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(54) Title: NOVEL SERPIN DERIVED FROM HUMAN HYPOTHALAMUS

(57) Abstract

The present invention provides nucleotide and amino acid sequences that identify and encode a novel serpin (CAPE) expressed in human hypothalamus. The present invention also provides for antisense molecules to the nucleotide sequences which encode CAPE, expression vectors for the production of purified CAPE, antibodies capable for binding specifically to CAPE, hybridization probes or oligonucleotides for the detection of CAPE-encoding nucleotide sequences, genetically engineered host cells for the expression of CAPE, a pharmaceutical composition containing biologically active CAPE, a diagnostic test based on CAPE-encoding nucleic acid molecules, and treatment methods comprising administration of biologically active CAPE.
NOVEL SERPIN DERIVED FROM HUMAN HYPOTHALAMUS

TECHNICAL FIELD

The present invention is in the field of molecular biology; more particularly, the present invention describes the nucleic acid and amino acid sequences of a novel serpin expressed in the hypothalamus.

BACKGROUND ART

Inhibitory Serpins

Serpins are irreversible serine protease inhibitors which are principally located extracellularly. As a group, they are defined on the basis of their structural and functional characteristics of a high molecular weight (between 370-420 amino acid residues), and a C-terminal reactive region. Proteins which have been assigned to the serpin family include $\alpha$-1 protease inhibitor, $\alpha$-1-antichymotrypsin, antithrombin III, $\alpha$-2-antiplasmin, heparin cofactor II, complement C1 inhibitor, plasminogen activator inhibitors 1 and 2, glia derived nexin, protein C inhibitor, rat hepatocyte inhibitors, crmA (a viral serpin which inhibits interleukin 1-ß cleavage enzyme), human squamous cell carcinoma antigen which may modulate the host immune response against tumor cells, human maspin which seems to function as a tumor suppressor, lepidopteran protease inhibitor, leukocyte elastase inhibitor (the only known intracellular serpin), and products from three orthopoxviruses (these products may be involved in the regulation of the blood clotting cascade and/or of the complement cascade in the mammalian host).

Serpins form tight complexes with their target proteases. The serpin region which binds to the target protease is a mobile, exposed reactive site loop (RSL) which contains the P1-P1' bond that is cleaved. When the characteristic serpin P1-P1' bond cleaves, the serpin structure changes profoundly, and stability to heat- or guanidine-induced denaturation increases markedly. These changes are referred to as the stressed-to-relaxed (S->R) transition, and are associated with tight complex formation with specific proteases. For the $\alpha$-1-proteinase inhibitor, cleavage of the P1-P1' bond results in a separation of about 69Å between the two residues (Loebermann H et al (1984) J Mol Biol 177:531-556). The ability of a serpin to function as an inhibitor may be directly related to its ability to undergo this S->R transition (Bruch M et al (1988) J Biol Chem 263:16626-30; Carrell RW et al (1992) Curr Opin Struct Biol 2:438-446).

In addition, the RSL sequence from P17 to P8 (hinge region) is highly conserved, and small amino acid with side chains are found at positions P9, P10, P11, P12, and P15 in active
inhibitors. The presence of small amino acids in this region allows the peptide loop from P14-P2 to be inserted into the middle of the protease inhibitor A-sheet. The insertion of this sequence into the A-sheet appears to be important in stabilizing the inhibitor, and consequently tightening the protease/serpin complex. Sequence divergence in the hinge region may convert an inhibitor to a substrate.

**NonInhibitory Serpins**

A number of proteins with no known inhibitory activity are also categorized as serpins on the basis of strong sequence and structural similarities. These proteins can be cleaved by specific proteases, but do not form the tight complexes that inhibit protease activity. Examples are bird ovalbumin, angiotensinogen, barley protein Z, corticosteroid binding globulin, thyroxine binding globulin, sheep uterine milk protein, pig uteroferrin-associated protein, an endoplasmic reticulum heat-shock protein (which binds strongly to collagen and could act as a chaperone), pigment epithelium-derived factor, and an estrogen-regulated protein from Xenopus.

The nature of the difference between inhibitory and noninhibitory serpins is not well understood. For example, ovalbumin is unable to undergo this S->R transition (Mottonen et al (1992) Nature 355: 270-273). However, hormone binding globulins, such as thyroxine or cortisol binding globulins, apparently do undergo the transition from the native stressed to relaxed conformation upon protease cleavage but do not form a tight complex with specific proteases (Pemberton et al (1988) Nature 336: 257-258). The S->R transition may confer an advantage for hormone binding molecules, and for small molecule binding proteins in general, in that the transition from a stressed to a relaxed conformation may provide a method for modulating hormone delivery. Both hormone binding globulins have a greater than 30% homology with the archetype of the serpin family, alpha-1-antitrypsin, and sequence matching infers that they all share a common secondary and tertiary structure.


**DISCLOSURE OF THE INVENTION**

The subject invention provides a unique nucleotide sequence (cape) which encodes a
novel serpin (CAPE). The nucleotide sequence, which was identified from Incyte Clone 84476 derived from hypothalamic cells, contains two ATG codons. The two ATGs predict the expression of the two different proteins: CAPE1 and CAPE2. However, only CAPE1 includes a signal sequence. The subject invention includes the antisense DNA of cape; cloning or expression vectors containing cape; host cells or organisms transformed with expression vectors containing cape; a method for the production and recovery of purified CAPE polypeptide from host cells; purified CAPE polypeptide; antibodies to both polypeptides; and pharmacological compounds using CAPE for the treatment of disease.

Furthermore, the subject invention also comprises diagnostic tests for pathologically compromised brain tissues including but not limited to the hypothalamus which include the steps of testing a sample or an extract thereof with cape DNA, fragments or oligomers thereof.

DESCRIPTION OF THE FIGURES

Figures 1A, 1B and 1C show the nucleotide sequence (SEQ ID NO:1) for cape including the entire coding sequence and the predicted amino acid sequences for CAPE1 and CAPE2 polypeptides (SEQ ID NO:2). The start codon for CAPE1 is at nucleotide 79; whereas the start codon for CAPE2 is at nucleotide 121.

Figures 2A, 2B, 2C, and 2D display the alignment of the CAPE molecules with plasminogen activator inhibitor 2 (PAI-2) (SEQ ID NO:3). Figures 2A-2B display the alignment of CAPE1 with PAI-2 and Figures 2C-2D display the alignment of CAPE2 with PAI-2. The majority sequences are consensus sequences (SEQ ID NO:4 and SEQ ID NO:5). Alignments shown were produced using the multisequence alignment program of DNASTAR software (DNASTAR Inc, Madison WI).

Figure 3 provides structural analysis of the cape sequence for determining putative alpha (A), beta (B), turn (T), and coil (C) regions; a hydrophilicity plot (H); alpha and beta amphipathic regions (*); flexible regions (F); a putative antigenic index (AI); and a surface probability plot (S) using the structural analysis program of DNASTAR software (DNASTAR Inc, Madison WI).

BRIEF DESCRIPTION OF DRAWINGS

Definitions

As used herein, CAPE1 and CAPE2 refer to novel serpins, which may be naturally
occurring or synthetically derived, or active fragments thereof, which are encoded by mRNAs transcribed from the cDNA (cape) of SEQ ID NO: 1. The amino acid sequence of CAPE 1 is shown in SEQ ID NO 2 starting at residue 1 and terminating at residue 407, and that of CAPE2 is shown in SEQ ID NO 2 starting at residue 15 and terminating at residue 407. As used herein, the term “CAPE” refers generally to both CAPE1 and CAPE2.

“Active” refers to those forms of CAPE which retain biologic and/or immunologic activities of any naturally occurring CAPE.

“Naturally occurring CAPE” refers to CAPE produced by human cells that have not been genetically engineered and specifically contemplates various forms arising from post-translational modifications of the polypeptide, including but not limited to acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

“Derivative” refers to polypeptides derived from naturally occurring CAPE by chemical modifications such as ubiquitination, labeling (e.g., with radionuclides, various enzymes, chromogenic or fluorogenic means), pegylation (derivatization with polyethylene glycol), or by insertion (or substitution by chemical synthesis) of amino acids such as ornithine, which do not normally occur in human proteins.

As used herein the term “variant” or “recombinant variant” or “mutant” refers to any polypeptide differing from naturally occurring CAPE by amino acid (aa) insertions, deletions, and substitutions, created using recombinant DNA techniques. Guidance in determining which aa residues may be replaced, added or deleted without abolishing activities of interest, such as protein proteolysis, protease inhibition, or small molecule binding properties, may be found by comparing the sequence of the particular CAPE with that of homologous inhibitory and noninhibitory serpins and minimizing the number of amino acid sequence changes made in regions of high homology.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with an isoleucine or valine, an aspartate with a glutamate, or a threonine with a serine, i.e., conservative amino acid replacements. "Insertions" or "deletions" are typically in the range of about 1 to 5 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of an amino acid in a CAPE molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.
Where desired, nucleic acid encoding a CAPE molecule can be genetically engineered to contain a "signal or a leader sequence" that can direct the polypeptide to a specific location in a cell or to a specific destination outside of the cell. Such a sequence may be naturally present on the polypeptide of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues which has sufficient length to display biologic and/or immunogenic activity on their own or when conjugated to a carrier protein such as keyhole limpet hemocyanin (KLH, Sigma). In a preferred embodiment a fragment portion or segment will contain at least about 5 amino acids, often at least about 7 amino acids, typically at least about 8 to 13 amino acids, and, in various embodiments, at least about 17 or more amino acids. To be active, any CAPE polypeptide must have sufficient length to display biologic and/or immunologic activity.

"Small molecules" are molecules with a molecular weight under 5000, more preferably under 2000. The small molecules of particular interest may be derived from the hypothalamus, such as oxytocin, vasopressin, dopamine, neuropeptide Y, somatostatin, or enkephalins. These small molecules may directly affect the hypothalamus or other target neuronal tissues, such as the pituitary gland. Alternatively, the small molecules may be derived from other tissues and affect the hypothalamus. These small molecules may include, but are not limited to, molecules such as serotonin, epinephrine, norepinephrine, gamma amino butyric acid, glutamate, or other neurotransmitters or hormones. These small molecules may be naturally occurring or synthetically made.

"Conditions associated with altered expression of CAPE" refer to physiological or pathological changes of the hypothalamus or other tissues. Pathological changes include inflammation, disease and tumors.

"Hypothalamic tissue" refers to tissue derived mostly from the hypothalamus, but which may include other tissue from organs that surround or are adjacent to the hypothalamus.

"Animal" as used herein may be defined to include human, domestic, or agricultural (cats, dogs, cows, sheep, etc.) or test species (mouse, rat, rabbit, etc.).

As used herein, an "oligonucleotide" or polynucleotide "fragment", "portion," or "segment" refers to any stretch of nucleic acids encoding a CAPE molecule which is of sufficient length to use as a primer in polymerase chain reaction (PCR) or various hybridization procedures known to those of skill in the art, for the purpose of identifying or amplifying identical or related
nucleic acids.

The present invention includes purified CAPE polypeptides from natural or recombinant sources, vectors and host cells transformed with recombinant nucleic acid molecules encoding CAPE. Various methods for the isolation of the CAPE polypeptides may be accomplished by procedures well known in the art. For example, such polypeptides may be purified by immunoaffinity chromatography by employing the antibodies provided by the present invention. Various other methods of protein purification well known in the art include those described in Deutscher M (1990) Methods in Enzymology, Vol 182, Academic Press, San Diego; and Scopes R (1982) Protein Purification: Principles and Practice. Springer-Verlag, New York City, both incorporated herein by reference.

As used herein the term “recombinant” refers to a polynucleotide which encodes CAPE and is prepared using recombinant DNA techniques. The polynucleotide which encodes CAPE may also include allelic or recombinant variants and mutants thereof.

As used herein the term “probe” or “nucleic acid probe” or “oligonucleotide probe” refers to a portion, fragment, or segment of a CAPE molecule that is capable of being hybridized to a desired target nucleotide sequence. A probe can be used to detect, amplify or quantify cDNAs or endogenous nucleic acid encoding CAPE by employing conventional techniques in molecular biology. A probe may be of variable length, preferably from about 10 nucleotides up to several hundred nucleotides. As will be understood by those of skill in the art, hybridization conditions and probe design will vary depending upon the intended use. For example, a probe intended for use in PCR will be from about 15 to 30 nucleotides in length and may be up to 60 nucleotides in length and may be part of a pool of degenerate probes, i.e., oligonucleotides which tolerate nucleotide mismatch but accommodate binding to an unknown sequence; whereas a probe for use in Southern or northern hybridizations may be a single, specific nucleotide sequence that is several hundred nucleotides in length. Accordingly, a preferred probe for the specific detection of a CAPE molecule will comprise a polynucleotide or oligonucleotide fragment from a non-conserved nucleotide region of SEQ ID NO:1. As used herein the term “non-conserved nucleotide region” refers to a nucleotide region that is unique to SEQ ID NO:1 and does not comprise a region that is conserved in the family of serpin genes. Probes may be single-stranded or double-stranded and may have specificity in solution, cell, tissue or membrane-based hybridizations including in situ and ELISA-like technologies. The present invention encompasses oligonucleotides, fragments or portions of the polynucleotides disclosed herein, or
their complementary strands used as probes.

Nucleic acid probes may comprise portions of the sequence having fewer nucleotides than about 6 kb and usually fewer than about 1 kb. The oligonucleotides and nucleic acid probes of the present invention may be used to determine whether nucleic acid encoding CAPE is present in a cell or tissue or to isolate identical or similar nucleic acid sequences from chromosomal DNA as described by Walsh PS et al (1992 PCR Methods Appl 1:241-250).

Nucleic acid probes of the present invention may be derived from naturally occurring or recombinant single- or double-stranded nucleic acids or be chemically synthesized. They may be labeled by nick translation, Klenow fill-in reaction, PCR or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook J et al (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel FM et al (1989) Current Protocols in Molecular Biology, John Wiley & Sons, NYC, both incorporated herein by reference.

Alternatively, recombinant variants encoding the polypeptides of the present invention or related polypeptides may be synthesized or identified through hybridization techniques known to those of skill in the art by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations may also be introduced to modify the properties of the polypeptide, to change ligand-binding affinities, interchain affinities, or polypeptide degradation or turnover rate.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations may also be introduced to modify the properties of the polypeptide, including but not limited to small molecule-binding affinities, or polypeptide degradation or turnover rate. The nucleotide sequence of recombinant variants can be determined by means known to those of skill in the art. Conventional enzymatic methods employed DNA polymerase Klenow fragment, SEQUENASE® (US Biochemical Corp, Cleveland, OH) or Taq polymerase to extend DNA chains from an oligonucleotide primer annealed to the DNA template of interest. Methods have been developed for the use of both
single- and double-stranded templates. The chain termination reaction products were
electrophoresed on urea-acrylamide gels and detected either by autoradiography (for
radionuclide-labeled precursors) or by fluorescence (for fluorescent-labeled precursors). Recent
improvements in mechanized reaction preparation, sequencing and analysis using the fluorescent
detection method have permitted expansion in the number of sequences that can be determined
per day (using machines such as the Catalyst 800 and the Applied Biosystems 377 or 373 DNA
sequencer).

The present invention includes purified CAPE polypeptide from natural or recombinant
sources, and cells transformed with recombinant nucleic acid molecules encoding CAPE.
Various methods for the isolation of the polypeptide may be accomplished by procedures well
known in the art. For example, such polypeptides may be purified by immunoaffinity
chromatography by employing the antibodies provided by the present invention. Various other
methods of protein purification well known in the art include those described in Deutscher M
Protein Purification: Principles and Practice. Springer-Verlag, New York City, both incorporated
herein by reference.

**Modes of Carrying Out the Invention**

The present invention provides a nucleotide sequence (cape) for a novel serpin, identified
in cDNA libraries made from hypothalamic cells, brain tissue and neonatal kidney cells. The
sequence is provided in SEQ ID NO 1. Figs. 1A-1C provide the cape nucleotide sequence, and
the polypeptide sequence it encodes. The nucleotide sequence of SEQ ID NO:1 contains two
alternative start sites (ATG codons). These start sites serve to express two novel serpins which
possess substantial overlap (> 95%) in the polypeptide sequence. One encoded protein (CAPE1)
is expressed from an ATG codon at nucleotide position 79; its sequence is presented in SEQ ID
NO 2 starting at residue 27. The second protein (CAPE2) is expressed from an ATG codon at
nucleotide position 121; its sequence is presented in SEQ ID NO 2 starting at residue 41.

Figs. 2A-2D provide an alignment of CAPE1 and CAPE2, respectively, with
plasminogen activation inhibitor-2 (PAI-2), an exemplary serpin family member. CAPE1
contains a signal sequence consisting of hydrophobic residues indicating that it may be
selectively transported from hypothalamic cells to another location such as the pituitary gland.
Alternatively, CAPE2, like other serpins, may be secreted from hypothalamic cells. Overall,
about 110 out of 406 residues of CAPE2 match exactly with those of PAI-2 (about 27% homology). For the reactive site loop (RSL) residues P10, and P12-16 match exactly, whereas P8, P11, and P17 are substituted by amino acids that are larger by either an extra carbon group, i.e. the presence of threonine versus serine at P11, or a hydroxyl group, i.e. the presence of serine versus alanine at P8.

Since CAPE appears to have an RSL that resembles that of inhibitory serpins, CAPE may inhibit unidentified proteases within or outside of cells. Alternatively, CAPE may serve to bind specific small molecules to maintain higher levels of these molecules inside or outside of a cell and to modulate their release. Therefore CAPE, the novel serpin of the subject invention, may function either to mask protease activity or to sequester small molecules.

In view of the fact that the cape nucleotide sequence has been identified in brain and hypothalamic cells, the nucleic acid (cape), polypeptide (CAPE), and antibody to CAPE may be useful in investigations of and the intervention in the normal and abnormal function of the numerous endocrine and nonendocrine functions of the hypothalamus. However, even though the cape sequence was found to be expressed in hypothalamic cells it should not be ruled out that cape may be expressed in other cells, particularly other neuronal or secretory cells.

The nucleotide sequence encoding cape has numerous applications in techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use in the construction of oligomers for PCR, use for chromosome and gene mapping, use in the recombinant production of CAPE and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like. Uses of nucleotides encoding the proteins disclosed herein are exemplary of known techniques and are not intended to limit their use in any technique known to a person of ordinary skill in the art. Furthermore, the nucleotide sequences disclosed herein may be used in molecular biology techniques that have not yet been developed, provided the new techniques rely on properties of nucleotide sequences that are currently known, eg, the triplet genetic code, specific base pair interactions, etc.

It will be appreciated by those skilled in the art that as a result of the degeneracy of the genetic code, a multitude of CAPE-encoding nucleotide sequences, some bearing minimal homology to the nucleotide sequence of any known and naturally occurring gene may be produced. The invention has specifically contemplated each and every possible variation of nucleotide sequence that could be made by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code as
applied to the nucleotide sequence of naturally occurring CAPE, and all such variations are to be considered as being specifically disclosed.

Although the nucleotide sequences which encode CAPE and/or its variants are preferably capable of hybridizing to the nucleotide sequence of naturally occurring CAPE under stringent conditions, it may be advantageous to produce nucleotide sequences encoding CAPE or its derivatives possessing a substantially different codon usage. Codons can be selected to increase the rate at which expression of the peptide occurs in a particular prokaryotic or eukaryotic expression host in accordance with the frequency with which particular codons are utilized by the host. Other reasons for substantially altering the nucleotide sequence encoding CAPE and/or its derivatives without altering the encoded amino acid sequence include the production of RNA transcripts having more desirable properties, such as a greater half-life, than transcripts produced from the naturally occurring sequence.

Nucleotide sequences encoding CAPE may be joined to a variety of other nucleotide sequences by means of well established recombinant DNA techniques (Sambrook J et al. supra). Useful nucleotide sequences for joining to cape include an assortment of cloning vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Vectors of interest include expression vectors, replication vectors, probe generation vectors, sequencing vectors, and the like. In general, vectors of interest may contain an origin of replication functional in at least one organism, convenient restriction endonuclease sensitive sites, and selectable markers for the host cell.

Another aspect of the subject invention is to provide for cape-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences encoding CAPE. Such probes may also be used for the detection of similar serpin encoding sequences and should preferably contain at least 50% of the nucleotides from the conserved region or active site. The hybridization probes of the subject invention may be derived from the nucleotide sequences of SEQ ID NO 1 or from genomic sequences including promoters, enhancer elements and/or possible introns of respective naturally occurring CAPE molecules. Hybridization probes may be labeled by a variety of reporter groups, including radionuclides such as $^{32}$P or $^{35}$S, or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

Other means of producing specific hybridization probes for cape DNAs include the cloning of nucleic acid sequences encoding CAPE or CAPE derivatives into vectors for the
production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides.

It is now possible to produce a DNA sequence, or portions thereof, encoding CAPE and their derivatives entirely by synthetic chemistry, after which the gene can be inserted into any of the many available DNA vectors using reagents, vectors and cells that are known in the art at the time of the filing of this application. Moreover, synthetic chemistry may be used to introduce mutations into the cape sequences or any portion thereof.

PCR as described in US Patent Nos 4,683,195; 4,800,195; and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequence which encodes CAPE. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both and comprise a discrete nucleotide sequence for diagnostic use or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Full length genes may be cloned from known sequence using a new method which employs XL-PCR (Perkin-Elmer, Foster City, CA) to amplify long pieces of DNA as disclosed in Guegler, United States Application Serial Number 08/487,112 filed June 7, 1995. This method was developed to allow a single researcher to process multiple genes (up to 20 or more) at a time and to obtain an extended (possibly full-length) sequence within 6-10 days. It replaces current methods which use labelled probes to screen libraries and allow one researcher to process only about 3-5 genes in 14-40 days.

In the first step, which can be performed in about two days, primers are designed and synthesized based on a known partial sequence. In step 2, which takes about six to eight hours, the sequence is extended by PCR amplification of a selected library. Steps 3 and 4, which take about one day, are purification of the amplified cDNA and its ligation into an appropriate vector. Step 5, which takes about one day, involves transforming and growing up host bacteria. In step 6, which takes approximately five hours, PCR is used to screen bacterial clones for extended sequence. The final steps, which take about one day, involve the preparation and sequencing of selected clones. If the full length cDNA has not been obtained, the entire procedure is repeated using either the original library or some other preferred library. The preferred library may be one that has been size-selected to include only larger cDNAs or may consist of single or combined commercially available libraries, eg. lung, liver, heart and brain from Gibco/BRL (Gaithersburg
The cDNA library may have been prepared with oligo dT or random primers. The advantage of using random primed libraries is that they will have more sequences which contain 5' ends of genes. A randomly primed library may be particularly useful if an oligo dT library does not yield a complete gene. Obviously, the larger the protein, the less likely it is that the complete gene will be found in a single plasmid.

The nucleotide sequence disclosed in SEQ ID NO:1 can be used in an assay to detect conditions associated with altered expression of CAPE. The nucleotide sequence can be labeled by methods known in the art and added to a fluid or tissue sample from a patient under hybridizing conditions. After an incubation period, the sample is washed with a compatible fluid which optionally contains a dye (or other label requiring a developer) if the nucleotide has been labeled with an enzyme. After the compatible fluid is rinsed off, the dye is quantitated and compared with a standard. If the amount of dye is significantly elevated, the nucleotide sequence has hybridized with the sample, and the assay indicates the presence of inflammation, tumor and/or disease.

The nucleotide sequence for cape can be used to construct hybridization probes for mapping that gene. The nucleotide sequence provided herein may be mapped to a particular chromosome or to specific regions of that chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries, flow-sorted chromosomal preparations, or artificial chromosome constructions YAC or P1 constructions. The technique of fluorescent in situ hybridization of chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York City.

Fluorescent in situ hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of cape on a physical chromosomal map and a specific disease (or predisposition to a specific disease) can help delimit the region of DNA associated with that genetic disease. The nucleotide sequence of the subject invention may be used to detect differences in gene sequence between normal and carrier or affected individuals.

Nucleotide sequences encoding CAPE may be used to produce purified CAPE using well known methods of recombinant DNA technology. Among the many publications that teach
methods for the expression of genes after they have been isolated is Goeddel (1990) Gene Expression Technology, Methods and Enzymology, Vol 185, Academic Press, San Diego CA. CAPE may be expressed in a variety of host cells, either prokaryotic or eukaryotic. Host cells may be from the same species in which cape nucleotide sequences are endogenous or from a different species. Advantages of producing CAPE by recombinant DNA technology include obtaining adequate amounts of the protein for purification and the availability of simplified purification procedures.

Cells transformed with DNA encoding CAPE may be cultured under conditions suitable for the expression of serpins and recovery of the protein from the cell culture. CAPE produced by a recombinant cell may be secreted or may be contained intracellularly, depending on the cape sequence and the genetic construction used. In general, it is more convenient to prepare recombinant proteins in secreted form. Purification steps vary with the production process and the particular protein produced.

In addition to recombinant production, fragments of CAPE may be produced by direct peptide synthesis using solid-phase techniques (cf Stewart et al (1969) Solid-Phase Peptide Synthesis, WH Freeman Co, San Francisco CA; Merrifield J (1963) J Am Chem Soc 85:2149-2154. In vitro protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be achieved, for example, using Applied Biosystems 431A Peptide Synthesizer (Foster City, California CA) in accordance with the instructions provided by the manufacturer. Various fragments of CAPE may be chemically synthesized separately and combined using chemical methods to produce the full length molecule.

CAPE for antibody induction does not require biological activity; however, the protein must be antigenic. Peptides used to induce specific antibodies may have an amino acid sequence consisting of at least five amino acids, preferably at least 10 amino acids. They should mimic an exposed portion of the amino acid sequence of the protein and may contain the entire amino acid sequence of a small naturally occurring molecule such as CAPE. Short stretches of CAPE amino acid may be fused with those of another protein such as keyhole limpet hemocyanin and the resulting chimeric molecule used for antibody production.

Antibodies specific for CAPE may be produced by inoculation of an appropriate animal with the polypeptide or an antigenic fragment. An antibody is specific for CAPE if it is produced against an epitope of the polypeptide and binds to at least part of the natural or recombinant protein. Antibody production includes not only the stimulation of an immune
response by injection into animals, but also analogous steps in the production of synthetic antibodies or other specific-binding molecules such as the screening of recombinant immunoglobulin libraries (Orlandi R et al (1989) PNAS 86:3833-3837, or Huse WD et al (1989) Science 256:1275-1281) or the in vitro stimulation of lymphocyte populations. Current technology (Winter G and Milstein C (1991) Nature 349:293-299) provides for a number of highly specific binding reagents based on the principles of antibody formation. These techniques may be adapted to produce molecules specifically binding CAPE.

Two approaches are utilized to raise antibodies to CAPE, and each approach is useful for generating either polyclonal or monoclonal antibodies. In one approach, denatured protein from the reverse phase HPLC separation is obtained in quantities up to 75 mg. This denatured protein can be used to immunize mice or rabbits using standard protocols; about 100 micrograms are adequate for immunization of a mouse, while up to 1 mg might be used to immunize a rabbit. For identifying mouse hybridomas, the denatured protein can be radioiodinated and used to screen potential murine B-cell hybridomas for those which produce antibody. This procedure requires only small quantities of protein, such that 20 mg would be sufficient for labeling and screening of several thousand clones.

In the second approach, the amino acid sequence of CAPE, as deduced from translation of the cDNA, is analyzed to determine regions of high immunogenicity. Oligopeptides comprising regions which are hydrophilic, highly antigenic, or highly likely to be on the serpin surface, as shown in Fig. 3, are synthesized and used in suitable immunization protocols to raise antibodies. Analysis to select appropriate epitopes is described by Ausubel FM et al (supra). The optimal amino acid sequences for immunization are usually at the C-terminus, the N-terminus and those intervening, hydrophilic regions of the polypeptide which are likely to be exposed to the external environment when the protein is in its natural conformation.

Typically, selected peptides, about 15 residues in length, are synthesized using an Applied Biosystems Peptide Synthesizer Model 431A using fmc-chemistry and coupled to keyhole limpet hemocyanin (KLH) by reaction with M-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS; cf. Ausubel FM et al, supra). If necessary, a cysteine may be introduced at the N-terminus of the peptide to permit coupling to KLH. Rabbits are immunized with the peptide-KLH complex in complete Freund's adjuvant. The resulting antisera are tested for antipeptide activity by binding the peptide to plastic, blocking with 1% BSA, reacting with antisera, washing and reacting with labeled (radioactive or fluorescent), affinity purified, specific
goat anti-rabbit IgG.

Hybridomas may also be prepared and screened using standard techniques. Hybridomas of interest are detected by screening with labeled CAPE to identify those fusions producing the monoclonal antibody with the desired specificity. In a typical protocol, wells of plates (FAST; Becton-Dickinson, Palo Alto CA) are coated with affinity purified, specific rabbit-anti-mouse (or suitable anti-species Ig) antibodies at 10 mg/ml. The coated wells are blocked with 1% BSA, washed and exposed to supernatants from hybridomas. After incubation the wells are exposed to labeled CAPE, 1 mg/ml. Clones producing antibodies will bind a quantity of labeled CAPE which is detectable above background. Such clones are expanded and subjected to 2 cycles of cloning at limiting dilution (1 cell/3 wells). Cloned hybridomas are injected into pristane mice to produce ascites, and monoclonal antibody is purified from mouse ascitic fluid by affinity chromatography on Protein A. Monoclonal antibodies with affinities of at least 10$^8$ M$^{-1}$, preferably 10$^9$ to 10$^{10}$ or stronger, will typically be made by standard procedures as described in Harlow and Lane (1988) Antibodies: A Laboratory Manual. Cold Spring Harbor Laboratory, Cold Spring Harbor NY; and in Goding (1986) Monoclonal Antibodies: Principles and Practice, Academic Press, New York City, both incorporated herein by reference.

An additional embodiment of the subject invention is the use of CAPE as a specific protease inhibitor to treat inflammatory or pathologic problems of the hypothalamus, or another target tissue. A further embodiment of the subject invention is the use of CAPE to specifically bind a small molecule and to modulate its release either within the hypothalamus, a target tissue or extracellularly.

CAPE as a bioactive agent or composition may be administered in a suitable therapeutic dose determined by any of several methodologies including clinical studies on mammalian species to determine maximal tolerable dose and on normal human subjects to determine safe dose. Additionally, the bioactive agent may be complexed with a variety of well established compounds or compositions which enhance stability or pharmacological properties such as half-life. It is contemplated that the therapeutic, bioactive composition may be delivered by intravenous infusion into the bloodstream or any other effective means which could be used for treating problems involving excess expression and activity of proteases. Alternatively, the compositions may be employed for treating problems associated with excessive levels of specific small molecules.

Since CAPE appears to be a protease inhibitor, it may be used to treat diseases associated
with it expression such as, tissue wasting associated with excessive protease production during inflammation or diseases associated with nervous tissue degeneration. The tissues that may be affected by wasting are the brain or hypothalamus, where the serpin may be expressed in tissues surrounding or adjacent to the hypothalamus. For example, neuronal loss associated with diseases such as Kallmann's and Down's syndromes, or in Alzheimer's and Huntington's diseases may be prevented by administration of CAPE molecules. Destruction of the posterior hypothalamus by ischemia, encephalitis, trauma or tumor may also be prevented by administration of CAPE molecules.

CAPE also appears to be a small molecule binding protein which can be used to modulate levels of specific small molecules in the treatment of disease. For example, anorexia, bulimia, depression, and some forms of diabetes may be related to the overproduction of one or more of the molecules, such as CRH, ACTH, TRH, TSH, GRH, GH, insulin, somatostatin, cholecystokinin, interleukins, oxytocin, insulin-like growth factors, glucagon, etc., which govern the nonendocrine intake and eating behaviors. CAPE may be employed to bind one of these molecules, thereby decreasing the symptoms of these diseases.

For therapeutic uses, CAPE will be formulated in a nontoxic, inert, pharmaceutically acceptable aqueous carrier medium preferably at a pH of about 5 to 8, more preferably 6 to 8, although the pH may vary according to the characteristics of the formulation and its administration. Characteristics such as solubility of the molecule, half-life and antigenicity/immunogenicity will aid in defining an effective carrier. Native CAPE human proteins are preferred as a treatments for diseases, but recombinant, organic or synthetic CAPE molecules may be equally effective in particular situations.

CAPE may be delivered by known routes of administration including but not limited to transmucosal spray and aerosol, transdermal patch and bandage, intravenous formulations, orally administered liquids and pills particularly formulated to resist stomach acid and enzymes. For higher specificity in administration, CAPE may be directly injected or implanted in the brain, close to the hypothalamus.

The particular formulation, exact dosage, and route of administration will be determined by the attending physician and will vary according to each specific situation. Such determinations are made by considering multiple variables such as the condition to be treated, the CAPE molecule to be administered, and the pharmacokinetic profile of the particular CAPE molecule. Additional factors which may be taken into account include disease state (e.g.
severity) of the patient, age, weight, gender, diet, time of administration, drug combination, reaction sensitivities, and tolerance/response to therapy. Long acting formulations might be administered every 3 to 4 days, every week, or once every two weeks depending on half-life and clearance rate of the particular molecule.

Normal dosage amounts may vary from 0.1 to 100,000 micrograms, up to a total dose of about 1 g, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature; see US Patent Nos. 4,657,760; 5,206,344; or 5,225,212. It is anticipated that different formulations will be effective for different uses of CAPE and that administration targeting a tissue or organ may necessitate delivery in a specific manner.

The examples below are provided to illustrate the subject invention. These examples are provided by way of illustration and are not included for the purpose of limiting the invention.

**EXAMPLES**

**I Isolation of mRNA and Construction of cDNA Libraries**

The hypothalamic library was constructed from a pooled sample of hypothalamic tissue taken from the normal human brains of 51 Caucasian males and females of different ages. The polyadenylated mRNA was obtained from Clontech Laboratories, Inc. (Catalogue No. #6579-2, Palo Alto CA)

The polyadenylated mRNA was used to construct a custom cDNA library (Stratagene, La Jolla CA). cDNA synthesis was primed using both oligo dT and random hexamers, and the two cDNA libraries produced were treated separately. Synthetic adapter oligonucleotides were ligated onto the cDNA enabling its insertion into the Stratagene Uni-ZAP™ vector system. This system allows high efficiency unidirectional (sense orientation) lambda library construction and the convenience of a plasmid system with blue/white color selection to detect clones with cDNA insertions. Finally, the two cDNA libraries were combined into a single library by mixing equal numbers of bacteriophage.

The hypothalamic cDNA library is screened with either DNA probes or antibody probes and the pBluescript® phagemid (Stratagene) can be rapidly excised in vivo. The phagemid allows the use of a plasmid system for easy insert characterization, sequencing, site directed mutagenesis, creation of unidirectional deletions, and expression of fusion proteins. The custom-constructed library phage particles were infected into E. Coli host strain XL1 Blue®
(Stratagene) which has a high transformation efficiency. This efficiency increases the probability of obtaining rare, under-represented clones in the cDNA library. Alternative unidirectional vectors include but are not limited to pcDNAI (Invitrogen, San Diego CA) and pSHlox-1 (Novagen, Madison WI).

II Isolation of cDNA Clones

The phagemid forms of individual cDNA clones were obtained by the in vivo excision process, in which XL1-BLUE was coinfected with an f1 helper phage. Proteins derived from both lambda phage and f1 helper phage initiated new DNA synthesis from defined sequences on the lambda target DNA and create a smaller, single-stranded circular phagemid DNA molecule that includes all DNA sequences of the pBluescript plasmid and the cDNA insert. The phagemid DNA was released from the cells and purified, then used to reinfect fresh bacterial host cells (SOLR, Stratagene Inc), where the double-stranded phagemid DNA was produced. Because the phagemid carries the gene for β-lactamase, the newly transformed bacteria were selected on medium containing ampicillin.

Phagemid DNA was purified using the QIAWELL-8 Plasmid Purification System® (QIAGEN Inc, Chatsworth CA). This technique provides a rapid and reliable high-throughput method for lysing the bacterial cells and isolating highly purified phagemid DNA. The DNA eluted from the purification resin was suitable for DNA sequencing and other analytical manipulations.

An alternate method of purifying phagemid has recently become available. It utilizes the Miniprep Kit (Catalog No. #77468, Advanced Genetic Technologies Corporation, Gaithersburg MD). This kit is in the 96-well format and provides enough reagents for 960 purifications. Each kit is provided with a recommended protocol, which has been employed except for the following changes. First, the 96 wells are each filled with only 1 ml of sterile terrific broth with carbenicillin at 25 mg/L and glycerol at 0.4%. After the wells are inoculated, the bacteria are cultured for 24 hours and lysed with 60 μl of lysis buffer. A centrifugation step (2900 rpm for 5 minutes) is performed before the contents of the block are added to the primary filter plate. The optional step of adding isopropanol to TRIS buffer is not routinely performed. After the last step in the protocol, samples are transferred to a Beckman 96-well block for storage.

III Sequencing of cDNA Clones
The cDNA inserts from random isolates of the hypothalamus library were sequenced in part. Methods for DNA sequencing are well known in the art. The cDNAs were sequenced by the method of Sanger F. and AR Coulson (1975; J. Mol. Biol.94:441f), using a Hamilton Micro Lab 2200 (Hamilton, Reno NV) in combination with four Peltier Thermal Cyclers (PTC200 from MJ Research, Watertown MA) and Applied Biosystems 377 or 373 DNA Sequencing Systems (Perkin Elmer) and reading frame determined.

IV Homology Searching of cDNA Clones and Deduced Proteins

Each sequence so obtained was compared to sequences in GenBank using a search algorithm developed by Applied Biosystems Inc. and incorporated into its INHERIT™ 670 Sequence Analysis System. In this algorithm, Pattern Specification Language (developed by TRW Inc.) was used to determine regions of homology. The three parameters that determine how the sequence comparisons run were window size, window offset, and error tolerance. Using a combination of these three parameters, the DNA database was searched for sequences containing regions of homology to the query sequence, and the appropriate sequences were scored with an initial value. Subsequently, these homologous regions were examined using dot matrix homology plots to distinguish regions of homology from chance matches. Smith-Waterman alignments of the protein sequence were used to display the results of the homology search.

Peptide and protein sequence homologies were ascertained using the INHERIT 670 Sequence Analysis System in a way similar to that used in DNA sequence homologies. Pattern Specification Language and parameter windows were used to search protein databases for sequences containing regions of homology which were scored with an initial value. Dot-matrix homology plots were examined to distinguish regions of significant homology from chance matches.

Alternatively, BLAST, which stands for Basic Local Alignment Search Tool, is used to search for local sequence alignments (Altschul, SF (1993) J Mol Evol 36:290-300; Altschul, SF et al (1990) J Mol Biol 215:403-10). BLAST produces alignments of both nucleotide and amino acid sequences to determine sequence similarity. Because of the local nature of the alignments, BLAST is especially useful in determining exact matches or in identifying homologues. Although it is ideal for matches which do not contain gaps, it is inappropriate for performing motif-style searching. The fundamental unit of BLAST algorithm output is the high-scoring
segment pair (HSP).

An HSP consists of two sequence fragments of arbitrary but equal lengths whose alignment is locally maximal and for which the alignment score meets or exceeds a threshold or cutoff score set by the user. The BLAST approach is to look for HSPs between a query sequence and a database sequence, to evaluate the statistical significance of any matches found, and to report only those matches which satisfy the user-selected threshold of significance. The parameter E establishes the statistically significant threshold for reporting database sequence matches. E is interpreted as the upper bound of the expected frequency of chance occurrence of an HSP (or set of HSPs) within the context of the entire database search. Any database sequence whose match satisfies E is reported in the program output.

V Identification and Full Length Sequencing of the Genes

The nucleotide sequence for the entire coding region of CAPE is shown in Figs. 1A-1C. The cDNA of Incyte 84476 was extended to full length using a modified XL-PCR (Perkin Elmer) procedure. Primers were designed based on known sequence; one primer was synthesized to initiate extension in the antisense direction (XLR) and the other to extend sequence in the sense direction (XLF). The sequences of these primers and their location are as follows: XLR (nucleotides 502-525 in SEQ ID NO 1) and XLF (nucleotides 609-632 in SEQ ID NO 1). The primers allowed the sequence to be extended "outward" generating amplicons containing new, unknown nucleotide sequence for the gene of interest (Guegler supra). The primers were designed using Oligo 4.0 (National Biosciences Inc, Plymouth MN) to be 22-30 nucleotides in length, to have a GC content of 50% or more, and to anneal to the target sequence at temperatures about 68°-72° C. Any stretch of nucleotides which would result in hairpin structures and primer primer dimerizations were avoided.

The hypothalamus cell cDNA library was used as a template, and XLR and XLF primers were used to extend and amplify the 84476 sequence. By following the instructions for the XL-PCR kit, the enzymes provided high fidelity in the amplification. Beginning with 25 pMol of each primer and the recommended concentrations of all other components of the kit, PCR was performed using the MJ PTC200 (MJ Research, Watertown MA) and the following parameters:

<table>
<thead>
<tr>
<th>Step</th>
<th>Temperature</th>
<th>Time</th>
</tr>
</thead>
<tbody>
<tr>
<td>Step 1</td>
<td>94° C</td>
<td>60 sec</td>
</tr>
<tr>
<td>Step 2</td>
<td>94° C</td>
<td>15 sec</td>
</tr>
<tr>
<td>Step 3</td>
<td>65° C</td>
<td>1 min</td>
</tr>
<tr>
<td>Step 4</td>
<td>68° C</td>
<td>7 min</td>
</tr>
</tbody>
</table>
Step 5 Repeat step 2-4 for 15 additional cycles
Step 6 94° C for 15 sec
Step 7 65° C for 1 min
Step 8 68° C for 7 min + 15 sec/cycle
Step 9 Repeat step 6-8 for 11 additional cycles
Step 10 72° C for 8 min
Step 11 4° C (and holding)

At the end of 28 cycles, 50 μl of the reaction mix was removed; and the remaining reaction mix was run for an additional 10 cycles as outlined below:

Step 1 94° C for 15 sec
Step 2 65° C for 1 min
Step 3 68° C for (10 min + 15 sec)/cycle
Step 4 Repeat step 1-3 for 9 additional cycles
Step 5 72° C for 10 min

A 5-10 μl aliquot of the reaction mixture was analyzed by electrophoresis on a low concentration, about 0.6-0.8%, agarose mini-gel to determine which reactions were successful in extending the sequence. Although all extensions potentially contain a full length gene, some of the largest products or bands were selected and cut out of the gel. Further purification involved using a commercial gel extraction method such as QIAQuick™ (QIAGEN Inc, Chatsworth CA).

After recovery of the DNA, Klenow enzyme was used to trim single stranded, nucleotide overhangs creating blunt ends which facilitated religation and cloning.

After ethanol precipitation, the products were redissolved in 13 μl of ligation buffer. Then, 1μl T4-DNA ligase (15 units) and 1μl T4 polynucleotide kinase were added, and the mixture was incubated at room temperature for 2-3 hours or overnight at 16° C. Competent E. coli cells (in 40 μl of appropriate media) were transformed with 3 μl of ligation mixture and cultured in 80 μl of SOC medium (Sambrook J et al, supra). After incubation for one hour at 37° C, the whole transformation mixture was plated on Luria Bertani (LB)-agar (Sambrook J et al, supra) containing carbenicillin at 25 mg/L. The following day, 12 colonies were randomly picked from each plate and cultured in 150 μl of liquid LB/carbenicillin medium placed in an individual well of an appropriate, commercially-available, sterile 96-well microtiter plate. The following day, 5 μl of each overnight culture was transferred into a non-sterile 96-well plate and after dilution 1:10 with water, 5 μl of each sample was transferred into a PCR array.

For PCR amplification, 15 μl of PCR mix (1.33x containing 0.75 units of Taq polymerase, a vector primer and one or both of the gene specific primers used for the extension reaction) were added to each well. Amplification was performed using the following conditions:
Step 1  94 °C for 60 sec
Step 2  94 °C for 20 sec
Step 3  55 °C for 30 sec
Step 4  72 °C for 90 sec
Step 5  Repeat steps 2-4 for an additional 29 cycles
Step 6  72 °C for 180 sec
Step 7  4 °C (and holding)

Aliquots of the PCR reactions were run on agarose gels together with molecular weight markers. The sizes of the PCR products were compared to the original partial cDNAs, and appropriate clones were selected, ligated into plasmid and sequenced.

VI Antisense analysis

Knowledge of the cDNA sequence of the novel serpin gene will enable its use in antisense technology in the investigation of gene function. Oligonucleotides, genomic or cDNA fragments comprising the antisense strand of cape are used either in vitro or in vivo to inhibit expression of the protein. Such technology is now well known in the art, and probes can be designed at various locations along the nucleotide sequence. By transfection of cells or whole test animals with such antisense sequences, the gene of interest can effectively be turned off. Frequently, the function of the gene can be ascertained by observing behavior at the cellular, tissue or organismal level (e.g. lethality, loss of differentiated function, changes in morphology, etc).

In addition to using sequences constructed to interrupt transcription of the open reading frame, modifications of gene expression can be obtained by designing antisense sequences to intron regions, promoter/enhancer elements, or even to trans-acting regulatory genes. Similarly, inhibition can be achieved using Hogeboom base-pairing methodology, also known as "triple helix" base pairing.

VII Expression of CAPE

Expression of CAPE is accomplished by subcloning the cDNAs into appropriate expression vectors and transfecting the vectors into appropriate expression hosts. In this particular case, the cloning vector used in the generation of the full length clone also provides for expression of the included cape sequence in E. coli. Upstream of the cloning site, this vector contains a promoter for β-galactosidase, followed by sequence containing the amino-terminal Met and the subsequent 7 residues of β-galactosidase. Immediately following these eight
residues is an engineered bacteriophage promoter useful for artificial priming and transcription and for providing a number of unique endonuclease restriction sites for cloning.

Induction of the isolated, transfected bacterial strain with IPTG using standard methods will produce a fusion protein corresponding to the first seven residues of β-galactosidase, about 15 residues of "linker", and the peptide encoded within the cDNA. Since cDNA clone inserts are generated by an essentially random process, there is one chance in three that the included cDNA will lie in the correct frame for proper translation. If the cDNA is not in the proper reading frame, it is obtained by deletion or insertion of the appropriate number of bases by methods known to those of skill in the art including in vitro mutagenesis, digestion with exonuclease III or mung bean nuclease, or oligonucleotide linker inclusion.

The Cape cDNA is shuttled into other vectors known to be useful for expression of protein in specific hosts. Oligonucleotide amplimers containing cloning sites as well as a segment of DNA sufficient to hybridize to stretches at both ends of the target cDNA (25 bases) are synthesized chemically by standard methods. These primers can then be used to amplify the desired gene segments by PCR. The resulting new gene segments can be digested with appropriate restriction enzymes under standard conditions and isolated by gel electrophoresis. Alternately, similar gene segments can be produced by digesting the cDNA with appropriate restriction enzymes and filling in the missing gene segments with chemically synthesized oligonucleotides. Segments of the coding sequence from more than one gene are ligated together and cloned in appropriate vectors to optimize expression of recombinant sequence.

Suitable expression hosts for such molecules include but are not limited to mammalian cells such as Chinese Hamster Ovary (CHO) and human 293 cells, insect cells such as Sf9 cells, yeast cells such as Saccharomyces cerevisiae, and bacteria such as E. coli. For each of these cell systems, a useful expression vector contains an origin of replication to allow propagation in bacteria and a selectable marker such as the β-lactamase antibiotic resistance gene to allow selection in bacteria. In addition, the vectors may include a second selectable marker such as the neomycin phosphotransferase gene to allow selection in transfected eukaryotic host cells. Vectors for use in eukaryotic expression hosts may require RNA processing elements such as 3' polyadenylation sequences if such are not part of the cDNA of interest.

Additionally, the vector may contain promoters or enhancers which increase gene expression. Such promoters are host specific and include MMTV, SV40, or metallothionine promoters for CHO cells; trp, lac, tac or T7 promoters for bacterial hosts, or alpha factor, alcohol
oxidase or PGH promoters for yeast. Transcription enhancers, such as the rous sarcoma virus (RSV) enhancer, are used in mammalian host cells. Once homogeneous cultures of recombinant cells are obtained through standard culture methods, large quantities of recombinantly produced CAPE is recovered from the conditioned medium and analyzed using chromatographic methods known in the art.

VIII Isolation of Recombinant CAPE

CAPE is expressed as a chimeric protein with one or more additional polypeptide domains added to the CAPE amino acids to facilitate protein purification. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp., Seattle WA). The inclusion of a cleavable linker sequence such as Factor XA or enterokinase (Invitrogen) between the purification domain and the cape sequence is used to facilitate expression of CAPE.

IX Diagnostic Test Using CAPE Specific Antibodies

Particular CAPE antibodies are used for the diagnosis of prepathologic conditions, and chronic or acute diseases which are characterized by differences in the amount or distribution of CAPE. CAPE has been found to be expressed in brain and hypothalamus cDNA libraries and thus is used to detect conditions that damage the hypothalamus.

Diagnostic tests for CAPE include methods utilizing the antibody and a label to detect CAPE in human body fluids, tissues or extracts of such tissues. The polypeptides and antibodies of the present invention are used with or without modification. Frequently, the polypeptides and antibodies will be labeled by joining them, either covalently or noncovalently, with a substance which provides for a detectable signal. A wide variety of labels and conjugation techniques are known and have been reported extensively in both the scientific and patent literature. Suitable labels include radionuclides, enzymes, substrates, cofactors, inhibitors, fluorescent agents, chemiluminescent agents, chromogenic agents, magnetic particles and the like. Patents teaching the use of such labels include US Patent Nos. 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149; and 4,366,241. Also, recombinant immunoglobulins may be produced as shown in US Patent No. 4,816,567, incorporated herein by reference.
A variety of protocols for measuring soluble or membrane-bound CAPE, using either polyclonal or monoclonal antibodies specific for the respective protein are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA) and fluorescent activated cell sorting (FACS). A two-site monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on CAPE is preferred, but a competitive binding assay may be employed. These assays are described, among other places, in Maddox, DE et al (1983, J Exp Med 158:1211).

X  Purification of Native CAPE Using Specific Antibodies

Native or recombinant CAPE is purified by immunoaffinity chromatography using antibodies specific for CAPE. In general, an immunoaffinity column is constructed by covalently coupling the anti-CAPE antibody to an activated chromatographic resin.

Polyclonal immunoglobulins are prepared from immune sera either by precipitation with ammonium sulfate or by purification on immobilized Protein A (Pharmacia LKB Biotechnology, Piscataway, NJ). Similarly, monoclonal antibodies are prepared from mouse ascites fluid by ammonium sulfate precipitation or chromatography on immobilized Protein A. Partially purified immunoglobulin is covalently attached to a chromatographic resin such as CNBr-activated Sepharose (Pharmacia LKB Biotechnology). The antibody is coupled to the resin, the resin is blocked, and the derivative resin is washed according to the manufacturer's instructions.

Such immunoaffinity columns are utilized in the purification of CAPE by preparing a fraction from cells containing CAPE in a soluble form. This preparation is derived by solubilization of the whole cell or of a subcellular fraction obtained via differential centrifugation by the addition of detergent or by other methods well known in the art. Alternatively, soluble CAPE containing a signal sequence is secreted in useful quantity into the medium in which the cells are grown.

A soluble CAPE-containing preparation is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of serpin (eg, high ionic strength buffers in the presence of detergent). Then, the column is eluted under conditions that disrupt antibody/CAPE binding (e.g., a buffer of pH 2-3 or a high concentration of a chaotrope such as urea or thiocyanate ion), and CAPE is collected.

XI  CAPE Activity
The activity of purified or expressed CAPE in protease inhibition is tested by mixing a known quantity of the enzyme with a potential substrate protease such as chymotrypsin and a purified protein which chymotrypsin usually cleaves. The ability of a given amount of CAPE to inhibit chymotrypsin is assayed by FPLC of the protein fragments produced under a given set of conditions in a specific period of time.

In another method to test CAPE activity as a protease inhibitor, a sample of the reaction materials are run on a nondenaturing gel which separates the protease inhibitor complex, protease, inhibitor, protein substrate and protein fragments as different sized peptides.

The activity of purified or expressed CAPE in small molecule binding is tested by incubating CAPE with various small molecules, preferably those derived from the hypothalamus or those that affect hypothalamus function, in radiolabeled form. After allowing a suitable time for binding, CAPE-bound small molecules may be separated from free small molecules by FPLC, and the binding affinity of CAPE for different small molecules is determined.

XII Rational Drug Design

The goal of rational drug design is to produce structural analogs of biologically active polypeptides of interest or of small molecules with which they interact, eg, inhibitors, agonists, antagonists, etc. Any of these examples are used to fashion drugs which are more active or stable forms of the polypeptide or which enhance or interfere with the function of a polypeptide in vivo (Hodgson J (1991) Bio/Technology 9:19-21, incorporated herein by reference).

In one approach, the three-dimensional structure of a protein of interest, or of a protein-inhibitor complex, is determined by x-ray crystallography, by computer modeling or, most typically, by a combination of the two approaches. Both the shape and charges of the polypeptide is ascertained to elucidate the structure and to determine active site(s) of the molecule. Useful information regarding the structure of a polypeptide may be gained by modeling based on the structure of homologous proteins. In both cases, relevant structural information is used to design analogous serpin-like molecules, to identify efficient inhibitors, or to identify small molecules that may bind serpins. Useful examples of rational drug design may include molecules which have improved activity or stability as shown by Braxton S and Wells JA (1992 Biochemistry 31:7796-7801) or which act as inhibitors, agonists, or antagonists of native peptides as shown by Athauda SB et al (1993 J Biochem 113:742-746), incorporated herein by reference.
It is also possible to isolate a target-specific antibody, selected by functional assay, as described above, and then to solve its crystal structure. This approach, in principle, yields a pharmacore upon which subsequent drug design can be based. It is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies (anti-ids) to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-ids is expected to be an analog of the original receptor. The anti-id is then used to identify and isolate peptides from banks of chemically or biologically produced peptides. The isolated peptides would then act as the pharmacore.

By virtue of the present invention, sufficient amount of polypeptide is made available to perform such analytical studies as X-ray crystallography. In addition, knowledge of the CAPE amino acid sequence provided herein will provide guidance to those employing computer modeling techniques in place of or in addition to x-ray crystallography.

All publications and patents mentioned in the above specification are herein incorporated by reference. The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. Indeed, various modifications of the above described modes for carrying out the invention which are readily apparent to those skilled in the field of molecular biology or related fields are intended to be within the scope of the following claims.
SUBSTITUTE SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Incyte Pharmaceuticals, Inc.

(ii) TITLE OF THE INVENTION: NOVEL SERPIN DERIVED FROM HUMAN HYPOTHALAMUS

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:
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(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: US
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Filed Herewith

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/487,823
(B) FILING DATE: 7-JUN-1995

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Luther, Barbara J.
(B) REGISTRATION NUMBER: 33,954
(C) REFERENCE/DOCKET NUMBER: PF-0039 PCT

(ix) TELECOMMUNICATION INFORMATION:
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(B) TELEFAX: 415-852-0195

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1558 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: Hypothalamus
(B) CLONE: 84476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
**WO 96/40922**

**PCT/US96/10179**

| AATTCGCCA | GAGGGAAGGG | AGAGGAGAAG | GGGGCCAAC | CTCACCTG | GCCAATCGAG |
| GTTTGAACCT | GTTACAATAT | GCTTTCCGCT | GAGCTCCCTC | TTTGGCTGTG | TCTGGCAGAT |
| ATGGCTACAG | GGAGCCATTT | CTCCTGAGGAA | GCCATTGTTG | ACTGTCGACT | GAATATGAT |
| AATGTCTTTA | GAGCCACCTG | TGAATGATAG | AATATCCTC | TCTTCACAT | GATTATGGC |
| CTGCTGCAAGG | GAATGAGTGA | ACTGGGGGGG | CAAAGATCTA | CCCAGAAGA | AATGCGAC |
| AGCAGCAGGT | AGGAAAGCTT | TATGGGAA | CTGATGCAAA | TGCATGGAAT | GAGATGAT |
| GCTGCTGCTA | TCTACACAGT | CTCAGAATAT | CCAATGGAAG | GAGATGGAAT | AGGATGAGT |
| CTGCTGCTGTT | CCAGAGCAGA | AGTCTCGCTC | GCTACTGCTG | AGCCATTAGT | CAAGACGCA |
| CAGGCAAGA | AATTCCGCTA | CTTCGTGGAAG | AACAAAGAAAG | TCTGTTCTA | TCTGGGAGG |
| ATCTCTTAAAA | ATCTCTM | TGAATGATAG | AGAGCAACTC | TCTGGGAGG | TCTGGGAGG |
| GCAATTCAC | AGTCCACCTC | AGAGGTTAAT | GAAGAGGCT | CAAAATCTC | TGCTGCAAG |
| ATGATCCAT | TGATGGGTTA | TCGTCTGAT | CTCAGAGTTA | TTGCGGACA | TCTGGGAGG |
| TCTTCATCA | GAAACGAGAG | AAGCTGCTAC | ATCTATGCA | TGGGAGGCT | ATGCACCC |
| GAAACAATGA | ACAAGTGC | AGATGGTTTTC | GAAGAATCTT | ATGGCTTTC | TATAATAC |
| CAGGGGAAAAC | AGTAGTTCAC | CACATTAGT | TGGCAATCT | TACTATATAT | GTAATGAGG |
| TTTGCTATG | ATCTCTTATA | ATGGTCCAAG | ATAAATCTT | ATATAGATAA | ATGATGAT |
| TTTGCTATG | GCTGTTCTGT | AAAATAAAAG | TACACTATTA | AAAATAAAAA | AAAATAAAAA |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 407 amino acids
(B) TYPE: protein
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 382 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE: N-terminal
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
Met Glu Asp Leu Cys Val Ala Asn Thr Leu Phe Ala Leu Asn Leu Phe
1   5   10   15
Lys His Leu Ala Lys Ala Ser Pro Thr Gln Asn Leu Phe Leu Ser Pro
20   25   30
Trp Ser Ile Ser Ser Thr Met Ala Met Val Tyr Met Gly Ser Arg Gly
30
(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 420 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Ala Phe Leu Gly Leu Phe Ser Leu Leu Leu Val Leu Glu Ser Leu Ala
1      5       10      15
Val Gly Ala Thr Leu Pro Glu Glu Ala Ile Val Asp Leu Ala Val Asn
20     25       30
Leu Phe Asn His Leu Ala Ala Ala Gly Glu Thr Glu Asn Leu Leu Leu
35     40       45
Ser Pro Leu Ser Ile Ala Leu Ala Met Gly Met Val Glu Leu Gly Ala
50     55       60
Gln Gly Ser Thr Glu Asp Glu Ile Ala Lys Val Leu Gly Phe Asp Ser
65     70       75     80
Val Gly Ala Gly Ala Asp Lys Ile His Ser Ser Leu Lys Ser Leu Ser
85     90
Ser Ala Val Thr Ala Ser Thr Gly Asn Tyr Val Leu Glu Ile Ala Asn
100    105      110
Ser Leu Phe Gly Glu Asn Gly Ala Ser Val Asn Glu Glu Phe Leu Gln
115    120      125
Leu Cys Glu Lys Tyr Phe Ser Ala Ala Val Asn Ala Val Asp Phe Leu
130    135      140
Glu Asn Ala Ala Val Ala Arg Asn Lys Ile Asn Ser Trp Val Glu Thr
145    150      155    160
Asn Thr Asn Gly Leu Val Lys Asp Leu Val Ser Glu Gly Ser Val Xaa
165    170      175
Gly Ala Thr Arg Leu Ala Leu Val Arg Ala Val Tyr Phe Lys Gly Asn
180    185      190
Trp Lys Ser Gln Phe Glu Lys Glu Leu Thr Gly Leu Phe Ser Phe Thr
195    200      205
Val Asp Ser Ala Ser Glu Val Gln Val Gln Met Met Tyr Leu Glu Gln
210    215      220
Glu Leu Asn Ile Gly Glu Phe Ile Asp Gly Leu Asn Ala Ala Gly
225    230      235    240
Ile Tyr Gln Val Leu Glu Leu Pro Tyr Ala Gly Asp Glu Val Ser Met
245    250      255
Phe Leu Val Leu Ser Asp Glu Ile Ala Asp Val Ala Thr Gly Leu Glu
260    265      270
Leu Leu Glu Ser Leu Val Thr Ala Asp Leu Val Glu Glu Trp Ala Ser
275    280      285
Ser Val Lys Lys Ala Glu Asp Glu Val Glu Tyr Leu Pro Gln Phe
290    295      300
Thr Val Glu Glu Ile Asp Leu Lys Ser Val Leu Lys Ala Leu Gly
305    310      315    320
Ile Thr Asp Ala Phe Ile Lys Gly Lys Ala Asn Phe Ser Gly Leu Ser
325    330      335
Asp Asn Asn Leu Phe Leu Ser Glu Ala Ile His Gln Ala Phe Val
340    345      350
Asp Val Asp Glu Glu Gly Ser Glu Ala Ala Ala Gly Gly Gly Val
355    360      365
Leu Val Gly Arg Thr Gly His Gly Gly Pro Gln Val Val Ala Asp His
370    375      380
Pro Phe Leu Phe Leu Ile Arg Asn Lys Ile Thr Gly Thr Ile Leu Phe
385    390      395    400
Phe Gly Arg Val Met His Pro Glu Thr Met Asn Thr Ser Gly His Asp
405    410      415
Phe Ser Ser Leu
420
(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 406 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE: N-terminal
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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

1. A purified polynucleotide comprising a nucleic acid sequence encoding the polypeptide having the sequence as depicted in SEQ ID NO:2, or its complement.

2. The polynucleotide of Claim 1 wherein the nucleic acid sequence consists of SEQ ID NO:1.

3. An expression vector comprising the polynucleotide of Claim 2.

4. A host cell comprising the expression vector of Claim 3.

5. A nucleic acid probe comprising a non-conserved fragment of the polynucleotide of Claim 2.

6. An antisense molecule comprising a polynucleotide sequence complementary to at least a portion of the polynucleotide of Claim 2.

7. A method for producing a polypeptide comprising the sequence as depicted in SEQ ID NO:2, said method comprising:

   a) culturing the host cells of Claim 4 under conditions suitable for the expression of the polypeptide, and

   b) recovering said polypeptide from the cell culture.

8. A purified CAPE molecule having the amino acid sequence as depicted in SEQ ID NO:2.


10. A diagnostic composition for the detection of nucleic acid sequences encoding CAPE comprising the nucleic acid probe of Claim 5.
11. A diagnostic test for the detection of nucleotide sequences encoding CAPE in a biological sample, comprising the steps of:

a) combining the biological sample with a polynucleotide which comprises the nucleotide sequence of SEQ ID NO:1 or a fragment thereof, wherein said fragment is derived from a non-conserved region of said nucleotide, under conditions suitable for the formation of a nucleic acid hybridization complex between the nucleic acid sequence of SEQ ID NO:1 and a complementary nucleic acid sequence in said sample;

b) detecting said hybridization complex; and

c) comparing the amount of said hybridization complex with a standard wherein the presence of an abnormal level of said hybridization complex correlates positively with a condition associated with inflammation.

12. The diagnostic test of Claim 11 wherein the polynucleotide is labeled with a reporter molecule and the hybridization complex is detected by measuring said reporter molecule.

13. A diagnostic test for the detection of nucleotide sequences encoding CAPE in a biological sample, comprising the steps of:

a) combining the biological sample with polymerase chain reaction primers under conditions suitable for nucleic acid amplification, wherein said primers comprise fragments from non-conserved regions of the nucleotide sequence of SEQ ID NO:1;

b) detecting amplified nucleotide sequences; and

c) comparing the amount of amplified nucleotide sequences in said biological sample with a standard thereby determining whether the amount of said nucleotide sequence varies from said standard, wherein the presence of an abnormal level of said nucleotide sequence correlates positively with a condition associated with inflammation.
14. A method of screening a plurality of compounds for specific binding affinity with the polypeptide of Claim 8 or any portion thereof, comprising the steps of:

   a) providing a plurality of compounds;

   b) combining CAPE with each of a plurality of compounds for a time sufficient to allow binding under suitable conditions; and

   c) detecting binding of CAPE to each of the plurality of compounds, thereby identifying the compounds which specifically bind CAPE.
FIGURE 1A

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FIGURE 1B

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LPQFTVEEETDLKSVLKAALGITDAFIKGA

NFSGLSDNNDLFLSEAIHQAFVDVNEEGSE

AAAGGGGVLVGRTHGGPQVADHPFLFLI

RNKITGTLFFGRVMHPETMNTSGHDPSL

RHERTGTLFMGKVMHPETMNTSGHDPEEL

FIGURE 2B

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Decoration 'Decoration #1': Shade (with solid black) residues that match 84476 exactly.

**FIGURE 2D**

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