CTTGGTCCTA TGTTCAAGAA
50601 CACCAGTGTT GGCCTTCTGT ACTCTGGCTG CAGACTGACC TTGCTCAGGT
50651 CCGAGAAGGA TGGAGCAGCC ACTGGAGTGG ATGCCATCTG CACCCACCGT
50701 CTTGACCCCA AAAGCCCTGG ACTGNACAGN GAGCNGCTNT ACTGGGAGCT
50751 NAGCCANCTG ACCAANNNCA TCNNNGAGCT GGGNCCCTAC ACCCTGGACA
50801 GGNACAGTCT CTATGTCAAT GGTTTCACCC ATCNGANCTC TGNGCCCACC
50851 ACCAGCACTC CTGGGACCTC CACAGTGNAC NTNGGNACCT CNGGGACTCC
50901 ATCCTCCNTC CCCNGCCNCA CANCNNCTGN CCCTCTCCTG NTNCCNTTCA
50951 CCNTCAACTT NACCATCACC AACCTGCANT ANGNGGANNA CATGCNNCNC
51001 CCNGGNTCCA GGAAGTTCAA CACCACNGAG AGAGTCCTTC AGGGTCTGCT
51051 CAGGCCTGTG TTCAAGAACA CCAGTGTTGG CCCTCTGTAC TCTGGCTGCA
51101 GACTGACCTT GCTCAGGCCC AAGAAGGATG GGGCAGCCAC CAAAGTGGAT
51151 GCCATCTGCA CCTACCGCCC TGATCCCAAA AGCCCTGGAC TGGACAGAGA
51201 GCAGCTATAC TGGGAGCTGA GCCAGCTAAC CCACAGCATC ACTGAGCTGG
51251 GCCCCTACAC CCAGGACAGG GACAGTCTCT ATGTCAATGG CTTCACCCAT
51301 CGGAGCTCTG TGCCAACCAC CAGTATTCCT GGGACCTCTG CAGTGCACCT
51351 GGAAACCACT GGGACTCCAT CCTCCTTCCC CGGCCACACA GAGCCTGGCC
51401 CTCTCCTGAT ACCATTCACT TTCAACTTTA CCATCACCAA CCTGCGTTAT
51451 GAGGAAAACA TGCAACACCC TGGTTCCAGG AAGTTCAACA CCACGGAGAG
51501 GGTTCTGCAG GGTCTGCTCA CGCCCTTGTT CAAGAACACC AGTGTTGGCC
51551 CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGACCTGA GAAGCAGGAG
51601 GCAGCCACTG GAGTGGACAC CATCTGTACC CACCGCGTTG ATCCCATCGG
51651 ACCTGGACTG GACAGAGAGC GGCTATACTG GGAGCTGAGC CAGCTGACCA
51701 ACAGCATCAC AGAGCTGGGA CCCTACACCC TGGATAGGGA CAGTCTCTAT
51751 GTCGATGGCT TCAACCCTTG GAGCTCTGTG CCAACCACCA GCACTCCTGG
51801 GACCTCCACA GTGCACCTGG CAACCTCTGG GACTCCATCC CCCCTGCCTG

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)					
51851	GCCACACAGC	CCCTGTCCCT	CTCTTGATAC	CATTCACCCT	CAACTTTACC
51901	ATCACCGACC	TGCATTATGA	AGAAAACATG	CAACACCCTG	GTTCCAGGAA
51951	GTTCAACACC	ACGGAGAGGG	TTCTGCAGGG	TCTGCTCAAG	CCCTTGTTCA
52001	AGAGCACCAG	CGTTGGCCCT	CTGTACTCTG	GCTGCAGACT	GACCTTGCTC
52051	AGACCTGAGA	AACATGGGGC	AGCCACTGGA	GTGGACGCCA	TCTGCACCCT
52101	CCGCCTTGAT	CCCACTGGTC	CTGGACTGGA	CAGAGAGCGG	CTATACTGGG
52151	AGCTGAGCCA	GCTGACCAAC	AGCATCACAG	AGCTGGGACC	CTACACCCTG
52201	GATAGGGACA	GTCTCTATGT	CAATGGCTTC	AACCCTTGGA	GCTCTGTGCC
52251	AACCACCAGC	ACTCCTGGGA	CCTCCACAGT	GCACCTGGCA	ACCTCTGGGA
52301	CTCCATCCTC	CCTGCCTGGC	CACACAACTG	CTGGCCCTCT	CCTGGTGCCG
52351	TTCACCCTCA	ACTTCACCAT	CACCAACCTG	AAGTACGAGG	AGGACATGCA
52401	TTGCCCTGGC	TCCAGGAAGT	TCAACACCAC	AGAGAGAGTC	CTGCAGAGTC
52451	TGCATGGTCC	CATGTTCAAG	AACACCAGTG	TTGGCCCTCT	GTACTCTGGC
52501	TGCAGACTGA	CCTTGCTCAG	GTCCGAGAAG	GATGGAGCAG	CCACTGGAGT
52551	GGATGCCATC	TGCACCCACC	GTCTTGACCC	CAAAAGCCCT	GGACTGNACA
52601	GNGAGCNGCT	NTACTGGGAG	CTNAGCCANC	TGACCAANNN	CATCNNNGAG
52651	CTGGGNCCCT	ACACCCTGGA	CAGGNACAGT	CTCTATGTCA	ATGGTTTCAC
52701	CCATCNGANC	TCTGNGCCCA	CCACCAGCAC	TCCTGGGACC	TCCACAGTGN
52751	ACNTNGGNAC	CTCNGGGACT	CCATCCTCCN	TCCCCNGCCN	CACANCNNCT
52801	GNCCCTCTCC	TGNTNCCNTT	CACCNTCAAC	TTNACCATCA	CCAACCTGCA
52851	NTANGNGGAN	NACATGCNNC	NCCCNGGNTC	CAGGAAGTTC	AACACCACNG
52901	AGNGNGTNCT	GCAGGGTCTG	CTNNNNCCCN	TNTTCAAGAA	CNCCAGTGTN
52951	GGCCNTCTGT	ACTCTGGCTG	CAGACTGACC	TNNCTCAGGN	CNGAGAAGNA
53001	TGGNGCAGCC	ACTGGANTGG	ATGCCATCTG	CANCCACCNN	CNTNANCCCA
53051	AAAGNCCTGG	ACTGNACAGN	GAGCNGCTNT	ACTGGGAGCT	NAGCCANCTG
53101	ACCAACAGCA	TCACAGAGCT	GGGACCCTAC	ACCCTGGATA	GGGACAGTCT
53151	CTATGTCAAT	GGTTTCACCC	ATCGAAGCTC	TATGCCCACC	ACCAGTATTC
53201	CTGGGACCTC	TGCAGTGCAC	CTGGAAACCT	CTGGGACTCC	AGCCTCCCTC
53251	CCTGGCCACA	CAGCCCCTGG	CCCTCTCCTG	GTGCCATTCA	CCCTCAACTT
53301	CACTATCACC	AACCTGCAGT	ATGAGGAGGA	CATGCGTCAC	CCTGGTTCCA
53351	GGAAGTTCAA	CACCACGGAG	AGAGTCCTGC	AGGGTCTGCT	CAAGCCCTTG
53401	TTCAAGAGCA	CCAGTGTTGG	CCCTCTGTAC	TCTGGCTGCA	GACTGACCTT
53451	GCTCAGGCCT	GAAAAACGTG	GGGCAGCCAC	CGGCGTGGAC	ACCATCTGCA
53501	CTCACCGCCT	TGACCCTCTA	AACCCTGGAC	TGNACAGNGA	GCNGCTNTAC
53551	TGGGAGCTNA	GCCANCTGAC	CAANNNCATC	NNNGAGCTGG	GNCCCTACAC
53601	CCTGGACAGG	NACAGTCTCT	ATGTCAATGG	TTTCACCCAT	CNGANCTCTG
53651	NGCCCACCAC	CAGCACTCCT	GGGACCTCCA	CAGTGNACNT	NGGNACCTCN

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)
53701 GGGACTCCAT CCTCCNTCCC CNGCCNCACA NCNNCTGNCC CTCTCCTGNT
53751 NCCNTTCACC NTCAACTTNA CCATCACCAA CCTGCANTAN GNGGANNACA
53801 TGCNNCNCCC NGGNTCCAGG AAGTTCAACA CCACNGAGNG NGTNCTGCAG
53851 GGTCTGCTNN NNCCCNTNTT CAAGAACNCC AGTGTNGGCC NTCTGTACTC
53901 TGGCTGCAGA CTGACCTNNC TCAGGNCNGA GAAGNATGGN GCAGCCACTG
53951 GANTGGATGC CATCTGCANC CACCNNCNTN ANCCCAAAAG NCCTGGACTG
54001 NACAGNGAGC NGCTNTACTG GGAGCTNAGC CANCTGACCA ANNNCATCNN
54051 NGAGCTGGGN CCCTACACCC TGGACAGGNA CAGTCTCTAT GTCAATGGTT
54101 TTCACCCTCG GAGCTCTGTG CCAACCACCA GCACTCCTGG GACCTCCACA
54151 GTGCACCTGG CAACCTCTGG GACTCCATCC TCCCTGCCTG GCCACACAGC
54201 CCCTGTCCCT CTCTTGATAC CATTCACCCT CAACTTTACC ATCACCAACC
54251 TGCATTATGA AGAAAACATG CAACACCCTG GTTCCAGGAA GTTCAACACC
54301 ACGGAGCGGG TCCTGCAGGG TCTGCTTGGT CCCATGTTCA AGAACACAAG
54351 TGTCGGCCTT CTGTACTCTG GCTGCAGACT GACCTTGCTC AGGCCTGAGA
54401 AGAATGGGGC AGCCACTGGA ATGGATGCCA TCTGCAGCCA CCGTCTTGAC
54451 CCCAAAAGCC CTGGACTGNA CAGNGAGCNG CTNTACTGGG AGCTNAGCCA
54501 NCTGACCAAN NNCATCNNNG AGCTGGGNCC CTACACCCTG GACAGGNACA
54551 GTCTCTATGT CAATGGTTTC ACCCATCNGA NCTCTGNGCC CACCACCAGC
54601 ACTCCTGGGA CCTCCACAGT GNACNTNGGN ACCTCNGGGA CTCCATCCTC
54651 CNTCCCCNGC CNCACANCNN CTGNCCCTCT CCTGNTNCCN TTCACCNTCA
54701 ACTTNACCAT CACCAACCTG CANTANGNGG ANNACATGCN NCNCCCNGGN
54751 TCCAGGAAGT TCAACACCAC NGAGNGNGTN CTGCAGGGTC TGCTNNNNCC
54801 CNTNTTCAAG AACNCCAGTG TNGGCCNTCT GTACTCTGGC TGCAGACTGA
54851 CCTNNCTCAG GNCNGAGAAG NATGGNGCAG CCACTGGANT GGATGCCATC
54901 TGCANCCACC NNCNTNANCC CAAAAGNCCT GGACTGNACA GNGAGCNGCT
54951 NTACTGGGAG CTNAGCCANC TGACCAANNN CATCNNNGAG CTGGGNCCCT
55001 ACACCCTGGA CAGGNACAGT CTCTATGTCA ATGGTTTCAC CCATCAGAAC
55051 TCTGTGCCCA CCACCAGTAC TCCTGGGACC TCCACAGTGT ACTGGGCAAC
55101 CACTGGGACT CCATCCTCCT TCCCCGGCCA CACAGAGCCT GGCCCTCTCC
55151 TGATACCATT CACTTTCAAC TTTACCATCA CCAACCTGCA TTATGAGGAA
55201 AACATGCAAC ACCCTGGTTC CAGGAAGTTC AACACCACGG AGAGGGTTCT
55251 GCAGGGTCTG CTCACGCCCT TGTTCAAGAA CACCAGTGTT GGCCCTCTGT
55301 ACTCTGGCTG CAGACTGACC TTGCTCAGAC CTGAGAAGCA GGAGGCAGCC
55351 ACTGGAGTGG ACACCATCTG TACCCACCGC GTTGATCCCA TCGGACCTGG
55401 ACTGNACAGN GAGCNGCTNT ACTGGGAGCT NAGCCANCTG ACCAANNNCA
55451 TCNNNGAGCT GGGNCCCTAC ACCCTGGACA GGNACAGTCT CTATGTCAAT

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)				
55501	GGTTTCACCC	ATCNGANCTC	TGNGCCCACC	ACCAGCACTC	CTGGGACCTC
55551	CACAGTGNAC	NTNGGNACCT	CNGGGACTCC	ATCCTCCNTC	CCCNGCCNCA
55601	CANCNNCTGN	CCCTCTCCTG	NTNCCNTTCA	CCNTCAACTT	NACCATCACC
55651	AACCTGCANT	ANGNGGANNA	CATGCNNCNC	CCNGGNTCCA	GGAAGTTCAA
55701	CACCACNGAG	NGNGTNCTGC	AGGGTCTGCT	NNNNCCCNTN	TTCAAGAACN
55751	CCAGTGTNGG	CCNTCTGTAC	TCTGGCTGCA	GACTGACCTN	NCTCAGGNCN
55801	GAGAAGNATG	GNGCAGCCAC	TGGANTGGAT	GCCATCTGCA	NCCACCNNCN
55851	TNANCCCAAA	AGNCCTGGAC	TGNACAGNGA	GCNGCTNTAC	TGGGAGCTNA
55901	GCCANCTGAC	CAANNNCATC	NNNGAGCTGG	GNCCCTACAC	CCTGGACAGG
55951	NACAGTCTCT	ATGTCAATGG	TTTCACCCAT	CGGAGCTCTG	TGCCAACCAC
56001	CAGCAGTCCT	GGGACCTCCA	CAGTGCACCT	GGCAACCTCT	GGGACTCCAT
56051	CCTCCCTGCC	TGGCCACACA	GCCCCTGTCC	CTCTCTTGAT	ACCATTCACC
56101	CTCAACTTTA	CCATCACCAA	CCTGCATTAT	GAAGAAAACA	TGCAACACCC
56151	TGGTTCCAGG	AAGTTCAACA	CCACGGAGAG	GGTTCTGCAG	GGTCTGCTCA
56201	AGCCCTTGTT	CAAGAGCACC	AGTGTTGGCC	CTCTGTACTC	TGGCTGCAGA
56251	CTGACCTTGC	TCAGACCTGA	GAAACATGGG	GCAGCCACTG	GAGTGGACGC
56301	CATCTGCACC	CTCCGCCTTG	ATCCCACTGG	TCCTGGACTG	NACAGNGAGC
56351	NGCTNTACTG	GGAGCTNAGC	CANCTGACCA	ANNNCATCNN	NGAGCTGGGN
56401	CCCTACACCC	TGGACAGGNA	CAGTCTCTAT	GTCAATGGTT	TCACCCATCN
56451	GANCTCTGNG	CCCACCACCA	GCACTCCTGG	GACCTCCACA	GTGNACNTNG
56501	GNACCTCNGG	GACTCCATCC	TCCNTCCCCN	GCCNCACANC	NNCTGNCCCT
56551	CTCCTGNTNC	CNTTCACCNT	CAACTTNACC	ATCACCAACC	TGCANTANGN
56601	GGANNACATG	CNNCNCCCNG	GNTCCAGGAA	GTTCAACACC	ACNGAGNGNG
56651	TNCTGCAGGG	TCTGCTNNNN	CCCNTNTTCA	AGAACNCCAG	TGTNGGCCNT
56701	CTGTACTCTG	GCTGCAGACT	GACCTNNCTC	AGGNCNGAGA	AGNATGGNGC
56751	AGCCACTGGA	NTGGATGCCA	TCTGCANCCA	CCNNCNTNAN	CCCAAAAGNC
56801	CTGGACTGNA	CAGNGAGCNG	CTNTACTGGG	AGCTNAGCCA	NCTGACCAAN
56851	NNCATCNNNG	AGCTGGGNCC	CTACACCCTG	GACAGGNACA	GTCTCTATGT
56901	CAATGGTTTC	ACCCATCGGA	CCTCTGTGCC	CACCACCAGC	ACTCCTGGGA
56951	CCTCCACAGT	GCACCTGGCA	ACCTCTGGGA	CTCCATCCTC	CCTGCCTGGC
57001	CACACAGCCC	CTGTCCCTCT	CTTGATACCA	TTCACCCTCA	ACTTTACCAT
57051	CACCAACCTG	CAGTATGAGG	AGGACATGCA	TCGCCCTGGA	TCTAGGAAGT
57101	TCAACACCAC	AGAGAGGGTC	CTGCAGGGTC	TGCTTAGTCC	CATTTTCAAG
57151	AACTCCAGTG	TTGGCCCTCT	GTACTCTGGC	TGCAGACTGA	CCTCTCTCAG
57201	GCCCGAGAAG	GATGGGGCAG	CAACTGGAAT	GGATGCTGTC	TGCCTCTACC
57251	ACCCTAATCC	CAAAAGACCT	GGGCTGGACA	GAGAGCAGCT	GTACTGCGAG
57301	CTAAGCCAGC	TGACCCACAA	CATCACTGAG	CTGGGCCCCT	ACAGCCTGGA

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)
57351 CAGGGACAGT CTCTATGTCA ATGGTTTCAC CCATCAGAAC TCTGTGCCCA
57401 CCACCAGTAC TCCTGGGACC TCCACAGTGT ACTGGGCAAC CACTGGGACT
57451 CCATCCTCCT TCCCCGGCCA CACANCNNCT GNCCCTCTCC TGNTNCCNTT
57501 CACCNTCAAC TTNACCATCA CCAACCTGCA NTANGNGGAN NACATGCNNC
57551 NCCCNGGNTC CAGGAAGTTC AACACCACNG AGNGNGTNCT GCAGGGTCTG
57601 CTNNNNCCCN TNTTCAAGAA CNCCAGTGTN GGCCNTCTGT ACTCTGGCTG
57651 CAGACTGACC TNNCTCAGGN CNGAGAAGNA TGGNGCAGCC ACTGGANTGG
57701 ATGCCATCTG CANCCACCNN CNTNANCCCA AAAGNCCTGG ACTGNACAGN
57751 GAGCNGCTNT ACTGGGAGCT NAGCCANCTG ACCAANNNCA TCNNNGAGCT
57801 GGGNCCCTAC ACCCTGGACA GGNACAGTCT CTATGTCAAT GGTTTCACCC
57851 ATTGGAGCTC TGGGCTCACC ACCAGCACTC CTTGGACTTC CACAGTTGAC
57901 CTTGGAACCT CAGGGACTCC ATCCCCCGTC CCCAGCCCCA CAACTGCTGG
57951 CCCTCTCCTG GTGCCATTCA CCCTAAACTT CACCATCACC AACCTGCAGT
58001 ATGAGGAGGA CATGCATCGC CCTGGATCTA GGAAGTTCAA CGCCACAGAG
58051 AGGGTCCTGC AGGGTCTGCT TAGTCCCATA TTCAAGAACA CCAGTGTTGG
58101 CCCTCTGTAC TCTGGCTGCA GACTGACCTT GCTCAGACCT GAGAAGCAGG
58151 AGGCAGCCAC TGGAGTGGAC ACCATCTGTA CCCACCGCGT TGATCCCATC
58201 GGACCTGGAC TGNACAGNGA GCNGCTNTAC TGGGAGCTNA GCCANCTGAC
58251 CAANNNCATC NNNGAGCTGG GNCCCTACAC CCTGGACAGG NACAGTCTCT
58301 ATGTCAATGG TTTCACCCAT CNGANCTCTG NGCCCACCAC CAGCACTCCT
58351 GGGACCTCCA CAGTGNACNT NGGNACCTCN GGGACTCCAT CCTCCNTCCC
58401 CNGCCNCACA NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA
58451 CCATCACCAA CCTGCANTAN GNGGANNACA TGCNNCNCCC NGGNTCCAGG
58501 AAGTTCAACA CCACNGAGNG NGTNCTGCAG GGTCTGCTNN NNCCCNTNTT
58551 CAAGAACNCC AGTGTNGGCC NTCTGTACTC TGGCTGCAGA CTGACCTNNC
58601 TCAGGNCNGA GAAGNATGGN GCAGCCACTG GANTGGATGC CATCTGCANC
58651 CACCNNCNTN ANCCCAAAAG NCCTGGACTG NACAGNGAGC NGCTNTACTG
58701 GGAGCTNAGC CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC
58751 TGGACAGGNA CAGTCTCTAT GTCAATGGTT TCACCCATCG GAGCTTTGGG
58801 CTCACCACCA GCACTCCTTG GACTTCCACA GTTGACCTTG GAACCTCAGG
58851 GACTCCATCC CCCGTCCCCA GCCCCACAAC TGCTGGCCCT CTCCTGGTGC
58901 CATTCACCCT AAACTTCACC ATCACCAACC TGCAGTATGA GGAGGACATG
58951 CATCGCCCTG GCTCCAGGAA GTTCAACACC ACGGAGAGGG TCCTTCAGGG
59001 TCTGCTTACG CCCTTGTTCA GGAACACCAG TGTCAGCTCT CTGTACTCTG
59051 GTTGCAGACT GACCTTGCTC AGGCCTGAGA AGGATGGGGC AGCCACCAGA
59101 GTGGATGCTG TCTGCACCCA TCGTCCTGAC CCCAAAAGCC CTGGACTGNA

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)
59151 CAGNGAGCNG CTNTACTGGG AGCTNAGCCA NCTGACCAAN NNCATCNNNG
59201 AGCTGGGNCC CTACACCCTG GACAGGNACA GTCTCTATGT CAATGGTTTC
59251 ACCCATCNGA NCTCTGNGCC CACCACCAGC ACTCCTGGGA CCTCCACAGT
59301 GNACNTNGGN ACCTCNGGGA CTCCATCCTC CNTCCCCNGC CNCACANCNN
59351 CTGNCCCTCT CCTGNTNCCN TTCACCNTCA ACTTNACCAT CACCAACCTG
59401 CANTANGNGG ANNACATGCN NCNCCCNGGN TCCAGGAAGT TCAACACCAC
59451 NGAGNGNGTN CTGCAGGGTC TGCTNNNNCC CNTNTTCAAG AACNCCAGTG
59501 TNGGCCNTCT GTACTCTGGC TGCAGACTGA CCTNNCTCAG GNCNGAGAAG
59551 NATGGNGCAG CCACTGGANT GGATGCCATC TGCANCCACC NNCNTNANCC
59601 CAAAAGNCCT GGACTGNACA GNGAGCNGCT NTACTGGGAG CTNAGCCANC
59651 TGACCAANNN CATCNNNGAG CTGGGNCCCT ACACCCTGGA CAGGNACAGT
59701 CTCTATGTCA ATGGTTTCAC CCATTGGATC CCTGTGCCCA CCAGCAGCAC
59751 TCCTGGGACC TCCACAGTGG ACCTTGGGTC AGGGACTCCA TCCTCCCTCC
59801 CCAGCCCCAC AACTGCTGGC CCTCTCCTGG TACCATTCAC CCTCAACTTC
59851 ACCATCACCA ACCTGCAGTA TGGGGAGGAC ATGGGTCACC CTGGCTCCAG
59901 GAAGTTCAAC ACCACAGAGA GGGTCCTGCA GGGTCTGCTT GGTCCCATAT
59951 TCAAGAACAC CAGTGTTGGC CCTCTGTACT CTGGCTGCAG ACTGACCTCT
60001 CTCAGGTCCG AGAAGGATGG AGCAGCCACT GGAGTGGATG CCATCTGCAT
60051 CCATCATCTT GACCCCAAAA GCCCTGGACT GNACAGNGAG CNGCTNTACT
60101 GGGAGCTNAG CCANCTGACC AANNNCATCN NNGAGCTGGG NCCCTACACC
60151 CTGGACAGGN ACAGTCTCTA TGTCAATGGT TTCACCCATC NGANCTCTGN
60201 GCCCACCACC AGCACTCCTG GGACCTCCAC AGTGNACNTN GGNACCTCNG
60251 GGACTCCATC CTCCNTCCCC NGCCNCACAN CNNCTGNCCC TCTCCTGNTN
60301 CCNTTCACCN TCAACTTNAC CATCACCAAC CTGCANTANG NGGANNACAT
60351 GCNNCNCCCN GGNTCCAGGA AGTTCAACAC CACNGAGNGN GTNCTGCAGG
60401 GTCTGCTNNN NCCCNTNTTC AAGAACNCCA GTGTNGGCCN TCTGTACTCT
60451 GGCTGCAGAC TGACCTNNCT CAGGNCNGAG AAGNATGGNG CAGCCACTGG
60501 ANTGGATGCC ATCTGCANCC ACCNNCNTNA NCCCAAAAGN CCTGGACTGN
60551 ACAGNGAGCN GCTNTACTGG GAGCTNAGCC ANCTGACCAA NNNCATCNNN
60601 GAGCTGGGNC CCTACACCCT GGACAGGNAC AGTCTCTATG TCAATGGTTT
60651 CACCCATCAG ACCTTTGCGC CCAACACCAG CACTCCTGGG ACCTCCACAG
60701 TGGACCTTGG GACCTCAGGG ACTCCATCCT CCCTCCCCAG CCCTACATCT
60751 GCTGGCCCTC TCCTGGTGCC ATTCACCCTC AACTTCACCA TCACCAACCT
60801 GCAGTACGAG GAGGACATGC ATCACCCAGG CTCCAGGAAG TTCAACACCA
60851 CGGAGCGGGT CCTGCAGGGT CTGCTTGGTC CCATGTTCAA GAACACCAGT
60901 GTCGGCCTTC TGTACTCTGG CTGCAGACTG ACCTTGCTCA GGCCTGAGAA
60951 GAATGGGGCA GCCACCAGAG TGGATGCTGT CTGCACCCAT CGTCCTGACC

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)
61001 CCAAAAGCCC TGGACTGNAC AGNGAGCNGC TNTACTGGGA GCTNAGCCAN
61051 CTGACCAANN NCATCNNNGA GCTGGGNCCC TACACCCTGG ACAGGNACAG
61101 TCTCTATGTC AATGGTTTCA CCCATCNGAN CTCTGNGCCC ACCACCAGCA
61151 CTCCTGGGAC CTCCACAGTG NACNTNGGNA CCTCNGGGAC TCCATCCTCC
61201 NTCCCCNGCC NCACAGCCCC TGTCCCTCTC TTGATACCAT TCACCCTCAA
61251 CTTTACCATC ACCAACCTGC ATTATGAAGA AAACATGCAA CACCCTGGTT
61301 CCAGGAAGTT CAACACCACG GAGAGGGTTC TGCAGGGTCT GCTCAAGCCC
61351 TTGTTCAAGA GCACCAGCGT TGGCCCTCTG TACTCTGGCT GCAGACTGAC
61401 CTTGCTCAGA CCTGAGAAAC ATGGGGCAGC CACTGGAGTG GACGCCATCT
61451 GCACCCTCCG CCTTGATCCC ACTGGTCCTG GACTGGACAG AGAGCGGCTA
61501 TACTGGGAGC TGAGCCAGCT GACCAACAGC GTTACAGAGC TGGGCCCCTA
61551 CACCCTGGAC AGGGACAGTC TCTATGTCAA TGGCTTCACC CAGCGGAGCT
61601 CTGTGCCAAC CACCAGTATT CCTGGGACCT CTGCAGTGCA CCTGGAAACC
61651 TCTGGGACTC CAGCCTCCCT CCCTGGCCAC ACAGCCCCTG GCCCTCTCCT
61701 GGTGCCATTC ACCCTCAACT TCACTATCAC CAACCTGCAG TATGAGGTGG
61751 ACATGCGTCA CCCTGGTTCC AGGAAGTTCA ACACCACGGA GAGAGTCCTG
61801 CAGGGTCTGC TCAAGCCCTT GTTCAAGAGC ACCAGTGTTG GCCCTCTGTA
61851 CTCTGGCTGC AGACTGACCT TGCTCAGGCC TGAAAAACGT GGGGCAGCCA
61901 CCGGCGTGGA CACCATCTGC ACTCACCGCC TTGACCCTCT AAACCCTGGA
61951 CTGGACAGAG AGCAGCTATA CTGGGAGCTG AGCAAACTGA CCCGTGGCAT
62001 CATCGAGCTG GGCCCCTACC TCCTGGACAG AGGCAGTCTC TATGTCAATG
62051 GTTTCACCCA TCGGAACTTT GTGCCCATCA CCAGCACTCC TGGGACCTCC
62101 ACAGTACACC TAGGAACCTC TGAAACTCCA TCCTCCCTAC CTAGACCCAT
62151 AGTGCCTGGC CCTCTCCTGG TGCCATTCAC CCTCAACTTC ACCATCACCA
62201 ACTTGCAGTA TGAGGAGGCC ATGCGACACC CTGGCTCCAG GAAGTTCAAT
62251 ACCACGGAGA GGGTCCTACA GGGTCTGCTC AGGCCCTTGT TCAAGAATAC
62301 CAGTATCGGC CCTCTGTACT CCAGCTGCAG ACTGACCTTG CTCAGGCCAG
62351 AGAAGGACAA GGCAGCCACC AGAGTGGATG CCATCTGTAC CCACCACCCT
62401 GACCCTCAAA GCCCTGGACT GAACAGAGAG CAGCTGTACT GGGAGCTGAG
62451 CCAGCTGACC CACGGCATCA CTGAGCTGGG CCCCTACACC CTGGACAGGG
62501 ACAGTCTCTA TGTCGATGGT TTCACTCATT GGAGCCCCAT ACCGACCACC
62551 AGCACTCCTG GGACCTCCAT AGTGAACCTG GGAACCTCTG GGATCCCACC
62601 TTCCCTCCCT GAAACTACAN CNNCTGNCCC TCTCCTGNTN CCNTTCACCN
62651 TCAACTTNAC CATCACCAAC CTGCANTANG NGGANNACAT GCNNCNCCCN
62701 GGNTCCAGGA AGTTCAACAC CACNGAGAGG GTTCTGCAGG GTCTGCTCAA
62751 GCCCTTGTTC AAGAGCACCA GTGTTGGCCC TCTGTATTCT GGCTGCAGAC

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)
62801 TGACCTTGCT CAGGCCTGAG AAGGACGGAG TAGCCACCAG AGTGGACGCC
62851 ATCTGCACCC ACCGCCCTGA CCCCAAAATC CCTGGGCTAG ACAGACAGCA
62901 GCTATACTGG GAGCTGAGCC AGCTGACCCA CAGCATCACT GAGCTGGGAC
62951 CCTACACCCT GGATAGGGAC AGTCTCTATG TCAATGGTTT CACCCAGCGG
63001 AGCTCTGTGC CCACCACCAG CACTCCTGGG ACTTTCACAG TACAGCCGGA
63051 AACCTCTGAG ACTCCATCAT CCCTCCCTGG CCCCACAGCC ACTGGCCCTG
63101 TCCTGCTGCC ATTCACCCTC AATTTTACCA TCACTAACCT GCAGTATGAG
63151 GAGGACATGC ATCGCCCTGG CTCCAGGAAG TTCAACACCA CGGAGAGGGT
63201 CCTTCAGGGT CTGCTTATGC CCTTGTTCAA GAACACCAGT GTCAGCTCTC
63251 TGTACTCTGG TTGCAGACTG ACCTTGCTCA GGCCTGAGAA GGATGGGGCA
63301 GCCACCAGAG TGGATGCTGT CTGCACCCAT CGTCCTGACC CCAAAAGCCC
63351 TGGACTGGAC AGAGAGCGGC TGTACTGGAA GCTGAGCCAG CTGACCCACG
63401 GCATCACTGA GCTGGGCCCC TACACCCTGG ACAGGCACAG TCTCTATGTC
63451 AATGGTTTCA CCCATCAGAG CTCTATGACG ACCACCAGAA CTCCTGATAC
63501 CTCCACAATG CACCTGGCAA CCTCGAGAAC TCCAGCCTCC CTGTCTGGAC
63551 CTACGACCGC CAGCCCTCTC CTGGTGCTAT TCACAATTAA CTTCACCATC
63601 ACTAACCTGC GGTATGAGGA GAACATGCAT CACCCTGGCT CTAGAAAGTT
63651 TAACACCACG GAGAGAGTCC TTCAGGGTCT GCTCAGGCCT GTGTTCAAGA
63701 ACACCAGTGT TGGCCCTCTG TACTCTGGCT GCAGACTGAC CTTGCTCAGG
63751 CCCAAGAAGG ATGGGGCAGC CACCAAAGTG GATGCCATCT GCACCTACCG
63801 CCCTGATCCC AAAAGCCCTG GACTGGACAG AGAGCAGCTA TACTGGGAGC
63851 TGAGCCAGCT AACCCACAGC ATCACTGAGC TGGGCCCCTA CACCCTGGAC
63901 AGGGACAGTC TCTATGTCAA TGGTTTCACA CAGCGGAGCT CTGTGCCCAC
63951 CACTAGCATT CCTGGGACCC CCACAGTGGA CCTGGGAACA TCTGGGACTC
64001 CAGTTTCTAA ACCTGGTCCC TCGGCTGCCA GCCCTCTCCT GGTGCTATTC
64051 ACTCTCAACT TCACCATCAC CAACCTGCGG TATGAGGAGA ACATGCAGCA
64101 CCCTGGCTCC AGGAAGTTCA ACACCACGGA GAGGGTCCTT CAGGGCCTGC
64151 TCAGGTCCCT GTTCAAGAGC ACCAGTGTTG GCCCTCTGTA CTCTGGCTGC
64201 AGACTGACTT TGCTCAGGCC TGAAAAGGAT GGGACAGCCA CTGGAGTGGA
64251 TGCCATCTGC ACCCACCACC CTGACCCCAA AAGCCCTAGG CTGGACAGAG
64301 AGCAGCTGTA TTGGGAGCTG AGCCAGCTGA CCCACAATAT CACTGAGCTG
64351 GGCCACTATG CCCTGGACAA CGACAGCCTC TTTGTCAATG GTTTCACTCA
64401 TCGGAGCTCT GTGTCCACCA CCAGCACTCC TGGGACCCCC ACAGTGTATC
64451 TGGGAGCATC TAAGACTCCA GCCTCGATAT TTGGCCCTTC AGCTGCCAGC
64501 CATCTCCTGA TACTATTCAC CCTCAACTTC ACCATCACTA ACCTGCGGTA
64551 TGAGGAGAAC ATGTGGCCTG GCTCCAGGAA GTTCAACACT ACAGAGAGGG
64601 TCCTTCAGGG CCTGCTAAGG CCCTTGTTCA AGAACACCAG TGTTGGCCCT

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)
64651 CTGTACTCTG GCTCCAGGCT GACCTTGCTC AGGCCAGAGA AAGATGGGGA
64701 AGCCACCGGA GTGGATGCCA TCTGCACCCA CCGCCCTGAC CCCACAGGCC
64751 CTGGGCTGGA CAGAGAGCAG CTGTATTTGG AGCTGAGCCA GCTGACCCAC
64801 AGCATCACTG AGCTGGGCCC CTACACACTG GACAGGGACA GTCTCTATGT
64851 CAATGGTTTC ACCCATCGGA GCTCTGTACC CACCACCAGC ACCGGGGTGG
64901 TCAGCGAGGA GCCATTCACA CTGAACTTCA CCATCAACAA CCTGCGCTAC
64951 ATGGCGGACA TGGGCCAACC CGGCTCCCTC AAGTTCAACA TCACAGACAA
65001 CGTCATGAAG CACCTGCTCA GTCCTTTGTT CCAGAGGAGC AGCCTGGGTG
65051 CACGGTACAC AGGCTGCAGG GTCATCGCAC TAAGGTCTGT GAAGAACGGT
65101 GCTGAGACAC GGGTGGACCT CCTCTGCACC TACCTGCAGC CCCTCAGCGG
65151 CCCAGGTCTG CCTATCAAGC AGGTGTTCCA TGAGCTGAGC CAGCAGACCC
65201 ATGGCATCAC CCGGCTGGGC CCCTACTCTC TGGACAAAGA CAGCCTCTAC
65251 CTTAACGGTT ACAATGAACC TGGTCTAGAT GAGCCTCCTA CAACTCCCAA
65301 GCCAGCCACC ACATTCCTGC CTCCTCTGTC AGAAGCCACA ACAGCCATGG
65351 GGTACCACCT GAAGACCCTC ACACTCAACT TCACCATCTC CAATCTCCAG
65401 TATTCACCAG ATATGGGCAA GGGCTCAGCT ACATTCAACT CCACCGAGGG
65451 GGTCCTTCAG CACCTGCTCA GACCCTTGTT CCAGAAGAGC AGCATGGGCC
65501 CCTTCTACTT GGGTTGCCAA CTGATCTCCC TCAGGCCTGA GAAGGATGGG
65551 GCAGCCACTG GTGTGGACAC CACCTGCACC TACCACCCTG ACCCTGTGGG
65601 CCCCGGGCTG GACATACAGC AGCTTTACTG GGAGCTGAGT CAGCTGACCC
65651 ATGGTGTCAC CCAACTGGGC TTCTATGTCC TGGACAGGGA TAGCCTCTTC
65701 ATCAATGGCT ATGCACCCCA GAATTTATCA ATCCGGGGCG AGTACCAGAT
65751 AAATTTCCAC ATTGTCAACT GGAACCTCAG TAATCCAGAC CCCACATCCT
65801 CAGAGTACAT CACCCTGCTG AGGGACATCC AGGACAAGGT CACCACACTC
65851 TACAAAGGCA GTCAACTACA TGACACATTC CGCTTCTGCC TGGTCACCAA
65901 CTTGACGATG GACTCCGTGT TGGTCACTGT CAAGGCATTG TTCTCCTCCA
65951 ATTTGGACCC CAGCCTGGTG GAGCAAGTCT TTCTAGATAA GACCCTGAAT
66001 GCCTCATTCC ATTGGCTGGG CTCCACCTAC CAGTTGGTGG ACATCCATGT
66051 GACAGAAATG GAGTCATCAG TTTATCAACC AACAAGCAGC TCCAGCACCC
66101 AGCACTTCTA CCTGAATTTC ACCATCACCA ACCTACCATA TTCCCAGGAC
66151 AAAGCCCAGC CAGGCACCAC CAATTACCAG AGGAACAAAA GGAATATTGA
66201 GGATGCGCTC AACCAACTCT TCCGAAACAG CAGCATCAAG AGTTATTTTT
66251 CTGACTGTCA AGTTTCAACA TTCAGGTCTG TCCCCAACAG GCACCACACC
66301 GGGGTGGACT CCCTGTGTAA CTTCTCGCCA CTGGCTCGGA GAGTAGACAG
66351 AGTTGCCATC TATGAGGAAT TTCTGCGGAT GACCCGGAAT GGTACCCAGC
66401 TGCAGAACTT CACCCTGGAC AGGAGCAGTG TCCTTGTGGA TGGGTATTCT

TABLE 4-continued

Human cDNA of CA125 (SEQ ID NO: 4)					
66451	CCCAACAGAA	ATGAGCCCTT	AACTGGGAAT	TCTGACCTTC	CCTTCTGGGC
66501	TGTCATCCTC	ATCGGCTTGG	CAGGACTCCT	GGGACTCATC	ACATGCCTGA
66551	TCTGCGGTGT	CCTGGTGACC	ACCCGCCGGC	GGAAGAAGGA	AGGAGAATAC
66601	AACGTCCAGC	AACAGTGCCC	AGGCTACTAC	CAGTCACACC	TAGACCTGGA
66651	GGATCTGCAA	TGACTGGAAC	TTGCCGGTGC	CTGGGGTGCC	TTTCCCCCAG
66701	CCAGGGTCCA	AAGAAGCTTG	GCTGGGGCAG	AAATAAACCA	TATTGGTCGG
66751	AAAAAAAAAA	AAAAA			

TABLE 5

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
1	MLKPSGLPGS	SSPTRSLMTG	SRSTKATPEM	DSGLTGATLS	PKTSTGAIVV
51	TEHTLPFTSP	DKTLASPTSS	VVGRTTQSLG	VMSSALPEST	SRGMTHSEQR
101	TSPSLSPQVN	GTPSRNYPAT	SMVSGLSSPR	TRTSSTEGNF	TKEASTYTLT
151	VETTSGPVTE	KYTVPTETST	TEGDSTETPW	DTRYIPVKIT	SPMKTFADST
201	ASKENAPVSM	TPAETTVTDS	HTPGRTNPSF	GTLYSSFLDL	SPKGTPNSRG
251	ETSLELILST	TGYPFSSPEP	GSAGHSRIST	SAPLSSSASV	LDNKISETSI
301	FSGQSLTSPL	SPGVPEARAS	TMPNSAIPFS	MTLSNAETSA	ERVRSTISSL
351	GTPSISTKQT	AETILTFHAF	AETMDIPSTH	IAKTLASEWL	GSPGTLGGTS
401	TSALTTTSPS	TTLVSEETNT	HHSTSGKETE	GTLNTSMTPL	ETSAPGEESE
451	MTATLVPTLG	FTTLDSKIRS	PSQVSSSHPT	RELRTTGSTS	GRQSSSTAAH
501	GSSDILRATT	SSTSKASSWT	SESTAQQFSE	PQHTQWVETS	PSMKTERPPA
551	STSVAAPITT	SVPSVVSGFT	TLKTSSTKGI	WLEETSADTL	IGESTAGPTT
601	HQFAVPTGIS	MTGGSSTRGS	QGTTHLLTRA	TASSETSADL	TLATNGVPVS
651	VSPAVSKTAA	GSSPPGGTKP	SYTMVSSVIP	ETSSLQSSAF	REGTSLGLTP
701	LNTRHPFSSP	EPDSAGHTKI	STSIPLLSSA	SVLEDKVSAT	STFSHHKATS
751	SITTGTPEIS	TKTKPSSAVL	SSMTLSNAAT	SPERVRNATS	PLTHPSPSGE
801	ETAGSVLTLS	TSAETTDSPN	IHPTGTLTSE	SSESPSTLSL	PSVSGVKTTF
851	SSSTPSTHLF	TSGEETEETS	NPSVSQPETS	VSRVRTTLAS	TSVPTPVFPT
901	MDTWPTRSAQ	FSSSHLVSEL	RATSSTSVTN	STGSALPKIS	HLTGTATMSQ
951	TNRDTFNDSA	APQSTTWPET	SPRFKTGLPS	ATTTVSTSAT	SLSATVMVSK
1001	FTSPATSSME	ATSIREPSTT	ILTTETTNGP	GSMAVASTNI	PIGKGYITEG
1051	RLDTSHLPIG	TTASSETSMD	FTMAKESVSM	SVSPSQSMDA	AGSSTPGRTS
1101	QFVDTFSDDV	YHLTSREITI	PRDGTSSALT	PQMTATHPPS	PDPGSARSTW
1151	LGILSSSPSS	PTPKVTMSST	FSTQRVTTSM	IMDTVETSRW	NMPNLPSTTS
1201	LTPSNIPTSG	AIGKSTLVPL	DTPSPATSLE	ASEGGLPTLS	TYPESTNTPS
1251	IHLGAHASSE	SPSTINLTMA	SVVKPGSYTP	LTFPSIETHI	HVSTARMAYS

TABLE 5-continued

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
1301	SGSSPEMTAP	GETNTGSTWD	PTTYITTTDP	KDTSSAQVST	PHSVRTLRTT
1351	ENHPKTESAT	PAAYSGSPKI	SSSPNLTSPA	TKAWTITDTT	EHSTQLHYTK
1401	LAEKSSGFET	QSAPGPVSVV	IPTSPTIGSS	TLELTSDVPG	EPLVLAPSEQ
1451	TTITLPMATW	LSTSLTEEMA	STDLDISSPS	SPMSTFAIFP	PMSTPSHELS
1501	KSEADTSAIR	NTDSTTLDQH	LGIRSLGRTG	DLTTVPITPL	TTTWTSVIEH
1551	STQAQDTLSA	TMSPTHVTQS	LKDQTSIPAS	ASPSHLTEVY	PELGTQGRSS
1601	SEATTFWKPS	TDTLSREIET	GPTNIQSTPP	MDNTTTGSSS	SGVTLGIAHL
1651	PIGTSSPAET	STNMALERRS	STATVSMAGT	MGLLVTSAPG	RSISQSLGRV
1701	SSVLSESTTE	GVTDSSKGSS	PRLNTQGNTA	LSSSLEPSYA	EGSQMSTSIP
1751	LTSSPTTPDV	EFIGGSTFWT	KEVTTVMTSD	ISKSSARTES	SSATLMSTAL
1801	GSTENTGKEK	LRTASMDLPS	PTPSMEVTPW	ISLTLSNAPN	TTDSLDLSHG
1851	VHTSSAGTLA	TDRSLNTGVT	RASRLENGSD	TSSKSLSMGN	STHTSMTDTE
1901	KSEVSSSIHP	RPETSAPGAE	TTLTSTPGNR	AISLTLPFSS	IPVEEVISTG
1951	ITSGPDINSA	PMTHSPITPP	TIVWTSTGTI	EQSTQPLHAV	SSEKVSVQTQ
2001	STPYVNSVAV	SASPTHENSV	SSGSSTSSPY	SSASLESLDS	TISRRNAITS
2051	WLWDLTTSLP	TTTWPSTSLS	EALSSGHSGV	SNPSSTTTEF	PLFSAASTSA
2101	AKQRNPETET	HGPQNTAAST	LNTDASSVTG	LSETPVGASI	SSEVPLPMAI
2151	TSRSDVSGLT	SESTANPSLG	TASSAGTKLT	RTISLPTSES	LVSFRMNKDP
2201	WTVSIPLGSH	PTTNTETSIP	VNSAGPPGLS	TVASDVIDTP	SDGAESIPTV
2251	SFSPSPDTEV	TTISHFPEKT	THSFRTISSL	THELTSRVTP	IPGDWMSSAM
2301	STKPTGASPS	ITLGERRTIT	SAAPTTSPIV	LTASFTETST	VSLDNETTVK
2351	TSDILDARKT	NELPSDSSSS	SDLINTSIAS	STMDVTKTAS	ISPTSISGMT
2401	ASSSPSLFSS	DRPQVPTSTT	ETNTATSPSV	SSNTYSLDGG	SNVGGTPSTL
2451	PPFTITHPVE	TSSALLAWSR	PVRTFSTMVS	TDTASGENPT	SSNSVVTSVP
2501	APGTWASVGS	TTDLPAMGFL	KTSPAGEAHS	LLASTIEPAT	AFTPHLSAAV
2551	VTGSSATSEA	SLLTTSESKA	IHSSPQTPTT	PTSGANWETS	ATPESLLVVT
2601	ETSDTTLTSK	ILVTDTILFS	TVSTPPSKFP	STGTLSGASF	PTLLPDTPAI
2651	PLTATEPTSS	LATSFDSTPL	VTIASDSLGT	VPETTLTMSE	TSNGDALVLK
2701	TVSNPDRSIP	GITIQGVTES	PLHPSSTSPS	KIVAPRNTTY	EGSITVALST
2751	LPAGTTGSLV	FSQSSENSET	TALVDSSAGL	ERASVMPLTT	GSQGMASSGG
2801	IRSGSTHSTG	TKTFSSLPLT	MNPGEVTAMS	EITTNRLTAT	QSTAPKGIPV
2851	KPTSAESGLL	TPVSASSSPS	KAFASLTTAP	PSTWGIPQST	LTFEFSEVPS
2901	LDTKSASLPT	PGQSLNTIPD	SDASTASSSL	SKSPEKNPRA	RMMTSTKAIS
2951	ASSFQSTGFT	ETPEGSASPS	MAGHEPRVPT	SGTGDPRYAS	ESMSYPDPSK
3001	ASSAMTSTSL	ASKLTTLFST	GQAARSGSSS	SPISLSTEKE	TSFLSPTAST
3051	SRKTSLFLGP	SMARQPNILV	HLQTSALTLS	PTSTLNMSQE	EPPELTSSQT

TABLE 5-continued

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
3101	IAEEEGTTAE	TQTLTFTPSE	TPTSLLPVSS	PTEPTARRKS	SPETWASSIS
3151	VPAKTSLVET	TDGTLVTTIK	MSSQAAQGNS	TWPAPAEETG	TSPAGTSPGS
3201	PEVSTTLKIM	SSKEPSISPE	IRSTVRNSPW	KTPETTVPME	TTVEPVTLQS
3251	TALGSGSTSI	SHLPTGTTSP	TKSPTENMLA	TERVSLSPSP	PEAWTNLYSG
3301	TPGGTRQSLA	TMSSVSLESP	TARSITGTGQ	QSSPELVSKT	TGMEFSMWHG
3351	STGGTTGDTH	VSLSTSSNIL	EDPVTSPNSV	SSLTDKSKHK	TETWVSTTAI
3401	PSTVLNNKIM	AAEQQTSRSV	DEAYSSTSSW	SDQTSGSDIT	LGASPDVTNT
3451	LYITSTAQTT	SLVSLPSGDQ	GITSLTNPSG	GKTSSASSVT	SPSIGLETLR
3501	ANVSAVKSDI	APTAGHLSQT	SSPAEVSILD	VTTAPTPGIS	TTITTMGTNS
3551	ISTTTPNPEV	GMSTMDSTPA	TERRTTSTEH	PSTWSSTAAS	DSWTVTDMTS
3601	NLKVARSPGT	ISTMHTTSFL	ASSTELDSMS	TPHGRITVIG	TSLVTPSSDA
3651	SAVKTETSTS	ERTLSPSDTT	ASTPISTFSR	VQRMSISVPD	ILSTSWTPSS
3701	TEAEDVPVSM	VPTDHASTKT	DPNTPLSTFL	FDSLSTLDWD	TGRSLSSATA
3751	TTSAPQGATT	PQELTLETMI	SPATSQLPFS	IGHITSAVTP	AAMARSSGVT
3801	FSRPDPTSKK	AEQTSTQLPT	TTSAHPGQVP	RSAATTLDVI	PHTAKTPDAT
3851	FQRQGQTALT	TEARATSDSW	NEKEKSTPSA	PWITEMMNSV	SEDTIKEVTS
3901	SSSVLKDPEY	AGHKLGIWDD	FIPKFGKAAH	MRELPLLSPP	QDKEAIHPST
3951	NTVETTGWVT	SSEHASHSTI	PAHSASSKLT	SPVVTTSTRE	QAIVSMSTTT
4001	WPESTRARTE	PNSFLTIELR	DVSPYMDTSS	TTQTSIISSP	GSTAITKGHR
4051	TEITSYKRIS	SSFLAQSMRS	SDSPSEAITR	LSNFPAMTES	GGMILAMQTS
4101	PPGATSISAP	TLDTSATASW	TGTPLATTQR	FTYSEKTTLF	SKGREDTSQP
4151	SPPCVEETSS	SSSVVPIHAT	TSPSNILLTS	QGHSPSSTPP	VTSVFLSETS
4201	GLGKTTDMSR	ISLEPGTSLP	PNLSSTAGEA	LSTYEASRDT	KAIHHSADTA
4251	VTNMEATSSE	YSPIPGHTKP	SKATSPLVTS	HIMGDITSST	SVFGSSETTE
4301	IETVSSVNQG	LQERSTSQVA	SSATETSTVI	THVSSGDATT	HVTKTQATFS
4351	SGTSISSPHQ	FITSTNTFTD	VSTNPSTSLI	MTESSGVTIT	TQTGPTGAAT
4401	QGPYLLDTST	MPYLTETPLA	VTPDFMQSEK	TTLISKGPKD	VTWTSPPSVA
4451	ETSYPSSLTP	FLVTTIPPAT	STLQGQHTSS	PVSATSVLTS	GLVKTTDMLN
4501	TSMEPVTNSP	QNLNNPSNEI	LATLAATTDI	ETIHPSINKA	VTNMGTASSA
4551	HVLHSTLPVS	SEPSTATSPM	VPASSMGDAL	ASISIPGSET	TDIEGEPTSS
4601	LTAGRKENST	LQEMNSTTES	NIILSNVSVG	AITEATKMEV	PSFDATFIPT
4651	PAQSTKFPDI	FSVASSRLSN	SPPMTISTHM	TTTQTGSSGA	TSKIPLALDT
4701	STLETSAGTP	SVVTEGFAHS	KITTAMNNDV	KDVSQTNPPF	QDEASSPSSQ
4751	APVLVTTLPS	SVAFTPQWHS	TSSPVSMSSV	LTSSLVKTAG	KVDTSLETVT
4801	SSPQSMSNTL	DDISVTSAAT	TDIETTHPSI	NTVVTNVGTT	GSAFESHSTV
4851	SAYPEPSKVT	SPNVTTSTME	DTTISRSIPK	SSKTTRTETE	TTSSLTPKLR
4901	ETSISQEITS	STETSTVPYK	ELTGATTEVS	RTDVTSSSST	SFPGPDQSTV

TABLE 5-continued

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
4951	SLDISTETNT	RLSTSPIMTE	SAEITITTQT	GPHGATSQDT	FTMDPSNTTP
5001	QAGIHSAMTH	GFSQLDVTTL	MSRIPQDVSW	TSPPSVDKTS	SPSSFLSSPA
5051	MTTPSLISST	LPEDKLSSPM	TSLLTSGLVK	ITDILRTRLE	PVTSSLPNFS
5101	STSDKILATS	KDSKDTKEIF	PSINTEETNV	KANNSGHESH	SPALADSETP
5151	KATTQMVITT	TVGDPAPSTS	MPVHGSSETT	NIKREPTYFL	TPRLRETSTS
5201	QESSFPTDTS	FLLSKVPTGT	ITEVSSTGVI	SSSKISTPDH	DKSTVPPDTF
5251	TGEIPRVFTS	SIKTKSAEMT	ITTQASPPES	ASHSTLPLDT	STTLSQGGTH
5301	STVSQGFPYS	EVTTLMGMGP	GNVSWMTTPP	VEETSSVSSL	MSSPAMTSPS
5351	PVSSTSPQSI	PSSPLPVTAL	PTSVLVTTTD	VLGTTSPESV	TSSPPNLSSI
5401	THERPATYKD	TAHTEAAMHH	STNTAVTNVG	TSGSGHKSQS	SVLADSETSK
5451	ATPLMSTAST	LGDTSVSTST	PNISQTNQIQ	TEPTASLSPR	LRESSTSEKT
5501	SSTTETNTAF	SYVPTGAITQ	ASRTEISSSR	TSISDLDRST	IAPDISTGMI
5551	TRLFTSPIMT	KSAEMTVTTQ	TTTPGATSQG	ILPWDTSTTL	FQGGTHSTVS
5601	QGFPHSEITT	LRSRTPGDVS	WMTTPPVEET	SSGFSLMSPS	MTSPSPVSST
5651	SPESIPSSPL	PVTALLTSVL	VTTTNVLGTT	SPEPVTSSPP	NLSSPTQERL
5701	TTYKDTAHTE	AMHASMHTNT	AVANVGTSIS	GHESQSSVPA	DSHTSKATSP
5751	MGITFAMGDT	SVYTSTPAFF	ETRIQSESTS	SLIPGLRDTR	TSEEINTVTE
5801	TSTVLSEVPT	TTTTEVSRTE	VITSSRTTIS	GPDHSKMSPY	ISTETITRLS
5851	TFPFVTGSTE	MAITNQTGPI	GTISQATLTL	DTSSTASWEG	THSPVTQRFP
5901	HSEETTTMSR	STKGVSWQSP	PSVEETSSPS	SPVPLPAITS	HSSLYSAVSG
5951	SSPTSALPVT	SLLTSGRRKT	IDMLDTHSEL	VTSSLPSASS	FSGEILTSEA
6001	STNTETIHFS	ENTAETNMGT	TNSMHKLHSS	VSIHSQPSGH	TPPKVTGSMM
6051	EDAIVSTSTP	GSPETKNVDR	DSTSPLTPEL	KEDSTALVMN	STTESNTVFS
6101	SVSLDAATEV	SRAEVTYYDP	TFMPASAQST	KSPDISPEAS	SSHSNSPPLT
6151	ISTHKTIATQ	TGPSGVTSLG	QLTLDTSTIA	TSAGTPSART	QDFVDSETTS
6201	VMNNDLNDVL	KTSPFSAEEA	NSLSSQAPLL	VTTSPSPVTS	TLQEHSTSSL
6251	VSVTSVPTPT	LAKITDMDTN	LEPVTRSPQN	LRNTLATSEA	TTDTHTMHPS
6301	INTAMANVGT	TSSPNEFYFT	VSPDSDPYKA	TSAVVITSTS	GDSIVSTSMP
6351	RSSAMKKIES	ETTFSLIFRL	RETSTSQKIG	SSSDTSTVFD	KAFTAATTEV
6401	SRTELTSSSR	TSIQGTEKPT	MSPDTSTRSV	TMLSTFAGLT	KSEERTIATQ
6451	TGPHRATSQG	TLTWDTSITT	SQAGTHSAMT	HGFSQLDLST	LTSRVPEYIS
6501	GTSPPSVEKT	SSSSSLLSLP	AITSPSPVPT	TLPESRPSSP	VHLTSLPTSG
6551	LVKTTDMLAS	VASLPPNLGS	TSHKIPTTSE	DIKDTEKMYP	STNIAVTNVG
6601	TTTSEKESYS	SVPAYSEPPK	VTSPMVTSFN	IRDTIVSTSM	PGSSEITRIE
6651	MESTFSLAHG	LKGTSTSQDP	IVSTEKSAVL	HKLTTGATET	SRTEVASSRR
6701	TSIPGPDHST	ESPDISTEVI	PSLPISLGIT	ESSNMTIITR	TGPPLGSTSQ

TABLE 5-continued

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
6751	GTFTLDTPTT	SSRAGTHSMA	TQEFPHSEMT	TVMNKDPEIL	SWTIPPSIEK
6801	TSFSSSLMPS	PAMTSPPVSS	TLPKTIHTTP	SPMTSLLTPS	LVMTTDTLGT
6851	SPEPTTSSPP	NLSSTSHVIL	TTDEDTTAIE	AMHPSTSTAA	TNVETTCSGH
6901	GSQSSVLTDS	EKTKATAPMD	TTSTMGHTTV	STSMSVSSET	TKIKRESTYS
6951	LTPGLRETSI	SQNASFSTDT	SIVLSEVPTG	TTAEVSRTEV	TSSGRTSIPG
7001	PSQSTVLPEI	STRTMTRLFA	SPTMTESAEM	TIPTQTGPSG	STSQDTLTLD
7051	TSTTKSQAKT	HSTLTQRFPH	SEMTTLMSRG	PGDMSWQSSP	SLENPSSLPS
7101	LLSLPATTSP	PPISSTLPVT	ISSSPLPVTS	LLTSSPVTTT	DMLHTSPELV
7151	TSSPPKLSHT	SDERLTTGKD	TTNTEAVHPS	TNTAASNVEI	PSFGHESPSS
7201	ALADSETSKA	TSPMFITSTQ	EDTTVAISTP	HFLETSRIQK	ESISSLSPKL
7251	RETGSSVETS	SAIETSAVLS	EVSIGATTEI	SRTEVTSSSR	TSISGSAEST
7301	MLPEISTTRK	IIKFPTSPIL	AESSEMTIKT	QTSPPGSTSE	STFTLDTSTT
7351	PSLVITHSTM	TQRLPHSEIT	TLVSRGAGDV	PRPSSLPVEE	TSPPSSQLSL
7401	SAMISPSPVS	STLPASSHSS	SASVTSPLTP	GQVKTTEVLD	ASAEPETSSP
7451	PSLSSTSVEI	LATSEVTTDT	EKIHPFPNTA	VTKVGTSSSG	HESPSSVLPD
7501	SETTKATSAM	GTISIMGDTS	VSTLTPALSN	TRKIQSEPAS	SLTTRLRETS
7551	TSEETSLATE	ANTVLSKVST	GATTEVSRTE	AISFSRTSMS	GPEQSTMSQD
7601	ISIGTIPRIS	ASSVLTESAK	MTITTQTGPS	ESTLESTLNL	NTATTPSWVE
7651	THSIVIQGFP	HPEMTTSMGR	GPGGVSWPSP	PFVKETSPPS	SPLSLPAVTS
7701	PHPVSTTFLA	HIPPSPLPVT	SLLTSGPATT	TDILGTSTEP	GTSSSSSLST
7751	TSHERLTTYK	DTAHTEAVHP	STNTGGTNVA	TTSSGYKSQS	SVLADSSPMC
7801	TTSTMGDTSV	LTSTPAFLET	RRIQTELASS	LTPGLRESSG	SEGTSSGTKM
7851	STVLSKVPTG	ATTEISKEDV	TSIPGPAQST	ISPDTSTRTV	SWFSTSPVMT
7901	ESAEITMNTH	TSPLGATTQG	TSTLDTSSTT	SLTMTHSTIS	QGFSHSQMST
7951	LMRRGPEDVS	WMSPPLLEKT	RPSFSLMSSP	ATTSPSPVSS	TLPESISSSP
8001	LPVTSLLTSG	LAKTTDMLHK	SSEPVTNSPA	NLSSTSVEIL	ATSEVTTDTE
8051	KTHPSSNRTV	TDVGTSSSGH	ESTSFVLADS	QTSKVTSPMV	ITSTMEDTSV
8101	STSTPGFFET	SRIQTEPTSS	LTLGLRKTSS	SEGTSLATEM	STVLSGVPTG
8151	ATAEVSRTEV	TSSSRTSISG	FAQLTVSPET	STETITRLPT	SSIMTESAEM
8201	MIKTQTDPPG	STPESTHTVD	ISTTPNWVET	HSTVTQRFSH	SEMTTLVSRS
8251	PGDMLWPSQS	SVEETSSASS	LLSLPATTSP	SPVSSTLVED	FPSASLPVTS
8301	LLTPGLVITT	DRMGISREPG	TSSTSNLSST	SHERLTTLED	TVDTEAMQPS
8351	THTAVTNVRT	SISGHESQSS	VLSDSETPKA	TSSMGTTYTM	GETSVSISTS
8401	DFFETSRVQI	EPTSSLTSGL	RETSSSERIS	SATEGSTVLS	EVPSGATTEV
8451	SRTEVISSRG	TSMSGPDQFT	ISPDISTEAI	TRLSTSPIMT	ESAESAITIE
8501	TGSPGATSEG	TLTLDTSTTT	FWSGTHSTAS	PGFSHSEMTT	LMSRTPGDVP
8551	WPSLPSVEEA	SSVSSSLSSP	AMTSTSFFSA	LPESISSSPH	PVTALLTLGP

TABLE 5-continued

Human Protein of CA125 Molecule (SEQ ID NO: 5)
8601 VKTTDMLRTS SEPETSSPPN LSSTSAEILA TSEVTKDREK IHPSSNTPVV
8651 NVGTVIYKHL SPSSVLADLV TTKPTSPMAT TSTLGNTSVS TSTPAFPETM
8701 MTQPTSSLTS GLREISTSQE TSSATERSAS LSGMPTGATT KVSRTEALSL
8751 GRTSTPGPAQ STISPEISTE TITRISTPLT TTGSAEMTIT PKTGHSGASS
8801 QGTFTLDTSS RASWPGTHSA ATHRSPHSGM TTPMSRGPED VSWPSRPSVE
8851 KTSPPSSLVS LSAVTSPSPL YSTPSESSHS SPLRVTSLFT PVMMKTTDML
8901 DTSLEPVTTS PPSMNITSDE SLATSKATME TEAIQLSENT AVTQMGTISA
8951 RQEFYSSYPG LPEPSKVTSP VVTSSTIKDI VSTTIPASSE ITRIEMESTS
9001 TLTPTPRETS TSQEIHSATK PSTVPYKALT SATIEDSMTQ VMSSSRGPSP
9051 DQSTMSQDIS TEVITRLSTS PIKAESTEMT ITTQTGSPGA TSRGTLTLDT
9101 STTFMSGTHS TASQGFSHSQ MTALMSRTPG DVPWLSHPSV EEASSASFSL
9151 SSPVMTSSSP VSSTLPDSIH SSSLPVTSLL TSGLVKTTEL LGTSSEPETS
9201 SPPNLSSTSA EILATTEVTT DTEKLEMTNV VTSGYTHESP SSVLADSVTT
9251 KATSSMGITY PTGDTNVLTS TPAFSDTSRI QTKSKLSLTP GLMETSISEE
9301 TSSATEKSTV LSSVPTGATT EVSRTEAISS SRTSIPGPAQ STMSSDTSME
9351 TITRISTPLT RKESTDMAIT PKTGPSGATS QGTFTLDSSS TASWPGTHSA
9401 TTQRFPQSVV TTPMSRGPED VSWPSPLSVE KNSPPSSLVS SSSVTSPSPL
9451 YSTPSGSSHS SPVPVTSLFT SIMMKATDML DASLEPETTS APNMNITSDE
9501 SLATSKATTE TEAIHVFENT AASHVETTSA TEELYSSSPG FSEPTKVISP
9551 VVTSSSIRDN MVSTTMPGSS GITRIEIESM SSLTPGLRET RTSQDITSST
9601 ETSTVLYKMS SGATPEVSRT EVMPSSRTSI PGPAQSTMSL DISDEVVTRL
9651 STSPIMTESA EITITTQTGY SLATSQVTLP LGTSMTFLSG THSTMSQGLS
9701 HSEMTNLMSR GPESLSWTSP RFVETTRSSS SLTSLPLTTS LSPVSSTLLD
9751 SSPSSPLPVT SLILPGLVKT TEVLDTSSEP KTSSSPNLSS TSVEIPATSE
9801 IMTDTEKIHP SSNTAVAKVR TSSSVHESHS SVLADSETTI TIPSMGITSA
9851 VDDTTVFTSN PAFSETRRIP TEPTFSLTPG FRETSTSEET TSITETSAVL
9901 YGVPTSATTE VSMTEIMSSN RTHIPDSDQS TMSPDIITEV ITRLSSSSMM
9951 SESTQMTITT QKSSPGATAQ STLTLATTTA PLARTHSTVP PRFLHSEMTT
10001 LMSRSPENPS WKSSPFVEKT SSSSSLLSLP VTTSPSVSST LPQSIPSSSF
10051 SVTSLLTPGM VKTTDTSTEP GTSLSPNLSG TSVEILAASE VTTDTEKIHP
10101 SSSMAVTNVG TTSSGHELYS SVSIHSEPSK ATYPVGTPSS MAETSISTSM
10151 PANFETTGFE AEPFSHLTSG FRKTNMSLDT SSVTPTNTPS SPGSTHLLQS
10201 SKTDFTSSAK TSSPDWPPAS QYTEIPVDII TPFNASPSIT ESTGITSFPE
10251 SRFTMSVTES THHLSTDLLP SAETISTGTV MPSLSEAMTS FATTGVPRAI
10301 SGSGSPFSRT ESGPGDATLS TIAESLPSST PVPFSSSTFT TTDSSTIPAL
10351 HEITSSSATP YRVDTSLGTE SSTTEGRLVM VSTLDTSSQP GRTSSTPILD

TABLE 5-continued

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
10401	TRMTESVELG	TVTSAYQVPS	LSTRLTRTDG	IMEHITKIPN	EAAHRGTIRP
10451	VKGPQTSTSP	ASPKGLHTGG	TKRMETTTTA	LKTTTTALKT	TSRATLTTSV
10501	YTPTLGTLTP	LNASRQMAST	ILTEMMITTP	YVFPDVPETT	SSLATSLGAE
10551	TSTALPRTTP	SVLNRESETT	ASLVSRSGAE	RSPVIQTLDV	SSSEPDTTAS
10601	WVIHPAETIP	TVSKTTPNFF	HSELDTVSST	ATSHGADVSS	AIPTNISPSE
10651	LDALTPLVTI	SGTDTSTTFP	TLTKSPHETE	TRTTWLTHPA	ETSSTIPRTI
10701	PNFSHHESDA	TPSIATSPGA	ETSSAIPIMT	VSPGAEDLVT	SQVTSSGTDR
10751	NMTIPTLTLS	PGEPKTIASL	VTHPEAQTSS	AIPTSTISPA	VSRLVTSMVT
10801	SLAAKTSTTN	RALTNSPGEP	ATTVSLVTHP	AQTSPTVPWT	TSIFFHSKSD
10851	TTPSMTTSHG	AESSSAVPTP	TVSTEVPGVV	TPLVTSSRAV	ISTTIPILTL
10901	SPGEPETTPS	MATSHGEEAS	SAIPTPTVSP	GVPGVVTSLV	TSSRAVTSTT
10951	IPILTFSLGE	PETTPSMATS	HGTEAGSAVP	TVLPEVPGMV	TSLVASSRAV
11001	TSTTLPTLTL	SPGEPETTPS	MATSHGAEAS	STVPTVSPEV	PGVVTSLVTS
11051	SSGVNSTSIP	TLILSPGELE	TTPSMATSHG	AEASSAVPTP	TVSPGVSGVV
11101	TPLVTSSRAV	TSTTIPILTL	SSSEPETTPS	MATSHGVEAS	SAVLTVSPEV
11151	PGMVTSLVTS	SRAVTSTTIP	TLTISSDEPE	TTTSLVTHSE	AKMISAIPTL
11201	AVSPTVQGLV	TSLVTSSGSE	TSAFSNLTVA	SSQPETIDSW	VAHPGTEASS
11251	VVPTLTVSTG	EPFTNISLVT	HPAESSSTLP	RTTSRFSHSE	LDTMPSTVTS
11301	PEAESSSAIS	TTISPGIPGV	LTSLVTSSGR	DISATFPTVP	ESPHESEATA
11351	SWVTHPAVTS	TTVPRTTPNY	SHSEPDTTPS	IATSPGAEAT	SDFPTITVSP
11401	DVPDMVTSQV	TSSGTDTSIT	IPTLTLSSGE	PETTTSFITY	SETHTSSAIP
11451	TLPVSPGASK	MLTSLVISSG	TDSTTTFPTL	TETPYEPETT	AIQLIHPAET
11501	NTMVPRTTPK	FSHSKSDTTL	PVAITSPGPE	ASSAVSTTTI	SPDMSDLVTS
11551	LVPSSGTDTS	TTFPTLSETP	YEPETTATWL	THPAETSTTV	SGTIPNFSHR
11601	GSDTAPSMVT	SPGVDTRSGV	PTTTIPPSIP	GVVTSQVTSS	ATDTSTAIPT
11651	LTPSPGEPET	TASSATHPGT	QTGFTVPIRT	VPSSEPDTMA	SWVTHPPQTS
11701	TPVSRTTSSF	SHSSPDATPV	MATSPRTEAS	SAVLTTISPG	APEMVTSQIT
11751	SSGAATSTTV	PTLTHSPGMP	ETTALLSTHP	RTETSKTFPA	STVFPQVSET
11801	TASLTIRPGA	ETSTALPTQT	TSSLFTLLVT	GTSRVDLSPT	ASPGVSAKTA
11851	PLSTHPGTET	STMIPTSTLS	LGLLETTGLL	ATSSSAETST	STLTLTVSPA
11901	VSGLSSASIT	TDKPQTVTSW	NTETSPSVTS	VGPPEFSRTV	TGTTMTLIPS
11951	EMPTPPKTSH	GEGVSPTTIL	RTTMVEATNL	ATTGSSPTVA	KTTTTFNTLA
12001	GSLFTPLTTP	GMSTLASESV	TSRTSYNHRS	WISTTSSYNR	RYWTPATSTP
12051	VTSTFSPGIS	TSSIPSSTAA	TVPFMVPFTL	NFTITNLQYE	EDMRHPGSRK
12101	FNATERELQG	LLKPLFRNSS	LEYLYSGCRL	ASLRPEKDSS	AMAVDAICTH
12151	RPDPEDLGLD	RERLYWELSN	LTNGIQELGP	YTLDRNSLYV	NGFTHRSSMP
12201	TTSTPGTSTV	DVGTSGTPSS	SPSPTAAGPL	LMPFTLNFTI	TNLQYEEDMR

TABLE 5-continued

Human Protein of CA125 Molecule (SEQ ID NO: 5)
12251 RTGSRKFNTM ESVLQGLLKP LFKNTSVGPL YSGCRLTLLR PEKDGAATGV
12301 DAICTHRLDP KSPGLNREQL YWELSKLTND IEELGPYTLD RNSLYVNGFT
12351 HQSSVSTTST PGTSTVDLRT SGTPSSLSSP TIMAAGPLLV PFTLNFTITN
12401 LQYGEDMGHP GSRKFNTTER VLQGLLGPIF KNTSVGPLYS GCRLTSLRSE
12451 KDGAATGVDA ICIHHLDPKS PGLNRERLYW ELSQLTNGIK ELGPYTLDRN
12501 SLYVNGFTHR TSVPTSSTPG TSTVDLGTSG TPFSLPSPAT AGPLLVLFTL
12551 NFTITNLKYE EDMHRPGSRK FNTTERVLQT LLGPMFKNTS VGLLYSGCRL
12601 TLLRSEKDGA ATGVDAICTH RLDPKSPGLD REQLYWELSQ LTNGIKELGP
12651 YTLDRNSLYV NGFTHWIPVP TSSTPGTSTV DLGSGTPSSL PSPTAAGPLL
12701 VPFTLNFTIT NLQYEEDMHH PGSRKFNTTE RVLQGLLGPM FKNTSVGLLY
12751 SGCRLTLLRS EKDGAATGVD AICTHRLDPK SPGVDREQLY WELSQLTNGI
12801 KELGPYTLDR NSLYVNGFTH QTSAPNTSTP GTSTVDLGTS GTPSSLPSPT
12851 SAGPLLVPFT LNFTITNLQY EEDMRHPGSR KFNTTERVLQ GLLKPLFKST
12901 SVGPLYSGCR LTLLRSEKDG AATGVDAICT HRLDPKSPGV DREQLYWELS
12951 QLTNGIKELG PYTLDRNSLY VNGFTHQTSA PNTSTPGTST VDLGTSGTPS
13001 SLPSPTSAGP LLVPFTLNFT ITNLQYEEDM HHPGSRKFNT TERVLQGLLG
13051 PMFKNTSVGL LYSGCRLTLL RPEKNGAATG MDAICSHRLD PKSPGLNREQ
13101 LYWELSQLTH GIKELGPYTL DRNSLYVNGF THRSSVAPTS TPGTSTVDLG
13151 TSGTPSSLPS PTTAVPLLVP FTLNFTITNL QYGEDMRHPG SRKFNTTERV
13201 LQGLLGPLFK NSSVGPLYSG CRLISLRSEK DGAATGVDAI CTHHLNPQSP
13251 GLDREQLYWQ LSQMTNGIKE LGPYTLDRNS LYVNGFTHRS SGLTTSTPWT
13301 STVDLGTSGT PSPVPSPTTA GPLLVPFTLN FTITNLQYEE DMHRPGSRKF
13351 NATERVLQGL LSPIFKNSSV GPLYSGCRLT SLRPEKDGAA TGMDAVCLYH
13401 PNPKRPGLDR EQLYWELSQL THNITELGPY SLDRDSLYVN GFTHQNSVPT
13451 TSTPGTSTVY WATTGTPSSF PGHTEPGPLL IPFTFNFTIT NLHYEENMQH
13501 PGSRKFNTTE RVLQGLLKPL FKNTSVGPLY SGCRLTSLRP EKDGAATGMD
13551 AVCLYHPNPK RPGLDREQLY CELSQLTHNI TELGPYSLDR DSLYVNGFTH
13601 QNSVPTTSTP GTSTVYWATT GTPSSFPGHT EPGPLLIPFT FNFTITNLHY
13651 EENMQHPGSR KFNTTERVLQ GLLKPLFKNT SVGPLYSGCR LTLLRPEKHE
13701 AATGVDTICT HRVDPIGPGL DRERLYWELS QLTNSITELG PYTLDRDSLY
13751 VNGFNPRSSV PTTSTPGTST VHLATSGTPS SLPGHTAPVP LLIPFTLNFT
13801 ITNLHYEENM QHPGSRKFNT TERVLQGLLK PLFKNTSVGP LYSGCRLTLL
13851 RPEKHEAATG VDTICTHRVD PIGPGLDREX LYWELSXLTX XIXELGPYXL
13901 DRXSLYVNGF XXXXXXXXTS TPGTSXVXLX TSGTPXXXPX XTSAGPLLVP
13951 FTLNFTITNL QYEEDMHHPG SRKFNTTERV LQGLLGPMFK NTSVGLLYSG
14001 CRLTLLRPEK NGAATGMDAI CSHRLDPKSP GLDREQLYWE LSQLTHGIKE

TABLE 5-continued

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
14051	LGPYTLDRNS	LYVNGFTHRS	SVAPTSTPGT	STVDLGTSGT	PSSLPSPTTA
14101	VPLLVPFTLN	FTITNLQYGE	DMRHPGSRKF	NTTERVLQGL	LGPLFKNSSV
14151	GPLYSGCRLI	SLRSEKDGAA	TGVDAICTHH	LNPQSPGLDR	EQLYWQLSQM
14201	TNGIKELGPY	TLDRNSLYVN	GFTHRSSGLT	TSTPWTSTVD	LGTSGTPSPV
14251	PSPTTAGPLL	VPFTLNFTIT	NLQYEEDMHR	PGSRKFNATE	RVLQGLLSPI
14301	FKNSSVGPLY	SGCRLTSLRP	EKDGAATGMD	AVCLYHPNPK	RPGLDREQLY
14351	WELSQLTHNI	TELGPYSLDR	DSLYVNGFTH	QSSMTTTRTP	DTSTMHLATS
14401	RTPASLSGPT	TASPLLVLFT	INCTITNLQY	EEDMRRTGSR	KFNTMESVLQ
14451	GLLKPLFKNT	SVGPLYSGCR	LTLLRPKKDG	AATGVDAICT	HRLDPKSPGL
14501	NREQLYWELS	KLTNDIEELG	PYTLDRNSLY	VNGFTHQSSV	STTSTPGTST
14551	VDLRTSGTPS	SLSSPTIMXX	XPLLXPFTLN	FTITNLXYEE	XMXXPGSRKF
14601	NTTERVLQGL	LRPLFKNTSV	SSLYSGCRLT	LLRPEKDGAA	TRVDAACTYR
14651	PDPKSPGLDR	EQLYWELSQL	THSITELGPY	TLDRVSLYVN	GFNPRSSVPT
14701	TSTPGTSTVH	LATSGTPSSL	PGHTXXXPLL	XPFTLNFTIT	NLXYEEXMXX
14751	PGSRKFNTTE	RVLQGLLKPL	FRNSSLEYLY	SGCRLASLRP	EKDSSAMAVD
14801	AICTHRPDPE	DLGLDRERLY	WELSNLTNGI	QELGPYTLDR	NSLYVNGFTH
14851	RSSFLTTSTP	WTSTVDLGTS	GTPSPVPSPT	TAGPLLVPFT	LNFTITNLQY
14901	EEDMHRPGSR	RFNTTERVLQ	GLLTPLFKNT	SVGPLYSGCR	LTLLRPEKQE
14951	AATGVDTICT	HRVDPIGPGL	DRERLYWELS	QLTNSITELG	PYTLDRDSLY
15001	VNGFNPWSSV	PTTSTPGTST	VHLATSGTPS	SLPGHTAPVP	LLIPFTLNFT
15051	ITDLHYEENM	QHPGSRKFNT	TERVLQGLLK	PLFKSTSVGP	LYSGCRLTLL
15101	RPEKHGAATG	VDAICTLRLD	PTGPGLDRER	LYWELSQLTN	SVTELGPYTL
15151	DRDSLYVNGF	THRSSVPTTS	IPGTSAVHLE	TSGTPASLPG	HTAPGPLLVP
15201	FTLNFTITNL	QYEEDMRHPG	SRKFSTTERV	LQGLLKPLFK	NTSVSSLYSG
15251	CRLTLLRPEK	DGAATRVDAV	CTHRPDPKSP	GLDRERLYWK	LSQLTHGITE
15301	LGPYTLDRHS	LYVNGFTHQS	SMTTTRTPDT	STMHLATSRT	PASLSGPTTA
15351	SPLLVLFTIN	FTITNQRYEE	NMHHPGSRKF	NTTERVLQGL	LRPVFKNTSV
15401	GPLYSGCRLT	LLRPKKDGAA	TKVDAICTYR	PDPKSPGLDR	EQLYWELSQL
15451	THSITELGPY	TQDRDSLYVN	GFTHRSSVPT	TSIPGTSAVH	LETSGTPASL
15501	PGHTAPGPLL	VPFTLNFTIT	NLQYEEDMRH	PGSRKFNTTE	RVLQGLLKPL
15551	FKSTSVGPLY	SGCRLTLLRP	EKRGAATGVD	TICTHRLDPL	NPGLDREQLY
15601	WELSKLTRGI	IELGPYLLDR	GSLYVNGFTH	RTSVPTTSTP	GTSTVDLGTS
15651	GTPFSLPSPA	XXXPLLXPFT	LNFTITNLXY	EEXMXXPGSR	KFNTTERVLQ
15701	TLLGPMFKNT	SVGLLYSGCR	LTLLRSEKDG	AATGVDAICT	HRLDPKSPGV
15751	DREQLYWELS	QLTNGIKELG	PYTLDRNSLY	VNGFTHWIPV	PTSSTPGTST
15801	VDLGSGTPSL	PSSPTTAGPL	LVPFTLNFTI	TNLKYEEDMH	CPGSRKFNTT
15851	ERVLQSLLGP	MFKNTSVGPL	YSGCRLTLLR	SEKDGAATGV	DAICTHRLDP

TABLE 5-continued

Human Protein of CA125 Molecule (SEQ ID NO: 5)
15901 KSPGVDREQL YWELSQLTNG IKELGPYTLD RNSLYVNGFT HQTSAPNTST
15951 PGTSTVDLGT SGTPSSLPSP TXXXPLLXPF TLNFTITNLX YEEXMXXPGS
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TABLE 5-continued

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
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17901	CRLTLLRXEK	XXAATXVDXX	CXXXXDPXXP	GLDREXLYWE	LSXLTXXIXE
17951	LGPYXLDRXS	LYVNGFHPRS	SVPTTSTPGT	STVHLATSGT	PSSLPGHTAP
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18301	GTPSSFPGHT	EPGPLLIPFT	FNFTITNLHY	EENMQHPGSR	KFNTTERVLQ
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18751	XXXXTSTPGT	SXVXLXTSGT	PXXXPXXTXX	XPLLXPFTLN	FTITNLXYEE
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19451	XTSVGXLYSG	CRLTLLRXEK	XXAATXVDXX	CXXXXDPXXP	GLDREXLYWE
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TABLE 5-continued

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21251 SVPGTPTVDL GTSGTPVSKP GPSAASPLLV LFTLNGTITN LRYEENMQHP
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TABLE 5-continued

Human Protein of CA125 Molecule (SEQ ID NO: 5)
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Ala Ser Pro Thr Ser Ser Val Val Gly Arg Thr Thr Gln Ser Leu Gly
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Val Met Ser Ser Ala Leu Pro Glu Ser Thr Ser Arg Gly Met Thr His
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Ser Glu Gln Arg Thr Ser Pro Ser Leu Ser Pro Gln Val Asn Gly Thr
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Pro Ser Arg Asn Tyr Pro Ala Thr Ser Met Val Ser Gly Leu Ser Ser
        115                 120                 125

Pro Arg Thr Arg Thr Ser Ser Thr Glu Gly Asn Phe Thr Lys Glu Ala
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Lys Tyr Thr Val Pro Thr Glu Thr Ser Thr Thr Glu Gly Asp Ser Thr
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Glu Thr Pro Trp Asp Thr Arg Tyr Ile Pro Val Lys Ile Thr Ser Pro
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Ser Met Thr Pro Ala Glu Thr Thr Val Thr Asp Ser His Thr Pro Gly
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Ile Leu Ser Thr Thr Gly Tyr Pro Phe Ser Ser Pro Glu Pro Gly Ser
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Ala Gly His Ser Arg Ile Ser Thr Ser Ala Pro Leu Ser Ser Ser Ala
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Ser Val Leu Asp Asn Lys Ile Ser Glu Thr Ser Ile Phe Ser Gly Gln
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Ser Leu Thr Ser Pro Leu Ser Pro Gly Val Pro Glu Ala Arg Ala Ser
305                 310                 315                 320

Thr Met Pro Asn Ser Ala Ile Pro Phe Ser Met Thr Leu Ser Asn Ala
                325                 330                 335

Glu Thr Ser Ala Glu Arg Val Arg Ser Thr Ile Ser Ser Leu Gly Thr
            340                 345                 350

Pro Ser Ile Ser Thr Lys Gln Thr Ala Glu Thr Ile Leu Thr Phe His
        355                 360                 365

Ala Phe Ala Glu Thr Met Asp Ile Pro Ser Thr His Ile Ala Lys Thr
    370                 375                 380

Leu Ala Ser Glu Trp Leu Gly Ser Pro Gly Thr Leu Gly Gly Thr Ser
385                 390                 395                 400

Thr Ser Ala Leu Thr Thr Thr Ser Pro Ser Thr Thr Leu Val Ser Glu
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                405                 410                 415

Glu Thr Asn Thr His His Ser Thr Ser Gly Lys Glu Thr Glu Gly Thr
            420                 425                 430

Leu Asn Thr Ser Met Thr Pro Leu Glu Thr Ser Ala Pro Gly Glu Glu
        435                 440                 445

Ser Glu Met Thr Ala Thr Leu Val Pro Thr Leu Gly Phe Thr Thr Leu
    450                 455                 460

Asp Ser Lys Ile Arg Ser Pro Ser Gln Val Ser Ser Ser His Pro Thr
465                 470                 475                 480

Arg Glu Leu Arg Thr Thr Gly Ser Thr Ser Gly Arg Gln Ser Ser Ser
                485                 490                 495

Thr Ala Ala His Gly Ser Ser Asp Ile Leu Arg Ala Thr Thr Ser Ser
            500                 505                 510

Thr Ser Lys Ala Ser Ser Trp Thr Ser Glu Ser Thr Ala Gln Gln Phe
        515                 520                 525

Ser Glu Pro Gln His Thr Gln Trp Val Glu Thr Ser Pro Ser Met Lys
    530                 535                 540

Thr Glu Arg Pro Pro Ala Ser Thr Ser Val Ala Ala Pro Ile Thr Thr
545                 550                 555                 560

Ser Val Pro Ser Val Val Ser Gly Phe Thr Thr Leu Lys Thr Ser Ser
                565                 570                 575

Thr Lys Gly Ile Trp Leu Glu Glu Thr Ser Ala Asp Thr Leu Ile Gly
            580                 585                 590

Glu Ser Thr Ala Gly Pro Thr Thr His Gln Phe Ala Val Pro Thr Gly
        595                 600                 605

Ile Ser Met Thr Gly Gly Ser Ser Thr Arg Gly Ser Gln Gly Thr Thr
    610                 615                 620

His Leu Leu Thr Arg Ala Thr Ala Ser Ser Glu Thr Ser Ala Asp Leu
625                 630                 635                 640

Thr Leu Ala Thr Asn Gly Val Pro Val Ser Val Ser Pro Ala Val Ser
                645                 650                 655

Lys Thr Ala Ala Gly Ser Ser Pro Pro Gly Gly Thr Lys Pro Ser Tyr
            660                 665                 670

Thr Met Val Ser Ser Val Ile Pro Glu Thr Ser Ser Leu Gln Ser Ser
        675                 680                 685

Ala Phe Arg Glu Gly Thr Ser Leu Gly Leu Thr Pro Leu Asn Thr Arg
    690                 695                 700

His Pro Phe Ser Ser Pro Glu Pro Asp Ser Ala Gly His Thr Lys Ile
705                 710                 715                 720

Ser Thr Ser Ile Pro Leu Leu Ser Ser Ala Ser Val Leu Glu Asp Lys
                725                 730                 735

Val Ser Ala Thr Ser Thr Phe Ser His His Lys Ala Thr Ser Ser Ile
            740                 745                 750

Thr Thr Gly Thr Pro Glu Ile Ser Thr Lys Thr Lys Pro Ser Ser Ala
        755                 760                 765

Val Leu Ser Ser Met Thr Leu Ser Asn Ala Ala Thr Ser Pro Glu Arg
    770                 775                 780

Val Arg Asn Ala Thr Ser Pro Leu Thr His Pro Ser Pro Ser Gly Glu
785                 790                 795                 800

Glu Thr Ala Gly Ser Val Leu Thr Leu Ser Thr Ser Ala Glu Thr Thr
                805                 810                 815
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Asp Ser Pro Asn Ile His Pro Thr Gly Thr Leu Thr Ser Glu Ser Ser
            820                 825                 830

Glu Ser Pro Ser Thr Leu Ser Leu Pro Ser Val Ser Gly Val Lys Thr
        835                 840                 845

Thr Phe Ser Ser Ser Thr Pro Ser Thr His Leu Phe Thr Ser Gly Glu
    850                 855                 860

Glu Thr Glu Glu Thr Ser Asn Pro Ser Val Ser Gln Pro Glu Thr Ser
865                 870                 875                 880

Val Ser Arg Val Arg Thr Thr Leu Ala Ser Thr Ser Val Pro Thr Pro
                885                 890                 895

Val Phe Pro Thr Met Asp Thr Trp Pro Thr Arg Ser Ala Gln Phe Ser
            900                 905                 910

Ser Ser His Leu Val Ser Glu Leu Arg Ala Thr Ser Ser Thr Ser Val
        915                 920                 925

Thr Asn Ser Thr Gly Ser Ala Leu Pro Lys Ile Ser His Leu Thr Gly
    930                 935                 940

Thr Ala Thr Met Ser Gln Thr Asn Arg Asp Thr Phe Asn Asp Ser Ala
945                 950                 955                 960

Ala Pro Gln Ser Thr Thr Trp Pro Glu Thr Ser Pro Arg Phe Lys Thr
                965                 970                 975

Gly Leu Pro Ser Ala Thr Thr Thr Val Ser Thr Ser Ala Thr Ser Leu
            980                 985                 990

Ser Ala Thr Val Met Val Ser Lys  Phe Thr Ser Pro Ala  Thr Ser Ser
        995                 1000                1005

Met Glu  Ala Thr Ser Ile Arg  Glu Pro Ser Thr Thr  Ile Leu Thr
    1010                1015                1020

Thr Glu  Thr Thr Asn Gly Pro  Gly Ser Met Ala Val  Ala Ser Thr
    1025                1030                1035

Asn Ile  Pro Ile Gly Lys Gly  Tyr Ile Thr Glu Gly  Arg Leu Asp
    1040                1045                1050

Thr Ser  His Leu Pro Ile Gly  Thr Thr Ala Ser Ser  Glu Thr Ser
    1055                1060                1065

Met Asp  Phe Thr Met Ala Lys  Glu Ser Val Ser Met  Ser Val Ser
    1070                1075                1080

Pro Ser  Gln Ser Met Asp Ala  Ala Gly Ser Ser Thr  Pro Gly Arg
    1085                1090                1095

Thr Ser  Gln Phe Val Asp Thr  Phe Ser Asp Asp Val  Tyr His Leu
    1100                1105                1110

Thr Ser  Arg Glu Ile Thr Ile  Pro Arg Asp Gly Thr  Ser Ser Ala
    1115                1120                1125

Leu Thr  Pro Gln Met Thr Ala  Thr His Pro Pro Ser  Pro Asp Pro
    1130                1135                1140

Gly Ser  Ala Arg Ser Thr Trp  Leu Gly Ile Leu Ser  Ser Ser Pro
    1145                1150                1155

Ser Ser  Pro Thr Pro Lys Val  Thr Met Ser Ser Thr  Phe Ser Thr
    1160                1165                1170

Gln Arg  Val Thr Thr Ser Met  Ile Met Asp Thr Val  Glu Thr Ser
    1175                1180                1185

Arg Trp  Asn Met Pro Asn Leu  Pro Ser Thr Thr Ser  Leu Thr Pro
    1190                1195                1200
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Ser Asn  Ile Pro Thr Ser Gly  Ala Ile Gly Lys Ser  Thr Leu Val
    1205                 1210                 1215

Pro Leu  Asp Thr Pro Ser Pro  Ala Thr Ser Leu Glu  Ala Ser Glu
    1220                 1225                 1230

Gly Gly  Leu Pro Thr Leu Ser  Thr Tyr Pro Glu Ser  Thr Asn Thr
    1235                 1240                 1245

Pro Ser  Ile His Leu Gly Ala  His Ala Ser Ser Glu  Ser Pro Ser
    1250                 1255                 1260

Thr Ile  Asn Leu Thr Met Ala  Ser Val Val Lys Pro  Gly Ser Tyr
    1265                 1270                 1275

Thr Pro  Leu Thr Phe Pro Ser  Ile Glu Thr His Ile  His Val Ser
    1280                 1285                 1290

Thr Ala  Arg Met Ala Tyr Ser  Ser Gly Ser Ser Pro  Glu Met Thr
    1295                 1300                 1305

Ala Pro  Gly Glu Thr Asn Thr  Gly Ser Thr Trp Asp  Pro Thr Thr
    1310                 1315                 1320

Tyr Ile  Thr Thr Thr Asp Pro  Lys Asp Thr Ser Ser  Ala Gln Val
    1325                 1330                 1335

Ser Thr  Pro His Ser Val Arg  Thr Leu Arg Thr Thr  Glu Asn His
    1340                 1345                 1350

Pro Lys  Thr Glu Ser Ala Thr  Pro Ala Ala Tyr Ser  Gly Ser Pro
    1355                 1360                 1365

Lys Ile  Ser Ser Ser Pro Asn  Leu Thr Ser Pro Ala  Thr Lys Ala
    1370                 1375                 1380

Trp Thr  Ile Thr Asp Thr Thr  Glu His Ser Thr Gln  Leu His Tyr
    1385                 1390                 1395

Thr Lys  Leu Ala Glu Lys Ser  Ser Gly Phe Glu Thr  Gln Ser Ala
    1400                 1405                 1410

Pro Gly  Pro Val Ser Val Val  Ile Pro Thr Ser Pro  Thr Ile Gly
    1415                 1420                 1425

Ser Ser  Thr Leu Glu Leu Thr  Ser Asp Val Pro Gly  Glu Pro Leu
    1430                 1435                 1440

Val Leu  Ala Pro Ser Glu Gln  Thr Thr Ile Thr Leu  Pro Met Ala
    1445                 1450                 1455

Thr Trp  Leu Ser Thr Ser Leu  Thr Glu Glu Met Ala  Ser Thr Asp
    1460                 1465                 1470

Leu Asp  Ile Ser Ser Pro Ser  Ser Pro Met Ser Thr  Phe Ala Ile
    1475                 1480                 1485

Phe Pro  Pro Met Ser Thr Pro  Ser His Glu Leu Ser  Lys Ser Glu
    1490                 1495                 1500

Ala Asp  Thr Ser Ala Ile Arg  Asn Thr Asp Ser Thr  Thr Leu Asp
    1505                 1510                 1515

Gln His  Leu Gly Ile Arg Ser  Leu Gly Arg Thr Gly  Asp Leu Thr
    1520                 1525                 1530

Thr Val  Pro Ile Thr Pro Leu  Thr Thr Thr Trp Thr  Ser Val Ile
    1535                 1540                 1545

Glu His  Ser Thr Gln Ala Gln  Asp Thr Leu Ser Ala  Thr Met Ser
    1550                 1555                 1560

Pro Thr  His Val Thr Gln Ser  Leu Lys Asp Gln Thr  Ser Ile Pro
    1565                 1570                 1575

Ala Ser  Ala Ser Pro Ser His  Leu Thr Glu Val Tyr  Pro Glu Leu
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    1580                1585                1590

Gly Thr  Gln Gly Arg Ser Ser  Ser Glu Ala Thr Thr  Phe Trp Lys
    1595                1600                1605

Pro Ser  Thr Asp Thr Leu Ser  Arg Glu Ile Glu Thr  Gly Pro Thr
    1610                1615                1620

Asn Ile  Gln Ser Thr Pro Pro  Met Asp Asn Thr Thr  Thr Gly Ser
    1625                1630                1635

Ser Ser  Ser Gly Val Thr Leu  Gly Ile Ala His Leu  Pro Ile Gly
    1640                1645                1650

Thr Ser  Ser Pro Ala Glu Thr  Ser Thr Asn Met Ala  Leu Glu Arg
    1655                1660                1665

Arg Ser  Ser Thr Ala Thr Val  Ser Met Ala Gly Thr  Met Gly Leu
    1670                1675                1680

Leu Val  Thr Ser Ala Pro Gly  Arg Ser Ile Ser Gln  Ser Leu Gly
    1685                1690                1695

Arg Val  Ser Ser Val Leu Ser  Glu Ser Thr Thr Glu  Gly Val Thr
    1700                1705                1710

Asp Ser  Ser Lys Gly Ser Ser  Pro Arg Leu Asn Thr  Gln Gly Asn
    1715                1720                1725

Thr Ala  Leu Ser Ser Ser Leu  Glu Pro Ser Tyr Ala  Glu Gly Ser
    1730                1735                1740

Gln Met  Ser Thr Ser Ile Pro  Leu Thr Ser Ser Pro  Thr Thr Pro
    1745                1750                1755

Asp Val  Glu Phe Ile Gly Gly  Ser Thr Phe Trp Thr  Lys Glu Val
    1760                1765                1770

Thr Thr  Val Met Thr Ser Asp  Ile Ser Lys Ser Ser  Ala Arg Thr
    1775                1780                1785

Glu Ser  Ser Ser Ala Thr Leu  Met Ser Thr Ala Leu  Gly Ser Thr
    1790                1795                1800

Glu Asn  Thr Gly Lys Glu Lys  Leu Arg Thr Ala Ser  Met Asp Leu
    1805                1810                1815

Pro Ser  Pro Thr Pro Ser Met  Glu Val Thr Pro Trp  Ile Ser Leu
    1820                1825                1830

Thr Leu  Ser Asn Ala Pro Asn  Thr Thr Asp Ser Leu  Asp Leu Ser
    1835                1840                1845

His Gly  Val His Thr Ser Ser  Ala Gly Thr Leu Ala  Thr Asp Arg
    1850                1855                1860

Ser Leu  Asn Thr Gly Val Thr  Arg Ala Ser Arg Leu  Glu Asn Gly
    1865                1870                1875

Ser Asp  Thr Ser Ser Lys Ser  Leu Ser Met Gly Asn  Ser Thr His
    1880                1885                1890

Thr Ser  Met Thr Asp Thr Glu  Lys Ser Glu Val Ser  Ser Ser Ile
    1895                1900                1905

His Pro  Arg Pro Glu Thr Ser  Ala Pro Gly Ala Glu  Thr Thr Leu
    1910                1915                1920

Thr Ser  Thr Pro Gly Asn Arg  Ala Ile Ser Leu Thr  Leu Pro Phe
    1925                1930                1935

Ser Ser  Ile Pro Val Glu Glu  Val Ile Ser Thr Gly  Ile Thr Ser
    1940                1945                1950

Gly Pro  Asp Ile Asn Ser Ala  Pro Met Thr His Ser  Pro Ile Thr
    1955                1960                1965
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Pro Pro  Thr Ile Val Trp Thr  Ser Thr Gly Thr Ile  Glu Gln Ser
    1970                 1975                 1980

Thr Gln  Pro Leu His Ala Val  Ser Ser Glu Lys Val  Ser Val Gln
    1985                 1990                 1995

Thr Gln  Ser Thr Pro Tyr Val  Asn Ser Val Ala Val  Ser Ala Ser
    2000                 2005                 2010

Pro Thr  His Glu Asn Ser Val  Ser Ser Gly Ser Ser  Thr Ser Ser
    2015                 2020                 2025

Pro Tyr  Ser Ser Ala Ser Leu  Glu Ser Leu Asp Ser  Thr Ile Ser
    2030                 2035                 2040

Arg Arg  Asn Ala Ile Thr Ser  Trp Leu Trp Asp Leu  Thr Thr Ser
    2045                 2050                 2055

Leu Pro  Thr Thr Thr Trp Pro  Ser Thr Ser Leu Ser  Glu Ala Leu
    2060                 2065                 2070

Ser Ser  Gly His Ser Gly Val  Ser Asn Pro Ser Ser  Thr Thr Thr
    2075                 2080                 2085

Glu Phe  Pro Leu Phe Ser Ala  Ala Ser Thr Ser Ala  Ala Lys Gln
    2090                 2095                 2100

Arg Asn  Pro Glu Thr Glu Thr  His Gly Pro Gln Asn  Thr Ala Ala
    2105                 2110                 2115

Ser Thr  Leu Asn Thr Asp Ala  Ser Ser Val Thr Gly  Leu Ser Glu
    2120                 2125                 2130

Thr Pro  Val Gly Ala Ser Ile  Ser Ser Glu Val Pro  Leu Pro Met
    2135                 2140                 2145

Ala Ile  Thr Ser Arg Ser Asp  Val Ser Gly Leu Thr  Ser Glu Ser
    2150                 2155                 2160

Thr Ala  Asn Pro Ser Leu Gly  Thr Ala Ser Ser Ala  Gly Thr Lys
    2165                 2170                 2175

Leu Thr  Arg Thr Ile Ser Leu  Pro Thr Ser Glu Ser  Leu Val Ser
    2180                 2185                 2190

Phe Arg  Met Asn Lys Asp Pro  Trp Thr Val Ser Ile  Pro Leu Gly
    2195                 2200                 2205

Ser His  Pro Thr Thr Asn Thr  Glu Thr Ser Ile Pro  Val Asn Ser
    2210                 2215                 2220

Ala Gly  Pro Pro Gly Leu Ser  Thr Val Ala Ser Asp  Val Ile Asp
    2225                 2230                 2235

Thr Pro  Ser Asp Gly Ala Glu  Ser Ile Pro Thr Val  Ser Phe Ser
    2240                 2245                 2250

Pro Ser  Pro Asp Thr Glu Val  Thr Thr Ile Ser His  Phe Pro Glu
    2255                 2260                 2265

Lys Thr  Thr His Ser Phe Arg  Thr Ile Ser Ser Leu  Thr His Glu
    2270                 2275                 2280

Leu Thr  Ser Arg Val Thr Pro  Ile Pro Gly Asp Trp  Met Ser Ser
    2285                 2290                 2295

Ala Met  Ser Thr Lys Pro Thr  Gly Ala Ser Pro Ser  Ile Thr Leu
    2300                 2305                 2310

Gly Glu  Arg Arg Thr Ile Thr  Ser Ala Ala Pro Thr  Thr Ser Pro
    2315                 2320                 2325

Ile Val  Leu Thr Ala Ser Phe  Thr Glu Thr Ser Thr  Val Ser Leu
    2330                 2335                 2340
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Asp Asn  Glu Thr Thr Val Lys  Thr Ser Asp Ile Leu  Asp Ala Arg
    2345                2350                2355

Lys Thr  Asn Glu Leu Pro Ser  Asp Ser Ser Ser Ser  Ser Asp Leu
    2360                2365                2370

Ile Asn  Thr Ser Ile Ala Ser  Ser Thr Met Asp Val  Thr Lys Thr
    2375                2380                2385

Ala Ser  Ile Ser Pro Thr Ser  Ile Ser Gly Met Thr  Ala Ser Ser
    2390                2395                2400

Ser Pro  Ser Leu Phe Ser Ser  Asp Arg Pro Gln Val  Pro Thr Ser
    2405                2410                2415

Thr Thr  Glu Thr Asn Thr Ala  Thr Ser Pro Ser Val  Ser Ser Asn
    2420                2425                2430

Thr Tyr  Ser Leu Asp Gly Gly  Ser Asn Val Gly Gly  Thr Pro Ser
    2435                2440                2445

Thr Leu  Pro Pro Phe Thr Ile  Thr His Pro Val Glu  Thr Ser Ser
    2450                2455                2460

Ala Leu  Leu Ala Trp Ser Arg  Pro Val Arg Thr Phe  Ser Thr Met
    2465                2470                2475

Val Ser  Thr Asp Thr Ala Ser  Gly Glu Asn Pro Thr  Ser Ser Asn
    2480                2485                2490

Ser Val  Val Thr Ser Val Pro  Ala Pro Gly Thr Trp  Ala Ser Val
    2495                2500                2505

Gly Ser  Thr Thr Asp Leu Pro  Ala Met Gly Phe Leu  Lys Thr Ser
    2510                2515                2520

Pro Ala  Gly Glu Ala His Ser  Leu Leu Ala Ser Thr  Ile Glu Pro
    2525                2530                2535

Ala Thr  Ala Phe Thr Pro His  Leu Ser Ala Ala Val  Val Thr Gly
    2540                2545                2550

Ser Ser  Ala Thr Ser Glu Ala  Ser Leu Leu Thr Thr  Ser Glu Ser
    2555                2560                2565

Lys Ala  Ile His Ser Ser Pro  Gln Thr Pro Thr Thr  Pro Thr Ser
    2570                2575                2580

Gly Ala  Asn Trp Glu Thr Ser  Ala Thr Pro Glu Ser  Leu Leu Val
    2585                2590                2595

Val Thr  Glu Thr Ser Asp Thr  Thr Leu Thr Ser Lys  Ile Leu Val
    2600                2605                2610

Thr Asp  Thr Ile Leu Phe Ser  Thr Val Ser Thr Pro  Pro Ser Lys
    2615                2620                2625

Phe Pro  Ser Thr Gly Thr Leu  Ser Gly Ala Ser Phe  Pro Thr Leu
    2630                2635                2640

Leu Pro  Asp Thr Pro Ala Ile  Pro Leu Thr Ala Thr  Glu Pro Thr
    2645                2650                2655

Ser Ser  Leu Ala Thr Ser Phe  Asp Ser Thr Pro Leu  Val Thr Ile
    2660                2665                2670

Ala Ser  Asp Ser Leu Gly Thr  Val Pro Glu Thr Thr  Leu Thr Met
    2675                2680                2685

Ser Glu  Thr Ser Asn Gly Asp  Ala Leu Val Leu Lys  Thr Val Ser
    2690                2695                2700

Asn Pro  Asp Arg Ser Ile Pro  Gly Ile Thr Ile Gln  Gly Val Thr
    2705                2710                2715

Glu Ser  Pro Leu His Pro Ser  Ser Thr Ser Pro Ser  Lys Ile Val
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    2720                2725                2730

Ala Pro  Arg Asn Thr Thr Tyr  Glu Gly Ser Ile Thr  Val Ala Leu
    2735                2740                2745

Ser Thr  Leu Pro Ala Gly Thr  Thr Gly Ser Leu Val  Phe Ser Gln
    2750                2755                2760

Ser Ser  Glu Asn Ser Glu Thr  Thr Ala Leu Val Asp  Ser Ser Ala
    2765                2770                2775

Gly Leu  Glu Arg Ala Ser Val  Met Pro Leu Thr Thr  Gly Ser Gln
    2780                2785                2790

Gly Met  Ala Ser Ser Gly Gly  Ile Arg Ser Gly Ser  Thr His Ser
    2795                2800                2805

Thr Gly  Thr Lys Thr Phe Ser  Ser Leu Pro Leu Thr  Met Asn Pro
    2810                2815                2820

Gly Glu  Val Thr Ala Met Ser  Glu Ile Thr Thr Asn  Arg Leu Thr
    2825                2830                2835

Ala Thr  Gln Ser Thr Ala Pro  Lys Gly Ile Pro Val  Lys Pro Thr
    2840                2845                2850

Ser Ala  Glu Ser Gly Leu Leu  Thr Pro Val Ser Ala  Ser Ser Ser
    2855                2860                2865

Pro Ser  Lys Ala Phe Ala Ser  Leu Thr Thr Ala Pro  Pro Ser Thr
    2870                2875                2880

Trp Gly  Ile Pro Gln Ser Thr  Leu Thr Phe Glu Phe  Ser Glu Val
    2885                2890                2895

Pro Ser  Leu Asp Thr Lys Ser  Ala Ser Leu Pro Thr  Pro Gly Gln
    2900                2905                2910

Ser Leu  Asn Thr Ile Pro Asp  Ser Asp Ala Ser Thr  Ala Ser Ser
    2915                2920                2925

Ser Leu  Ser Lys Ser Pro Glu  Lys Asn Pro Arg Ala  Arg Met Met
    2930                2935                2940

Thr Ser  Thr Lys Ala Ile Ser  Ala Ser Ser Phe Gln  Ser Thr Gly
    2945                2950                2955

Phe Thr  Glu Thr Pro Glu Gly  Ser Ala Ser Pro Ser  Met Ala Gly
    2960                2965                2970

His Glu  Pro Arg Val Pro Thr  Ser Gly Thr Gly Asp  Pro Arg Tyr
    2975                2980                2985

Ala Ser  Glu Ser Met Ser Tyr  Pro Asp Pro Ser Lys  Ala Ser Ser
    2990                2995                3000

Ala Met  Thr Ser Thr Ser Leu  Ala Ser Lys Leu Thr  Thr Leu Phe
    3005                3010                3015

Ser Thr  Gly Gln Ala Ala Arg  Ser Gly Ser Ser Ser  Ser Pro Ile
    3020                3025                3030

Ser Leu  Ser Thr Glu Lys Glu  Thr Ser Phe Leu Ser  Pro Thr Ala
    3035                3040                3045

Ser Thr  Ser Arg Lys Thr Ser  Leu Phe Leu Gly Pro  Ser Met Ala
    3050                3055                3060

Arg Gln  Pro Asn Ile Leu Val  His Leu Gln Thr Ser  Ala Leu Thr
    3065                3070                3075

Leu Ser  Pro Thr Ser Thr Leu  Asn Met Ser Gln Glu  Glu Pro Pro
    3080                3085                3090

Glu Leu  Thr Ser Ser Gln Thr  Ile Ala Glu Glu Glu  Gly Thr Thr
    3095                3100                3105
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Ala Glu  Thr Gln Thr Leu Thr  Phe Thr Pro Ser Glu  Thr Pro Thr
    3110                 3115                 3120

Ser Leu  Leu Pro Val Ser Ser  Pro Thr Glu Pro Thr  Ala Arg Arg
    3125                 3130                 3135

Lys Ser  Ser Pro Glu Thr Trp  Ala Ser Ser Ile Ser  Val Pro Ala
    3140                 3145                 3150

Lys Thr  Ser Leu Val Glu Thr  Thr Asp Gly Thr Leu  Val Thr Thr
    3155                 3160                 3165

Ile Lys  Met Ser Ser Gln Ala  Ala Gln Gly Asn Ser  Thr Trp Pro
    3170                 3175                 3180

Ala Pro  Ala Glu Glu Thr Gly  Thr Ser Pro Ala Gly  Thr Ser Pro
    3185                 3190                 3195

Gly Ser  Pro Glu Val Ser Thr  Thr Leu Lys Ile Met  Ser Ser Lys
    3200                 3205                 3210

Glu Pro  Ser Ile Ser Pro Glu  Ile Arg Ser Thr Val  Arg Asn Ser
    3215                 3220                 3225

Pro Trp  Lys Thr Pro Glu Thr  Thr Val Pro Met Glu  Thr Thr Val
    3230                 3235                 3240

Glu Pro  Val Thr Leu Gln Ser  Thr Ala Leu Gly Ser  Gly Ser Thr
    3245                 3250                 3255

Ser Ile  Ser His Leu Pro Thr  Gly Thr Thr Ser Pro  Thr Lys Ser
    3260                 3265                 3270

Pro Thr  Glu Asn Met Leu Ala  Thr Glu Arg Val Ser  Leu Ser Pro
    3275                 3280                 3285

Ser Pro  Pro Glu Ala Trp Thr  Asn Leu Tyr Ser Gly  Thr Pro Gly
    3290                 3295                 3300

Gly Thr  Arg Gln Ser Leu Ala  Thr Met Ser Ser Val  Ser Leu Glu
    3305                 3310                 3315

Ser Pro  Thr Ala Arg Ser Ile  Thr Gly Thr Gly Gln  Gln Ser Ser
    3320                 3325                 3330

Pro Glu  Leu Val Ser Lys Thr  Thr Gly Met Glu Phe  Ser Met Trp
    3335                 3340                 3345

His Gly  Ser Thr Gly Gly Thr  Thr Gly Asp Thr His  Val Ser Leu
    3350                 3355                 3360

Ser Thr  Ser Ser Asn Ile Leu  Glu Asp Pro Val Thr  Ser Pro Asn
    3365                 3370                 3375

Ser Val  Ser Ser Leu Thr Asp  Lys Ser Lys His Lys  Thr Glu Thr
    3380                 3385                 3390

Trp Val  Ser Thr Thr Ala Ile  Pro Ser Thr Val Leu  Asn Asn Lys
    3395                 3400                 3405

Ile Met  Ala Ala Glu Gln Gln  Thr Ser Arg Ser Val  Asp Glu Ala
    3410                 3415                 3420

Tyr Ser  Ser Thr Ser Ser Trp  Ser Asp Gln Thr Ser  Gly Ser Asp
    3425                 3430                 3435

Ile Thr  Leu Gly Ala Ser Pro  Asp Val Thr Asn Thr  Leu Tyr Ile
    3440                 3445                 3450

Thr Ser  Thr Ala Gln Thr Thr  Ser Leu Val Ser Leu  Pro Ser Gly
    3455                 3460                 3465

Asp Gln  Gly Ile Thr Ser Leu  Thr Asn Pro Ser Gly  Gly Lys Thr
    3470                 3475                 3480
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Ser Ser  Ala Ser Ser Val Thr  Ser Pro Ser Ile Gly  Leu Glu Thr
    3485                 3490                 3495

Leu Arg  Ala Asn Val Ser Ala  Val Lys Ser Asp Ile  Ala Pro Thr
    3500                 3505                 3510

Ala Gly  His Leu Ser Gln Thr  Ser Ser Pro Ala Glu  Val Ser Ile
    3515                 3520                 3525

Leu Asp  Val Thr Thr Ala Pro  Thr Pro Gly Ile Ser  Thr Thr Ile
    3530                 3535                 3540

Thr Thr  Met Gly Thr Asn Ser  Ile Ser Thr Thr Thr  Pro Asn Pro
    3545                 3550                 3555

Glu Val  Gly Met Ser Thr Met  Asp Ser Thr Pro Ala  Thr Glu Arg
    3560                 3565                 3570

Arg Thr  Thr Ser Thr Glu His  Pro Ser Thr Trp Ser  Ser Thr Ala
    3575                 3580                 3585

Ala Ser  Asp Ser Trp Thr Val  Thr Asp Met Thr Ser  Asn Leu Lys
    3590                 3595                 3600

Val Ala  Arg Ser Pro Gly Thr  Ile Ser Thr Met His  Thr Thr Ser
    3605                 3610                 3615

Phe Leu  Ala Ser Ser Thr Glu  Leu Asp Ser Met Ser  Thr Pro His
    3620                 3625                 3630

Gly Arg  Ile Thr Val Ile Gly  Thr Ser Leu Val Thr  Pro Ser Ser
    3635                 3640                 3645

Asp Ala  Ser Ala Val Lys Thr  Glu Thr Ser Thr Ser  Glu Arg Thr
    3650                 3655                 3660

Leu Ser  Pro Ser Asp Thr Thr  Ala Ser Thr Pro Ile  Ser Thr Phe
    3665                 3670                 3675

Ser Arg  Val Gln Arg Met Ser  Ile Ser Val Pro Asp  Ile Leu Ser
    3680                 3685                 3690

Thr Ser  Trp Thr Pro Ser Ser  Thr Glu Ala Glu Asp  Val Pro Val
    3695                 3700                 3705

Ser Met  Val Pro Thr Asp His  Ala Ser Thr Lys Thr  Asp Pro Asn
    3710                 3715                 3720

Thr Pro  Leu Ser Thr Phe Leu  Phe Asp Ser Leu Ser  Thr Leu Asp
    3725                 3730                 3735

Trp Asp  Thr Gly Arg Ser Leu  Ser Ser Ala Thr Ala  Thr Thr Ser
    3740                 3745                 3750

Ala Pro  Gln Gly Ala Thr Thr  Pro Gln Glu Leu Thr  Leu Glu Thr
    3755                 3760                 3765

Met Ile  Ser Pro Ala Thr Ser  Gln Leu Pro Phe Ser  Ile Gly His
    3770                 3775                 3780

Ile Thr  Ser Ala Val Thr Pro  Ala Ala Met Ala Arg  Ser Ser Gly
    3785                 3790                 3795

Val Thr  Phe Ser Arg Pro Asp  Pro Thr Ser Lys Lys  Ala Glu Gln
    3800                 3805                 3810

Thr Ser  Thr Gln Leu Pro Thr  Thr Thr Ser Ala His  Pro Gly Gln
    3815                 3820                 3825

Val Pro  Arg Ser Ala Ala Thr  Thr Leu Asp Val Ile  Pro His Thr
    3830                 3835                 3840

Ala Lys  Thr Pro Asp Ala Thr  Phe Gln Arg Gln Gly  Gln Thr Ala
    3845                 3850                 3855

Leu Thr  Thr Glu Ala Arg Ala  Thr Ser Asp Ser Trp  Asn Glu Lys
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    3860                3865                3870

Glu Lys  Ser Thr Pro Ser Ala  Pro Trp Ile Thr Glu  Met Met Asn
    3875                3880                3885

Ser Val  Ser Glu Asp Thr Ile  Lys Glu Val Thr Ser  Ser Ser Ser
    3890                3895                3900

Val Leu  Lys Asp Pro Glu Tyr  Ala Gly His Lys Leu  Gly Ile Trp
    3905                3910                3915

Asp Asp  Phe Ile Pro Lys Phe  Gly Lys Ala Ala His  Met Arg Glu
    3920                3925                3930

Leu Pro  Leu Leu Ser Pro Pro  Gln Asp Lys Glu Ala  Ile His Pro
    3935                3940                3945

Ser Thr  Asn Thr Val Glu Thr  Thr Gly Trp Val Thr  Ser Ser Glu
    3950                3955                3960

His Ala  Ser His Ser Thr Ile  Pro Ala His Ser Ala  Ser Ser Lys
    3965                3970                3975

Leu Thr  Ser Pro Val Val Thr  Thr Ser Thr Arg Glu  Gln Ala Ile
    3980                3985                3990

Val Ser  Met Ser Thr Thr Thr  Trp Pro Glu Ser Thr  Arg Ala Arg
    3995                4000                4005

Thr Glu  Pro Asn Ser Phe Leu  Thr Ile Glu Leu Arg  Asp Val Ser
    4010                4015                4020

Pro Tyr  Met Asp Thr Ser Ser  Thr Thr Gln Thr Ser  Ile Ile Ser
    4025                4030                4035

Ser Pro  Gly Ser Thr Ala Ile  Thr Lys Gly His Arg  Thr Glu Ile
    4040                4045                4050

Thr Ser  Tyr Lys Arg Ile Ser  Ser Ser Phe Leu Ala  Gln Ser Met
    4055                4060                4065

Arg Ser  Ser Asp Ser Pro Ser  Glu Ala Ile Thr Arg  Leu Ser Asn
    4070                4075                4080

Phe Pro  Ala Met Thr Glu Ser  Gly Gly Met Ile Leu  Ala Met Gln
    4085                4090                4095

Thr Ser  Pro Pro Gly Ala Thr  Ser Ile Ser Ala Pro  Thr Leu Asp
    4100                4105                4110

Thr Ser  Ala Thr Ala Ser Trp  Thr Gly Thr Pro Leu  Ala Thr Thr
    4115                4120                4125

Gln Arg  Phe Thr Tyr Ser Glu  Lys Thr Thr Leu Phe  Ser Lys Gly
    4130                4135                4140

Arg Glu  Asp Thr Ser Gln Pro  Ser Pro Pro Cys Val  Glu Glu Thr
    4145                4150                4155

Ser Ser  Ser Ser Ser Val Val  Pro Ile His Ala Thr  Thr Ser Pro
    4160                4165                4170

Ser Asn  Ile Leu Leu Thr Ser  Gln Gly His Ser Pro  Ser Ser Thr
    4175                4180                4185

Pro Pro  Val Thr Ser Val Phe  Leu Ser Glu Thr Ser  Gly Leu Gly
    4190                4195                4200

Lys Thr  Thr Asp Met Ser Arg  Ile Ser Leu Glu Pro  Gly Thr Ser
    4205                4210                4215

Leu Pro  Pro Asn Leu Ser Ser  Thr Ala Gly Glu Ala  Leu Ser Thr
    4220                4225                4230

Tyr Glu  Ala Ser Arg Asp Thr  Lys Ala Ile His His  Ser Ala Asp
    4235                4240                4245
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Thr Ala  Val Thr Asn Met Glu  Ala Thr Ser Ser Glu  Tyr Ser Pro
    4250                 4255                 4260

Ile Pro  Gly His Thr Lys Pro  Ser Lys Ala Thr Ser  Pro Leu Val
    4265                 4270                 4275

Thr Ser  His Ile Met Gly Asp  Ile Thr Ser Ser Thr  Ser Val Phe
    4280                 4285                 4290

Gly Ser  Ser Glu Thr Thr Glu  Ile Glu Thr Val Ser  Ser Val Asn
    4295                 4300                 4305

Gln Gly  Leu Gln Glu Arg Ser  Thr Ser Gln Val Ala  Ser Ser Ala
    4310                 4315                 4320

Thr Glu  Thr Ser Thr Val Ile  Thr His Val Ser Ser  Gly Asp Ala
    4325                 4330                 4335

Thr Thr  His Val Thr Lys Thr  Gln Ala Thr Phe Ser  Ser Gly Thr
    4340                 4345                 4350

Ser Ile  Ser Ser Pro His Gln  Phe Ile Thr Ser Thr  Asn Thr Phe
    4355                 4360                 4365

Thr Asp  Val Ser Thr Asn Pro  Ser Thr Ser Leu Ile  Met Thr Glu
    4370                 4375                 4380

Ser Ser  Gly Val Thr Ile Thr  Thr Gln Thr Gly Pro  Thr Gly Ala
    4385                 4390                 4395

Ala Thr  Gln Gly Pro Tyr Leu  Leu Asp Thr Ser Thr  Met Pro Tyr
    4400                 4405                 4410

Leu Thr  Glu Thr Pro Leu Ala  Val Thr Pro Asp Phe  Met Gln Ser
    4415                 4420                 4425

Glu Lys  Thr Thr Leu Ile Ser  Lys Gly Pro Lys Asp  Val Thr Trp
    4430                 4435                 4440

Thr Ser  Pro Pro Ser Val Ala  Glu Thr Ser Tyr Pro  Ser Ser Leu
    4445                 4450                 4455

Thr Pro  Phe Leu Val Thr Thr  Ile Pro Pro Ala Thr  Ser Thr Leu
    4460                 4465                 4470

Gln Gly  Gln His Thr Ser Ser  Pro Val Ser Ala Thr  Ser Val Leu
    4475                 4480                 4485

Thr Ser  Gly Leu Val Lys Thr  Thr Asp Met Leu Asn  Thr Ser Met
    4490                 4495                 4500

Glu Pro  Val Thr Asn Ser Pro  Gln Asn Leu Asn Asn  Pro Ser Asn
    4505                 4510                 4515

Glu Ile  Leu Ala Thr Leu Ala  Ala Thr Thr Asp Ile  Glu Thr Ile
    4520                 4525                 4530

His Pro  Ser Ile Asn Lys Ala  Val Thr Asn Met Gly  Thr Ala Ser
    4535                 4540                 4545

Ser Ala  His Val Leu His Ser  Thr Leu Pro Val Ser  Ser Glu Pro
    4550                 4555                 4560

Ser Thr  Ala Thr Ser Pro Met  Val Pro Ala Ser Ser  Met Gly Asp
    4565                 4570                 4575

Ala Leu  Ala Ser Ile Ser Ile  Pro Gly Ser Glu Thr  Thr Asp Ile
    4580                 4585                 4590

Glu Gly  Glu Pro Thr Ser Ser  Leu Thr Ala Gly Arg  Lys Glu Asn
    4595                 4600                 4605

Ser Thr  Leu Gln Glu Met Asn  Ser Thr Thr Glu Ser  Asn Ile Ile
    4610                 4615                 4620
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Leu Ser  Asn Val Ser Val Gly  Ala Ile Thr Glu Ala  Thr Lys Met
    4625                4630                4635

Glu Val  Pro Ser Phe Asp Ala  Thr Phe Ile Pro Thr  Pro Ala Gln
    4640                4645                4650

Ser Thr  Lys Phe Pro Asp Ile  Phe Ser Val Ala Ser  Ser Arg Leu
    4655                4660                4665

Ser Asn  Ser Pro Pro Met Thr  Ile Ser Thr His Met  Thr Thr Thr
    4670                4675                4680

Gln Thr  Gly Ser Ser Gly Ala  Thr Ser Lys Ile Pro  Leu Ala Leu
    4685                4690                4695

Asp Thr  Ser Thr Leu Glu Thr  Ser Ala Gly Thr Pro  Ser Val Val
    4700                4705                4710

Thr Glu  Gly Phe Ala His Ser  Lys Ile Thr Thr Ala  Met Asn Asn
    4715                4720                4725

Asp Val  Lys Asp Val Ser Gln  Thr Asn Pro Pro Phe  Gln Asp Glu
    4730                4735                4740

Ala Ser  Ser Pro Ser Ser Gln  Ala Pro Val Leu Val  Thr Thr Leu
    4745                4750                4755

Pro Ser  Ser Val Ala Phe Thr  Pro Gln Trp His Ser  Thr Ser Ser
    4760                4765                4770

Pro Val  Ser Met Ser Ser Val  Leu Thr Ser Ser Leu  Val Lys Thr
    4775                4780                4785

Ala Gly  Lys Val Asp Thr Ser  Leu Glu Thr Val Thr  Ser Ser Pro
    4790                4795                4800

Gln Ser  Met Ser Asn Thr Leu  Asp Asp Ile Ser Val  Thr Ser Ala
    4805                4810                4815

Ala Thr  Thr Asp Ile Glu Thr  Thr His Pro Ser Ile  Asn Thr Val
    4820                4825                4830

Val Thr  Asn Val Gly Thr Thr  Gly Ser Ala Phe Glu  Ser His Ser
    4835                4840                4845

Thr Val  Ser Ala Tyr Pro Glu  Pro Ser Lys Val Thr  Ser Pro Asn
    4850                4855                4860

Val Thr  Thr Ser Thr Met Glu  Asp Thr Thr Ile Ser  Arg Ser Ile
    4865                4870                4875

Pro Lys  Ser Ser Lys Thr Thr  Arg Thr Glu Thr Glu  Thr Thr Ser
    4880                4885                4890

Ser Leu  Thr Pro Lys Leu Arg  Glu Thr Ser Ile Ser  Gln Glu Ile
    4895                4900                4905

Thr Ser  Ser Thr Glu Thr Ser  Thr Val Pro Tyr Lys  Glu Leu Thr
    4910                4915                4920

Gly Ala  Thr Thr Glu Val Ser  Arg Thr Asp Val Thr  Ser Ser Ser
    4925                4930                4935

Ser Thr  Ser Phe Pro Gly Pro  Asp Gln Ser Thr Val  Ser Leu Asp
    4940                4945                4950

Ile Ser  Thr Glu Thr Asn Thr  Arg Leu Ser Thr Ser  Pro Ile Met
    4955                4960                4965

Thr Glu  Ser Ala Glu Ile Thr  Ile Thr Thr Gln Thr  Gly Pro His
    4970                4975                4980

Gly Ala  Thr Ser Gln Asp Thr  Phe Thr Met Asp Pro  Ser Asn Thr
    4985                4990                4995

Thr Pro  Gln Ala Gly Ile His  Ser Ala Met Thr His  Gly Phe Ser
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    5000                5005                5010

Gln Leu  Asp Val Thr Thr Leu  Met Ser Arg Ile Pro  Gln Asp Val
    5015                5020                5025

Ser Trp  Thr Ser Pro Pro Ser  Val Asp Lys Thr Ser  Ser Pro Ser
    5030                5035                5040

Ser Phe  Leu Ser Ser Pro Ala  Met Thr Thr Pro Ser  Leu Ile Ser
    5045                5050                5055

Ser Thr  Leu Pro Glu Asp Lys  Leu Ser Ser Pro Met  Thr Ser Leu
    5060                5065                5070

Leu Thr  Ser Gly Leu Val Lys  Ile Thr Asp Ile Leu  Arg Thr Arg
    5075                5080                5085

Leu Glu  Pro Val Thr Ser Ser  Leu Pro Asn Phe Ser  Ser Thr Ser
    5090                5095                5100

Asp Lys  Ile Leu Ala Thr Ser  Lys Asp Ser Lys Asp  Thr Lys Glu
    5105                5110                5115

Ile Phe  Pro Ser Ile Asn Thr  Glu Glu Thr Asn Val  Lys Ala Asn
    5120                5125                5130

Asn Ser  Gly His Glu Ser His  Ser Pro Ala Leu Ala  Asp Ser Glu
    5135                5140                5145

Thr Pro  Lys Ala Thr Thr Gln  Met Val Ile Thr Thr  Thr Val Gly
    5150                5155                5160

Asp Pro  Ala Pro Ser Thr Ser  Met Pro Val His Gly  Ser Ser Glu
    5165                5170                5175

Thr Thr  Asn Ile Lys Arg Glu  Pro Thr Tyr Phe Leu  Thr Pro Arg
    5180                5185                5190

Leu Arg  Glu Thr Ser Thr Ser  Gln Glu Ser Ser Phe  Pro Thr Asp
    5195                5200                5205

Thr Ser  Phe Leu Leu Ser Lys  Val Pro Thr Gly Thr  Ile Thr Glu
    5210                5215                5220

Val Ser  Ser Thr Gly Val Ile  Ser Ser Ser Lys Ile  Ser Thr Pro
    5225                5230                5235

Asp His  Asp Lys Ser Thr Val  Pro Pro Asp Thr Phe  Thr Gly Glu
    5240                5245                5250

Ile Pro  Arg Val Phe Thr Ser  Ser Ile Lys Thr Lys  Ser Ala Glu
    5255                5260                5265

Met Thr  Ile Thr Thr Gln Ala  Ser Pro Pro Glu Ser  Ala Ser His
    5270                5275                5280

Ser Thr  Leu Pro Leu Asp Thr  Ser Thr Thr Leu Ser  Gln Gly Gly
    5285                5290                5295

Thr His  Ser Thr Val Ser Gln  Gly Phe Pro Tyr Ser  Glu Val Thr
    5300                5305                5310

Thr Leu  Met Gly Met Gly Pro  Gly Asn Val Ser Trp  Met Thr Thr
    5315                5320                5325

Pro Pro  Val Glu Glu Thr Ser  Ser Val Ser Ser Leu  Met Ser Ser
    5330                5335                5340

Pro Ala  Met Thr Ser Pro Ser  Pro Val Ser Ser Thr  Ser Pro Gln
    5345                5350                5355

Ser Ile  Pro Ser Ser Pro Leu  Pro Val Thr Ala Leu  Pro Thr Ser
    5360                5365                5370

Val Leu  Val Thr Thr Thr Asp  Val Leu Gly Thr Thr  Ser Pro Glu
    5375                5380                5385
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Ser Val  Thr Ser Ser Pro Pro  Asn Leu Ser Ser Ile  Thr His Glu
    5390                 5395                 5400

Arg Pro  Ala Thr Tyr Lys Asp  Thr Ala His Thr Glu  Ala Ala Met
    5405                 5410                 5415

His His  Ser Thr Asn Thr Ala  Val Thr Asn Val Gly  Thr Ser Gly
    5420                 5425                 5430

Ser Gly  His Lys Ser Gln Ser  Ser Val Leu Ala Asp  Ser Glu Thr
    5435                 5440                 5445

Ser Lys  Ala Thr Pro Leu Met  Ser Thr Ala Ser Thr  Leu Gly Asp
    5450                 5455                 5460

Thr Ser  Val Ser Thr Ser Thr  Pro Asn Ile Ser Gln  Thr Asn Gln
    5465                 5470                 5475

Ile Gln  Thr Glu Pro Thr Ala  Ser Leu Ser Pro Arg  Leu Arg Glu
    5480                 5485                 5490

Ser Ser  Thr Ser Glu Lys Thr  Ser Ser Thr Thr Glu  Thr Asn Thr
    5495                 5500                 5505

Ala Phe  Ser Tyr Val Pro Thr  Gly Ala Ile Thr Gln  Ala Ser Arg
    5510                 5515                 5520

Thr Glu  Ile Ser Ser Ser Arg  Thr Ser Ile Ser Asp  Leu Asp Arg
    5525                 5530                 5535

Ser Thr  Ile Ala Pro Asp Ile  Ser Thr Gly Met Ile  Thr Arg Leu
    5540                 5545                 5550

Phe Thr  Ser Pro Ile Met Thr  Lys Ser Ala Glu Met  Thr Val Thr
    5555                 5560                 5565

Thr Gln  Thr Thr Thr Pro Gly  Ala Thr Ser Gln Gly  Ile Leu Pro
    5570                 5575                 5580

Trp Asp  Thr Ser Thr Thr Leu  Phe Gln Gly Gly Thr  His Ser Thr
    5585                 5590                 5595

Val Ser  Gln Gly Phe Pro His  Ser Glu Ile Thr Thr  Leu Arg Ser
    5600                 5605                 5610

Arg Thr  Pro Gly Asp Val Ser  Trp Met Thr Thr Pro  Pro Val Glu
    5615                 5620                 5625

Glu Thr  Ser Ser Gly Phe Ser  Leu Met Ser Pro Ser  Met Thr Ser
    5630                 5635                 5640

Pro Ser  Pro Val Ser Ser Thr  Ser Pro Glu Ser Ile  Pro Ser Ser
    5645                 5650                 5655

Pro Leu  Pro Val Thr Ala Leu  Leu Thr Ser Val Leu  Val Thr Thr
    5660                 5665                 5670

Thr Asn  Val Leu Gly Thr Thr  Ser Pro Glu Pro Val  Thr Ser Ser
    5675                 5680                 5685

Pro Pro  Asn Leu Ser Ser Pro  Thr Gln Glu Arg Leu  Thr Thr Tyr
    5690                 5695                 5700

Lys Asp  Thr Ala His Thr Glu  Ala Met His Ala Ser  Met His Thr
    5705                 5710                 5715

Asn Thr  Ala Val Ala Asn Val  Gly Thr Ser Ile Ser  Gly His Glu
    5720                 5725                 5730

Ser Gln  Ser Ser Val Pro Ala  Asp Ser His Thr Ser  Lys Ala Thr
    5735                 5740                 5745

Ser Pro  Met Gly Ile Thr Phe  Ala Met Gly Asp Thr  Ser Val Tyr
    5750                 5755                 5760
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Thr Ser  Thr Pro Ala Phe Phe  Glu Thr Arg Ile Gln  Ser Glu Ser
    5765                 5770                 5775

Thr Ser  Ser Leu Ile Pro Gly  Leu Arg Asp Thr Arg  Thr Ser Glu
    5780                 5785                 5790

Glu Ile  Asn Thr Val Thr Glu  Thr Ser Thr Val Leu  Ser Glu Val
    5795                 5800                 5805

Pro Thr  Thr Thr Thr Thr Glu  Val Ser Arg Thr Glu  Val Ile Thr
    5810                 5815                 5820

Ser Ser  Arg Thr Thr Ile Ser  Gly Pro Asp His Ser  Lys Met Ser
    5825                 5830                 5835

Pro Tyr  Ile Ser Thr Glu Thr  Ile Thr Arg Leu Ser  Thr Phe Pro
    5840                 5845                 5850

Phe Val  Thr Gly Ser Thr Glu  Met Ala Ile Thr Asn  Gln Thr Gly
    5855                 5860                 5865

Pro Ile  Gly Thr Ile Ser Gln  Ala Thr Leu Thr Leu  Asp Thr Ser
    5870                 5875                 5880

Ser Thr  Ala Ser Trp Glu Gly  Thr His Ser Pro Val  Thr Gln Arg
    5885                 5890                 5895

Phe Pro  His Ser Glu Glu Thr  Thr Thr Met Ser Arg  Ser Thr Lys
    5900                 5905                 5910

Gly Val  Ser Trp Gln Ser Pro  Pro Ser Val Glu Glu  Thr Ser Ser
    5915                 5920                 5925

Pro Ser  Ser Pro Val Pro Leu  Pro Ala Ile Thr Ser  His Ser Ser
    5930                 5935                 5940

Leu Tyr  Ser Ala Val Ser Gly  Ser Ser Pro Thr Ser  Ala Leu Pro
    5945                 5950                 5955

Val Thr  Ser Leu Leu Thr Ser  Gly Arg Arg Lys Thr  Ile Asp Met
    5960                 5965                 5970

Leu Asp  Thr His Ser Glu Leu  Val Thr Ser Ser Leu  Pro Ser Ala
    5975                 5980                 5985

Ser Ser  Phe Ser Gly Glu Ile  Leu Thr Ser Glu Ala  Ser Thr Asn
    5990                 5995                 6000

Thr Glu  Thr Ile His Phe Ser  Glu Asn Thr Ala Glu  Thr Asn Met
    6005                 6010                 6015

Gly Thr  Thr Asn Ser Met His  Lys Leu His Ser Ser  Val Ser Ile
    6020                 6025                 6030

His Ser  Gln Pro Ser Gly His  Thr Pro Pro Lys Val  Thr Gly Ser
    6035                 6040                 6045

Met Met  Glu Asp Ala Ile Val  Ser Thr Ser Thr Pro  Gly Ser Pro
    6050                 6055                 6060

Glu Thr  Lys Asn Val Asp Arg  Asp Ser Thr Ser Pro  Leu Thr Pro
    6065                 6070                 6075

Glu Leu  Lys Glu Asp Ser Thr  Ala Leu Val Met Asn  Ser Thr Thr
    6080                 6085                 6090

Glu Ser  Asn Thr Val Phe Ser  Ser Val Ser Leu Asp  Ala Ala Thr
    6095                 6100                 6105

Glu Val  Ser Arg Ala Glu Val  Thr Tyr Tyr Asp Pro  Thr Phe Met
    6110                 6115                 6120

Pro Ala  Ser Ala Gln Ser Thr  Lys Ser Pro Asp Ile  Ser Pro Glu
    6125                 6130                 6135

Ala Ser  Ser Ser His Ser Asn  Ser Pro Pro Leu Thr  Ile Ser Thr
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    6140                6145                6150

His Lys  Thr Ile Ala Thr Gln  Thr Gly Pro Ser Gly  Val Thr Ser
    6155                6160                6165

Leu Gly  Gln Leu Thr Leu Asp  Thr Ser Thr Ile Ala  Thr Ser Ala
    6170                6175                6180

Gly Thr  Pro Ser Ala Arg Thr  Gln Asp Phe Val Asp  Ser Glu Thr
    6185                6190                6195

Thr Ser  Val Met Asn Asn Asp  Leu Asn Asp Val Leu  Lys Thr Ser
    6200                6205                6210

Pro Phe  Ser Ala Glu Glu Ala  Asn Ser Leu Ser Ser  Gln Ala Pro
    6215                6220                6225

Leu Leu  Val Thr Thr Ser Pro  Ser Pro Val Thr Ser  Thr Leu Gln
    6230                6235                6240

Glu His  Ser Thr Ser Ser Leu  Val Ser Val Thr Ser  Val Pro Thr
    6245                6250                6255

Pro Thr  Leu Ala Lys Ile Thr  Asp Met Asp Thr Asn  Leu Glu Pro
    6260                6265                6270

Val Thr  Arg Ser Pro Gln Asn  Leu Arg Asn Thr Leu  Ala Thr Ser
    6275                6280                6285

Glu Ala  Thr Thr Asp Thr His  Thr Met His Pro Ser  Ile Asn Thr
    6290                6295                6300

Ala Met  Ala Asn Val Gly Thr  Thr Ser Ser Pro Asn  Glu Phe Tyr
    6305                6310                6315

Phe Thr  Val Ser Pro Asp Ser  Asp Pro Tyr Lys Ala  Thr Ser Ala
    6320                6325                6330

Val Val  Ile Thr Ser Thr Ser  Gly Asp Ser Ile Val  Ser Thr Ser
    6335                6340                6345

Met Pro  Arg Ser Ser Ala Met  Lys Lys Ile Glu Ser  Glu Thr Thr
    6350                6355                6360

Phe Ser  Leu Ile Phe Arg Leu  Arg Glu Thr Ser Thr  Ser Gln Lys
    6365                6370                6375

Ile Gly  Ser Ser Ser Asp Thr  Ser Thr Val Phe Asp  Lys Ala Phe
    6380                6385                6390

Thr Ala  Ala Thr Thr Glu Val  Ser Arg Thr Glu Leu  Thr Ser Ser
    6395                6400                6405

Ser Arg  Thr Ser Ile Gln Gly  Thr Glu Lys Pro Thr  Met Ser Pro
    6410                6415                6420

Asp Thr  Ser Thr Arg Ser Val  Thr Met Leu Ser Thr  Phe Ala Gly
    6425                6430                6435

Leu Thr  Lys Ser Glu Glu Arg  Thr Ile Ala Thr Gln  Thr Gly Pro
    6440                6445                6450

His Arg  Ala Thr Ser Gln Gly  Thr Leu Thr Trp Asp  Thr Ser Ile
    6455                6460                6465

Thr Thr  Ser Gln Ala Gly Thr  His Ser Ala Met Thr  His Gly Phe
    6470                6475                6480

Ser Gln  Leu Asp Leu Ser Thr  Leu Thr Ser Arg Val  Pro Glu Tyr
    6485                6490                6495

Ile Ser  Gly Thr Ser Pro Pro  Ser Val Glu Lys Thr  Ser Ser Ser
    6500                6505                6510

Ser Ser  Leu Leu Ser Leu Pro  Ala Ile Thr Ser Pro  Ser Pro Val
    6515                6520                6525
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Pro Thr  Thr Leu Pro Glu Ser  Arg Pro Ser Ser Pro  Val His Leu
    6530                 6535                 6540

Thr Ser  Leu Pro Thr Ser Gly  Leu Val Lys Thr Thr  Asp Met Leu
    6545                 6550                 6555

Ala Ser  Val Ala Ser Leu Pro  Pro Asn Leu Gly Ser  Thr Ser His
    6560                 6565                 6570

Lys Ile  Pro Thr Thr Ser Glu  Asp Ile Lys Asp Thr  Glu Lys Met
    6575                 6580                 6585

Tyr Pro  Ser Thr Asn Ile Ala  Val Thr Asn Val Gly  Thr Thr Thr
    6590                 6595                 6600

Ser Glu  Lys Glu Ser Tyr Ser  Ser Val Pro Ala Tyr  Ser Glu Pro
    6605                 6610                 6615

Pro Lys  Val Thr Ser Pro Met  Val Thr Ser Phe Asn  Ile Arg Asp
    6620                 6625                 6630

Thr Ile  Val Ser Thr Ser Met  Pro Gly Ser Ser Glu  Ile Thr Arg
    6635                 6640                 6645

Ile Glu  Met Glu Ser Thr Phe  Ser Leu Ala His Gly  Leu Lys Gly
    6650                 6655                 6660

Thr Ser  Thr Ser Gln Asp Pro  Ile Val Ser Thr Glu  Lys Ser Ala
    6665                 6670                 6675

Val Leu  His Lys Leu Thr Thr  Gly Ala Thr Glu Thr  Ser Arg Thr
    6680                 6685                 6690

Glu Val  Ala Ser Ser Arg Arg  Thr Ser Ile Pro Gly  Pro Asp His
    6695                 6700                 6705

Ser Thr  Glu Ser Pro Asp Ile  Ser Thr Glu Val Ile  Pro Ser Leu
    6710                 6715                 6720

Pro Ile  Ser Leu Gly Ile Thr  Glu Ser Ser Asn Met  Thr Ile Ile
    6725                 6730                 6735

Thr Arg  Thr Gly Pro Pro Leu  Gly Ser Thr Ser Gln  Gly Thr Phe
    6740                 6745                 6750

Thr Leu  Asp Thr Pro Thr Thr  Ser Ser Arg Ala Gly  Thr His Ser
    6755                 6760                 6765

Met Ala  Thr Gln Glu Phe Pro  His Ser Glu Met Thr  Thr Val Met
    6770                 6775                 6780

Asn Lys  Asp Pro Glu Ile Leu  Ser Trp Thr Ile Pro  Pro Ser Ile
    6785                 6790                 6795

Glu Lys  Thr Ser Phe Ser Ser  Ser Leu Met Pro Ser  Pro Ala Met
    6800                 6805                 6810

Thr Ser  Pro Pro Val Ser Ser  Thr Leu Pro Lys Thr  Ile His Thr
    6815                 6820                 6825

Thr Pro  Ser Pro Met Thr Ser  Leu Leu Thr Pro Ser  Leu Val Met
    6830                 6835                 6840

Thr Thr  Asp Thr Leu Gly Thr  Ser Pro Glu Pro Thr  Thr Ser Ser
    6845                 6850                 6855

Pro Pro  Asn Leu Ser Ser Thr  Ser His Val Ile Leu  Thr Thr Asp
    6860                 6865                 6870

Glu Asp  Thr Thr Ala Ile Glu  Ala Met His Pro Ser  Thr Ser Thr
    6875                 6880                 6885

Ala Ala  Thr Asn Val Glu Thr  Thr Cys Ser Gly His  Gly Ser Gln
    6890                 6895                 6900
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Ser Ser  Val Leu Thr Asp Ser  Glu Lys Thr Lys Ala  Thr Ala Pro
    6905                6910                6915

Met Asp  Thr Thr Ser Thr Met  Gly His Thr Thr Val  Ser Thr Ser
    6920                6925                6930

Met Ser  Val Ser Ser Glu Thr  Thr Lys Ile Lys Arg  Glu Ser Thr
    6935                6940                6945

Tyr Ser  Leu Thr Pro Gly Leu  Arg Glu Thr Ser Ile  Ser Gln Asn
    6950                6955                6960

Ala Ser  Phe Ser Thr Asp Thr  Ser Ile Val Leu Ser  Glu Val Pro
    6965                6970                6975

Thr Gly  Thr Thr Ala Glu Val  Ser Arg Thr Glu Val  Thr Ser Ser
    6980                6985                6990

Gly Arg  Thr Ser Ile Pro Gly  Pro Ser Gln Ser Thr  Val Leu Pro
    6995                7000                7005

Glu Ile  Ser Thr Arg Thr Met  Thr Arg Leu Phe Ala  Ser Pro Thr
    7010                7015                7020

Met Thr  Glu Ser Ala Glu Met  Thr Ile Pro Thr Gln  Thr Gly Pro
    7025                7030                7035

Ser Gly  Ser Thr Ser Gln Asp  Thr Leu Thr Leu Asp  Thr Ser Thr
    7040                7045                7050

Thr Lys  Ser Gln Ala Lys Thr  His Ser Thr Leu Thr  Gln Arg Phe
    7055                7060                7065

Pro His  Ser Glu Met Thr Thr  Leu Met Ser Arg Gly  Pro Gly Asp
    7070                7075                7080

Met Ser  Trp Gln Ser Ser Pro  Ser Leu Glu Asn Pro  Ser Ser Leu
    7085                7090                7095

Pro Ser  Leu Leu Ser Leu Pro  Ala Thr Thr Ser Pro  Pro Pro Ile
    7100                7105                7110

Ser Ser  Thr Leu Pro Val Thr  Ile Ser Ser Ser Pro  Leu Pro Val
    7115                7120                7125

Thr Ser  Leu Leu Thr Ser Ser  Pro Val Thr Thr Thr  Asp Met Leu
    7130                7135                7140

His Thr  Ser Pro Glu Leu Val  Thr Ser Ser Pro Pro  Lys Leu Ser
    7145                7150                7155

His Thr  Ser Asp Glu Arg Leu  Thr Thr Gly Lys Asp  Thr Thr Asn
    7160                7165                7170

Thr Glu  Ala Val His Pro Ser  Thr Asn Thr Ala Ala  Ser Asn Val
    7175                7180                7185

Glu Ile  Pro Ser Phe Gly His  Glu Ser Pro Ser Ser  Ala Leu Ala
    7190                7195                7200

Asp Ser  Glu Thr Ser Lys Ala  Thr Ser Pro Met Phe  Ile Thr Ser
    7205                7210                7215

Thr Gln  Glu Asp Thr Thr Val  Ala Ile Ser Thr Pro  His Phe Leu
    7220                7225                7230

Glu Thr  Ser Arg Ile Gln Lys  Glu Ser Ile Ser Ser  Leu Ser Pro
    7235                7240                7245

Lys Leu  Arg Glu Thr Gly Ser  Ser Val Glu Thr Ser  Ser Ala Ile
    7250                7255                7260

Glu Thr  Ser Ala Val Leu Ser  Glu Val Ser Ile Gly  Ala Thr Thr
    7265                7270                7275

Glu Ile  Ser Arg Thr Glu Val  Thr Ser Ser Ser Arg  Thr Ser Ile
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    7280                7285                7290

Ser Gly  Ser Ala Glu Ser Thr  Met Leu Pro Glu Ile  Ser Thr Thr
    7295                7300                7305

Arg Lys  Ile Ile Lys Phe Pro  Thr Ser Pro Ile Leu  Ala Glu Ser
    7310                7315                7320

Ser Glu  Met Thr Ile Lys Thr  Gln Thr Ser Pro Pro  Gly Ser Thr
    7325                7330                7335

Ser Glu  Ser Thr Phe Thr Leu  Asp Thr Ser Thr Thr  Pro Ser Leu
    7340                7345                7350

Val Ile  Thr His Ser Thr Met  Thr Gln Arg Leu Pro  His Ser Glu
    7355                7360                7365

Ile Thr  Thr Leu Val Ser Arg  Gly Ala Gly Asp Val  Pro Arg Pro
    7370                7375                7380

Ser Ser  Leu Pro Val Glu Glu  Thr Ser Pro Pro Ser  Ser Gln Leu
    7385                7390                7395

Ser Leu  Ser Ala Met Ile Ser  Pro Ser Pro Val Ser  Ser Thr Leu
    7400                7405                7410

Pro Ala  Ser Ser His Ser Ser  Ser Ala Ser Val Thr  Ser Pro Leu
    7415                7420                7425

Thr Pro  Gly Gln Val Lys Thr  Thr Glu Val Leu Asp  Ala Ser Ala
    7430                7435                7440

Glu Pro  Glu Thr Ser Ser Pro  Pro Ser Leu Ser Ser  Thr Ser Val
    7445                7450                7455

Glu Ile  Leu Ala Thr Ser Glu  Val Thr Thr Asp Thr  Glu Lys Ile
    7460                7465                7470

His Pro  Phe Pro Asn Thr Ala  Val Thr Lys Val Gly  Thr Ser Ser
    7475                7480                7485

Ser Gly  His Glu Ser Pro Ser  Ser Val Leu Pro Asp  Ser Glu Thr
    7490                7495                7500

Thr Lys  Ala Thr Ser Ala Met  Gly Thr Ile Ser Ile  Met Gly Asp
    7505                7510                7515

Thr Ser  Val Ser Thr Leu Thr  Pro Ala Leu Ser Asn  Thr Arg Lys
    7520                7525                7530

Ile Gln  Ser Glu Pro Ala Ser  Ser Leu Thr Thr Arg  Leu Arg Glu
    7535                7540                7545

Thr Ser  Thr Ser Glu Glu Thr  Ser Leu Ala Thr Glu  Ala Asn Thr
    7550                7555                7560

Val Leu  Ser Lys Val Ser Thr  Gly Ala Thr Thr Glu  Val Ser Arg
    7565                7570                7575

Thr Glu  Ala Ile Ser Phe Ser  Arg Thr Ser Met Ser  Gly Pro Glu
    7580                7585                7590

Gln Ser  Thr Met Ser Gln Asp  Ile Ser Ile Gly Thr  Ile Pro Arg
    7595                7600                7605

Ile Ser  Ala Ser Ser Val Leu  Thr Glu Ser Ala Lys  Met Thr Ile
    7610                7615                7620

Thr Thr  Gln Thr Gly Pro Ser  Glu Ser Thr Leu Glu  Ser Thr Leu
    7625                7630                7635

Asn Leu  Asn Thr Ala Thr Thr  Pro Ser Trp Val Glu  Thr His Ser
    7640                7645                7650

Ile Val  Ile Gln Gly Phe Pro  His Pro Glu Met Thr  Thr Ser Met
    7655                7660                7665
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Gly Arg  Gly Pro Gly Gly Val  Ser Trp Pro Ser Pro  Pro Phe Val
    7670                 7675                 7680

Lys Glu  Thr Ser Pro Pro Ser  Ser Pro Leu Ser Leu  Pro Ala Val
    7685                 7690                 7695

Thr Ser  Pro His Pro Val Ser  Thr Thr Phe Leu Ala  His Ile Pro
    7700                 7705                 7710

Pro Ser  Pro Leu Pro Val Thr  Ser Leu Leu Thr Ser  Gly Pro Ala
    7715                 7720                 7725

Thr Thr  Thr Asp Ile Leu Gly  Thr Ser Thr Glu Pro  Gly Thr Ser
    7730                 7735                 7740

Ser Ser  Ser Ser Leu Ser Thr  Thr Ser His Glu Arg  Leu Thr Thr
    7745                 7750                 7755

Tyr Lys  Asp Thr Ala His Thr  Glu Ala Val His Pro  Ser Thr Asn
    7760                 7765                 7770

Thr Gly  Gly Thr Asn Val Ala  Thr Thr Ser Ser Gly  Tyr Lys Ser
    7775                 7780                 7785

Gln Ser  Ser Val Leu Ala Asp  Ser Ser Pro Met Cys  Thr Thr Ser
    7790                 7795                 7800

Thr Met  Gly Asp Thr Ser Val  Leu Thr Ser Thr Pro  Ala Phe Leu
    7805                 7810                 7815

Glu Thr  Arg Arg Ile Gln Thr  Glu Leu Ala Ser Ser  Leu Thr Pro
    7820                 7825                 7830

Gly Leu  Arg Glu Ser Ser Gly  Ser Glu Gly Thr Ser  Ser Gly Thr
    7835                 7840                 7845

Lys Met  Ser Thr Val Leu Ser  Lys Val Pro Thr Gly  Ala Thr Thr
    7850                 7855                 7860

Glu Ile  Ser Lys Glu Asp Val  Thr Ser Ile Pro Gly  Pro Ala Gln
    7865                 7870                 7875

Ser Thr  Ile Ser Pro Asp Thr  Ser Thr Arg Thr Val  Ser Trp Phe
    7880                 7885                 7890

Ser Thr  Ser Pro Val Met Thr  Glu Ser Ala Glu Ile  Thr Met Asn
    7895                 7900                 7905

Thr His  Thr Ser Pro Leu Gly  Ala Thr Thr Gln Gly  Thr Ser Thr
    7910                 7915                 7920

Leu Asp  Thr Ser Ser Thr Thr  Ser Leu Thr Met Thr  His Ser Thr
    7925                 7930                 7935

Ile Ser  Gln Gly Phe Ser His  Ser Gln Met Ser Thr  Leu Met Arg
    7940                 7945                 7950

Arg Gly  Pro Glu Asp Val Ser  Trp Met Ser Pro Pro  Leu Leu Glu
    7955                 7960                 7965

Lys Thr  Arg Pro Ser Phe Ser  Leu Met Ser Ser Pro  Ala Thr Thr
    7970                 7975                 7980

Ser Pro  Ser Pro Val Ser Ser  Thr Leu Pro Glu Ser  Ile Ser Ser
    7985                 7990                 7995

Ser Pro  Leu Pro Val Thr Ser  Leu Leu Thr Ser Gly  Leu Ala Lys
    8000                 8005                 8010

Thr Thr  Asp Met Leu His Lys  Ser Ser Glu Pro Val  Thr Asn Ser
    8015                 8020                 8025

Pro Ala  Asn Leu Ser Ser Thr  Ser Val Glu Ile Leu  Ala Thr Ser
    8030                 8035                 8040
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Glu Val  Thr Thr Asp Thr Glu  Lys Thr His Pro Ser  Ser Asn Arg
    8045                 8050                 8055

Thr Val  Thr Asp Val Gly Thr  Ser Ser Ser Gly His  Glu Ser Thr
    8060                 8065                 8070

Ser Phe  Val Leu Ala Asp Ser  Gln Thr Ser Lys Val  Thr Ser Pro
    8075                 8080                 8085

Met Val  Ile Thr Ser Thr Met  Glu Asp Thr Ser Val  Ser Thr Ser
    8090                 8095                 8100

Thr Pro  Gly Phe Phe Glu Thr  Ser Arg Ile Gln Thr  Glu Pro Thr
    8105                 8110                 8115

Ser Ser  Leu Thr Leu Gly Leu  Arg Lys Thr Ser Ser  Ser Glu Gly
    8120                 8125                 8130

Thr Ser  Leu Ala Thr Glu Met  Ser Thr Val Leu Ser  Gly Val Pro
    8135                 8140                 8145

Thr Gly  Ala Thr Ala Glu Val  Ser Arg Thr Glu Val  Thr Ser Ser
    8150                 8155                 8160

Ser Arg  Thr Ser Ile Ser Gly  Phe Ala Gln Leu Thr  Val Ser Pro
    8165                 8170                 8175

Glu Thr  Ser Thr Glu Thr Ile  Thr Arg Leu Pro Thr  Ser Ser Ile
    8180                 8185                 8190

Met Thr  Glu Ser Ala Glu Met  Met Ile Lys Thr Gln  Thr Asp Pro
    8195                 8200                 8205

Pro Gly  Ser Thr Pro Glu Ser  Thr His Thr Val Asp  Ile Ser Thr
    8210                 8215                 8220

Thr Pro  Asn Trp Val Glu Thr  His Ser Thr Val Thr  Gln Arg Phe
    8225                 8230                 8235

Ser His  Ser Glu Met Thr Thr  Leu Val Ser Arg Ser  Pro Gly Asp
    8240                 8245                 8250

Met Leu  Trp Pro Ser Gln Ser  Ser Val Glu Glu Thr  Ser Ser Ala
    8255                 8260                 8265

Ser Ser  Leu Leu Ser Leu Pro  Ala Thr Thr Ser Pro  Ser Pro Val
    8270                 8275                 8280

Ser Ser  Thr Leu Val Glu Asp  Phe Pro Ser Ala Ser  Leu Pro Val
    8285                 8290                 8295

Thr Ser  Leu Leu Thr Pro Gly  Leu Val Ile Thr Thr  Asp Arg Met
    8300                 8305                 8310

Gly Ile  Ser Arg Glu Pro Gly  Thr Ser Ser Thr Ser  Asn Leu Ser
    8315                 8320                 8325

Ser Thr  Ser His Glu Arg Leu  Thr Thr Leu Glu Asp  Thr Val Asp
    8330                 8335                 8340

Thr Glu  Ala Met Gln Pro Ser  Thr His Thr Ala Val  Thr Asn Val
    8345                 8350                 8355

Arg Thr  Ser Ile Ser Gly His  Glu Ser Gln Ser Ser  Val Leu Ser
    8360                 8365                 8370

Asp Ser  Glu Thr Pro Lys Ala  Thr Ser Ser Met Gly  Thr Thr Tyr
    8375                 8380                 8385

Thr Met  Gly Glu Thr Ser Val  Ser Ile Ser Thr Ser  Asp Phe Phe
    8390                 8395                 8400

Glu Thr  Ser Arg Val Gln Ile  Glu Pro Thr Ser Ser  Leu Thr Ser
    8405                 8410                 8415

Gly Leu  Arg Glu Thr Ser Ser  Ser Glu Arg Ile Ser  Ser Ala Thr
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    8420                8425                8430

Glu Gly  Ser Thr Val Leu Ser  Glu Val Pro Ser Gly  Ala Thr Thr
    8435                8440                8445

Glu Val  Ser Arg Thr Glu Val  Ile Ser Ser Arg Gly  Thr Ser Met
    8450                8455                8460

Ser Gly  Pro Asp Gln Phe Thr  Ile Ser Pro Asp Ile  Ser Thr Glu
    8465                8470                8475

Ala Ile  Thr Arg Leu Ser Thr  Ser Pro Ile Met Thr  Glu Ser Ala
    8480                8485                8490

Glu Ser  Ala Ile Thr Ile Glu  Thr Gly Ser Pro Gly  Ala Thr Ser
    8495                8500                8505

Glu Gly  Thr Leu Thr Leu Asp  Thr Ser Thr Thr Thr  Phe Trp Ser
    8510                8515                8520

Gly Thr  His Ser Thr Ala Ser  Pro Gly Phe Ser His  Ser Glu Met
    8525                8530                8535

Thr Thr  Leu Met Ser Arg Thr  Pro Gly Asp Val Pro  Trp Pro Ser
    8540                8545                8550

Leu Pro  Ser Val Glu Glu Ala  Ser Ser Val Ser Ser  Ser Leu Ser
    8555                8560                8565

Ser Pro  Ala Met Thr Ser Thr  Ser Phe Phe Ser Ala  Leu Pro Glu
    8570                8575                8580

Ser Ile  Ser Ser Ser Pro His  Pro Val Thr Ala Leu  Leu Thr Leu
    8585                8590                8595

Gly Pro  Val Lys Thr Thr Asp  Met Leu Arg Thr Ser  Ser Glu Pro
    8600                8605                8610

Glu Thr  Ser Ser Pro Pro Asn  Leu Ser Ser Thr Ser  Ala Glu Ile
    8615                8620                8625

Leu Ala  Thr Ser Glu Val Thr  Lys Asp Arg Glu Lys  Ile His Pro
    8630                8635                8640

Ser Ser  Asn Thr Pro Val Val  Asn Val Gly Thr Val  Ile Tyr Lys
    8645                8650                8655

His Leu  Ser Pro Ser Ser Val  Leu Ala Asp Leu Val  Thr Thr Lys
    8660                8665                8670

Pro Thr  Ser Pro Met Ala Thr  Thr Ser Thr Leu Gly  Asn Thr Ser
    8675                8680                8685

Val Ser  Thr Ser Thr Pro Ala  Phe Pro Glu Thr Met  Met Thr Gln
    8690                8695                8700

Pro Thr  Ser Ser Leu Thr Ser  Gly Leu Arg Glu Ile  Ser Thr Ser
    8705                8710                8715

Gln Glu  Thr Ser Ser Ala Thr  Glu Arg Ser Ala Ser  Leu Ser Gly
    8720                8725                8730

Met Pro  Thr Gly Ala Thr Thr  Lys Val Ser Arg Thr  Glu Ala Leu
    8735                8740                8745

Ser Leu  Gly Arg Thr Ser Thr  Pro Gly Pro Ala Gln  Ser Thr Ile
    8750                8755                8760

Ser Pro  Glu Ile Ser Thr Glu  Thr Ile Thr Arg Ile  Ser Thr Pro
    8765                8770                8775

Leu Thr  Thr Thr Gly Ser Ala  Glu Met Thr Ile Thr  Pro Lys Thr
    8780                8785                8790

Gly His  Ser Gly Ala Ser Ser  Gln Gly Thr Phe Thr  Leu Asp Thr
    8795                8800                8805
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Ser Ser  Arg Ala Ser Trp Pro  Gly Thr His Ser Ala  Ala Thr His
    8810                 8815                 8820

Arg Ser  Pro His Ser Gly Met  Thr Thr Pro Met Ser  Arg Gly Pro
    8825                 8830                 8835

Glu Asp  Val Ser Trp Pro Ser  Arg Pro Ser Val Glu  Lys Thr Ser
    8840                 8845                 8850

Pro Pro  Ser Ser Leu Val Ser  Leu Ser Ala Val Thr  Ser Pro Ser
    8855                 8860                 8865

Pro Leu  Tyr Ser Thr Pro Ser  Glu Ser Ser His Ser  Ser Pro Leu
    8870                 8875                 8880

Arg Val  Thr Ser Leu Phe Thr  Pro Val Met Met Lys  Thr Thr Asp
    8885                 8890                 8895

Met Leu  Asp Thr Ser Leu Glu  Pro Val Thr Thr Ser  Pro Pro Ser
    8900                 8905                 8910

Met Asn  Ile Thr Ser Asp Glu  Ser Leu Ala Thr Ser  Lys Ala Thr
    8915                 8920                 8925

Met Glu  Thr Glu Ala Ile Gln  Leu Ser Glu Asn Thr  Ala Val Thr
    8930                 8935                 8940

Gln Met  Gly Thr Ile Ser Ala  Arg Gln Glu Phe Tyr  Ser Ser Tyr
    8945                 8950                 8955

Pro Gly  Leu Pro Glu Pro Ser  Lys Val Thr Ser Pro  Val Val Thr
    8960                 8965                 8970

Ser Ser  Thr Ile Lys Asp Ile  Val Ser Thr Thr Ile  Pro Ala Ser
    8975                 8980                 8985

Ser Glu  Ile Thr Arg Ile Glu  Met Glu Ser Thr Ser  Thr Leu Thr
    8990                 8995                 9000

Pro Thr  Pro Arg Glu Thr Ser  Thr Ser Gln Glu Ile  His Ser Ala
    9005                 9010                 9015

Thr Lys  Pro Ser Thr Val Pro  Tyr Lys Ala Leu Thr  Ser Ala Thr
    9020                 9025                 9030

Ile Glu  Asp Ser Met Thr Gln  Val Met Ser Ser Ser  Arg Gly Pro
    9035                 9040                 9045

Ser Pro  Asp Gln Ser Thr Met  Ser Gln Asp Ile Ser  Thr Glu Val
    9050                 9055                 9060

Ile Thr  Arg Leu Ser Thr Ser  Pro Ile Lys Ala Glu  Ser Thr Glu
    9065                 9070                 9075

Met Thr  Ile Thr Thr Gln Thr  Gly Ser Pro Gly Ala  Thr Ser Arg
    9080                 9085                 9090

Gly Thr  Leu Thr Leu Asp Thr  Ser Thr Thr Phe Met  Ser Gly Thr
    9095                 9100                 9105

His Ser  Thr Ala Ser Gln Gly  Phe Ser His Ser Gln  Met Thr Ala
    9110                 9115                 9120

Leu Met  Ser Arg Thr Pro Gly  Asp Val Pro Trp Leu  Ser His Pro
    9125                 9130                 9135

Ser Val  Glu Glu Ala Ser Ser  Ala Ser Phe Ser Leu  Ser Ser Pro
    9140                 9145                 9150

Val Met  Thr Ser Ser Ser Pro  Val Ser Ser Thr Leu  Pro Asp Ser
    9155                 9160                 9165

Ile His  Ser Ser Ser Leu Pro  Val Thr Ser Leu Leu  Thr Ser Gly
    9170                 9175                 9180
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Leu Val  Lys Thr Thr Glu Leu  Leu Gly Thr Ser Ser  Glu Pro Glu
    9185                 9190                 9195

Thr Ser  Ser Pro Pro Asn Leu  Ser Ser Thr Ser Ala  Glu Ile Leu
    9200                 9205                 9210

Ala Thr  Thr Glu Val Thr Thr  Asp Thr Glu Lys Leu  Glu Met Thr
    9215                 9220                 9225

Asn Val  Val Thr Ser Gly Tyr  Thr His Glu Ser Pro  Ser Ser Val
    9230                 9235                 9240

Leu Ala  Asp Ser Val Thr Thr  Lys Ala Thr Ser Ser  Met Gly Ile
    9245                 9250                 9255

Thr Tyr  Pro Thr Gly Asp Thr  Asn Val Leu Thr Ser  Thr Pro Ala
    9260                 9265                 9270

Phe Ser  Asp Thr Ser Arg Ile  Gln Thr Lys Ser Lys  Leu Ser Leu
    9275                 9280                 9285

Thr Pro  Gly Leu Met Glu Thr  Ser Ile Ser Glu Glu  Thr Ser Ser
    9290                 9295                 9300

Ala Thr  Glu Lys Ser Thr Val  Leu Ser Ser Val Pro  Thr Gly Ala
    9305                 9310                 9315

Thr Thr  Glu Val Ser Arg Thr  Glu Ala Ile Ser Ser  Ser Arg Thr
    9320                 9325                 9330

Ser Ile  Pro Gly Pro Ala Gln  Ser Thr Met Ser Ser  Asp Thr Ser
    9335                 9340                 9345

Met Glu  Thr Ile Thr Arg Ile  Ser Thr Pro Leu Thr  Arg Lys Glu
    9350                 9355                 9360

Ser Thr  Asp Met Ala Ile Thr  Pro Lys Thr Gly Pro  Ser Gly Ala
    9365                 9370                 9375

Thr Ser  Gln Gly Thr Phe Thr  Leu Asp Ser Ser Ser  Thr Ala Ser
    9380                 9385                 9390

Trp Pro  Gly Thr His Ser Ala  Thr Thr Gln Arg Phe  Pro Gln Ser
    9395                 9400                 9405

Val Val  Thr Thr Pro Met Ser  Arg Gly Pro Glu Asp  Val Ser Trp
    9410                 9415                 9420

Pro Ser  Pro Leu Ser Val Glu  Lys Asn Ser Pro Pro  Ser Ser Leu
    9425                 9430                 9435

Val Ser  Ser Ser Ser Val Thr  Ser Pro Ser Pro Leu  Tyr Ser Thr
    9440                 9445                 9450

Pro Ser  Gly Ser Ser His Ser  Ser Pro Val Pro Val  Thr Ser Leu
    9455                 9460                 9465

Phe Thr  Ser Ile Met Met Lys  Ala Thr Asp Met Leu  Asp Ala Ser
    9470                 9475                 9480

Leu Glu  Pro Glu Thr Thr Ser  Ala Pro Asn Met Asn  Ile Thr Ser
    9485                 9490                 9495

Asp Glu  Ser Leu Ala Thr Ser  Lys Ala Thr Thr Glu  Thr Glu Ala
    9500                 9505                 9510

Ile His  Val Phe Glu Asn Thr  Ala Ala Ser His Val  Glu Thr Thr
    9515                 9520                 9525

Ser Ala  Thr Glu Glu Leu Tyr  Ser Ser Ser Pro Gly  Phe Ser Glu
    9530                 9535                 9540

Pro Thr  Lys Val Ile Ser Pro  Val Val Thr Ser Ser  Ser Ile Arg
    9545                 9550                 9555

Asp Asn  Met Val Ser Thr Thr  Met Pro Gly Ser Ser  Gly Ile Thr
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    9560                9565                9570

Arg Ile  Glu Ile Glu Ser Met  Ser Ser Leu Thr Pro  Gly Leu Arg
    9575                9580                9585

Glu Thr  Arg Thr Ser Gln Asp  Ile Thr Ser Ser Thr  Glu Thr Ser
    9590                9595                9600

Thr Val  Leu Tyr Lys Met Ser  Ser Gly Ala Thr Pro  Glu Val Ser
    9605                9610                9615

Arg Thr  Glu Val Met Pro Ser  Ser Arg Thr Ser Ile  Pro Gly Pro
    9620                9625                9630

Ala Gln  Ser Thr Met Ser Leu  Asp Ile Ser Asp Glu  Val Val Thr
    9635                9640                9645

Arg Leu  Ser Thr Ser Pro Ile  Met Thr Glu Ser Ala  Glu Ile Thr
    9650                9655                9660

Ile Thr  Thr Gln Thr Gly Tyr  Ser Leu Ala Thr Ser  Gln Val Thr
    9665                9670                9675

Leu Pro  Leu Gly Thr Ser Met  Thr Phe Leu Ser Gly  Thr His Ser
    9680                9685                9690

Thr Met  Ser Gln Gly Leu Ser  His Ser Glu Met Thr  Asn Leu Met
    9695                9700                9705

Ser Arg  Gly Pro Glu Ser Leu  Ser Trp Thr Ser Pro  Arg Phe Val
    9710                9715                9720

Glu Thr  Thr Arg Ser Ser Ser  Ser Leu Thr Ser Leu  Pro Leu Thr
    9725                9730                9735

Thr Ser  Leu Ser Pro Val Ser  Ser Thr Leu Leu Asp  Ser Ser Pro
    9740                9745                9750

Ser Ser  Pro Leu Pro Val Thr  Ser Leu Ile Leu Pro  Gly Leu Val
    9755                9760                9765

Lys Thr  Thr Glu Val Leu Asp  Thr Ser Ser Glu Pro  Lys Thr Ser
    9770                9775                9780

Ser Ser  Pro Asn Leu Ser Ser  Thr Ser Val Glu Ile  Pro Ala Thr
    9785                9790                9795

Ser Glu  Ile Met Thr Asp Thr  Glu Lys Ile His Pro  Ser Ser Asn
    9800                9805                9810

Thr Ala  Val Ala Lys Val Arg  Thr Ser Ser Ser Val  His Glu Ser
    9815                9820                9825

His Ser  Ser Val Leu Ala Asp  Ser Glu Thr Thr Ile  Thr Ile Pro
    9830                9835                9840

Ser Met  Gly Ile Thr Ser Ala  Val Asp Asp Thr Thr  Val Phe Thr
    9845                9850                9855

Ser Asn  Pro Ala Phe Ser Glu  Thr Arg Arg Ile Pro  Thr Glu Pro
    9860                9865                9870

Thr Phe  Ser Leu Thr Pro Gly  Phe Arg Glu Thr Ser  Thr Ser Glu
    9875                9880                9885

Glu Thr  Thr Ser Ile Thr Glu  Thr Ser Ala Val Leu  Tyr Gly Val
    9890                9895                9900

Pro Thr  Ser Ala Thr Thr Glu  Val Ser Met Thr Glu  Ile Met Ser
    9905                9910                9915

Ser Asn  Arg Thr His Ile Pro  Asp Ser Asp Gln Ser  Thr Met Ser
    9920                9925                9930

Pro Asp  Ile Ile Thr Glu Val  Ile Thr Arg Leu Ser  Ser Ser Ser
    9935                9940                9945
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Met Met  Ser Glu Ser Thr Gln  Met Thr Ile Thr Thr  Gln Lys Ser
    9950                 9955                 9960

Ser Pro  Gly Ala Thr Ala Gln  Ser Thr Leu Thr Leu  Ala Thr Thr
    9965                 9970                 9975

Thr Ala  Pro Leu Ala Arg Thr  His Ser Thr Val Pro  Pro Arg Phe
    9980                 9985                 9990

Leu His  Ser Glu Met Thr Thr   Leu Met Ser Arg Ser   Pro Glu Asn
    9995                 10000                 10005

Pro Ser   Trp Lys Ser Ser Pro   Phe Val Glu Lys Thr   Ser Ser Ser
    10010                 10015                 10020

Ser Ser   Leu Leu Ser Leu Pro   Val Thr Thr Ser Pro   Ser Val Ser
    10025                 10030                 10035

Ser Thr   Leu Pro Gln Ser Ile   Pro Ser Ser Ser Phe   Ser Val Thr
    10040                 10045                 10050

Ser Leu   Leu Thr Pro Gly Met   Val Lys Thr Thr Asp   Thr Ser Thr
    10055                 10060                 10065

Glu Pro   Gly Thr Ser Leu Ser   Pro Asn Leu Ser Gly   Thr Ser Val
    10070                 10075                 10080

Glu Ile   Leu Ala Ala Ser Glu   Val Thr Thr Asp Thr   Glu Lys Ile
    10085                 10090                 10095

His Pro   Ser Ser Ser Met Ala   Val Thr Asn Val Gly   Thr Thr Ser
    10100                 10105                 10110

Ser Gly   His Glu Leu Tyr Ser   Ser Val Ser Ile His   Ser Glu Pro
    10115                 10120                 10125

Ser Lys   Ala Thr Tyr Pro Val   Gly Thr Pro Ser Ser   Met Ala Glu
    10130                 10135                 10140

Thr Ser   Ile Ser Thr Ser Met   Pro Ala Asn Phe Glu   Thr Thr Gly
    10145                 10150                 10155

Phe Glu   Ala Glu Pro Phe Ser   His Leu Thr Ser Gly   Phe Arg Lys
    10160                 10165                 10170

Thr Asn   Met Ser Leu Asp Thr   Ser Ser Val Thr Pro   Thr Asn Thr
    10175                 10180                 10185

Pro Ser   Ser Pro Gly Ser Thr   His Leu Leu Gln Ser   Ser Lys Thr
    10190                 10195                 10200

Asp Phe   Thr Ser Ser Ala Lys   Thr Ser Ser Pro Asp   Trp Pro Pro
    10205                 10210                 10215

Ala Ser   Gln Tyr Thr Glu Ile   Pro Val Asp Ile Ile   Thr Pro Phe
    10220                 10225                 10230

Asn Ala   Ser Pro Ser Ile Thr   Glu Ser Thr Gly Ile   Thr Ser Phe
    10235                 10240                 10245

Pro Glu   Ser Arg Phe Thr Met   Ser Val Thr Glu Ser   Thr His His
    10250                 10255                 10260

Leu Ser   Thr Asp Leu Leu Pro   Ser Ala Glu Thr Ile   Ser Thr Gly
    10265                 10270                 10275

Thr Val   Met Pro Ser Leu Ser   Glu Ala Met Thr Ser   Phe Ala Thr
    10280                 10285                 10290

Thr Gly   Val Pro Arg Ala Ile   Ser Gly Ser Gly Ser   Pro Phe Ser
    10295                 10300                 10305

Arg Thr   Glu Ser Gly Pro Gly   Asp Ala Thr Leu Ser   Thr Ile Ala
    10310                 10315                 10320
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Glu Ser   Leu Pro Ser Ser Thr   Pro Val Pro Phe Ser   Ser Ser Thr
    10325                 10330                 10335

Phe Thr   Thr Thr Asp Ser Ser   Thr Ile Pro Ala Leu   His Glu Ile
    10340                 10345                 10350

Thr Ser   Ser Ser Ala Thr Pro   Tyr Arg Val Asp Thr   Ser Leu Gly
    10355                 10360                 10365

Thr Glu   Ser Ser Thr Thr Glu   Gly Arg Leu Val Met   Val Ser Thr
    10370                 10375                 10380

Leu Asp   Thr Ser Ser Gln Pro   Gly Arg Thr Ser Ser   Thr Pro Ile
    10385                 10390                 10395

Leu Asp   Thr Arg Met Thr Glu   Ser Val Glu Leu Gly   Thr Val Thr
    10400                 10405                 10410

Ser Ala   Tyr Gln Val Pro Ser   Leu Ser Thr Arg Leu   Thr Arg Thr
    10415                 10420                 10425

Asp Gly   Ile Met Glu His Ile   Thr Lys Ile Pro Asn   Glu Ala Ala
    10430                 10435                 10440

His Arg   Gly Thr Ile Arg Pro   Val Lys Gly Pro Gln   Thr Ser Thr
    10445                 10450                 10455

Ser Pro   Ala Ser Pro Lys Gly   Leu His Thr Gly Gly   Thr Lys Arg
    10460                 10465                 10470

Met Glu   Thr Thr Thr Thr Ala   Leu Lys Thr Thr Thr   Thr Ala Leu
    10475                 10480                 10485

Lys Thr   Thr Ser Arg Ala Thr   Leu Thr Thr Ser Val   Tyr Thr Pro
    10490                 10495                 10500

Thr Leu   Gly Thr Leu Thr Pro   Leu Asn Ala Ser Arg   Gln Met Ala
    10505                 10510                 10515

Ser Thr   Ile Leu Thr Glu Met   Met Ile Thr Thr Pro   Tyr Val Phe
    10520                 10525                 10530

Pro Asp   Val Pro Glu Thr Thr   Ser Ser Leu Ala Thr   Ser Leu Gly
    10535                 10540                 10545

Ala Glu   Thr Ser Thr Ala Leu   Pro Arg Thr Thr Pro   Ser Val Leu
    10550                 10555                 10560

Asn Arg   Glu Ser Glu Thr Thr   Ala Ser Leu Val Ser   Arg Ser Gly
    10565                 10570                 10575

Ala Glu   Arg Ser Pro Val Ile   Gln Thr Leu Asp Val   Ser Ser Ser
    10580                 10585                 10590

Glu Pro   Asp Thr Thr Ala Ser   Trp Val Ile His Pro   Ala Glu Thr
    10595                 10600                 10605

Ile Pro   Thr Val Ser Lys Thr   Thr Pro Asn Phe Phe   His Ser Glu
    10610                 10615                 10620

Leu Asp   Thr Val Ser Ser Thr   Ala Thr Ser His Gly   Ala Asp Val
    10625                 10630                 10635

Ser Ser   Ala Ile Pro Thr Asn   Ile Ser Pro Ser Glu   Leu Asp Ala
    10640                 10645                 10650

Leu Thr   Pro Leu Val Thr Ile   Ser Gly Thr Asp Thr   Ser Thr Thr
    10655                 10660                 10665

Phe Pro   Thr Leu Thr Lys Ser   Pro His Glu Thr Glu   Thr Arg Thr
    10670                 10675                 10680

Thr Trp   Leu Thr His Pro Ala   Glu Thr Ser Ser Thr   Ile Pro Arg
    10685                 10690                 10695

Thr Ile   Pro Asn Phe Ser His   His Glu Ser Asp Ala   Thr Pro Ser
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    10700                10705                10710

Ile Ala   Thr Ser Pro Gly Ala   Glu Thr Ser Ser Ala   Ile Pro Ile
    10715                10720                10725

Met Thr   Val Ser Pro Gly Ala   Glu Asp Leu Val Thr   Ser Gln Val
    10730                10735                10740

Thr Ser   Ser Gly Thr Asp Arg   Asn Met Thr Ile Pro   Thr Leu Thr
    10745                10750                10755

Leu Ser   Pro Gly Glu Pro Lys   Thr Ile Ala Ser Leu   Val Thr His
    10760                10765                10770

Pro Glu   Ala Gln Thr Ser Ser   Ala Ile Pro Thr Ser   Thr Ile Ser
    10775                10780                10785

Pro Ala   Val Ser Arg Leu Val   Thr Ser Met Val Thr   Ser Leu Ala
    10790                10795                10800

Ala Lys   Thr Ser Thr Thr Asn   Arg Ala Leu Thr Asn   Ser Pro Gly
    10805                10810                10815

Glu Pro   Ala Thr Thr Val Ser   Leu Val Thr His Pro   Ala Gln Thr
    10820                10825                10830

Ser Pro   Thr Val Pro Trp Thr   Thr Ser Ile Phe Phe   His Ser Lys
    10835                10840                10845

Ser Asp   Thr Thr Pro Ser Met   Thr Thr Ser His Gly   Ala Glu Ser
    10850                10855                10860

Ser Ser   Ala Val Pro Thr Pro   Thr Val Ser Thr Glu   Val Pro Gly
    10865                10870                10875

Val Val   Thr Pro Leu Val Thr   Ser Ser Arg Ala Val   Ile Ser Thr
    10880                10885                10890

Thr Ile   Pro Ile Leu Thr Leu   Ser Pro Gly Glu Pro   Glu Thr Thr
    10895                10900                10905

Pro Ser   Met Ala Thr Ser His   Gly Glu Glu Ala Ser   Ser Ala Ile
    10910                10915                10920

Pro Thr   Pro Thr Val Ser Pro   Gly Val Pro Gly Val   Val Thr Ser
    10925                10930                10935

Leu Val   Thr Ser Ser Arg Ala   Val Thr Ser Thr Thr   Ile Pro Ile
    10940                10945                10950

Leu Thr   Phe Ser Leu Gly Glu   Pro Glu Thr Thr Pro   Ser Met Ala
    10955                10960                10965

Thr Ser   His Gly Thr Glu Ala   Gly Ser Ala Val Pro   Thr Val Leu
    10970                10975                10980

Pro Glu   Val Pro Gly Met Val   Thr Ser Leu Val Ala   Ser Ser Arg
    10985                10990                10995

Ala Val   Thr Ser Thr Thr Leu   Pro Thr Leu Thr Leu   Ser Pro Gly
    11000                11005                11010

Glu Pro   Glu Thr Thr Pro Ser   Met Ala Thr Ser His   Gly Ala Glu
    11015                11020                11025

Ala Ser   Ser Thr Val Pro Thr   Val Ser Pro Glu Val   Pro Gly Val
    11030                11035                11040

Val Thr   Ser Leu Val Thr Ser   Ser Ser Gly Val Asn   Ser Thr Ser
    11045                11050                11055

Ile Pro   Thr Leu Ile Leu Ser   Pro Gly Glu Leu Glu   Thr Thr Pro
    11060                11065                11070

Ser Met   Ala Thr Ser His Gly   Ala Glu Ala Ser Ser   Ala Val Pro
    11075                11080                11085
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Thr Pro   Thr Val Ser Pro Gly   Val Ser Gly Val Val   Thr Pro Leu
    11090                 11095                 11100

Val Thr   Ser Ser Arg Ala Val   Thr Ser Thr Thr Ile   Pro Ile Leu
    11105                 11110                 11115

Thr Leu   Ser Ser Ser Glu Pro   Glu Thr Thr Pro Ser   Met Ala Thr
    11120                 11125                 11130

Ser His   Gly Val Glu Ala Ser   Ser Ala Val Leu Thr   Val Ser Pro
    11135                 11140                 11145

Glu Val   Pro Gly Met Val Thr   Ser Leu Val Thr Ser   Ser Arg Ala
    11150                 11155                 11160

Val Thr   Ser Thr Thr Ile Pro   Thr Leu Thr Ile Ser   Ser Asp Glu
    11165                 11170                 11175

Pro Glu   Thr Thr Thr Ser Leu   Val Thr His Ser Glu   Ala Lys Met
    11180                 11185                 11190

Ile Ser   Ala Ile Pro Thr Leu   Ala Val Ser Pro Thr   Val Gln Gly
    11195                 11200                 11205

Leu Val   Thr Ser Leu Val Thr   Ser Ser Gly Ser Glu   Thr Ser Ala
    11210                 11215                 11220

Phe Ser   Asn Leu Thr Val Ala   Ser Ser Gln Pro Glu   Thr Ile Asp
    11225                 11230                 11235

Ser Trp   Val Ala His Pro Gly   Thr Glu Ala Ser Ser   Val Val Pro
    11240                 11245                 11250

Thr Leu   Thr Val Ser Thr Gly   Glu Pro Phe Thr Asn   Ile Ser Leu
    11255                 11260                 11265

Val Thr   His Pro Ala Glu Ser   Ser Ser Thr Leu Pro   Arg Thr Thr
    11270                 11275                 11280

Ser Arg   Phe Ser His Ser Glu   Leu Asp Thr Met Pro   Ser Thr Val
    11285                 11290                 11295

Thr Ser   Pro Glu Ala Glu Ser   Ser Ser Ala Ile Ser   Thr Thr Ile
    11300                 11305                 11310

Ser Pro   Gly Ile Pro Gly Val   Leu Thr Ser Leu Val   Thr Ser Ser
    11315                 11320                 11325

Gly Arg   Asp Ile Ser Ala Thr   Phe Pro Thr Val Pro   Glu Ser Pro
    11330                 11335                 11340

His Glu   Ser Glu Ala Thr Ala   Ser Trp Val Thr His   Pro Ala Val
    11345                 11350                 11355

Thr Ser   Thr Thr Val Pro Arg   Thr Thr Pro Asn Tyr   Ser His Ser
    11360                 11365                 11370

Glu Pro   Asp Thr Thr Pro Ser   Ile Ala Thr Ser Pro   Gly Ala Glu
    11375                 11380                 11385

Ala Thr   Ser Asp Phe Pro Thr   Ile Thr Val Ser Pro   Asp Val Pro
    11390                 11395                 11400

Asp Met   Val Thr Ser Gln Val   Thr Ser Ser Gly Thr   Asp Thr Ser
    11405                 11410                 11415

Ile Thr   Ile Pro Thr Leu Thr   Leu Ser Ser Gly Glu   Pro Glu Thr
    11420                 11425                 11430

Thr Thr   Ser Phe Ile Thr Tyr   Ser Glu Thr His Thr   Ser Ser Ala
    11435                 11440                 11445

Ile Pro   Thr Leu Pro Val Ser   Pro Gly Ala Ser Lys   Met Leu Thr
    11450                 11455                 11460
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Ser Leu   Val Ile Ser Ser Gly   Thr Asp Ser Thr Thr   Thr Phe Pro
    11465                 11470                 11475

Thr Leu   Thr Glu Thr Pro Tyr   Glu Pro Glu Thr Thr   Ala Ile Gln
    11480                 11485                 11490

Leu Ile   His Pro Ala Glu Thr   Asn Thr Met Val Pro   Arg Thr Thr
    11495                 11500                 11505

Pro Lys   Phe Ser His Ser Lys   Ser Asp Thr Thr Leu   Pro Val Ala
    11510                 11515                 11520

Ile Thr   Ser Pro Gly Pro Glu   Ala Ser Ser Ala Val   Ser Thr Thr
    11525                 11530                 11535

Thr Ile   Ser Pro Asp Met Ser   Asp Leu Val Thr Ser   Leu Val Pro
    11540                 11545                 11550

Ser Ser   Gly Thr Asp Thr Ser   Thr Thr Phe Pro Thr   Leu Ser Glu
    11555                 11560                 11565

Thr Pro   Tyr Glu Pro Glu Thr   Thr Ala Thr Trp Leu   Thr His Pro
    11570                 11575                 11580

Ala Glu   Thr Ser Thr Thr Val   Ser Gly Thr Ile Pro   Asn Phe Ser
    11585                 11590                 11595

His Arg   Gly Ser Asp Thr Ala   Pro Ser Met Val Thr   Ser Pro Gly
    11600                 11605                 11610

Val Asp   Thr Arg Ser Gly Val   Pro Thr Thr Thr Ile   Pro Pro Ser
    11615                 11620                 11625

Ile Pro   Gly Val Val Thr Ser   Gln Val Thr Ser Ser   Ala Thr Asp
    11630                 11635                 11640

Thr Ser   Thr Ala Ile Pro Thr   Leu Thr Pro Ser Pro   Gly Glu Pro
    11645                 11650                 11655

Glu Thr   Thr Ala Ser Ser Ala   Thr His Pro Gly Thr   Gln Thr Gly
    11660                 11665                 11670

Phe Thr   Val Pro Ile Arg Thr   Val Pro Ser Ser Glu   Pro Asp Thr
    11675                 11680                 11685

Met Ala   Ser Trp Val Thr His   Pro Pro Gln Thr Ser   Thr Pro Val
    11690                 11695                 11700

Ser Arg   Thr Thr Ser Ser Phe   Ser His Ser Ser Pro   Asp Ala Thr
    11705                 11710                 11715

Pro Val   Met Ala Thr Ser Pro   Arg Thr Glu Ala Ser   Ser Ala Val
    11720                 11725                 11730

Leu Thr   Thr Ile Ser Pro Gly   Ala Pro Glu Met Val   Thr Ser Gln
    11735                 11740                 11745

Ile Thr   Ser Ser Gly Ala Ala   Thr Ser Thr Thr Val   Pro Thr Leu
    11750                 11755                 11760

Thr His   Ser Pro Gly Met Pro   Glu Thr Thr Ala Leu   Leu Ser Thr
    11765                 11770                 11775

His Pro   Arg Thr Glu Thr Ser   Lys Thr Phe Pro Ala   Ser Thr Val
    11780                 11785                 11790

Phe Pro   Gln Val Ser Glu Thr   Thr Ala Ser Leu Thr   Ile Arg Pro
    11795                 11800                 11805

Gly Ala   Glu Thr Ser Thr Ala   Leu Pro Thr Gln Thr   Thr Ser Ser
    11810                 11815                 11820

Leu Phe   Thr Leu Leu Val Thr   Gly Thr Ser Arg Val   Asp Leu Ser
    11825                 11830                 11835

Pro Thr   Ala Ser Pro Gly Val   Ser Ala Lys Thr Ala   Pro Leu Ser
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    11840                   11845                   11850

Thr His   Pro Gly Thr Glu Thr   Ser Thr Met Ile Pro   Thr Ser Thr
    11855                   11860                   11865

Leu Ser   Leu Gly Leu Leu Glu   Thr Thr Gly Leu Leu   Ala Thr Ser
    11870                   11875                   11880

Ser Ser   Ala Glu Thr Ser Thr   Ser Thr Leu Thr Leu   Thr Val Ser
    11885                   11890                   11895

Pro Ala   Val Ser Gly Leu Ser   Ser Ala Ser Ile Thr   Thr Asp Lys
    11900                   11905                   11910

Pro Gln   Thr Val Thr Ser Trp   Asn Thr Glu Thr Ser   Pro Ser Val
    11915                   11920                   11925

Thr Ser   Val Gly Pro Pro Glu   Phe Ser Arg Thr Val   Thr Gly Thr
    11930                   11935                   11940

Thr Met   Thr Leu Ile Pro Ser   Glu Met Pro Thr Pro   Pro Lys Thr
    11945                   11950                   11955

Ser His   Gly Glu Gly Val Ser   Pro Thr Thr Ile Leu   Arg Thr Thr
    11960                   11965                   11970

Met Val   Glu Ala Thr Asn Leu   Ala Thr Thr Gly Ser   Ser Pro Thr
    11975                   11980                   11985

Val Ala   Lys Thr Thr Thr Thr   Phe Asn Thr Leu Ala   Gly Ser Leu
    11990                   11995                   12000

Phe Thr   Pro Leu Thr Thr Pro   Gly Met Ser Thr Leu   Ala Ser Glu
    12005                   12010                   12015

Ser Val   Thr Ser Arg Thr Ser   Tyr Asn His Arg Ser   Trp Ile Ser
    12020                   12025                   12030

Thr Thr   Ser Ser Tyr Asn Arg   Arg Tyr Trp Thr Pro   Ala Thr Ser
    12035                   12040                   12045

Thr Pro   Val Thr Ser Thr Phe   Ser Pro Gly Ile Ser   Thr Ser Ser
    12050                   12055                   12060

Ile Pro   Ser Ser Thr Ala Ala   Thr Val Pro Phe Met   Val Pro Phe
    12065                   12070                   12075

Thr Leu   Asn Phe Thr Ile Thr   Asn Leu Gln Tyr Glu   Glu Asp Met
    12080                   12085                   12090

Arg His   Pro Gly Ser Arg Lys   Phe Asn Ala Thr Glu   Arg Glu Leu
    12095                   12100                   12105

Gln Gly   Leu Leu Lys Pro Leu   Phe Arg Asn Ser Ser   Leu Glu Tyr
    12110                   12115                   12120

Leu Tyr   Ser Gly Cys Arg Leu   Ala Ser Leu Arg Pro   Glu Lys Asp
    12125                   12130                   12135

Ser Ser   Ala Met Ala Val Asp   Ala Ile Cys Thr His   Arg Pro Asp
    12140                   12145                   12150

Pro Glu   Asp Leu Gly Leu Asp   Arg Glu Arg Leu Tyr   Trp Glu Leu
    12155                   12160                   12165

Ser Asn   Leu Thr Asn Gly Ile   Gln Glu Leu Gly Pro   Tyr Thr Leu
    12170                   12175                   12180

Asp Arg   Asn Ser Leu Tyr Val   Asn Gly Phe Thr His   Arg Ser Ser
    12185                   12190                   12195

Met Pro   Thr Thr Ser Thr Pro   Gly Thr Ser Thr Val   Asp Val Gly
    12200                   12205                   12210

Thr Ser   Gly Thr Pro Ser Ser   Ser Pro Ser Pro Thr   Ala Ala Gly
    12215                   12220                   12225
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Pro Leu   Leu Met Pro Phe Thr   Leu Asn Phe Thr Ile   Thr Asn Leu
    12230                 12235                 12240

Gln Tyr   Glu Glu Asp Met Arg   Arg Thr Gly Ser Arg   Lys Phe Asn
    12245                 12250                 12255

Thr Met   Glu Ser Val Leu Gln   Gly Leu Leu Lys Pro   Leu Phe Lys
    12260                 12265                 12270

Asn Thr   Ser Val Gly Pro Leu   Tyr Ser Gly Cys Arg   Leu Thr Leu
    12275                 12280                 12285

Leu Arg   Pro Glu Lys Asp Gly   Ala Ala Thr Gly Val   Asp Ala Ile
    12290                 12295                 12300

Cys Thr   His Arg Leu Asp Pro   Lys Ser Pro Gly Leu   Asn Arg Glu
    12305                 12310                 12315

Gln Leu   Tyr Trp Glu Leu Ser   Lys Leu Thr Asn Asp   Ile Glu Glu
    12320                 12325                 12330

Leu Gly   Pro Tyr Thr Leu Asp   Arg Asn Ser Leu Tyr   Val Asn Gly
    12335                 12340                 12345

Phe Thr   His Gln Ser Ser Val   Ser Thr Thr Ser Thr   Pro Gly Thr
    12350                 12355                 12360

Ser Thr   Val Asp Leu Arg Thr   Ser Gly Thr Pro Ser   Ser Leu Ser
    12365                 12370                 12375

Ser Pro   Thr Ile Met Ala Ala   Gly Pro Leu Leu Val   Pro Phe Thr
    12380                 12385                 12390

Leu Asn   Phe Thr Ile Thr Asn   Leu Gln Tyr Gly Glu   Asp Met Gly
    12395                 12400                 12405

His Pro   Gly Ser Arg Lys Phe   Asn Thr Thr Glu Arg   Val Leu Gln
    12410                 12415                 12420

Gly Leu   Leu Gly Pro Ile Phe   Lys Asn Thr Ser Val   Gly Pro Leu
    12425                 12430                 12435

Tyr Ser   Gly Cys Arg Leu Thr   Ser Leu Arg Ser Glu   Lys Asp Gly
    12440                 12445                 12450

Ala Ala   Thr Gly Val Asp Ala   Ile Cys Ile His His   Leu Asp Pro
    12455                 12460                 12465

Lys Ser   Pro Gly Leu Asn Arg   Glu Arg Leu Tyr Trp   Glu Leu Ser
    12470                 12475                 12480

Gln Leu   Thr Asn Gly Ile Lys   Glu Leu Gly Pro Tyr   Thr Leu Asp
    12485                 12490                 12495

Arg Asn   Ser Leu Tyr Val Asn   Gly Phe Thr His Arg   Thr Ser Val
    12500                 12505                 12510

Pro Thr   Ser Ser Thr Pro Gly   Thr Ser Thr Val Asp   Leu Gly Thr
    12515                 12520                 12525

Ser Gly   Thr Pro Phe Ser Leu   Pro Ser Pro Ala Thr   Ala Gly Pro
    12530                 12535                 12540

Leu Leu   Val Leu Phe Thr Leu   Asn Phe Thr Ile Thr   Asn Leu Lys
    12545                 12550                 12555

Tyr Glu   Glu Asp Met His Arg   Pro Gly Ser Arg Lys   Phe Asn Thr
    12560                 12565                 12570

Thr Glu   Arg Val Leu Gln Thr   Leu Leu Gly Pro Met   Phe Lys Asn
    12575                 12580                 12585

Thr Ser   Val Gly Leu Leu Tyr   Ser Gly Cys Arg Leu   Thr Leu Leu
    12590                 12595                 12600
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Arg Ser   Glu Lys Asp Gly Ala   Ala Thr Gly Val Asp   Ala Ile Cys
    12605                 12610                 12615

Thr His   Arg Leu Asp Pro Lys   Ser Pro Gly Leu Asp   Arg Glu Gln
    12620                 12625                 12630

Leu Tyr   Trp Glu Leu Ser Gln   Leu Thr Asn Gly Ile   Lys Glu Leu
    12635                 12640                 12645

Gly Pro   Tyr Thr Leu Asp Arg   Asn Ser Leu Tyr Val   Asn Gly Phe
    12650                 12655                 12660

Thr His   Trp Ile Pro Val Pro   Thr Ser Ser Thr Pro   Gly Thr Ser
    12665                 12670                 12675

Thr Val   Asp Leu Gly Ser Gly   Thr Pro Ser Ser Leu   Pro Ser Pro
    12680                 12685                 12690

Thr Ala   Ala Gly Pro Leu Leu   Val Pro Phe Thr Leu   Asn Phe Thr
    12695                 12700                 12705

Ile Thr   Asn Leu Gln Tyr Glu   Glu Asp Met His His   Pro Gly Ser
    12710                 12715                 12720

Arg Lys   Phe Asn Thr Thr Glu   Arg Val Leu Gln Gly   Leu Leu Gly
    12725                 12730                 12735

Pro Met   Phe Lys Asn Thr Ser   Val Gly Leu Leu Tyr   Ser Gly Cys
    12740                 12745                 12750

Arg Leu   Thr Leu Leu Arg Ser   Glu Lys Asp Gly Ala   Ala Thr Gly
    12755                 12760                 12765

Val Asp   Ala Ile Cys Thr His   Arg Leu Asp Pro Lys   Ser Pro Gly
    12770                 12775                 12780

Val Asp   Arg Glu Gln Leu Tyr   Trp Glu Leu Ser Gln   Leu Thr Asn
    12785                 12790                 12795

Gly Ile   Lys Glu Leu Gly Pro   Tyr Thr Leu Asp Arg   Asn Ser Leu
    12800                 12805                 12810

Tyr Val   Asn Gly Phe Thr His   Gln Thr Ser Ala Pro   Asn Thr Ser
    12815                 12820                 12825

Thr Pro   Gly Thr Ser Thr Val   Asp Leu Gly Thr Ser   Gly Thr Pro
    12830                 12835                 12840

Ser Ser   Leu Pro Ser Pro Thr   Ser Ala Gly Pro Leu   Leu Val Pro
    12845                 12850                 12855

Phe Thr   Leu Asn Phe Thr Ile   Thr Asn Leu Gln Tyr   Glu Glu Asp
    12860                 12865                 12870

Met Arg   His Pro Gly Ser Arg   Lys Phe Asn Thr Thr   Glu Arg Val
    12875                 12880                 12885

Leu Gln   Gly Leu Leu Lys Pro   Leu Phe Lys Ser Thr   Ser Val Gly
    12890                 12895                 12900

Pro Leu   Tyr Ser Gly Cys Arg   Leu Thr Leu Leu Arg   Ser Glu Lys
    12905                 12910                 12915

Asp Gly   Ala Ala Thr Gly Val   Asp Ala Ile Cys Thr   His Arg Leu
    12920                 12925                 12930

Asp Pro   Lys Ser Pro Gly Val   Asp Arg Glu Gln Leu   Tyr Trp Glu
    12935                 12940                 12945

Leu Ser   Gln Leu Thr Asn Gly   Ile Lys Glu Leu Gly   Pro Tyr Thr
    12950                 12955                 12960

Leu Asp   Arg Asn Ser Leu Tyr   Val Asn Gly Phe Thr   His Gln Thr
    12965                 12970                 12975

Ser Ala   Pro Asn Thr Ser Thr   Pro Gly Thr Ser Thr   Val Asp Leu
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    12980                   12985                   12990

Gly Thr   Ser Gly Thr Pro Ser   Ser Leu Pro Ser Pro   Thr Ser Ala
    12995                   13000                   13005

Gly Pro   Leu Leu Val Pro Phe   Thr Leu Asn Phe Thr   Ile Thr Asn
    13010                   13015                   13020

Leu Gln   Tyr Glu Glu Asp Met   His His Pro Gly Ser   Arg Lys Phe
    13025                   13030                   13035

Asn Thr   Thr Glu Arg Val Leu   Gln Gly Leu Leu Gly   Pro Met Phe
    13040                   13045                   13050

Lys Asn   Thr Ser Val Gly Leu   Leu Tyr Ser Gly Cys   Arg Leu Thr
    13055                   13060                   13065

Leu Leu   Arg Pro Glu Lys Asn   Gly Ala Ala Thr Gly   Met Asp Ala
    13070                   13075                   13080

Ile Cys   Ser His Arg Leu Asp   Pro Lys Ser Pro Gly   Leu Asn Arg
    13085                   13090                   13095

Glu Gln   Leu Tyr Trp Glu Leu   Ser Gln Leu Thr His   Gly Ile Lys
    13100                   13105                   13110

Glu Leu   Gly Pro Tyr Thr Leu   Asp Arg Asn Ser Leu   Tyr Val Asn
    13115                   13120                   13125

Gly Phe   Thr His Arg Ser Ser   Val Ala Pro Thr Ser   Thr Pro Gly
    13130                   13135                   13140

Thr Ser   Thr Val Asp Leu Gly   Thr Ser Gly Thr Pro   Ser Ser Leu
    13145                   13150                   13155

Pro Ser   Pro Thr Thr Ala Val   Pro Leu Leu Val Pro   Phe Thr Leu
    13160                   13165                   13170

Asn Phe   Thr Ile Thr Asn Leu   Gln Tyr Gly Glu Asp   Met Arg His
    13175                   13180                   13185

Pro Gly   Ser Arg Lys Phe Asn   Thr Thr Glu Arg Val   Leu Gln Gly
    13190                   13195                   13200

Leu Leu   Gly Pro Leu Phe Lys   Asn Ser Ser Val Gly   Pro Leu Tyr
    13205                   13210                   13215

Ser Gly   Cys Arg Leu Ile Ser   Leu Arg Ser Glu Lys   Asp Gly Ala
    13220                   13225                   13230

Ala Thr   Gly Val Asp Ala Ile   Cys Thr His His Leu   Asn Pro Gln
    13235                   13240                   13245

Ser Pro   Gly Leu Asp Arg Glu   Gln Leu Tyr Trp Gln   Leu Ser Gln
    13250                   13255                   13260

Met Thr   Asn Gly Ile Lys Glu   Leu Gly Pro Tyr Thr   Leu Asp Arg
    13265                   13270                   13275

Asn Ser   Leu Tyr Val Asn Gly   Phe Thr His Arg Ser   Ser Gly Leu
    13280                   13285                   13290

Thr Thr   Ser Thr Pro Trp Thr   Ser Thr Val Asp Leu   Gly Thr Ser
    13295                   13300                   13305

Gly Thr   Pro Ser Pro Val Pro   Ser Pro Thr Thr Ala   Gly Pro Leu
    13310                   13315                   13320

Leu Val   Pro Phe Thr Leu Asn   Phe Thr Ile Thr Asn   Leu Gln Tyr
    13325                   13330                   13335

Glu Glu   Asp Met His Arg Pro   Gly Ser Arg Lys Phe   Asn Ala Thr
    13340                   13345                   13350

Glu Arg   Val Leu Gln Gly Leu   Leu Ser Pro Ile Phe   Lys Asn Ser
    13355                   13360                   13365
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Ser Val   Gly Pro Leu Tyr Ser   Gly Cys Arg Leu Thr   Ser Leu Arg
    13370                 13375                 13380

Pro Glu   Lys Asp Gly Ala Ala   Thr Gly Met Asp Ala   Val Cys Leu
    13385                 13390                 13395

Tyr His   Pro Asn Pro Lys Arg   Pro Gly Leu Asp Arg   Glu Gln Leu
    13400                 13405                 13410

Tyr Trp   Glu Leu Ser Gln Leu   Thr His Asn Ile Thr   Glu Leu Gly
    13415                 13420                 13425

Pro Tyr   Ser Leu Asp Arg Asp   Ser Leu Tyr Val Asn   Gly Phe Thr
    13430                 13435                 13440

His Gln   Asn Ser Val Pro Thr   Thr Ser Thr Pro Gly   Thr Ser Thr
    13445                 13450                 13455

Val Tyr   Trp Ala Thr Thr Gly   Thr Pro Ser Ser Phe   Pro Gly His
    13460                 13465                 13470

Thr Glu   Pro Gly Pro Leu Leu   Ile Pro Phe Thr Phe   Asn Phe Thr
    13475                 13480                 13485

Ile Thr   Asn Leu His Tyr Glu   Glu Asn Met Gln His   Pro Gly Ser
    13490                 13495                 13500

Arg Lys   Phe Asn Thr Thr Glu   Arg Val Leu Gln Gly   Leu Leu Lys
    13505                 13510                 13515

Pro Leu   Phe Lys Asn Thr Ser   Val Gly Pro Leu Tyr   Ser Gly Cys
    13520                 13525                 13530

Arg Leu   Thr Ser Leu Arg Pro   Glu Lys Asp Gly Ala   Ala Thr Gly
    13535                 13540                 13545

Met Asp   Ala Val Cys Leu Tyr   His Pro Asn Pro Lys   Arg Pro Gly
    13550                 13555                 13560

Leu Asp   Arg Glu Gln Leu Tyr   Cys Glu Leu Ser Gln   Leu Thr His
    13565                 13570                 13575

Asn Ile   Thr Glu Leu Gly Pro   Tyr Ser Leu Asp Arg   Asp Ser Leu
    13580                 13585                 13590

Tyr Val   Asn Gly Phe Thr His   Gln Asn Ser Val Pro   Thr Thr Ser
    13595                 13600                 13605

Thr Pro   Gly Thr Ser Thr Val   Tyr Trp Ala Thr Thr   Gly Thr Pro
    13610                 13615                 13620

Ser Ser   Phe Pro Gly His Thr   Glu Pro Gly Pro Leu   Leu Ile Pro
    13625                 13630                 13635

Phe Thr   Phe Asn Phe Thr Ile   Thr Asn Leu His Tyr   Glu Glu Asn
    13640                 13645                 13650

Met Gln   His Pro Gly Ser Arg   Lys Phe Asn Thr Thr   Glu Arg Val
    13655                 13660                 13665

Leu Gln   Gly Leu Leu Lys Pro   Leu Phe Lys Asn Thr   Ser Val Gly
    13670                 13675                 13680

Pro Leu   Tyr Ser Gly Cys Arg   Leu Thr Leu Leu Arg   Pro Glu Lys
    13685                 13690                 13695

His Glu   Ala Ala Thr Gly Val   Asp Thr Ile Cys Thr   His Arg Val
    13700                 13705                 13710

Asp Pro   Ile Gly Pro Gly Leu   Asp Arg Glu Arg Leu   Tyr Trp Glu
    13715                 13720                 13725

Leu Ser   Gln Leu Thr Asn Ser   Ile Thr Glu Leu Gly   Pro Tyr Thr
    13730                 13735                 13740
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Leu Asp   Arg Asp Ser Leu Tyr   Val Asn Gly Phe Asn   Pro Arg Ser
    13745                 13750                 13755

Ser Val   Pro Thr Thr Ser Thr   Pro Gly Thr Ser Thr   Val His Leu
    13760                 13765                 13770

Ala Thr   Ser Gly Thr Pro Ser   Ser Leu Pro Gly His   Thr Ala Pro
    13775                 13780                 13785

Val Pro   Leu Leu Ile Pro Phe   Thr Leu Asn Phe Thr   Ile Thr Asn
    13790                 13795                 13800

Leu His   Tyr Glu Glu Asn Met   Gln His Pro Gly Ser   Arg Lys Phe
    13805                 13810                 13815

Asn Thr   Thr Glu Arg Val Leu   Gln Gly Leu Leu Lys   Pro Leu Phe
    13820                 13825                 13830

Lys Asn   Thr Ser Val Gly Pro   Leu Tyr Ser Gly Cys   Arg Leu Thr
    13835                 13840                 13845

Leu Leu   Arg Pro Glu Lys His   Glu Ala Ala Thr Gly   Val Asp Thr
    13850                 13855                 13860

Ile Cys   Thr His Arg Val Asp   Pro Ile Gly Pro Gly   Leu Asp Arg
    13865                 13870                 13875

Glu Xaa   Leu Tyr Trp Glu Leu   Ser Xaa Leu Thr Xaa   Xaa Ile Xaa
    13880                 13885                 13890

Glu Leu   Gly Pro Tyr Xaa Leu   Asp Arg Xaa Ser Leu   Tyr Val Asn
    13895                 13900                 13905

Gly Phe   Xaa Xaa Xaa Xaa Xaa   Xaa Xaa Xaa Thr Ser   Thr Pro Gly
    13910                 13915                 13920

Thr Ser   Xaa Val Xaa Leu Xaa   Thr Ser Gly Thr Pro   Xaa Xaa Xaa
    13925                 13930                 13935

Pro Xaa   Xaa Thr Ser Ala Gly   Pro Leu Leu Val Pro   Phe Thr Leu
    13940                 13945                 13950

Asn Phe   Thr Ile Thr Asn Leu   Gln Tyr Glu Glu Asp   Met His His
    13955                 13960                 13965

Pro Gly   Ser Arg Lys Phe Asn   Thr Thr Glu Arg Val   Leu Gln Gly
    13970                 13975                 13980

Leu Leu   Gly Pro Met Phe Lys   Asn Thr Ser Val Gly   Leu Leu Tyr
    13985                 13990                 13995

Ser Gly   Cys Arg Leu Thr Leu   Leu Arg Pro Glu Lys   Asn Gly Ala
    14000                 14005                 14010

Ala Thr   Gly Met Asp Ala Ile   Cys Ser His Arg Leu   Asp Pro Lys
    14015                 14020                 14025

Ser Pro   Gly Leu Asp Arg Glu   Gln Leu Tyr Trp Glu   Leu Ser Gln
    14030                 14035                 14040

Leu Thr   His Gly Ile Lys Glu   Leu Gly Pro Tyr Thr   Leu Asp Arg
    14045                 14050                 14055

Asn Ser   Leu Tyr Val Asn Gly   Phe Thr His Arg Ser   Ser Val Ala
    14060                 14065                 14070

Pro Thr   Ser Thr Pro Gly Thr   Ser Thr Val Asp Leu   Gly Thr Ser
    14075                 14080                 14085

Gly Thr   Pro Ser Ser Leu Pro   Ser Pro Thr Thr Ala   Val Pro Leu
    14090                 14095                 14100

Leu Val   Pro Phe Thr Leu Asn   Phe Thr Ile Thr Asn   Leu Gln Tyr
    14105                 14110                 14115

Gly Glu   Asp Met Arg His Pro   Gly Ser Arg Lys Phe   Asn Thr Thr
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    14120                   14125                   14130

Glu Arg   Val Leu Gln Gly Leu   Leu Gly Pro Leu Phe   Lys Asn Ser
    14135                   14140                   14145

Ser Val   Gly Pro Leu Tyr Ser   Gly Cys Arg Leu Ile   Ser Leu Arg
    14150                   14155                   14160

Ser Glu   Lys Asp Gly Ala Ala   Thr Gly Val Asp Ala   Ile Cys Thr
    14165                   14170                   14175

His His   Leu Asn Pro Gln Ser   Pro Gly Leu Asp Arg   Glu Gln Leu
    14180                   14185                   14190

Tyr Trp   Gln Leu Ser Gln Met   Thr Asn Gly Ile Lys   Glu Leu Gly
    14195                   14200                   14205

Pro Tyr   Thr Leu Asp Arg Asn   Ser Leu Tyr Val Asn   Gly Phe Thr
    14210                   14215                   14220

His Arg   Ser Ser Gly Leu Thr   Thr Ser Thr Pro Trp   Thr Ser Thr
    14225                   14230                   14235

Val Asp   Leu Gly Thr Ser Gly   Thr Pro Ser Pro Val   Pro Ser Pro
    14240                   14245                   14250

Thr Thr   Ala Gly Pro Leu Leu   Val Pro Phe Thr Leu   Asn Phe Thr
    14255                   14260                   14265

Ile Thr   Asn Leu Gln Tyr Glu   Glu Asp Met His Arg   Pro Gly Ser
    14270                   14275                   14280

Arg Lys   Phe Asn Ala Thr Glu   Arg Val Leu Gln Gly   Leu Leu Ser
    14285                   14290                   14295

Pro Ile   Phe Lys Asn Ser Ser   Val Gly Pro Leu Tyr   Ser Gly Cys
    14300                   14305                   14310

Arg Leu   Thr Ser Leu Arg Pro   Glu Lys Asp Gly Ala   Ala Thr Gly
    14315                   14320                   14325

Met Asp   Ala Val Cys Leu Tyr   His Pro Asn Pro Lys   Arg Pro Gly
    14330                   14335                   14340

Leu Asp   Arg Glu Gln Leu Tyr   Trp Glu Leu Ser Gln   Leu Thr His
    14345                   14350                   14355

Asn Ile   Thr Glu Leu Gly Pro   Tyr Ser Leu Asp Arg   Asp Ser Leu
    14360                   14365                   14370

Tyr Val   Asn Gly Phe Thr His   Gln Ser Ser Met Thr   Thr Thr Arg
    14375                   14380                   14385

Thr Pro   Asp Thr Ser Thr Met   His Leu Ala Thr Ser   Arg Thr Pro
    14390                   14395                   14400

Ala Ser   Leu Ser Gly Pro Thr   Thr Ala Ser Pro Leu   Leu Val Leu
    14405                   14410                   14415

Phe Thr   Ile Asn Cys Thr Ile   Thr Asn Leu Gln Tyr   Glu Glu Asp
    14420                   14425                   14430

Met Arg   Arg Thr Gly Ser Arg   Lys Phe Asn Thr Met   Glu Ser Val
    14435                   14440                   14445

Leu Gln   Gly Leu Leu Lys Pro   Leu Phe Lys Asn Thr   Ser Val Gly
    14450                   14455                   14460

Pro Leu   Tyr Ser Gly Cys Arg   Leu Thr Leu Leu Arg   Pro Lys Lys
    14465                   14470                   14475

Asp Gly   Ala Ala Thr Gly Val   Asp Ala Ile Cys Thr   His Arg Leu
    14480                   14485                   14490

Asp Pro   Lys Ser Pro Gly Leu   Asn Arg Glu Gln Leu   Tyr Trp Glu
    14495                   14500                   14505
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Leu Ser   Lys Leu Thr Asn Asp   Ile Glu Glu Leu Gly   Pro Tyr Thr
    14510                 14515                 14520

Leu Asp   Arg Asn Ser Leu Tyr   Val Asn Gly Phe Thr   His Gln Ser
    14525                 14530                 14535

Ser Val   Ser Thr Thr Ser Thr   Pro Gly Thr Ser Thr   Val Asp Leu
    14540                 14545                 14550

Arg Thr   Ser Gly Thr Pro Ser   Ser Leu Ser Ser Pro   Thr Ile Met
    14555                 14560                 14565

Xaa Xaa   Xaa Pro Leu Leu Xaa   Pro Phe Thr Leu Asn   Phe Thr Ile
    14570                 14575                 14580

Thr Asn   Leu Xaa Tyr Glu Glu   Xaa Met Xaa Xaa Pro   Gly Ser Arg
    14585                 14590                 14595

Lys Phe   Asn Thr Thr Glu Arg   Val Leu Gln Gly Leu   Leu Arg Pro
    14600                 14605                 14610

Leu Phe   Lys Asn Thr Ser Val   Ser Ser Leu Tyr Ser   Gly Cys Arg
    14615                 14620                 14625

Leu Thr   Leu Leu Arg Pro Glu   Lys Asp Gly Ala Ala   Thr Arg Val
    14630                 14635                 14640

Asp Ala   Ala Cys Thr Tyr Arg   Pro Asp Pro Lys Ser   Pro Gly Leu
    14645                 14650                 14655

Asp Arg   Glu Gln Leu Tyr Trp   Glu Leu Ser Gln Leu   Thr His Ser
    14660                 14665                 14670

Ile Thr   Glu Leu Gly Pro Tyr   Thr Leu Asp Arg Val   Ser Leu Tyr
    14675                 14680                 14685

Val Asn   Gly Phe Asn Pro Arg   Ser Ser Val Pro Thr   Thr Ser Thr
    14690                 14695                 14700

Pro Gly   Thr Ser Thr Val His   Leu Ala Thr Ser Gly   Thr Pro Ser
    14705                 14710                 14715

Ser Leu   Pro Gly His Thr Xaa   Xaa Xaa Pro Leu Leu   Xaa Pro Phe
    14720                 14725                 14730

Thr Leu   Asn Phe Thr Ile Thr   Asn Leu Xaa Tyr Glu   Glu Xaa Met
    14735                 14740                 14745

Xaa Xaa   Pro Gly Ser Arg Lys   Phe Asn Thr Thr Glu   Arg Val Leu
    14750                 14755                 14760

Gln Gly   Leu Leu Lys Pro Leu   Phe Arg Asn Ser Ser   Leu Glu Tyr
    14765                 14770                 14775

Leu Tyr   Ser Gly Cys Arg Leu   Ala Ser Leu Arg Pro   Glu Lys Asp
    14780                 14785                 14790

Ser Ser   Ala Met Ala Val Asp   Ala Ile Cys Thr His   Arg Pro Asp
    14795                 14800                 14805

Pro Glu   Asp Leu Gly Leu Asp   Arg Glu Arg Leu Tyr   Trp Glu Leu
    14810                 14815                 14820

Ser Asn   Leu Thr Asn Gly Ile   Gln Glu Leu Gly Pro   Tyr Thr Leu
    14825                 14830                 14835

Asp Arg   Asn Ser Leu Tyr Val   Asn Gly Phe Thr His   Arg Ser Ser
    14840                 14845                 14850

Phe Leu   Thr Thr Ser Thr Pro   Trp Thr Ser Thr Val   Asp Leu Gly
    14855                 14860                 14865

Thr Ser   Gly Thr Pro Ser Pro   Val Pro Ser Pro Thr   Thr Ala Gly
    14870                 14875                 14880
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Pro Leu   Leu Val Pro Phe Thr   Leu Asn Phe Thr Ile   Thr Asn Leu
    14885                 14890                 14895

Gln Tyr   Glu Glu Asp Met His   Arg Pro Gly Ser Arg   Arg Phe Asn
    14900                 14905                 14910

Thr Thr   Glu Arg Val Leu Gln   Gly Leu Leu Thr Pro   Leu Phe Lys
    14915                 14920                 14925

Asn Thr   Ser Val Gly Pro Leu   Tyr Ser Gly Cys Arg   Leu Thr Leu
    14930                 14935                 14940

Leu Arg   Pro Glu Lys Gln Glu   Ala Ala Thr Gly Val   Asp Thr Ile
    14945                 14950                 14955

Cys Thr   His Arg Val Asp Pro   Ile Gly Pro Gly Leu   Asp Arg Glu
    14960                 14965                 14970

Arg Leu   Tyr Trp Glu Leu Ser   Gln Leu Thr Asn Ser   Ile Thr Glu
    14975                 14980                 14985

Leu Gly   Pro Tyr Thr Leu Asp   Arg Asp Ser Leu Tyr   Val Asn Gly
    14990                 14995                 15000

Phe Asn   Pro Trp Ser Ser Val   Pro Thr Thr Ser Thr   Pro Gly Thr
    15005                 15010                 15015

Ser Thr   Val His Leu Ala Thr   Ser Gly Thr Pro Ser   Ser Leu Pro
    15020                 15025                 15030

Gly His   Thr Ala Pro Val Pro   Leu Leu Ile Pro Phe   Thr Leu Asn
    15035                 15040                 15045

Phe Thr   Ile Thr Asp Leu His   Tyr Glu Glu Asn Met   Gln His Pro
    15050                 15055                 15060

Gly Ser   Arg Lys Phe Asn Thr   Thr Glu Arg Val Leu   Gln Gly Leu
    15065                 15070                 15075

Leu Lys   Pro Leu Phe Lys Ser   Thr Ser Val Gly Pro   Leu Tyr Ser
    15080                 15085                 15090

Gly Cys   Arg Leu Thr Leu Leu   Arg Pro Glu Lys His   Gly Ala Ala
    15095                 15100                 15105

Thr Gly   Val Asp Ala Ile Cys   Thr Leu Arg Leu Asp   Pro Thr Gly
    15110                 15115                 15120

Pro Gly   Leu Asp Arg Glu Arg   Leu Tyr Trp Glu Leu   Ser Gln Leu
    15125                 15130                 15135

Thr Asn   Ser Val Thr Glu Leu   Gly Pro Tyr Thr Leu   Asp Arg Asp
    15140                 15145                 15150

Ser Leu   Tyr Val Asn Gly Phe   Thr His Arg Ser Ser   Val Pro Thr
    15155                 15160                 15165

Thr Ser   Ile Pro Gly Thr Ser   Ala Val His Leu Glu   Thr Ser Gly
    15170                 15175                 15180

Thr Pro   Ala Ser Leu Pro Gly   His Thr Ala Pro Gly   Pro Leu Leu
    15185                 15190                 15195

Val Pro   Phe Thr Leu Asn Phe   Thr Ile Thr Asn Leu   Gln Tyr Glu
    15200                 15205                 15210

Glu Asp   Met Arg His Pro Gly   Ser Arg Lys Phe Ser   Thr Thr Glu
    15215                 15220                 15225

Arg Val   Leu Gln Gly Leu Leu   Lys Pro Leu Phe Lys   Asn Thr Ser
    15230                 15235                 15240

Val Ser   Ser Leu Tyr Ser Gly   Cys Arg Leu Thr Leu   Leu Arg Pro
    15245                 15250                 15255

Glu Lys   Asp Gly Ala Ala Thr   Arg Val Asp Ala Val   Cys Thr His
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    15260                15265                15270

Arg Pro   Asp Pro Lys Ser Pro   Gly Leu Asp Arg Glu   Arg Leu Tyr
    15275                15280                15285

Trp Lys   Leu Ser Gln Leu Thr   His Gly Ile Thr Glu   Leu Gly Pro
    15290                15295                15300

Tyr Thr   Leu Asp Arg His Ser   Leu Tyr Val Asn Gly   Phe Thr His
    15305                15310                15315

Gln Ser   Ser Met Thr Thr Thr   Arg Thr Pro Asp Thr   Ser Thr Met
    15320                15325                15330

His Leu   Ala Thr Ser Arg Thr   Pro Ala Ser Leu Ser   Gly Pro Thr
    15335                15340                15345

Thr Ala   Ser Pro Leu Leu Val   Leu Phe Thr Ile Asn   Phe Thr Ile
    15350                15355                15360

Thr Asn   Gln Arg Tyr Glu Glu   Asn Met His His Pro   Gly Ser Arg
    15365                15370                15375

Lys Phe   Asn Thr Thr Glu Arg   Val Leu Gln Gly Leu   Leu Arg Pro
    15380                15385                15390

Val Phe   Lys Asn Thr Ser Val   Gly Pro Leu Tyr Ser   Gly Cys Arg
    15395                15400                15405

Leu Thr   Leu Leu Arg Pro Lys   Lys Asp Gly Ala Ala   Thr Lys Val
    15410                15415                15420

Asp Ala   Ile Cys Thr Tyr Arg   Pro Asp Pro Lys Ser   Pro Gly Leu
    15425                15430                15435

Asp Arg   Glu Gln Leu Tyr Trp   Glu Leu Ser Gln Leu   Thr His Ser
    15440                15445                15450

Ile Thr   Glu Leu Gly Pro Tyr   Thr Gln Asp Arg Asp   Ser Leu Tyr
    15455                15460                15465

Val Asn   Gly Phe Thr His Arg   Ser Ser Val Pro Thr   Thr Ser Ile
    15470                15475                15480

Pro Gly   Thr Ser Ala Val His   Leu Glu Thr Ser Gly   Thr Pro Ala
    15485                15490                15495

Ser Leu   Pro Gly His Thr Ala   Pro Gly Pro Leu Leu   Val Pro Phe
    15500                15505                15510

Thr Leu   Asn Phe Thr Ile Thr   Asn Leu Gln Tyr Glu   Glu Asp Met
    15515                15520                15525

Arg His   Pro Gly Ser Arg Lys   Phe Asn Thr Thr Glu   Arg Val Leu
    15530                15535                15540

Gln Gly   Leu Leu Lys Pro Leu   Phe Lys Ser Thr Ser   Val Gly Pro
    15545                15550                15555

Leu Tyr   Ser Gly Cys Arg Leu   Thr Leu Leu Arg Pro   Glu Lys Arg
    15560                15565                15570

Gly Ala   Ala Thr Gly Val Asp   Thr Ile Cys Thr His   Arg Leu Asp
    15575                15580                15585

Pro Leu   Asn Pro Gly Leu Asp   Arg Glu Gln Leu Tyr   Trp Glu Leu
    15590                15595                15600

Ser Lys   Leu Thr Arg Gly Ile   Ile Glu Leu Gly Pro   Tyr Leu Leu
    15605                15610                15615

Asp Arg   Gly Ser Leu Tyr Val   Asn Gly Phe Thr His   Arg Thr Ser
    15620                15625                15630

Val Pro   Thr Thr Ser Thr Pro   Gly Thr Ser Thr Val   Asp Leu Gly
    15635                15640                15645
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Thr Ser   Gly Thr Pro Phe Ser   Leu Pro Ser Pro Ala   Xaa Xaa Xaa
    15650                 15655                 15660

Pro Leu   Leu Xaa Pro Phe Thr   Leu Asn Phe Thr Ile   Thr Asn Leu
    15665                 15670                 15675

Xaa Tyr   Glu Glu Xaa Met Xaa   Xaa Pro Gly Ser Arg   Lys Phe Asn
    15680                 15685                 15690

Thr Thr   Glu Arg Val Leu Gln   Thr Leu Leu Gly Pro   Met Phe Lys
    15695                 15700                 15705

Asn Thr   Ser Val Gly Leu Leu   Tyr Ser Gly Cys Arg   Leu Thr Leu
    15710                 15715                 15720

Leu Arg   Ser Glu Lys Asp Gly   Ala Ala Thr Gly Val   Asp Ala Ile
    15725                 15730                 15735

Cys Thr   His Arg Leu Asp Pro   Lys Ser Pro Gly Val   Asp Arg Glu
    15740                 15745                 15750

Gln Leu   Tyr Trp Glu Leu Ser   Gln Leu Thr Asn Gly   Ile Lys Glu
    15755                 15760                 15765

Leu Gly   Pro Tyr Thr Leu Asp   Arg Asn Ser Leu Tyr   Val Asn Gly
    15770                 15775                 15780

Phe Thr   His Trp Ile Pro Val   Pro Thr Ser Ser Thr   Pro Gly Thr
    15785                 15790                 15795

Ser Thr   Val Asp Leu Gly Ser   Gly Thr Pro Ser Leu   Pro Ser Ser
    15800                 15805                 15810

Pro Thr   Thr Ala Gly Pro Leu   Leu Val Pro Phe Thr   Leu Asn Phe
    15815                 15820                 15825

Thr Ile   Thr Asn Leu Lys Tyr   Glu Glu Asp Met His   Cys Pro Gly
    15830                 15835                 15840

Ser Arg   Lys Phe Asn Thr Thr   Glu Arg Val Leu Gln   Ser Leu Leu
    15845                 15850                 15855

Gly Pro   Met Phe Lys Asn Thr   Ser Val Gly Pro Leu   Tyr Ser Gly
    15860                 15865                 15870

Cys Arg   Leu Thr Leu Leu Arg   Ser Glu Lys Asp Gly   Ala Ala Thr
    15875                 15880                 15885

Gly Val   Asp Ala Ile Cys Thr   His Arg Leu Asp Pro   Lys Ser Pro
    15890                 15895                 15900

Gly Val   Asp Arg Glu Gln Leu   Tyr Trp Glu Leu Ser   Gln Leu Thr
    15905                 15910                 15915

Asn Gly   Ile Lys Glu Leu Gly   Pro Tyr Thr Leu Asp   Arg Asn Ser
    15920                 15925                 15930

Leu Tyr   Val Asn Gly Phe Thr   His Gln Thr Ser Ala   Pro Asn Thr
    15935                 15940                 15945

Ser Thr   Pro Gly Thr Ser Thr   Val Asp Leu Gly Thr   Ser Gly Thr
    15950                 15955                 15960

Pro Ser   Ser Leu Pro Ser Pro   Thr Xaa Xaa Xaa Pro   Leu Leu Xaa
    15965                 15970                 15975

Pro Phe   Thr Leu Asn Phe Thr   Ile Thr Asn Leu Xaa   Tyr Glu Glu
    15980                 15985                 15990

Xaa Met   Xaa Xaa Pro Gly Ser   Arg Lys Phe Asn Thr   Thr Glu Arg
    15995                 16000                 16005

Val Leu   Gln Gly Leu Leu Xaa   Pro Xaa Phe Lys Xaa   Thr Ser Val
    16010                 16015                 16020
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Gly Xaa   Leu Tyr Ser Gly Cys   Arg Leu Thr Leu Leu   Arg Xaa Glu
    16025                 16030                 16035

Lys Xaa   Xaa Ala Ala Thr Xaa   Val Asp Xaa Xaa Cys   Xaa Xaa Xaa
    16040                 16045                 16050

Xaa Asp   Pro Xaa Xaa Pro Gly   Leu Asp Arg Glu Xaa   Leu Tyr Trp
    16055                 16060                 16065

Glu Leu   Ser Xaa Leu Thr Xaa   Xaa Ile Xaa Glu Leu   Gly Pro Tyr
    16070                 16075                 16080

Xaa Leu   Asp Arg Xaa Ser Leu   Tyr Val Asn Gly Phe   Thr His Trp
    16085                 16090                 16095

Ile Pro   Val Pro Thr Ser Ser   Thr Pro Gly Thr Ser   Thr Val Asp
    16100                 16105                 16110

Leu Gly   Ser Gly Thr Pro Ser   Ser Leu Pro Ser Pro   Thr Thr Ala
    16115                 16120                 16125

Gly Pro   Leu Leu Val Pro Phe   Thr Leu Asn Phe Thr   Ile Thr Asn
    16130                 16135                 16140

Leu Lys   Tyr Glu Glu Asp Met   His Cys Pro Gly Ser   Arg Lys Phe
    16145                 16150                 16155

Asn Thr   Thr Glu Arg Val Leu   Gln Ser Leu Leu Gly   Pro Met Phe
    16160                 16165                 16170

Lys Asn   Thr Ser Val Gly Pro   Leu Tyr Ser Gly Cys   Arg Leu Thr
    16175                 16180                 16185

Ser Leu   Arg Ser Glu Lys Asp   Gly Ala Ala Thr Gly   Val Asp Ala
    16190                 16195                 16200

Ile Cys   Thr His Arg Val Asp   Pro Lys Ser Pro Gly   Val Asp Arg
    16205                 16210                 16215

Glu Gln   Leu Tyr Trp Glu Leu   Ser Gln Leu Thr Asn   Gly Ile Lys
    16220                 16225                 16230

Glu Leu   Gly Pro Tyr Thr Leu   Asp Arg Asn Ser Leu   Tyr Val Asn
    16235                 16240                 16245

Gly Phe   Thr His Gln Thr Ser   Ala Pro Asn Thr Ser   Thr Pro Gly
    16250                 16255                 16260

Thr Ser   Thr Val Asp Leu Gly   Thr Ser Gly Thr Pro   Ser Ser Leu
    16265                 16270                 16275

Pro Ser   Pro Thr Ser Ala Gly   Pro Leu Leu Val Pro   Phe Thr Leu
    16280                 16285                 16290

Asn Phe   Thr Ile Thr Asn Leu   Gln Tyr Glu Glu Asp   Met His His
    16295                 16300                 16305

Pro Gly   Ser Arg Lys Phe Asn   Thr Thr Glu Arg Val   Leu Gln Gly
    16310                 16315                 16320

Leu Leu   Gly Pro Met Phe Lys   Asn Thr Ser Val Gly   Leu Leu Tyr
    16325                 16330                 16335

Ser Gly   Cys Arg Leu Thr Leu   Leu Arg Pro Glu Lys   Asn Gly Ala
    16340                 16345                 16350

Ala Thr   Gly Met Asp Ala Ile   Cys Thr His Arg Leu   Asp Pro Lys
    16355                 16360                 16365

Ser Pro   Gly Leu Asp Arg Glu   Xaa Leu Tyr Trp Glu   Leu Ser Xaa
    16370                 16375                 16380

Leu Thr   Xaa Xaa Ile Xaa Glu   Leu Gly Pro Tyr Xaa   Leu Asp Arg
    16385                 16390                 16395

Xaa Ser   Leu Tyr Val Asn Gly   Phe Xaa Xaa Xaa Xaa   Xaa Xaa Xaa
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    16400                   16405                   16410

Xaa Thr   Ser Thr Pro Gly Thr   Ser Xaa Val Xaa Leu   Xaa Thr Ser
    16415                   16420                   16425

Gly Thr   Pro Xaa Xaa Xaa Pro   Xaa Xaa Thr Xaa Xaa   Xaa Pro Leu
    16430                   16435                   16440

Leu Xaa   Pro Phe Thr Leu Asn   Phe Thr Ile Thr Asn   Leu Xaa Tyr
    16445                   16450                   16455

Glu Glu   Xaa Met Xaa Xaa Pro   Gly Ser Arg Lys Phe   Asn Thr Thr
    16460                   16465                   16470

Glu Arg   Val Leu Gln Gly Leu   Leu Lys Pro Leu Phe   Arg Asn Ser
    16475                   16480                   16485

Ser Leu   Glu Tyr Leu Tyr Ser   Gly Cys Arg Leu Ala   Ser Leu Arg
    16490                   16495                   16500

Pro Glu   Lys Asp Ser Ser Ala   Met Ala Val Asp Ala   Ile Cys Thr
    16505                   16510                   16515

His Arg   Pro Asp Pro Glu Asp   Leu Gly Leu Asp Arg   Glu Arg Leu
    16520                   16525                   16530

Tyr Trp   Glu Leu Ser Asn Leu   Thr Asn Gly Ile Gln   Glu Leu Gly
    16535                   16540                   16545

Pro Tyr   Thr Leu Asp Arg Asn   Ser Leu Tyr Val Asn   Gly Phe Thr
    16550                   16555                   16560

His Arg   Ser Ser Met Pro Thr   Thr Ser Thr Pro Gly   Thr Ser Thr
    16565                   16570                   16575

Val Asp   Val Gly Thr Ser Gly   Thr Pro Ser Ser Ser   Pro Ser Pro
    16580                   16585                   16590

Thr Thr   Ala Gly Pro Leu Leu   Ile Pro Phe Thr Leu   Asn Phe Thr
    16595                   16600                   16605

Ile Thr   Asn Leu Gln Tyr Gly   Glu Asp Met Gly His   Pro Gly Ser
    16610                   16615                   16620

Arg Lys   Phe Asn Thr Thr Glu   Arg Val Leu Gln Gly   Leu Leu Gly
    16625                   16630                   16635

Pro Ile   Phe Lys Asn Thr Ser   Val Gly Pro Leu Tyr   Ser Gly Cys
    16640                   16645                   16650

Arg Leu   Thr Ser Leu Arg Ser   Glu Lys Asp Gly Ala   Ala Thr Gly
    16655                   16660                   16665

Val Asp   Ala Ile Cys Ile His   His Leu Asp Pro Lys   Ser Pro Gly
    16670                   16675                   16680

Leu Asn   Arg Glu Arg Leu Tyr   Trp Glu Leu Ser Gln   Leu Thr Asn
    16685                   16690                   16695

Gly Ile   Lys Glu Leu Gly Pro   Tyr Thr Leu Asp Arg   Asn Ser Leu
    16700                   16705                   16710

Tyr Val   Asn Gly Phe Thr His   Arg Thr Ser Val Pro   Thr Thr Ser
    16715                   16720                   16725

Thr Pro   Gly Thr Ser Thr Val   Asp Leu Gly Thr Ser   Gly Thr Pro
    16730                   16735                   16740

Phe Ser   Leu Pro Ser Pro Ala   Thr Ala Gly Pro Leu   Leu Val Leu
    16745                   16750                   16755

Phe Thr   Leu Asn Phe Thr Ile   Thr Asn Leu Lys Tyr   Glu Glu Asp
    16760                   16765                   16770

Met His   Arg Pro Gly Ser Arg   Lys Phe Asn Thr Thr   Glu Arg Val
    16775                   16780                   16785
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Leu Gln   Thr Leu Leu Gly Pro   Met Phe Lys Asn Thr   Ser Val Gly
    16790                 16795                 16800

Leu Leu   Tyr Ser Gly Cys Arg   Leu Thr Leu Leu Arg   Ser Glu Lys
    16805                 16810                 16815

Asp Gly   Ala Ala Thr Gly Val   Asp Ala Ile Cys Thr   His Arg Leu
    16820                 16825                 16830

Asp Pro   Lys Ser Pro Gly Leu   Asp Arg Glu Xaa Leu   Tyr Trp Glu
    16835                 16840                 16845

Leu Ser   Xaa Leu Thr Xaa Xaa   Ile Xaa Glu Leu Gly   Pro Tyr Xaa
    16850                 16855                 16860

Leu Asp   Arg Xaa Ser Leu Tyr   Val Asn Gly Phe Xaa   Xaa Xaa Xaa
    16865                 16870                 16875

Xaa Xaa   Xaa Xaa Thr Ser Thr   Pro Gly Thr Ser Xaa   Val Xaa Leu
    16880                 16885                 16890

Xaa Thr   Ser Gly Thr Pro Xaa   Xaa Xaa Pro Xaa Xaa   Thr Xaa Xaa
    16895                 16900                 16905

Xaa Pro   Leu Leu Xaa Pro Phe   Thr Leu Asn Phe Thr   Ile Thr Asn
    16910                 16915                 16920

Leu Xaa   Tyr Glu Glu Xaa Met   Xaa Xaa Pro Gly Ser   Arg Lys Phe
    16925                 16930                 16935

Asn Thr   Thr Glu Arg Val Leu   Gln Gly Leu Leu Arg   Pro Val Phe
    16940                 16945                 16950

Lys Asn   Thr Ser Val Gly Pro   Leu Tyr Ser Gly Cys   Arg Leu Thr
    16955                 16960                 16965

Leu Leu   Arg Pro Lys Lys Asp   Gly Ala Ala Thr Lys   Val Asp Ala
    16970                 16975                 16980

Ile Cys   Thr Tyr Arg Pro Asp   Pro Lys Ser Pro Gly   Leu Asp Arg
    16985                 16990                 16995

Glu Gln   Leu Tyr Trp Glu Leu   Ser Gln Leu Thr His   Ser Ile Thr
    17000                 17005                 17010

Glu Leu   Gly Pro Tyr Thr Gln   Asp Arg Asp Ser Leu   Tyr Val Asn
    17015                 17020                 17025

Gly Phe   Thr His Arg Ser Ser   Val Pro Thr Thr Ser   Ile Pro Gly
    17030                 17035                 17040

Thr Ser   Ala Val His Leu Glu   Thr Thr Gly Thr Pro   Ser Ser Phe
    17045                 17050                 17055

Pro Gly   His Thr Glu Pro Gly   Pro Leu Leu Ile Pro   Phe Thr Phe
    17060                 17065                 17070

Asn Phe   Thr Ile Thr Asn Leu   Arg Tyr Glu Glu Asn   Met Gln His
    17075                 17080                 17085

Pro Gly   Ser Arg Lys Phe Asn   Thr Thr Glu Arg Val   Leu Gln Gly
    17090                 17095                 17100

Leu Leu   Thr Pro Leu Phe Lys   Asn Thr Ser Val Gly   Pro Leu Tyr
    17105                 17110                 17115

Ser Gly   Cys Arg Leu Thr Leu   Leu Arg Pro Glu Lys   Gln Glu Ala
    17120                 17125                 17130

Ala Thr   Gly Val Asp Thr Ile   Cys Thr His Arg Val   Asp Pro Ile
    17135                 17140                 17145

Gly Pro   Gly Leu Asp Arg Glu   Arg Leu Tyr Trp Glu   Leu Ser Gln
    17150                 17155                 17160
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Leu Thr   Asn Ser Ile Thr Glu   Leu Gly Pro Tyr Thr   Leu Asp Arg
    17165                 17170                 17175

Asp Ser   Leu Tyr Val Asp Gly   Phe Asn Pro Trp Ser   Ser Val Pro
    17180                 17185                 17190

Thr Thr   Ser Thr Pro Gly Thr   Ser Thr Val His Leu   Ala Thr Ser
    17195                 17200                 17205

Gly Thr   Pro Ser Pro Leu Pro   Gly His Thr Ala Pro   Val Pro Leu
    17210                 17215                 17220

Leu Ile   Pro Phe Thr Leu Asn   Phe Thr Ile Thr Asp   Leu His Tyr
    17225                 17230                 17235

Glu Glu   Asn Met Gln His Pro   Gly Ser Arg Lys Phe   Asn Thr Thr
    17240                 17245                 17250

Glu Arg   Val Leu Gln Gly Leu   Leu Lys Pro Leu Phe   Lys Ser Thr
    17255                 17260                 17265

Ser Val   Gly Pro Leu Tyr Ser   Gly Cys Arg Leu Thr   Leu Leu Arg
    17270                 17275                 17280

Pro Glu   Lys His Gly Ala Ala   Thr Gly Val Asp Ala   Ile Cys Thr
    17285                 17290                 17295

Leu Arg   Leu Asp Pro Thr Gly   Pro Gly Leu Asp Arg   Glu Arg Leu
    17300                 17305                 17310

Tyr Trp   Glu Leu Ser Gln Leu   Thr Asn Ser Ile Thr   Glu Leu Gly
    17315                 17320                 17325

Pro Tyr   Thr Leu Asp Arg Asp   Ser Leu Tyr Val Asn   Gly Phe Asn
    17330                 17335                 17340

Pro Trp   Ser Ser Val Pro Thr   Thr Ser Thr Pro Gly   Thr Ser Thr
    17345                 17350                 17355

Val His   Leu Ala Thr Ser Gly   Thr Pro Ser Ser Leu   Pro Gly His
    17360                 17365                 17370

Thr Thr   Ala Gly Pro Leu Leu   Val Pro Phe Thr Leu   Asn Phe Thr
    17375                 17380                 17385

Ile Thr   Asn Leu Lys Tyr Glu   Glu Asp Met His Cys   Pro Gly Ser
    17390                 17395                 17400

Arg Lys   Phe Asn Thr Thr Glu   Arg Val Leu Gln Ser   Leu His Gly
    17405                 17410                 17415

Pro Met   Phe Lys Asn Thr Ser   Val Gly Pro Leu Tyr   Ser Gly Cys
    17420                 17425                 17430

Arg Leu   Thr Leu Leu Arg Ser   Glu Lys Asp Gly Ala   Ala Thr Gly
    17435                 17440                 17445

Val Asp   Ala Ile Cys Thr His   Arg Leu Asp Pro Lys   Ser Pro Gly
    17450                 17455                 17460

Leu Asp   Arg Glu Xaa Leu Tyr   Trp Glu Leu Ser Xaa   Leu Thr Xaa
    17465                 17470                 17475

Xaa Ile   Xaa Glu Leu Gly Pro   Tyr Xaa Leu Asp Arg   Xaa Ser Leu
    17480                 17485                 17490

Tyr Val   Asn Gly Phe Xaa Xaa   Xaa Xaa Xaa Xaa Xaa   Xaa Thr Ser
    17495                 17500                 17505

Thr Pro   Gly Thr Ser Xaa Val   Xaa Leu Xaa Thr Ser   Gly Thr Pro
    17510                 17515                 17520

Xaa Xaa   Xaa Pro Xaa Xaa Thr   Xaa Xaa Xaa Pro Leu   Leu Xaa Pro
    17525                 17530                 17535

Phe Thr   Leu Asn Phe Thr Ile   Thr Asn Leu Xaa Tyr   Glu Glu Xaa
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    17540                17545                17550

Met Xaa   Xaa Pro Gly Ser Arg   Lys Phe Asn Thr Thr   Glu Arg Val
    17555                17560                17565

Leu Gln   Gly Leu Leu Xaa Pro   Xaa Phe Lys Xaa Thr   Ser Val Gly
    17570                17575                17580

Xaa Leu   Tyr Ser Gly Cys Arg   Leu Thr Leu Leu Arg   Xaa Glu Lys
    17585                17590                17595

Xaa Xaa   Ala Ala Thr Xaa Val   Asp Xaa Xaa Cys Xaa   Xaa Xaa Xaa
    17600                17605                17610

Asp Pro   Xaa Xaa Pro Gly Leu   Asp Arg Glu Xaa Leu   Tyr Trp Glu
    17615                17620                17625

Leu Ser   Xaa Leu Thr Asn Ser   Ile Thr Glu Leu Gly   Pro Tyr Thr
    17630                17635                17640

Leu Asp   Arg Asp Ser Leu Tyr   Val Asn Gly Phe Thr   His Arg Ser
    17645                17650                17655

Ser Met   Pro Thr Thr Ser Ile   Pro Gly Thr Ser Ala   Val His Leu
    17660                17665                17670

Glu Thr   Ser Gly Thr Pro Ala   Ser Leu Pro Gly His   Thr Ala Pro
    17675                17680                17685

Gly Pro   Leu Leu Val Pro Phe   Thr Leu Asn Phe Thr   Ile Thr Asn
    17690                17695                17700

Leu Gln   Tyr Glu Glu Asp Met   Arg His Pro Gly Ser   Arg Lys Phe
    17705                17710                17715

Asn Thr   Thr Glu Arg Val Leu   Gln Gly Leu Leu Lys   Pro Leu Phe
    17720                17725                17730

Lys Ser   Thr Ser Val Gly Pro   Leu Tyr Ser Gly Cys   Arg Leu Thr
    17735                17740                17745

Leu Leu   Arg Pro Glu Lys Arg   Gly Ala Ala Thr Gly   Val Asp Thr
    17750                17755                17760

Ile Cys   Thr His Arg Leu Asp   Pro Leu Asn Pro Gly   Leu Asp Arg
    17765                17770                17775

Glu Xaa   Leu Tyr Trp Glu Leu   Ser Xaa Leu Thr Xaa   Xaa Ile Xaa
    17780                17785                17790

Glu Leu   Gly Pro Tyr Xaa Leu   Asp Arg Xaa Ser Leu   Tyr Val Asn
    17795                17800                17805

Gly Phe   Xaa Xaa Xaa Xaa Xaa   Xaa Xaa Xaa Thr Ser   Thr Pro Gly
    17810                17815                17820

Thr Ser   Xaa Val Xaa Leu Xaa   Thr Ser Gly Thr Pro   Xaa Xaa Xaa
    17825                17830                17835

Pro Xaa   Xaa Thr Xaa Xaa Xaa   Pro Leu Leu Xaa Pro   Phe Thr Leu
    17840                17845                17850

Asn Phe   Thr Ile Thr Asn Leu   Xaa Tyr Glu Glu Xaa   Met Xaa Xaa
    17855                17860                17865

Pro Gly   Ser Arg Lys Phe Asn   Thr Thr Glu Arg Val   Leu Gln Gly
    17870                17875                17880

Leu Leu   Xaa Pro Xaa Phe Lys   Xaa Thr Ser Val Gly   Xaa Leu Tyr
    17885                17890                17895

Ser Gly   Cys Arg Leu Thr Leu   Leu Arg Xaa Glu Lys   Xaa Xaa Ala
    17900                17905                17910

Ala Thr   Xaa Val Asp Xaa Xaa   Cys Xaa Xaa Xaa Xaa   Asp Pro Xaa
    17915                17920                17925
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Xaa Pro   Gly Leu Asp Arg Glu   Xaa Leu Tyr Trp Glu   Leu Ser Xaa
    17930                 17935                 17940

Leu Thr   Xaa Xaa Ile Xaa Glu   Leu Gly Pro Tyr Xaa   Leu Asp Arg
    17945                 17950                 17955

Xaa Ser   Leu Tyr Val Asn Gly   Phe His Pro Arg Ser   Ser Val Pro
    17960                 17965                 17970

Thr Thr   Ser Thr Pro Gly Thr   Ser Thr Val His Leu   Ala Thr Ser
    17975                 17980                 17985

Gly Thr   Pro Ser Ser Leu Pro   Gly His Thr Ala Pro   Val Pro Leu
    17990                 17995                 18000

Leu Ile   Pro Phe Thr Leu Asn   Phe Thr Ile Thr Asn   Leu His Tyr
    18005                 18010                 18015

Glu Glu   Asn Met Gln His Pro   Gly Ser Arg Lys Phe   Asn Thr Thr
    18020                 18025                 18030

Glu Arg   Val Leu Gln Gly Leu   Leu Gly Pro Met Phe   Lys Asn Thr
    18035                 18040                 18045

Ser Val   Gly Leu Leu Tyr Ser   Gly Cys Arg Leu Thr   Leu Leu Arg
    18050                 18055                 18060

Pro Glu   Lys Asn Gly Ala Ala   Thr Gly Met Asp Ala   Ile Cys Ser
    18065                 18070                 18075

His Arg   Leu Asp Pro Lys Ser   Pro Gly Leu Asp Arg   Glu Xaa Leu
    18080                 18085                 18090

Tyr Trp   Glu Leu Ser Xaa Leu   Thr Xaa Xaa Ile Xaa   Glu Leu Gly
    18095                 18100                 18105

Pro Tyr   Xaa Leu Asp Arg Xaa   Ser Leu Tyr Val Asn   Gly Phe Xaa
    18110                 18115                 18120

Xaa Xaa   Xaa Xaa Xaa Xaa Xaa   Thr Ser Thr Pro Gly   Thr Ser Xaa
    18125                 18130                 18135

Val Xaa   Leu Xaa Thr Ser Gly   Thr Pro Xaa Xaa Xaa   Pro Xaa Xaa
    18140                 18145                 18150

Thr Xaa   Xaa Xaa Pro Leu Leu   Xaa Pro Phe Thr Leu   Asn Phe Thr
    18155                 18160                 18165

Ile Thr   Asn Leu Xaa Tyr Glu   Glu Xaa Met Xaa Xaa   Pro Gly Ser
    18170                 18175                 18180

Arg Lys   Phe Asn Thr Thr Glu   Arg Val Leu Gln Gly   Leu Leu Xaa
    18185                 18190                 18195

Pro Xaa   Phe Lys Xaa Thr Ser   Val Gly Xaa Leu Tyr   Ser Gly Cys
    18200                 18205                 18210

Arg Leu   Thr Leu Leu Arg Xaa   Glu Lys Xaa Xaa Ala   Ala Thr Xaa
    18215                 18220                 18225

Val Asp   Xaa Xaa Cys Xaa Xaa   Xaa Xaa Asp Pro Xaa   Xaa Pro Gly
    18230                 18235                 18240

Leu Asp   Arg Glu Xaa Leu Tyr   Trp Glu Leu Ser Xaa   Leu Thr Xaa
    18245                 18250                 18255

Xaa Ile   Xaa Glu Leu Gly Pro   Tyr Xaa Leu Asp Arg   Xaa Ser Leu
    18260                 18265                 18270

Tyr Val   Asn Gly Phe Thr His   Gln Asn Ser Val Pro   Thr Thr Ser
    18275                 18280                 18285

Thr Pro   Gly Thr Ser Thr Val   Tyr Trp Ala Thr Thr   Gly Thr Pro
    18290                 18295                 18300
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Ser Ser   Phe Pro Gly His Thr   Glu Pro Gly Pro Leu   Leu Ile Pro
    18305                 18310                 18315

Phe Thr   Phe Asn Phe Thr Ile   Thr Asn Leu His Tyr   Glu Glu Asn
    18320                 18325                 18330

Met Gln   His Pro Gly Ser Arg   Lys Phe Asn Thr Thr   Glu Arg Val
    18335                 18340                 18345

Leu Gln   Gly Leu Leu Thr Pro   Leu Phe Lys Asn Thr   Ser Val Gly
    18350                 18355                 18360

Pro Leu   Tyr Ser Gly Cys Arg   Leu Thr Leu Leu Arg   Pro Glu Lys
    18365                 18370                 18375

Gln Glu   Ala Ala Thr Gly Val   Asp Thr Ile Cys Thr   His Arg Val
    18380                 18385                 18390

Asp Pro   Ile Gly Pro Gly Leu   Asp Arg Glu Xaa Leu   Tyr Trp Glu
    18395                 18400                 18405

Leu Ser   Xaa Leu Thr Xaa Xaa   Ile Xaa Glu Leu Gly   Pro Tyr Xaa
    18410                 18415                 18420

Leu Asp   Arg Xaa Ser Leu Tyr   Val Asn Gly Phe Xaa   Xaa Xaa Xaa
    18425                 18430                 18435

Xaa Xaa   Xaa Xaa Thr Ser Thr   Pro Gly Thr Ser Xaa   Val Xaa Leu
    18440                 18445                 18450

Xaa Thr   Ser Gly Thr Pro Xaa   Xaa Xaa Pro Xaa Xaa   Thr Xaa Xaa
    18455                 18460                 18465

Xaa Pro   Leu Leu Xaa Pro Phe   Thr Leu Asn Phe Thr   Ile Thr Asn
    18470                 18475                 18480

Leu Xaa   Tyr Glu Glu Xaa Met   Xaa Xaa Pro Gly Ser   Arg Lys Phe
    18485                 18490                 18495

Asn Thr   Thr Glu Arg Val Leu   Gln Gly Leu Leu Xaa   Pro Xaa Phe
    18500                 18505                 18510

Lys Xaa   Thr Ser Val Gly Xaa   Leu Tyr Ser Gly Cys   Arg Leu Thr
    18515                 18520                 18525

Leu Leu   Arg Xaa Glu Lys Xaa   Xaa Ala Ala Thr Xaa   Val Asp Xaa
    18530                 18535                 18540

Xaa Cys   Xaa Xaa Xaa Xaa Asp   Pro Xaa Xaa Pro Gly   Leu Asp Arg
    18545                 18550                 18555

Glu Xaa   Leu Tyr Trp Glu Leu   Ser Xaa Leu Thr Xaa   Xaa Ile Xaa
    18560                 18565                 18570

Glu Leu   Gly Pro Tyr Xaa Leu   Asp Arg Xaa Ser Leu   Tyr Val Asn
    18575                 18580                 18585

Gly Phe   Thr His Arg Ser Ser   Val Pro Thr Thr Ser   Ser Pro Gly
    18590                 18595                 18600

Thr Ser   Thr Val His Leu Ala   Thr Ser Gly Thr Pro   Ser Ser Leu
    18605                 18610                 18615

Pro Gly   His Thr Ala Pro Val   Pro Leu Leu Ile Pro   Phe Thr Leu
    18620                 18625                 18630

Asn Phe   Thr Ile Thr Asn Leu   His Tyr Glu Glu Asn   Met Gln His
    18635                 18640                 18645

Pro Gly   Ser Arg Lys Phe Asn   Thr Thr Glu Arg Val   Leu Gln Gly
    18650                 18655                 18660

Leu Leu   Lys Pro Leu Phe Lys   Ser Thr Ser Val Gly   Pro Leu Tyr
    18665                 18670                 18675

Ser Gly   Cys Arg Leu Thr Leu   Leu Arg Pro Glu Lys   His Gly Ala
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    18680                   18685                   18690

Ala Thr   Gly Val Asp Ala Ile   Cys Thr Leu Arg Leu   Asp Pro Thr
    18695                   18700                   18705

Gly Pro   Gly Leu Asp Arg Glu   Xaa Leu Tyr Trp Glu   Leu Ser Xaa
    18710                   18715                   18720

Leu Thr   Xaa Xaa Ile Xaa Glu   Leu Gly Pro Tyr Xaa   Leu Asp Arg
    18725                   18730                   18735

Xaa Ser   Leu Tyr Val Asn Gly   Phe Xaa Xaa Xaa Xaa   Xaa Xaa Xaa
    18740                   18745                   18750

Xaa Thr   Ser Thr Pro Gly Thr   Ser Xaa Val Xaa Leu   Xaa Thr Ser
    18755                   18760                   18765

Gly Thr   Pro Xaa Xaa Xaa Pro   Xaa Xaa Thr Xaa Xaa   Xaa Pro Leu
    18770                   18775                   18780

Leu Xaa   Pro Phe Thr Leu Asn   Phe Thr Ile Thr Asn   Leu Xaa Tyr
    18785                   18790                   18795

Glu Glu   Xaa Met Xaa Xaa Pro   Gly Ser Arg Lys Phe   Asn Thr Thr
    18800                   18805                   18810

Glu Arg   Val Leu Gln Gly Leu   Leu Xaa Pro Xaa Phe   Lys Xaa Thr
    18815                   18820                   18825

Ser Val   Gly Xaa Leu Tyr Ser   Gly Cys Arg Leu Thr   Leu Leu Arg
    18830                   18835                   18840

Xaa Glu   Lys Xaa Xaa Ala Ala   Thr Xaa Val Asp Xaa   Xaa Cys Xaa
    18845                   18850                   18855

Xaa Xaa   Xaa Asp Pro Xaa Xaa   Pro Gly Leu Asp Arg   Glu Xaa Leu
    18860                   18865                   18870

Tyr Trp   Glu Leu Ser Xaa Leu   Thr Xaa Xaa Ile Xaa   Glu Leu Gly
    18875                   18880                   18885

Pro Tyr   Xaa Leu Asp Arg Xaa   Ser Leu Tyr Val Asn   Gly Phe Thr
    18890                   18895                   18900

His Arg   Thr Ser Val Pro Thr   Thr Ser Thr Pro Gly   Thr Ser Thr
    18905                   18910                   18915

Val His   Leu Ala Thr Ser Gly   Thr Pro Ser Ser Leu   Pro Gly His
    18920                   18925                   18930

Thr Ala   Pro Val Pro Leu Leu   Ile Pro Phe Thr Leu   Asn Phe Thr
    18935                   18940                   18945

Ile Thr   Asn Leu Gln Tyr Glu   Glu Asp Met His Arg   Pro Gly Ser
    18950                   18955                   18960

Arg Lys   Phe Asn Thr Thr Glu   Arg Val Leu Gln Gly   Leu Leu Ser
    18965                   18970                   18975

Pro Ile   Phe Lys Asn Ser Ser   Val Gly Pro Leu Tyr   Ser Gly Cys
    18980                   18985                   18990

Arg Leu   Thr Ser Leu Arg Pro   Glu Lys Asp Gly Ala   Ala Thr Gly
    18995                   19000                   19005

Met Asp   Ala Val Cys Leu Tyr   His Pro Asn Pro Lys   Arg Pro Gly
    19010                   19015                   19020

Leu Asp   Arg Glu Gln Leu Tyr   Cys Glu Leu Ser Gln   Leu Thr His
    19025                   19030                   19035

Asn Ile   Thr Glu Leu Gly Pro   Tyr Ser Leu Asp Arg   Asp Ser Leu
    19040                   19045                   19050

Tyr Val   Asn Gly Phe Thr His   Gln Asn Ser Val Pro   Thr Thr Ser
    19055                   19060                   19065
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Thr Pro   Gly Thr Ser Thr Val   Tyr Trp Ala Thr Thr   Gly Thr Pro
    19070                 19075                 19080

Ser Ser   Phe Pro Gly His Thr   Xaa Xaa Xaa Pro Leu   Leu Xaa Pro
    19085                 19090                 19095

Phe Thr   Leu Asn Phe Thr Ile   Thr Asn Leu Xaa Tyr   Glu Glu Xaa
    19100                 19105                 19110

Met Xaa   Xaa Pro Gly Ser Arg   Lys Phe Asn Thr Thr   Glu Arg Val
    19115                 19120                 19125

Leu Gln   Gly Leu Leu Xaa Pro   Xaa Phe Lys Xaa Thr   Ser Val Gly
    19130                 19135                 19140

Xaa Leu   Tyr Ser Gly Cys Arg   Leu Thr Leu Leu Arg   Xaa Glu Lys
    19145                 19150                 19155

Xaa Xaa   Ala Ala Thr Xaa Val   Asp Xaa Xaa Cys Xaa   Xaa Xaa Xaa
    19160                 19165                 19170

Asp Pro   Xaa Xaa Pro Gly Leu   Asp Arg Glu Xaa Leu   Tyr Trp Glu
    19175                 19180                 19185

Leu Ser   Xaa Leu Thr Xaa Xaa   Ile Xaa Glu Leu Gly   Pro Tyr Xaa
    19190                 19195                 19200

Leu Asp   Arg Xaa Ser Leu Tyr   Val Asn Gly Phe Thr   His Trp Ser
    19205                 19210                 19215

Ser Gly   Leu Thr Thr Ser Thr   Pro Trp Thr Ser Thr   Val Asp Leu
    19220                 19225                 19230

Gly Thr   Ser Gly Thr Pro Ser   Pro Val Pro Ser Pro   Thr Thr Ala
    19235                 19240                 19245

Gly Pro   Leu Leu Val Pro Phe   Thr Leu Asn Phe Thr   Ile Thr Asn
    19250                 19255                 19260

Leu Gln   Tyr Glu Glu Asp Met   His Arg Pro Gly Ser   Arg Lys Phe
    19265                 19270                 19275

Asn Ala   Thr Glu Arg Val Leu   Gln Gly Leu Leu Ser   Pro Ile Phe
    19280                 19285                 19290

Lys Asn   Thr Ser Val Gly Pro   Leu Tyr Ser Gly Cys   Arg Leu Thr
    19295                 19300                 19305

Leu Leu   Arg Pro Glu Lys Gln   Glu Ala Ala Thr Gly   Val Asp Thr
    19310                 19315                 19320

Ile Cys   Thr His Arg Val Asp   Pro Ile Gly Pro Gly   Leu Asp Arg
    19325                 19330                 19335

Glu Xaa   Leu Tyr Trp Glu Leu   Ser Xaa Leu Thr Xaa   Xaa Ile Xaa
    19340                 19345                 19350

Glu Leu   Gly Pro Tyr Xaa Leu   Asp Arg Xaa Ser Leu   Tyr Val Asn
    19355                 19360                 19365

Gly Phe   Xaa Xaa Xaa Xaa Xaa   Xaa Xaa Xaa Thr Ser   Thr Pro Gly
    19370                 19375                 19380

Thr Ser   Xaa Val Xaa Leu Xaa   Thr Ser Gly Thr Pro   Xaa Xaa Xaa
    19385                 19390                 19395

Pro Xaa   Xaa Thr Xaa Xaa Xaa   Pro Leu Leu Xaa Pro   Phe Thr Leu
    19400                 19405                 19410

Asn Phe   Thr Ile Thr Asn Leu   Xaa Tyr Glu Glu Xaa   Met Xaa Xaa
    19415                 19420                 19425

Pro Gly   Ser Arg Lys Phe Asn   Thr Thr Glu Arg Val   Leu Gln Gly
    19430                 19435                 19440
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Leu Leu   Xaa Pro Xaa Phe Lys   Xaa Thr Ser Val Gly   Xaa Leu Tyr
    19445                 19450                 19455

Ser Gly   Cys Arg Leu Thr Leu   Leu Arg Xaa Glu Lys   Xaa Xaa Ala
    19460                 19465                 19470

Ala Thr   Xaa Val Asp Xaa Xaa   Cys Xaa Xaa Xaa Xaa   Asp Pro Xaa
    19475                 19480                 19485

Xaa Pro   Gly Leu Asp Arg Glu   Xaa Leu Tyr Trp Glu   Leu Ser Xaa
    19490                 19495                 19500

Leu Thr   Xaa Xaa Ile Xaa Glu   Leu Gly Pro Tyr Xaa   Leu Asp Arg
    19505                 19510                 19515

Xaa Ser   Leu Tyr Val Asn Gly   Phe Thr His Arg Ser   Phe Gly Leu
    19520                 19525                 19530

Thr Thr   Ser Thr Pro Trp Thr   Ser Thr Val Asp Leu   Gly Thr Ser
    19535                 19540                 19545

Gly Thr   Pro Ser Pro Val Pro   Ser Pro Thr Thr Ala   Gly Pro Leu
    19550                 19555                 19560

Leu Val   Pro Phe Thr Leu Asn   Phe Thr Ile Thr Asn   Leu Gln Tyr
    19565                 19570                 19575

Glu Glu   Asp Met His Arg Pro   Gly Ser Arg Lys Phe   Asn Thr Thr
    19580                 19585                 19590

Glu Arg   Val Leu Gln Gly Leu   Leu Thr Pro Leu Phe   Arg Asn Thr
    19595                 19600                 19605

Ser Val   Ser Ser Leu Tyr Ser   Gly Cys Arg Leu Thr   Leu Leu Arg
    19610                 19615                 19620

Pro Glu   Lys Asp Gly Ala Ala   Thr Arg Val Asp Ala   Val Cys Thr
    19625                 19630                 19635

His Arg   Pro Asp Pro Lys Ser   Pro Gly Leu Asp Arg   Glu Xaa Leu
    19640                 19645                 19650

Tyr Trp   Glu Leu Ser Xaa Leu   Thr Xaa Xaa Ile Xaa   Glu Leu Gly
    19655                 19660                 19665

Pro Tyr   Xaa Leu Asp Arg Xaa   Ser Leu Tyr Val Asn   Gly Phe Xaa
    19670                 19675                 19680

Xaa Xaa   Xaa Xaa Xaa Xaa Xaa   Thr Ser Thr Pro Gly   Thr Ser Xaa
    19685                 19690                 19695

Val Xaa   Leu Xaa Thr Ser Gly   Thr Pro Xaa Xaa Xaa   Pro Xaa Xaa
    19700                 19705                 19710

Thr Xaa   Xaa Xaa Pro Leu Leu   Xaa Pro Phe Thr Leu   Asn Phe Thr
    19715                 19720                 19725

Ile Thr   Asn Leu Xaa Tyr Glu   Glu Xaa Met Xaa Xaa   Pro Gly Ser
    19730                 19735                 19740

Arg Lys   Phe Asn Thr Thr Glu   Arg Val Leu Gln Gly   Leu Leu Xaa
    19745                 19750                 19755

Pro Xaa   Phe Lys Xaa Thr Ser   Val Gly Xaa Leu Tyr   Ser Gly Cys
    19760                 19765                 19770

Arg Leu   Thr Leu Leu Arg Xaa   Glu Lys Xaa Xaa Ala   Ala Thr Xaa
    19775                 19780                 19785

Val Asp   Xaa Xaa Cys Xaa Xaa   Xaa Xaa Asp Pro Xaa   Xaa Pro Gly
    19790                 19795                 19800

Leu Asp   Arg Glu Xaa Leu Tyr   Trp Glu Leu Ser Xaa   Leu Thr Xaa
    19805                 19810                 19815

Xaa Ile   Xaa Glu Leu Gly Pro   Tyr Xaa Leu Asp Arg   Xaa Ser Leu
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    19820                19825                19830

Tyr Val   Asn Gly Phe Thr His   Trp Ile Pro Val Pro   Thr Ser Ser
    19835                19840                19845

Thr Pro   Gly Thr Ser Thr Val   Asp Leu Gly Ser Gly   Thr Pro Ser
    19850                19855                19860

Ser Leu   Pro Ser Pro Thr Thr   Ala Gly Pro Leu Leu   Val Pro Phe
    19865                19870                19875

Thr Leu   Asn Phe Thr Ile Thr   Asn Leu Gln Tyr Gly   Glu Asp Met
    19880                19885                19890

Gly His   Pro Gly Ser Arg Lys   Phe Asn Thr Thr Glu   Arg Val Leu
    19895                19900                19905

Gln Gly   Leu Leu Gly Pro Ile   Phe Lys Asn Thr Ser   Val Gly Pro
    19910                19915                19920

Leu Tyr   Ser Gly Cys Arg Leu   Thr Ser Leu Arg Ser   Glu Lys Asp
    19925                19930                19935

Gly Ala   Ala Thr Gly Val Asp   Ala Ile Cys Ile His   His Leu Asp
    19940                19945                19950

Pro Lys   Ser Pro Gly Leu Asp   Arg Glu Xaa Leu Tyr   Trp Glu Leu
    19955                19960                19965

Ser Xaa   Leu Thr Xaa Xaa Ile   Xaa Glu Leu Gly Pro   Tyr Xaa Leu
    19970                19975                19980

Asp Arg   Xaa Ser Leu Tyr Val   Asn Gly Phe Xaa Xaa   Xaa Xaa Xaa
    19985                19990                19995

Xaa Xaa   Xaa Thr Ser Thr Pro   Gly Thr Ser Xaa Val   Xaa Leu Xaa
    20000                20005                20010

Thr Ser   Gly Thr Pro Xaa Xaa   Xaa Pro Xaa Xaa Thr   Xaa Xaa Xaa
    20015                20020                20025

Pro Leu   Leu Xaa Pro Phe Thr   Leu Asn Phe Thr Ile   Thr Asn Leu
    20030                20035                20040

Xaa Tyr   Glu Glu Xaa Met Xaa   Xaa Pro Gly Ser Arg   Lys Phe Asn
    20045                20050                20055

Thr Thr   Glu Arg Val Leu Gln   Gly Leu Leu Xaa Pro   Xaa Phe Lys
    20060                20065                20070

Xaa Thr   Ser Val Gly Xaa Leu   Tyr Ser Gly Cys Arg   Leu Thr Leu
    20075                20080                20085

Leu Arg   Xaa Glu Lys Xaa Xaa   Ala Ala Thr Xaa Val   Asp Xaa Xaa
    20090                20095                20100

Cys Xaa   Xaa Xaa Xaa Asp Pro   Xaa Xaa Pro Gly Leu   Asp Arg Glu
    20105                20110                20115

Xaa Leu   Tyr Trp Glu Leu Ser   Xaa Leu Thr Xaa Xaa   Ile Xaa Glu
    20120                20125                20130

Leu Gly   Pro Tyr Xaa Leu Asp   Arg Xaa Ser Leu Tyr   Val Asn Gly
    20135                20140                20145

Phe Thr   His Gln Thr Phe Ala   Pro Asn Thr Ser Thr   Pro Gly Thr
    20150                20155                20160

Ser Thr   Val Asp Leu Gly Thr   Ser Gly Thr Pro Ser   Ser Leu Pro
    20165                20170                20175

Ser Pro   Thr Ser Ala Gly Pro   Leu Leu Val Pro Phe   Thr Leu Asn
    20180                20185                20190

Phe Thr   Ile Thr Asn Leu Gln   Tyr Glu Glu Asp Met   His His Pro
    20195                20200                20205
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Gly Ser   Arg Lys Phe Asn Thr   Thr Glu Arg Val Leu   Gln Gly Leu
    20210                 20215                 20220

Leu Gly   Pro Met Phe Lys Asn   Thr Ser Val Gly Leu   Leu Tyr Ser
    20225                 20230                 20235

Gly Cys   Arg Leu Thr Leu Leu   Arg Pro Glu Lys Asn   Gly Ala Ala
    20240                 20245                 20250

Thr Arg   Val Asp Ala Val Cys   Thr His Arg Pro Asp   Pro Lys Ser
    20255                 20260                 20265

Pro Gly   Leu Asp Arg Glu Xaa   Leu Tyr Trp Glu Leu   Ser Xaa Leu
    20270                 20275                 20280

Thr Xaa   Xaa Ile Xaa Glu Leu   Gly Pro Tyr Xaa Leu   Asp Arg Xaa
    20285                 20290                 20295

Ser Leu   Tyr Val Asn Gly Phe   Xaa Xaa Xaa Xaa Xaa   Xaa Xaa Xaa
    20300                 20305                 20310

Thr Ser   Thr Pro Gly Thr Ser   Xaa Val Xaa Leu Xaa   Thr Ser Gly
    20315                 20320                 20325

Thr Pro   Xaa Xaa Xaa Pro Xaa   Xaa Thr Ala Pro Val   Pro Leu Leu
    20330                 20335                 20340

Ile Pro   Phe Thr Leu Asn Phe   Thr Ile Thr Asn Leu   His Tyr Glu
    20345                 20350                 20355

Glu Asn   Met Gln His Pro Gly   Ser Arg Lys Phe Asn   Thr Thr Glu
    20360                 20365                 20370

Arg Val   Leu Gln Gly Leu Leu   Arg Pro Leu Phe Lys   Ser Thr Ser
    20375                 20380                 20385

Val Gly   Pro Leu Tyr Ser Gly   Cys Arg Leu Thr Leu   Leu Arg Pro
    20390                 20395                 20400

Glu Lys   His Gly Ala Ala Thr   Gly Val Asp Ala Ile   Cys Thr Leu
    20405                 20410                 20415

Arg Leu   Asp Pro Thr Gly Pro   Gly Leu Asp Arg Glu   Arg Leu Tyr
    20420                 20425                 20430

Trp Glu   Leu Ser Gln Leu Thr   Asn Ser Val Thr Glu   Leu Gly Pro
    20435                 20440                 20445

Tyr Thr   Leu Asp Arg Asp Ser   Leu Tyr Val Asn Gly   Phe Thr Gln
    20450                 20455                 20460

Arg Ser   Ser Val Pro Thr Thr   Ser Ile Pro Gly Thr   Ser Ala Val
    20465                 20470                 20475

His Leu   Glu Thr Ser Gly Thr   Pro Ala Ser Leu Pro   Gly His Thr
    20480                 20485                 20490

Ala Pro   Gly Pro Leu Leu Val   Pro Phe Thr Leu Asn   Phe Thr Ile
    20495                 20500                 20505

Thr Asn   Leu Gln Tyr Glu Val   Asp Met Arg His Pro   Gly Ser Arg
    20510                 20515                 20520

Lys Phe   Asn Thr Thr Glu Arg   Val Leu Gln Gly Leu   Leu Lys Pro
    20525                 20530                 20535

Leu Phe   Lys Ser Thr Ser Val   Gly Pro Leu Tyr Ser   Gly Cys Arg
    20540                 20545                 20550

Leu Thr   Leu Leu Arg Pro Glu   Lys Arg Gly Ala Ala   Thr Gly Val
    20555                 20560                 20565

Asp Thr   Ile Cys Thr His Arg   Leu Asp Pro Leu Asn   Pro Gly Leu
    20570                 20575                 20580
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Asp Arg   Glu Gln Leu Tyr Trp   Glu Leu Ser Lys Leu   Thr Arg Gly
    20585                 20590                 20595

Ile Ile   Glu Leu Gly Pro Tyr   Leu Leu Asp Arg Gly   Ser Leu Tyr
    20600                 20605                 20610

Val Asn   Gly Phe Thr His Arg   Asn Phe Val Pro Ile   Thr Ser Thr
    20615                 20620                 20625

Pro Gly   Thr Ser Thr Val His   Leu Gly Thr Ser Glu   Thr Pro Ser
    20630                 20635                 20640

Ser Leu   Pro Arg Pro Ile Val   Pro Gly Pro Leu Leu   Val Pro Phe
    20645                 20650                 20655

Thr Leu   Asn Phe Thr Ile Thr   Asn Leu Gln Tyr Glu   Glu Ala Met
    20660                 20665                 20670

Arg His   Pro Gly Ser Arg Lys   Phe Asn Thr Thr Glu   Arg Val Leu
    20675                 20680                 20685

Gln Gly   Leu Leu Arg Pro Leu   Phe Lys Asn Thr Ser   Ile Gly Pro
    20690                 20695                 20700

Leu Tyr   Ser Ser Cys Arg Leu   Thr Leu Leu Arg Pro   Glu Lys Asp
    20705                 20710                 20715

Lys Ala   Ala Thr Arg Val Asp   Ala Ile Cys Thr His   His Pro Asp
    20720                 20725                 20730

Pro Gln   Ser Pro Gly Leu Asn   Arg Glu Gln Leu Tyr   Trp Glu Leu
    20735                 20740                 20745

Ser Gln   Leu Thr His Gly Ile   Thr Glu Leu Gly Pro   Tyr Thr Leu
    20750                 20755                 20760

Asp Arg   Asp Ser Leu Tyr Val   Asp Gly Phe Thr His   Trp Ser Pro
    20765                 20770                 20775

Ile Pro   Thr Thr Ser Thr Pro   Gly Thr Ser Ile Val   Asn Leu Gly
    20780                 20785                 20790

Thr Ser   Gly Ile Pro Pro Ser   Leu Pro Glu Thr Thr   Xaa Xaa Xaa
    20795                 20800                 20805

Pro Leu   Leu Xaa Pro Phe Thr   Leu Asn Phe Thr Ile   Thr Asn Leu
    20810                 20815                 20820

Xaa Tyr   Glu Glu Xaa Met Xaa   Xaa Pro Gly Ser Arg   Lys Phe Asn
    20825                 20830                 20835

Thr Thr   Glu Arg Val Leu Gln   Gly Leu Leu Lys Pro   Leu Phe Lys
    20840                 20845                 20850

Ser Thr   Ser Val Gly Pro Leu   Tyr Ser Gly Cys Arg   Leu Thr Leu
    20855                 20860                 20865

Leu Arg   Pro Glu Lys Asp Gly   Val Ala Thr Arg Val   Asp Ala Ile
    20870                 20875                 20880

Cys Thr   His Arg Pro Asp Pro   Lys Ile Pro Gly Leu   Asp Arg Gln
    20885                 20890                 20895

Gln Leu   Tyr Trp Glu Leu Ser   Gln Leu Thr His Ser   Ile Thr Glu
    20900                 20905                 20910

Leu Gly   Pro Tyr Thr Leu Asp   Arg Asp Ser Leu Tyr   Val Asn Gly
    20915                 20920                 20925

Phe Thr   Gln Arg Ser Ser Val   Pro Thr Thr Ser Thr   Pro Gly Thr
    20930                 20935                 20940

Phe Thr   Val Gln Pro Glu Thr   Ser Glu Thr Pro Ser   Ser Leu Pro
    20945                 20950                 20955

Gly Pro   Thr Ala Thr Gly Pro   Val Leu Leu Pro Phe   Thr Leu Asn
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    20960                20965                20970

Phe Thr   Ile Thr Asn Leu Gln   Tyr Glu Glu Asp Met   His Arg Pro
    20975                20980                20985

Gly Ser   Arg Lys Phe Asn Thr   Thr Glu Arg Val Leu   Gln Gly Leu
    20990                20995                21000

Leu Met   Pro Leu Phe Lys Asn   Thr Ser Val Ser Ser   Leu Tyr Ser
    21005                21010                21015

Gly Cys   Arg Leu Thr Leu Leu   Arg Pro Glu Lys Asp   Gly Ala Ala
    21020                21025                21030

Thr Arg   Val Asp Ala Val Cys   Thr His Arg Pro Asp   Pro Lys Ser
    21035                21040                21045

Pro Gly   Leu Asp Arg Glu Arg   Leu Tyr Trp Lys Leu   Ser Gln Leu
    21050                21055                21060

Thr His   Gly Ile Thr Glu Leu   Gly Pro Tyr Thr Leu   Asp Arg His
    21065                21070                21075

Ser Leu   Tyr Val Asn Gly Phe   Thr His Gln Ser Ser   Met Thr Thr
    21080                21085                21090

Thr Arg   Thr Pro Asp Thr Ser   Thr Met His Leu Ala   Thr Ser Arg
    21095                21100                21105

Thr Pro   Ala Ser Leu Ser Gly   Pro Thr Thr Ala Ser   Pro Leu Leu
    21110                21115                21120

Val Leu   Phe Thr Ile Asn Phe   Thr Ile Thr Asn Leu   Arg Tyr Glu
    21125                21130                21135

Glu Asn   Met His His Pro Gly   Ser Arg Lys Phe Asn   Thr Thr Glu
    21140                21145                21150

Arg Val   Leu Gln Gly Leu Leu   Arg Pro Val Phe Lys   Asn Thr Ser
    21155                21160                21165

Val Gly   Pro Leu Tyr Ser Gly   Cys Arg Leu Thr Leu   Leu Arg Pro
    21170                21175                21180

Lys Lys   Asp Gly Ala Ala Thr   Lys Val Asp Ala Ile   Cys Thr Tyr
    21185                21190                21195

Arg Pro   Asp Pro Lys Ser Pro   Gly Leu Asp Arg Glu   Gln Leu Tyr
    21200                21205                21210

Trp Glu   Leu Ser Gln Leu Thr   His Ser Ile Thr Glu   Leu Gly Pro
    21215                21220                21225

Tyr Thr   Gln Asp Arg Asp Ser   Leu Tyr Asn Val Gly   Phe Thr Gln
    21230                21235                21240

Arg Ser   Ser Val Pro Thr Thr   Ser Val Pro Gly Thr   Pro Thr Val
    21245                21250                21255

Asp Leu   Gly Thr Ser Gly Thr   Pro Val Ser Lys Pro   Gly Pro Ser
    21260                21265                21270

Ala Ala   Ser Pro Leu Leu Val   Leu Phe Thr Leu Asn   Gly Thr Ile
    21275                21280                21285

Thr Asn   Leu Arg Tyr Glu Glu   Asn Met Gln His Pro   Gly Ser Arg
    21290                21295                21300

Lys Phe   Asn Thr Thr Glu Arg   Val Leu Gln Gly Leu   Leu Arg Ser
    21305                21310                21315

Leu Phe   Lys Ser Thr Ser Val   Gly Pro Leu Tyr Ser   Gly Cys Arg
    21320                21325                21330

Leu Thr   Leu Leu Arg Pro Glu   Lys Asp Gly Thr Ala   Thr Gly Val
    21335                21340                21345
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Asp Ala   Ile Cys Thr His His   Pro Asp Pro Lys Ser   Pro Arg Leu
    21350                 21355                 21360

Asp Arg   Glu Gln Leu Tyr Trp   Glu Leu Ser Gln Leu   Thr His Asn
    21365                 21370                 21375

Ile Thr   Glu Leu Gly His Tyr   Ala Leu Asp Asn Asp   Ser Leu Phe
    21380                 21385                 21390

Val Asn   Gly Phe Thr His Arg   Ser Ser Val Ser Thr   Thr Ser Thr
    21395                 21400                 21405

Pro Gly   Thr Pro Thr Val Tyr   Leu Gly Ala Ser Lys   Thr Pro Ala
    21410                 21415                 21420

Ser Ile   Phe Gly Pro Ser Ala   Ala Ser His Leu Leu   Ile Leu Phe
    21425                 21430                 21435

Thr Leu   Asn Phe Thr Ile Thr   Asn Leu Arg Tyr Glu   Glu Asn Met
    21440                 21445                 21450

Trp Pro   Gly Ser Arg Lys Phe   Asn Thr Thr Glu Arg   Val Leu Gln
    21455                 21460                 21465

Gly Leu   Leu Arg Pro Leu Phe   Lys Asn Thr Ser Val   Gly Pro Leu
    21470                 21475                 21480

Tyr Ser   Gly Ser Arg Leu Thr   Leu Leu Arg Pro Glu   Lys Asp Gly
    21485                 21490                 21495

Glu Ala   Thr Gly Val Asp Ala   Ile Cys Thr His Arg   Pro Asp Pro
    21500                 21505                 21510

Thr Gly   Pro Gly Leu Asp Arg   Glu Gln Leu Tyr Leu   Glu Leu Ser
    21515                 21520                 21525

Gln Leu   Thr His Ser Ile Thr   Glu Leu Gly Pro Tyr   Thr Leu Asp
    21530                 21535                 21540

Arg Asp   Ser Leu Tyr Val Asn   Gly Phe Thr His Arg   Ser Ser Val
    21545                 21550                 21555

Pro Thr   Thr Ser Thr Gly Val   Val Ser Glu Glu Pro   Phe Thr Leu
    21560                 21565                 21570

Asn Phe   Thr Ile Asn Asn Leu   Arg Tyr Met Ala Asp   Met Gly Gln
    21575                 21580                 21585

Pro Gly   Ser Leu Lys Phe Asn   Ile Thr Asp Asn Val   Met Lys His
    21590                 21595                 21600

Leu Leu   Ser Pro Leu Phe Gln   Arg Ser Ser Leu Gly   Ala Arg Tyr
    21605                 21610                 21615

Thr Gly   Cys Arg Val Ile Ala   Leu Arg Ser Val Lys   Asn Gly Ala
    21620                 21625                 21630

Glu Thr   Arg Val Asp Leu Leu   Cys Thr Tyr Leu Gln   Pro Leu Ser
    21635                 21640                 21645

Gly Pro   Gly Leu Pro Ile Lys   Gln Val Phe His Glu   Leu Ser Gln
    21650                 21655                 21660

Gln Thr   His Gly Ile Thr Arg   Leu Gly Pro Tyr Ser   Leu Asp Lys
    21665                 21670                 21675

Asp Ser   Leu Tyr Leu Asn Gly   Tyr Asn Glu Pro Gly   Leu Asp Glu
    21680                 21685                 21690

Pro Pro   Thr Thr Pro Lys Pro   Ala Thr Thr Phe Leu   Pro Pro Leu
    21695                 21700                 21705

Ser Glu   Ala Thr Thr Ala Met   Gly Tyr His Leu Lys   Thr Leu Thr
    21710                 21715                 21720
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Leu Asn   Phe Thr Ile Ser Asn   Leu Gln Tyr Ser Pro   Asp Met Gly
    21725                 21730                 21735

Lys Gly   Ser Ala Thr Phe Asn   Ser Thr Glu Gly Val   Leu Gln His
    21740                 21745                 21750

Leu Leu   Arg Pro Leu Phe Gln   Lys Ser Ser Met Gly   Pro Phe Tyr
    21755                 21760                 21765

Leu Gly   Cys Gln Leu Ile Ser   Leu Arg Pro Glu Lys   Asp Gly Ala
    21770                 21775                 21780

Ala Thr   Gly Val Asp Thr Thr   Cys Thr Tyr His Pro   Asp Pro Val
    21785                 21790                 21795

Gly Pro   Gly Leu Asp Ile Gln   Gln Leu Tyr Trp Glu   Leu Ser Gln
    21800                 21805                 21810

Leu Thr   His Gly Val Thr Gln   Leu Gly Phe Tyr Val   Leu Asp Arg
    21815                 21820                 21825

Asp Ser   Leu Phe Ile Asn Gly   Tyr Ala Pro Gln Asn   Leu Ser Ile
    21830                 21835                 21840

Arg Gly   Glu Tyr Gln Ile Asn   Phe His Ile Val Asn   Trp Asn Leu
    21845                 21850                 21855

Ser Asn   Pro Asp Pro Thr Ser   Ser Glu Tyr Ile Thr   Leu Leu Arg
    21860                 21865                 21870

Asp Ile   Gln Asp Lys Val Thr   Thr Leu Tyr Lys Gly   Ser Gln Leu
    21875                 21880                 21885

His Asp   Thr Phe Arg Phe Cys   Leu Val Thr Asn Leu   Thr Met Asp
    21890                 21895                 21900

Ser Val   Leu Val Thr Val Lys   Ala Leu Phe Ser Ser   Asn Leu Asp
    21905                 21910                 21915

Pro Ser   Leu Val Glu Gln Val   Phe Leu Asp Lys Thr   Leu Asn Ala
    21920                 21925                 21930

Ser Phe   His Trp Leu Gly Ser   Thr Tyr Gln Leu Val   Asp Ile His
    21935                 21940                 21945

Val Thr   Glu Met Glu Ser Ser   Val Tyr Gln Pro Thr   Ser Ser Ser
    21950                 21955                 21960

Ser Thr   Gln His Phe Tyr Leu   Asn Phe Thr Ile Thr   Asn Leu Pro
    21965                 21970                 21975

Tyr Ser   Gln Asp Lys Ala Gln   Pro Gly Thr Thr Asn   Tyr Gln Arg
    21980                 21985                 21990

Asn Lys   Arg Asn Ile Glu Asp   Ala Leu Asn Gln Leu   Phe Arg Asn
    21995                 22000                 22005

Ser Ser   Ile Lys Ser Tyr Phe   Ser Asp Cys Gln Val   Ser Thr Phe
    22010                 22015                 22020

Arg Ser   Val Pro Asn Arg His   His Thr Gly Val Asp   Ser Leu Cys
    22025                 22030                 22035

Asn Phe   Ser Pro Leu Ala Arg   Arg Val Asp Arg Val   Ala Ile Tyr
    22040                 22045                 22050

Glu Glu   Phe Leu Arg Met Thr   Arg Asn Gly Thr Gln   Leu Gln Asn
    22055                 22060                 22065

Phe Thr   Leu Asp Arg Ser Ser   Val Leu Val Asp Gly   Tyr Ser Pro
    22070                 22075                 22080

Asn Arg   Asn Glu Pro Leu Thr   Gly Asn Ser Asp Leu   Pro Phe Trp
    22085                 22090                 22095

Ala Val   Ile Leu Ile Gly Leu   Ala Gly Leu Leu Gly   Leu Ile Thr
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    22100                 22105                 22110

Cys Leu   Ile Cys Gly Val Leu   Val Thr Thr Arg Arg   Arg Lys Lys
    22115                 22120                 22125

Glu Gly   Glu Tyr Asn Val Gln   Gln Gln Cys Pro Gly   Tyr Tyr Gln
    22130                 22135                 22140

Ser His   Leu Asp Leu Glu Asp   Leu Gln
    22145                 22150


<210> SEQ ID NO 6
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<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
<223> OTHER INFORMATION: PCR primer

<400> SEQUENCE: 6

accggatcca tgggccacac agagcctggc cc                                  32


<210> SEQ ID NO 7
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<220> FEATURE:
<223> OTHER INFORMATION: PCR primer

<400> SEQUENCE: 7

tgtaagctta ggcagggagg atggagtcc                                      29
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1. (canceled)

2. The isolated nucleic acid molecule of claim **23** comprising the sequence of SEQ ID NO: 4.

3-20. (canceled)

21. The isolated nucleic acid molecule of claim **24** wherein the isolated nucleic acid molecule comprises SEQ ID NO:1 or a fragment thereof.

22. The isolated nucleic acid molecule of claim **24** wherein the isolated nucleic acid molecule encodes and is adapted to express in a cell residues 1-10,427 of SEQ ID NO:5 or a fragment of residues 1-10,427 of SEQ ID NO:5.

23. An isolated nucleic acid molecule encoding residues 10,432 to 22,152 of SEQ ID NO:5 or a fragment of residues 10,432 to 22,152 of SEQ ID NO:5;

wherein the isolated nucleic acid molecule is an expression vector and is adapted to express in a cell residues 10,432 to 22,152 of SEQ ID NO:5 or a fragment of residues 10,432 to 22,152 of SEQ ID NO:5;

wherein the fragment of residues 10,432 to 22,152 of SEQ ID NO:5 is an antigenic fragment that can be used to make monoclonal antibodies that specifically recognize CA125.

24. An isolated nucleic acid molecule encoding CA125 (SEQ ID NO:5) or a fragment thereof;

wherein the isolated nucleic acid molecule is an expression vector and is adapted to express in a cell CA125 (SEQ ID NO:5) or a fragment thereof;

wherein the fragment thereof is an antigenic fragment that can be used to make monoclonal antibodies that specifically recognize CA125 (SEQ ID NO:5);

wherein the isolated nucleic acid molecule encodes residues 1 to 10,431 of SEQ ID NO:5 or a fragment of residues 1 to 10,431 of SEQ ID NO:5.

25. The isolated nucleic acid molecule of claim **24** comprising the sequence of SEQ ID NO: 4.

26. The isolated nucleic acid molecule of claim **24** wherein the isolated nucleic acid molecule encodes and is adapted to express residues 1-10,431 of SEQ ID NO:5 or an antigenic fragment of residues 1 to 10,431 of SEQ ID NO:5.

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