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(73) Applicant(s):
VERTEX PHARMACEUTICALS INCORPORATED
130 Waverly Street, Cambridge
Massachusetts 02139-4242
United States Of America

(72) Inventors:
GUY BEMIS
256 Appleton Street
Arlington
MA 02174
United States Of America
(See Overleaf)

(74) Representative
FISHER CORMACK & BOTHA
P O BOX 74
BLANTYRE
MALAWI

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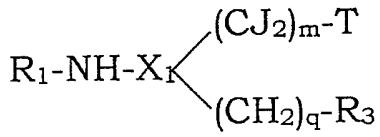
(54) Title: Inhibitors Of Interleukin-1β Converting Enzyme

(57) Abstract:

Compounds that are inhibitors of interleuken-1β converting enzyme and are representing by the formula:



The ICE inhibitors have specific structural and physicochemical features. The compounds and compositions thereof are suited for inhibiting ICE activity and may be used as agents against interleukin-1 mediated diseases, including inflammatory diseases, autoimmune diseases and neurodegenerative diseases.

(56) Documents Cited: EP 0519748 A; WO 93/09135 A; WO 93/14777 A; WO 93/16710 A; EP 0529713 A

Inventors Continued

2. JULIAN M GOLEC
   8 Manor Farm
   Chapel Road, Ashbury
   Swindon, Wiltshire SN6 8LS
   England

3. DAVID J LAUFFER
   254 Taylor Road, Stow
   MA 01775
   United States of America

4. MICHAEL D MULLICAN
   110 Parker Road
   Needham
   MA 02194
   United States of America

5. MARK A MURCKO
   520 Marshall Street
   Holliston
   MA 01746
   United States of America

6. DAVID J LIVINGSTON
   20 Madison Avenue
   Newtonville
   MA 02160
   United States of America

INHIBITORS OF INTERLEUKIN-1ß CONVERTING ENZYME

TECHNICAL FIELD OF THE INVENTION

The present invention relates to novel classes of compounds which are inhibitors of interleukin-1ß converting enzyme ("ICE"). The ICE inhibitors of this invention are characterized by specific structural and physicochemical features. This invention also relates to pharmaceutical compositions comprising these compounds. The compounds and pharmaceutical compositions of this invention are particularly well suited for inhibiting ICE activity and consequently, may be advantageously used as agents against interleukin-1 ("IL-1") mediated diseases, including inflammatory diseases, autoimmune diseases and neurodegenerative diseases. This invention also relates to methods for inhibiting ICE activity and methods for treating interleukin-1 mediated diseases using the compounds and compositions of this invention.

AP/P/97/00960

BACKGROUND OF THE INVENTION

Interleukin 1 ("IL-1") is a major pro-inflammatory and immunoregulatory protein that stimulates fibroblast differentiation and proliferation, the production of prostaglandins, collagenase and phospholipase by synovial cells and chondrocytes, basophil and eosinophil degranulation and

neutrophil activation. Oppenheim, J.H. et al, Immunology Today, 7, pp. 45-56 (1986). As such, it is involved in the pathogenesis of chronic and acute inflammatory and autoimmune diseases. IL-1 is predominantly produced by peripheral blood monocytes as part of the inflammatory response and exists in two distinct agonist forms, IL-1α and IL-1ß. Mosely, B.S. et al., Proc. Nat. Acad. Sci., 84, pp. 4572-4576 (1987); Lonnemann, G. et al., Eur.J. Immunol., 19, pp. 1531-1536 (1989).

IL-1ß is synthesized as a biologically inactive precursor, pIL-1ß. pIL-1ß lacks a conventional leader sequence and is not processed by a signal peptidase. March, C.J., Nature, 315, pp. 641-647 (1985). Instead, pIL-1ß is cleaved by interleukin-1ß converting enzyme ("ICE") between Asp-116 and Ala-117 to produce the biologically active C-terminal fragment found in human serum and synovial fluid. Sleath, P.R., et al., J. Biol. Chem., 265, pp. 14526-14528 (1992); A.D. Howard et al., J. Immunol., 147, pp. 2964-2969 (1991). Processing by ICE is also necessary for the transport of mature IL-1ß through the cell membrane.

ICE is a cysteine protease localized primarily in monocytes. It converts precursor IL-1ß to the mature form. Black, R.A. et al., FEBS Lett., 247, pp. 386-390 (1989); Kostura, M.J. et al., Proc. Natl. Acad. Sci. USA, 86, pp. 5227-5231 (1989). ICE, or its homologues, also appears to be involved in the regulation of cell death or apoptosis. Yuan, J. et al., Cell, 75, pp. 641-652 (1993); Miura, M. et al., Cell, 75, pp. 653-660 (1993); Nett-Fiordalisi, M.A. et al., J. Cell Biochem., 17B, p. 117 (1993). In particular, ICE or ICE homologues are thought to be associated with the regulation of apoptosis in

neurogenerative diseases, such as Alzheimer's and Parkinson's disease. Marx, J. and M. Baringa, Science, 259, pp. 760-762 (1993); Gagliardini, V. et al., Science, 263, pp. 826-828 (1994).

ICE has been previously described as a heterodimer composed of two subunits, p20 and p10 (20kDa and 10kDa molecular weight, respectively). These subunits are derived from a 45kDa proenzyme (p45) by way of a p30 form, through an activation mechanism that is autocatalytic. Thornberry, N.A. et al., Nature, 356, pp. 768-774 (1992). The ICE proenzyme has been divided into several functional domains: a prodomain (p14), a p22/20 subunit, a polypeptide linker and a p10 subunit. Thornberry et al., supra; Casano et al., Genomics, 20, pp. 474-481 (1994).

Full length p45 has been characterized by its cDNA and amino acid sequences. PCT patent applications WO 91/15577 and WO 94/00154. The p20 and p10 cDNA and amino acid sequences are also known. Thornberry et al., supra. Murine and rat ICE have also been sequenced and cloned. They have high amino acid and nucleic acid sequence homology to human ICE. Miller, D.K. et al., Ann. N.Y. Acad. Sci., 696, pp. 133-148 (1993); Molineaux, S.M. et al., Proc. Nat. Acad. Sci., 90, pp. 1809-1813 (1993). Knowledge of the primary structure of ICE, however, does not allow prediction of its tertiary structure. Nor does it afford an understanding of the structural, conformational and chemical interactions of ICE and its substrate pIL-1ß or other substrates or inhibitors.

ICE inhibitors represent a class of compounds useful for the control of inflammation or apoptosis or both. Peptide and peptidyl inhibitors of ICE have been described. PCT patent applications WO 91/15577; WO 93/05071; WO 93/09135; WO 93/14777 and WO 93/16710; and

European patent application 0 547 699. However, due to their peptidic nature, such inhibitors are typically characterized by undesirable pharmacologic properties, such as poor oral absorption, poor stability and rapid metabolism. Plattner, J.J. and D.W. Norbeck, in Drug Discovery Technologies, C.R. Clark and W.H. Moos, Eds. (Ellis Horwood, Chichester, England, 1990), pp. 92-126. This has hampered their development into effective drugs.

Accordingly, the need exists for compounds that can effectively inhibit the action of ICE, for use as agents for preventing and treating chronic and acute forms of IL-1 mediated diseases, including various cancers, as well as inflammatory, autoimmune or neurodegenerative diseases.

SUMMARY OF THE INVENTION

The present invention provides novel classes of compounds, and pharmaceutically acceptable derivatives thereof, that are useful as inhibitors of ICE. These compounds can be used alone or in combination with other therapeutic or prophylactic agents, such as antibiotics, immunomodulators or other anti-inflammatory agents, for the treatment or prophylaxis of diseases mediated by IL-1. According to a preferred embodiment, the compounds of this invention are capable of binding to the active site of ICE and inhibiting the activity of that enzyme.

It is a principal object of this invention to provide novel classes of inhibitors of ICE. These novel classes of ICE inhibitors are characterized by the following structural and physicochemical features:

a) a first and a second hydrogen bonding moiety, each of said moieties being capable of forming a hydrogen bond with a different backbone atom

of ICE, said backbone atom being selected from the group consisting of the carbonyl oxygen of Arg-341, the amide -NH- group of Arg-341, the carbonyl oxygen of Ser-339 and the amide -NH- group of Ser-339;

b) a first and a second moderately hydrophobic moiety, said moieties each being capable of associating with a separate binding pocket of ICE when the inhibitor is bound thereto, said binding pocket being selected from the group consisting of the P2 binding pocket, the P3 binding pocket, the P4 binding pocket and the P' binding pocket; and

c) an electronegative moiety comprising one or more electronegative atoms, said atoms being attached to the same atom or to adjacent atoms in the moiety and said moiety being capable of forming one or more hydrogen bonds or salt bridges with residues in the P1 binding pocket of ICE.

It is also an object of this invention to provide a method for identification, design or prediction of ICE inhibitors comprising the steps of:

a) selecting a candidate compound of defined chemical structure comprising at least two hydrogen bonding moieties, at least two moderately hydrophobic moieties and one electronegative moiety comprising one or more electronegative atoms attached either to the same atom or to adjacent atoms in the electronegative moiety;

b) determining a low-energy conformation for binding of said compound to the active site of ICE;

c) evaluating the capability of said compound in said conformation to form at least two hydrogen bonds with the non-carbon backbone atoms of Arg-341 and Ser-339 of ICE;

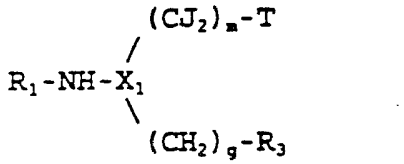
d) evaluating the capability of said compound in said conformation to associate with at

least two of the binding pockets of ICE selected from the group consisting of the P2 binding pocket, the P3 binding pocket, the P4 binding pocket and the P' binding pocket;

e) evaluating the capability of said compound in said conformation to interact with the P1 binding pocket of ICE; and

f) accepting or rejecting said candidate compound as an ICE inhibitor based on the determinations and evaluations carried out in the preceding steps.

It is a further object of this invention to provide novel classes of ICE inhibitors represented by formulas:

α 

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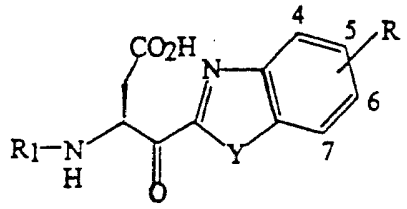
α 

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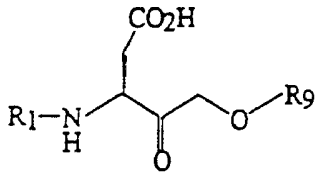
Π 

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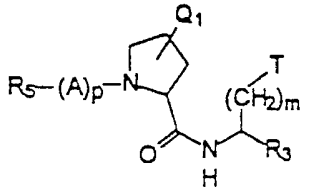
Υ 

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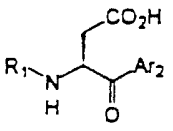
δ 

ABBREVIATIONS AND DEFINITIONS

Abbreviations

Designation	Reagent or Fragment
Ala	alanine
Arg	arginine
Asn	asparagine
Asp	aspartic acid
Cys	cysteine
Gln	glutamine
Glu	glutamic acid
Gly	glycine
His	histidine
Ile	isoleucine
Leu	leucine
Lys	lysine
Met	methionine
Phe	phenylalanine
Pro	proline
Ser	serine
Thr	threonine
Trp	tryptophan
Tyr	tyrosine
Val	valine.

Definitions

The following terms are employed herein:

The term "active site" refers to any or all of the following sites in ICE: the substrate binding site, the site where an inhibitor binds and the site where the cleavage of substrate occurs. The active site is characterized by at least amino acid residues: 173, 176, 177, 178, 179, 180, 236, 237, 238, 239, 244, 248, 283, 284, 285, 290, 338, 339, 340, 341, 342, 343,

344, 345, 348, 352, 381, 383, using the sequence and numbering according to Thornberry et al., supra.

The terms "P binding pocket", "S subsite", "S pocket", and the like, refer to binding subsites, or portions of the substrate binding site on the ICE molecule. The amino acid residues of the substrate are given designations according to their position relative to the scissile bond, i.e. the bond which is broken by the protease. The residues are designated P1, P2, etc., for those extending toward the N-terminus of the substrate and P1', P2', etc., for those extending toward the C-terminus of the substrate. The portions of an inhibitor which correspond to the P or P' residues of the substrate are also labeled P1, P1', etc., by analogy with the substrate. The binding subsites of the ICE molecule which receive the residues labeled P1, P1', etc., are designated S1, S1', etc., or may alternately be designated "the P1 binding pocket", "the P1' binding pocket", etc. [I. Schechter and A. Berger, "On the Size of the Active Site in Proteases", Biochem. Biophys. Res. Commun., vol. 27, pp. 157-162 (1967).]

The terms "P2 binding pocket" or "S2 subsite" of the ICE active site are equivalent and are defined as the space surrounded by amino acid residues Pro-290, Val-338 or Trp-340.

The terms "P3 binding pocket" or "S3 subsite" of the ICE active site are equivalent and are defined as the space surrounded by amino acid residues Pro-177, Arg-178, Thr-180, Arg-341 or Pro-343.

The terms "P4 binding pocket" or "S4 subsite" of the ICE active site are equivalent and are defined as the space surrounded by amino acid residues His-342, Met-345, Val-348, Arg-352, Asp-381, Arg-383 or Trp-340.

The terms "P1 binding pocket" or "S1 subsite" of the ICE active site are equivalent and are defined as the space surrounded by amino acid residues Arg-179, His-237, Gln-283, or Arg-341.

The terms "P' binding pocket" or "S' subsite" of the ICE active site are equivalent and are defined as the space surrounded by amino acid residues Phe-173, Ile-176, His-237, Gly-238, Ile-239, Cys-244 or His-248.

The term "hydrophobic" refers to a moiety which tends not to dissolve in water and is fat-soluble. Hydrophobic moieties include, but are not limited to, hydrocarbons, such as alkanes, alkenes, alkynes, cycloalkanes, cycloalkenes, cycloalkynes and aromatic compounds, such as aryls, certain saturated and unsaturated heterocycles and moieties that are substantially similar to the side chains of hydrophobic natural and unnatural α-amino acids, including valine, leucine, isoleucine, methionine, phenylanine, α-amino isobutyric acid, alloisoleucine, tyrosine, and tryptophan.

The term "moderately hydrophobic" refers to a hydrophobic moiety in which one or two carbon atoms have been replaced with more polar atoms, such as oxygen or nitrogen.

The term "heterocycle" or "heterocyclic" refers to a stable mono- or polycyclic compound which may optionally contain one or two double bonds or may optionally contain one or more aromatic rings. Each heterocycle consists of carbon atoms and from one to four heteroatoms independently selected from a group including nitrogen, oxygen, and sulfur. As used herein, the terms "nitrogen heteroatoms" and "sulphur heteroatoms" include any oxidized form of nitrogen or sulfur and the quaternized form of any basic nitrogen. Heterocycles defined above include, for example,

pyrimidinyl, tetrahydroquinolyl, tetrahydroisoquinonlinyl, purinyl, pyrimidyl, indolinyl, benzimidazolyl, imidazolyl, imidazolinoyl, imidazolidinyl, quinolyl, isoquinolyl, indolyl, pyridyl, pyrrolyl, pyrrolinyl, pyrazolyl, pyrazinyl, quinoxolyl, piperidinyl, morpholinyl, thiamorpholinyl, furyl, thienyl, triazolyl, thiazolyl, ß-carbolinyl, tetrazolyl, thiazolidinyl, benzofuranoyl, thiamorpholinyl sulfone, benzoxazolyl, oxopiperidinyl, oxopyrrolidinyl, oxoazepinyl, azepinyl, isoxazolyl, tetrahydropyranyl, tetrahydrofuranyl, thiadiazolyl, benzodioxolyl, benzothienyl, tetrahydrothiophenyl and sulfolanyl. Further heterocycles are described in A.R. Katritzky and C.W. Rees, eds., Comprehensive Heterocyclic Chemistry: The Structure, Reactions, Synthesis and Use of Heterocyclic Compounds, Vol. 1-8, Pergamon Press, NY (1984).

The term "cycloalkyl" refers to a mono- or polycyclic group which contains 3 to 15 carbons and may optionally contain one or two double bonds. Examples include cyclohexyl, adamantyl and norbornyl.

The term "aryl" refers to a mono- or polycyclic group which contains 6, 10, 12, or 14 carbons in which at least one ring is aromatic. Examples include phenyl, naphthyl and biphenyl.

The term "heteroaromatic" refers to a mono- or polycyclic group which contains 1 to 15 carbon atoms and from 1 to 4 heteroatoms, each of which is selected independently from a group including sulphur, nitrogen and oxygen, and which additionally contains from 1 to 3 five or six membered rings, at least one of which is aromatic.

The term "alpha-amino acid" (α-amino acid) refers to both the naturally occurring amino acids and other "non-protein" α-amino acids commonly utilized by

those in the peptide chemistry arts when preparing synthetic analogues of naturally occurring peptides, including D and L forms. The naturally occurring amino acids are glycine, alanine, valine, leucine, isoleucine, serine, methionine, threonine, phenylalanine, tyrosine, tryptophan, cysteine, proline, histidine, aspartic acid, asparagine, glutamic acid, glutamine, γ-carboxyglutamic acid, arginine, ornithine and lysine. Examples of "non-protein" alpha-amino acids include hydroxylysine, homoserine, homotyrosine, homophenylalanine, citrulline, kynurenine, 4-aminophenylalanine, 3-(2-naphthyl)-alanine, 3-(1-naphthyl)-alanine, methionine sulfone, t-butyl-alanine, t-butylglycine, 4-hydroxyphenylglycine, aminoalanine, phenylglycine, vinylalanine, propargyl-glycine, 1,2,4-triazolo-3-alanine, 4,4,4-trifluoro-threonine, thyronine, 6-hydroxytryptophan, 5-hydro-xytryptophan, 3-hydroxykynurenine, 3-aminotyrosine, trifuoromethyl-alanine, 2-thienylalanine, (2-(4-pyridyl)ethyl)-cysteine, 3,4-dimethoxy-phenylalanine, 3-(2-thiazolyl)-alanine, ibotenic acid, 1-amino-1-cyclopentane-carboxylic acid, 1-amino-1-cyclohexanecarboxylic acid, quisqualic acid, 3-trifuoromethylphenylalanine, 4-trifuoro-methylphenylalanine, cyclohexylalanine, cyclo-hexylglycine, thiohistidine, 3-methoxytyrosine, elastatinal, norleucine, norvaline, alloisoleucine, homoarginine, thioproline, dehydroproline, hydroxy-proline, isonipectotic acid, homoproline, cyclohexyl-glycine, α-amino-n-butyric acid, cyclohexylalanine, aminophenylbutyric acid, phenylalanines substituted at the ortho, meta, or para position of the phenyl moiety with one or two of the following: a (C_1-C_4) alkyl, a (C_1-C_4) alkoxy, halogen or nitro groups or substituted with a methylenedioxy group; ß-2- and 3-thienyl-alanine, ß-2- and 3-furanylalanine, ß-2-, 3- and

4-pyridylalanine, ß-(benzothienyl-2- and 3-yl)alanine, ß-(1- and 2-naphthyl)alanine, O-alkylated derivatives of serine, threonine or tyrosine, S-alkylated cysteine, S-alkylated homocysteine, O-sulfate, O-phosphate and O-carboxylate esters of tyrosine, 3-sulfo-tyrosine, 3-carboxy-tyrosine, 3-phospho-tyrosine, 4-methane sulfonic acid ester of tyrosine, 4-methane phosphonic acid ester of tyrosine, 3,5-diiodotyrosine, 3-nitro-tyrosine, ε-alkyl lysine, and delta-alkyl ornithine. Any of these α-amino acids may be substituted with a methyl group at the alpha position, a halogen at any aromatic residue on the α-amino side chain, or an appropriate protective group at the O, N, or S atoms of the side chain residues. Appropriate protective groups are disclosed in "Protective Groups In Organic Synthesis," T.W. Greene and P.G.M. Wuts, J. Wiley & Sons, NY, NY, 1991.

The term "α-amino acid side chain residue" refers to a chemical moiety which is attached to the α-carbon of an alpha-amino acid.

The term "bioisosteric replacement for $-CO_2H$" refers to group which may substitute for a carboxylic acid group in bioactive molecules. Examples of such groups are disclosed in Christopher A. Lipinski, "Bioisosteres in Drug Design" Annual Reports In Medical Chemistry, 21, pp. 286-88 (1986), and in C.W. Thornber, "Isosterism and Molecular Modification in Drug Design" Chemical Society Reviews, pp. 563-580 (1979).

The term "association" is used in reference to a condition of proximity between an inhibitor or portions thereof to an ICE molecule or portions thereof wherein the juxtaposition is energetically favored by electrostatic or van der Waals interactions.

The term "hydrogen bond" refers to a favorable interaction that occurs whenever a suitable

donor atom, X, bearing a proton, H, and a suitable acceptor atom, Y, have a separation of between 2.5Å and 3.5Å and where the angle X-H - - - Y is greater than 90 degrees. Suitable donor and acceptor atoms are well understood in medicinal chemistry (G.C. Pimentel and A.L. McClellan, The Hydrogen Bond, Freeman, San Francisco, 1960; R. Taylor and O. Kennard, "Hydrogen Bond Geometry in Organic Crystals", Accounts of Chemical Research, 17, pp. 320-326 (1984)).

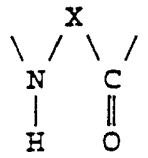
The term "salt bridge" refers to the non-covalent attractive interaction between a positively charged moiety (P) and a negatively charged moiety (N) when the distance between the centers of mass of P and N is between 2 and 6 Angstroms. In calculating the center of mass, atoms which may contain a formal charge and atoms immediately adjacent to these are included. For example, a salt bridge may be formed between the positively charged guanidinium side chain of an arginine residue and the negative charged carboxylate side chain of a glutamate residue. Salt bridges are well understood in medicinal chemistry (L. Stryer, Biochemistry, Freeman, San Francisco, (1975); K.A. Dill, "Dominant Forces in Protein Folding", Biochemistry, 29, No. 31, pp. 7133-7155, (1990)).

The term "center of mass" refers to a point in three-dimensional space which represents a weighted average position of the masses that make up an object.

The terms "backbone chain" and "backbone" refer to the portion of a polypeptide which comprises the repeating unit -CO-CH-NH-.

The term "scaffold" refers to a structural building block which forms the basis of an ICE inhibitor according to this invention. Various moieties and functional groups are intended to be appended to the scaffold. The scaffolds of this

invention are thus depicted having open valences. Various scaffolds of ICE inhibitors according to this invention include the portions:



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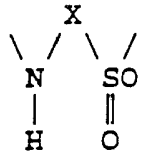


In those scaffolds, the NH and CO or SO_2 moieties represent a first and a second hydrogen bonding moiety, said moieties each being capable of forming a hydrogen bond with a backbone atom of ICE, said backbone atom being selected from the group consisting of the carbonyl oxygen of Arg-341, the amide -NH- of Arg-341, the carbonyl oxygen of Ser-339 and the amide -NH- of Ser-339.

The term "substitute" refers to the replacement of a hydrogen atom in a compound with a substituent group. In the present invention, those hydrogen atoms which form a part of a hydrogen bonding moiety which is capable of forming a hydrogen bond with the carbonyl oxygen of Arg-341 of ICE or the carbonyl oxygen of Ser-339 of ICE are excluded from substitution. These excluded hydrogen atoms include those which comprise an -NH- group which is alpha to a Z or a -CO- group and are depicted as -NH- rather than an X group or some other designation in the following diagrams: (a) through (t), (v) through (y), and (I) through (VIID).

The term "straight chain" refers to a contiguous unbranching string of covalently bound members, i.e. atoms, which form a portion of a ring. The straight chain and the ring of which it forms a part may be substituted, but these substituents are not a part of the straight chain.

The term "K_i" refers to a numerical measure of the effectiveness of a compound in inhibiting the activity of a target enzyme such as ICE. Lower values of K_i reflect higher effectiveness. The K_i value is a derived by fitting experimentally determined rate data to standard enzyme kinetic equations (see I. H. Segel, Enzyme Kinetics, Wiley-Interscience, 1975).

The term "minimize" refers to the systematic altering of the atomic geometry of a molecule or molecular complex so that any further minor perturbation of the atomic geometry would cause the total energy of the system as measured by a molecular mechanics force-field to increase. Minimization and molecular mechanics force-fields are well understood in computational chemistry [U. Burkert and N.L. Allinger, Molecular Mechanics, ACS Monograph 177, American Chemical Society, Washington, D.C. 1982 pages 59-78].

The term "strain energy" is used in this application to refer to the difference between the free conformation energy of a compound and the bound conformation energy of that compound when bound to ICE. The strain energy can be determined by the following steps: Evaluate the energy of the molecule when it has the conformation necessary for binding to ICE. Then minimize and reevaluate the energy -- this is the free conformation energy. The strain energy for binding of a potential inhibitor to ICE is the difference between the free conformation energy and the bound conformation energy. In a preferred embodiment, the strain energy

of an inhibitor of the present invention is less than about 10 kcal/mol.

The term "patient" as used in this application refers to any mammal, especially humans.

The term "pharmaceutically effective amount" refers to an amount effective in treating or ameliorating an IL-1 mediated disease in a patient. The term "prophylactically effective amount" refers to an amount effective in preventing or substantially lessening IL-1 mediated disease in a patient.

The term "pharmaceutically acceptable carrier or adjuvant" refers to a non-toxic carrier or adjuvant that may be administered to a patient, together with a compound of this invention, and which does not destroy the pharmacological activity thereof.

The term "pharmaceutically acceptable derivative" means any pharmaceutically acceptable salt, ester, or salt of such ester, of a compound of this invention or any other compound which, upon administration to a recipient, is capable of providing (directly or indirectly) a compound of this invention or an anti-ICE active metabolite or residue thereof.

Pharmaceutically acceptable salts of the compounds of this invention include, for example, those derived from pharmaceutically acceptable inorganic and organic acids and bases. Examples of suitable acids include hydrochloric, hydrobromic, sulfuric, nitric, perchloric, fumaric, maleic, phosphoric, glycolic, lactic, salicylic, succinic, toluene-p-sulfonic, tartaric, acetic, citric, methanesulfonic, formic, benzoic, malonic, naphthalene-2-sulfonic and benzenesulfonic acids. Other acids, such as oxalic, while not in themselves pharmaceutically acceptable, may be employed in the preparation of salts useful as intermediates in obtaining the compounds of the

invention and their pharmaceutically acceptable acid addition salts. Salts derived from appropriate bases include alkali metal (e.g., sodium), alkaline earth metal (e.g., magnesium), ammonium and N-(C_{1-4} alkyl)$_4^+$ salts.

This invention also envisions the "quaternization" of any basic nitrogen-containing groups of the compounds disclosed herein. The basic nitrogen can be quaternized with any agents known to those of ordinary skill in the art including, for example, lower alkyl halides, such as methyl, ethyl, propyl and butyl chloride, bromides and iodides; dialkyl sulfates including dimethyl, diethyl, dibutyl and diamyl sulfates; long chain halides such as decyl, lauryl, myristyl and stearyl chlorides, bromides and iodides; and aralkyl halides including benzyl and phenethyl bromides. Water or oil-soluble or dispersible products may be obtained by such quaternization.

The ICE inhibitors of this invention may contain one or more "asymmetric" carbon atoms and thus may occur as racemates and racemic mixtures, single enantiomers, diastereomeric mixtures and individual diastereomers. All such isomeric forms of these compounds are expressly included in the present invention. Each stereogenic carbon may be of the R or S configuration. Although specific compounds and scaffolds exemplified in this application may be depicted in a particular stereochemical configuration, compounds and scaffolds having either the opposite stereochemistry at any given chiral center or mixtures thereof are also envisioned.

The ICE inhibitors of this invention may comprise ring structures which may optionally be substituted at carbon, nitrogen or other atoms by

various substituents. Such ring structures may be singly or multiply substituted. Preferably, the ring structures contain between 0 and 3 substituents. When multiply substituted, each substituent may be picked independently of any other substituent as long as the combination of substituents results in the formation of a stable compound.

Combinations of substituents and variables envisioned by this invention are only those that result in the formation of stable compounds. The term "stable", as used herein, refers to compounds which possess stability sufficient to allow manufacture and administration to a mammal by methods known in the art. Typically, such compounds are stable at a temperature of 40°C or less, in the absence of moisture or other chemically reactive conditions, for at least a week.

DETAILED DESCRIPTION OF THE INVENTION

In order that the invention herein described may be more fully understood, the following detailed description is set forth.

We have discovered that compounds possessing the following novel combination of features are surprisingly effective ICE inhibitors:

a) a first and a second hydrogen bonding moiety, each of said moieties being capable of forming a hydrogen bond with a different backbone atom of ICE, said backbone atom being selected from the group consisting of the carbonyl oxygen of Arg-341, the amide -NH- group of Arg-341, the carbonyl oxygen of Ser-339 and the amide -NH- group of Ser-339;

b) a first and a second moderately hydrophobic moiety, said moieties each being capable of associating with a separate binding pocket of ICE when the inhibitor is bound thereto, said binding pocket

being selected from the group consisting of the P2 binding pocket, the P3 binding pocket, the P4 binding pocket and the P' binding pocket; and

c) an electronegative moiety comprising one or more electronegative atoms, said atoms being attached to the same atom or to adjacent atoms in the moiety and said moiety being capable of forming one or more hydrogen bonds or salt bridges with residues in the P1 binding pocket of ICE.

Preferably, any moderately hydrophobic moiety associating with the P2 binding pocket of ICE does so in such a way that:

a) the distance from the center of mass of the moderately hydrophobic moiety in the P2 binding pocket to the carbonyl oxygen of Arg-341 of ICE is between about 7.1Å and about 12.5Å;

b) the distance from the center of mass of the moderately hydrophobic moiety in the P2 binding pocket to the amide nitrogen of Arg-341 of ICE is between about 6.0Å and about 12Å; and

c) the distance from the center of mass of the moderately hydrophobic moiety in the P2 binding pocket to the carbonyl oxygen of Ser-339 of ICE is between about 3.7Å and about 9.5Å.

Preferably, any moderately hydrophobic moiety associating with the P3 binding pocket of ICE does so in such a way that:

a) the distance from the center of mass of the moderately hydrophobic moiety in the P3 binding pocket to the carbonyl oxygen of Arg-341 of ICE is between about 3.9Å and about 9.5Å;

b) the distance from the center of mass of the moderately hydrophobic moiety in the P3 binding pocket to the amide nitrogen of Arg-341 of ICE is between about 5.4Å and about 11Å; and

c) the distance from the center of mass of the moderately hydrophobic moiety in the P3 binding pocket to the carbonyl oxygen of Ser-339 of ICE is between about 7.0Å and about 13Å.

Preferably, any moderately hydrophobic moiety associating with the P4 binding pocket of ICE does so in such a way that:

a) the distance from the center of mass of the moderately hydrophobic moiety in the P4 binding pocket to the carbonyl oxygen of Arg-341 of ICE is between about 4.5Å and about 7.5Å;

b) the distance from the center of mass of the moderately hydrophobic moiety in the P4 binding pocket to the amide nitrogen of Arg-341 of ICE is between about 5.5Å and about 8.5Å; and

c) the distance from the center of mass of the moderately hydrophobic moiety in the P4 binding pocket to the carbonyl oxygen of Ser-339 of ICE is between about 8Å and about 11Å.

Preferably, any moderately hydrophobic moiety associating with the P' binding pocket of ICE does so in such a way that:

a) the distance from the center of mass of the moderately hydrophobic moiety in the P' binding pocket to the carbonyl oxygen of Arg-341 of ICE is between about 11Å and about 16Å;

b) the distance from the center of mass of the moderately hydrophobic moiety in the P' binding pocket to the amide nitrogen of Arg-341 of ICE is between about 10Å and about 15Å; and

c) the distance from the center of mass of the moderately hydrophobic moiety in the P' binding pocket to the carbonyl oxygen of Ser-339 of ICE is between about 8Å and about 12Å.

More preferably, all of the above associative conditions are met in the compounds of this invention.

The practitioner skilled in the art will appreciate that there are a number of means to design the inhibitors of the present invention. These same means may be used to select a candidate compound for screening as an ICE inhibitor. This design or selection may begin with selection of the various moieties which fill binding pockets.

There are a number of ways to select moieties to fill individual binding pockets. These include visual inspection of a physical model or computer model of the active site and manual docking of models of selected moieties into various binding pockets. Modeling software that is well known and available in the art may be used. These include QUANTA [Molecular Simulations, Inc., Burlington, MA, 1992], SYBYL [Molecular Modeling Software, Tripos Associates, Inc., St. Louis, MO, 1992], AMBER [S.J. Weiner, P.A. Kollman, D.A. Case, U.C. Singh, C. Ghio, G. Alagona, and P. Weiner, J. Am. Chem. Soc., vol. 106, pp. 765-784 (1984)], or CHARMM [B.R. Brooks, R.E. Bruccoleri, B.D. Olafson, D.J. States, S Swaminathan, and M. Karplus, J. Comp. Chem. vol. 4, pp. 187-217 (1983)]. This modelling step may be followed by energy minimization with standard molecular mechanics forcefields such as CHARMM and AMBER. In addition, there are a number of more specialized computer programs to assist in the process of selecting the binding moieties of this invention. These include:

1. GRID (Goodford, P.J. A Computational Procedure for Determining Energetically Favorable Binding Sites on Biologically Important Macromolecules. J. Med. Chem., 28, pp. 849-857 (1985)). GRID is available from Oxford University, Oxford, UK.

2. MCSS (Miranker, A.; Karplus, M. Functionality Maps of Binding Sites: A Multiple Copy Simultaneous Search Method. Proteins: Structure, Function and Genetics, 11, pp. 29-34 (1991)). MCSS is available from Molecular Simulations, Burlington, MA.

3. AUTODOCK (Goodsell, D.S.; Olsen, A.J. Automated Docking of Substrates to Proteins by Simmulated Annealing. PROTEINS: Structure, Function and Genetics, 8, pp. 195-202 (1990)). AUTODOCK is available from the Scripps Research Institute, La Jolla, CA.

4. DOCK (Kuntz, I.D.; Blaney, J.M.; Oatley, S.J.; Langridge, R.; Ferrin, T.E. A Geometric Approach to Macromolecule-Ligand Interactions. J. Mol. Biol., 161, pp. 269-288 (1982)). DOCK is available from the University of California, San Francisco, CA.

Once suitable binding moieties have been selected, they can be assembled into a single inhibitor. This assembly may be accomplished by connecting the various moieties to a central scaffold. The assembly process may, for example, be done by visual inspection followed by manual model building, again using software such as Quanta or Sybyl. A number of other programs may also be used to help select ways to connect the various moieties. These include:

1. CAVEAT (Bartlett, P.A.; Shea, G.T.; Telfer, S.J.; Waterman, S. CAVEAT: A Program to Facilitate the Structure-Derived Design of Biologically Active Molecules. In "Molecular Recognition in Chemical and Biological Problems," Special Pub., Royal Chem. Soc., 78, pp. 182-196 (1989)). CAVEAT is available from the University of California, Berkeley, CA.

2. 3D Database systems such as MACCS-3D (MDL Information Systems, San Leandro, CA). This area has been recently reviewed by Martin (Martin, Y.C. 3D Database Searching in Drug Design. J. Med. Chem., 35, pp. 2145-2154 (1992)).

3. HOOK (available from Molecular Simulations, Burlington, MA).

In addition to the above computer assisted modeling of inhibitor compounds, the inhibitors of this invention may be constructed "de novo" using either an empty active site or optionally including some portions of a known inhibitor. Such methods are well known in the art. They include, for example:

1. LUDI (Bohm, H.J. The Computer Program LUDI: A New Method for the De Novo Design of Enzyme Inhibitors. J. Comp. Aid. Molec. Design., 6, 61-78 (1992)). LUDI is available from Biosym Technologies, San Diego, CA.

2. LEGEND (Nishibata, Y., Itai, A., Tetrahedron, 47, 8985 (1991)). LEGEND is available from Molecular Simultations, Burlington, MA.

3. LeapFrog (available from Tripos associates, St. Louis, MO).

A number of techniques commonly used for modeling drugs may be employed (For a review, see: Cohen, N.C.; Blaney, J.M.; Humblet, C.; Gund, P.; Barry, D.C., "Molecular Modeling Software and Methods for Medicinal Chemistry", J. Med. Chem., 33, pp. 883-894 (1990)). There are likewise a number of examples in the chemical literature of techniques that can be applied to specific drug design projects. For a review, see: Navia, M.A. and Murcko, M.A., "The Use of Structural Information in Drug Design", Current Opinions in Structural Biology, 2, pp. 202-210 (1992). Some examples of these specific applications include: Baldwin, J.J. et al., "Thienothiopyran-2-sulfonamides: Novel Topically Active Carbonic Anhydrase Inhibitors for the Treatment of Glaucoma", J. Med. Chem., 32, pp. 2510-2513 (1989); Appelt, K. et al., "Design of Enzyme Inhibitors Using Iterative Protein Crystallographic Analysis", J. Med. Chem., 34, pp. 1925-1934 (1991); and

Ealick, S.E. et al., "Application of Crystallographic and Modeling Methods in the Design of Purine Nucleotide Phosphorylase Inhibitors" Proc. Nat. Acad. Sci. USA, 88, pp. 11540-11544 (1991).

Using the novel combination of steps of the present invention, the skilled artisan can advantageously avoid time consuming and expensive experimentation to determine enzymatic inhibition activity of particular compounds. The method also is useful to facilitate rational design of ICE inhibitors and therapeutic and prophylactic agents against IL-1-mediated diseases. Accordingly, the present invention relates to such inhibitors.

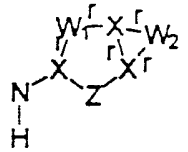
A variety of conventional techniques may be used to carry out each of the above evaluations as well as the evaluations necessary in screening a candidate compound for ICE inhibiting activity. Generally, these techniques involve determining the location and binding proximity of a given moiety, the occupied space of a bound inhibitor, the deformation energy of binding of a given compound and electrostatic interaction energies. Examples of conventional techniques useful in the above evaluations include: quantum mechanics, molecular mechanics, molecular dynamics, Monte Carlo sampling, systematic searches and distance geometry methods (G.R. Marshall, Ann. Rev. Pharmacol. Toxicol., 27, p. 193 (1987)). Specific computer software has been developed for use in carrying out these methods. Examples of programs designed for such uses include: Gaussian 92, revision E.2 (M.J. Frisch, Gaussian, Inc., Pittsburgh, PA ©1993); AMBER, version 4.0 (P.A. Kollman, University of California at San Francisco, ©1993); QUANTA/CHARMM [Molecular Simulations, Inc., Burlington, MA ©1992]; and Insight II/Discover (Biosysm Technologies Inc., San Diego, CA ©1992). These programs may be implemented,

for instance, using a Silicon Graphics Indigo 2 workstation or IBM RISC/6000 workstation model 550. Other hardware systems and software packages will be known and of evident applicability to those skilled in the art.

Different classes of active ICE inhibitors, according to this invention, may interact in similar ways with the various binding pockets of the ICE active site. The spatial arrangement of these important groups is often referred to as a pharmacophore. The concept of the pharmacophore has been well described in the literature (D. Mayer, C.B. Naylor, I. Motoc, and G.R. Marshall, J. Comp. Aided Molec. Design vol. 1, pp. 3-16 (1987); A. Hopfinger and B.J. Burke, in Concepts and Applications of Molecular Similarity, M.A. Johnson and G.M. Maggiora, ed., Wiley (1990)).

Different classes of ICE inhibitors of this invention may also use different scaffolds or core structures, but all of these cores will allow the necessary moieties to be placed in the active site such that the specific interactions necessary for binding may be obtained. These compounds are best defined in terms of their ability to match the pharmacophore, i.e., their structural identity relative to the shape and properties of the active site of ICE.

The ICE inhibitors of one embodiment of this invention comprise a first and a second hydrogen bonding moiety, a first and a second moderately hydrophobic moiety, and an electronegative moiety which comprise or are covalently bound to one of the following scaffolds:

(I) 

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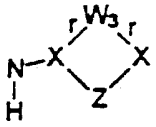
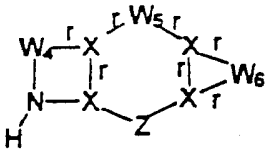
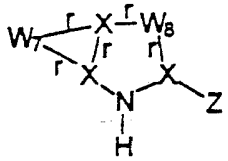
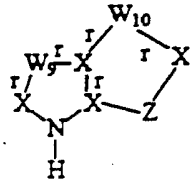
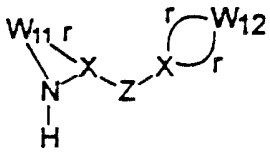
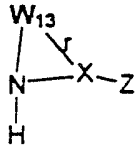
(II)  ;

(III)  ;

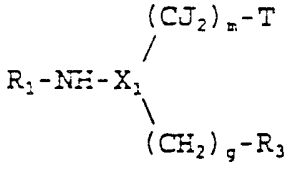
(IV)  ;

(V)  ;

(VI)  ; and

(VII)  .

The ICE inhibitors of another embodiment (A) of this invention are those of formula α:

α  ,

wherein:

X_1 is CH or N;

g is 0 or 1;

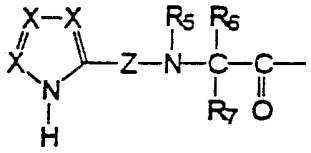
each J is independently selected from the group consisting of -H, -OH, and -F, provided that when a first and second J are bound to a C and said first J is -OH, said second J is -H;

m is 0, 1, or 2;

T is $-Ar_3$, -OH, $-CF_3$, $-CO-CO_2H$, $-CO_2H$ or any bioisosteric replacement for $-CO_2H$;

R_1 is selected from the group consisting of the following formulae, in which any ring may optionally be singly or multiply substituted at any carbon by Q_1, at any nitrogen by R_5, or at any atom by =O, -OH, $-CO_2H$, or halogen, and in which any saturated ring may optionally be unsaturated at one or two bonds:

(a)



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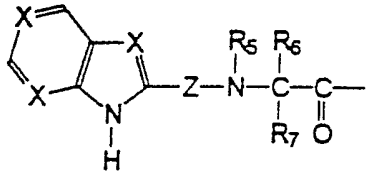

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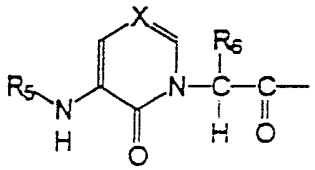

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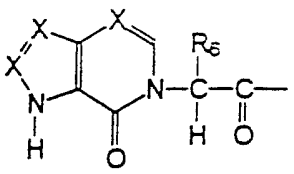

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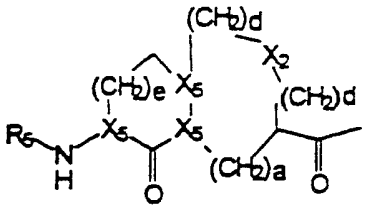
(e) 

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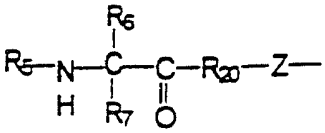
(f) 

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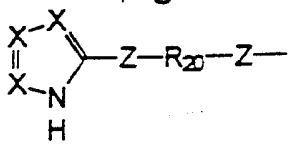
(g) 

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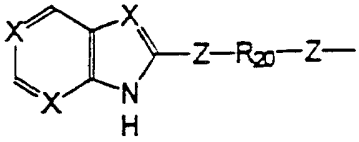
(h) 

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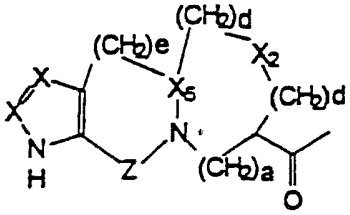
(i) 

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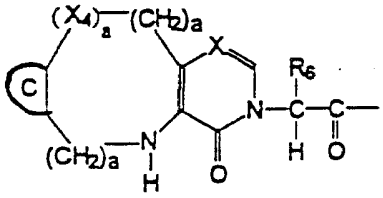
(j) 

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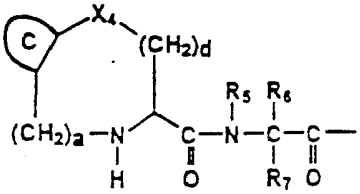
(k) 

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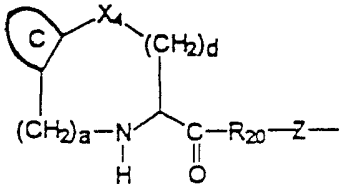
(l) 

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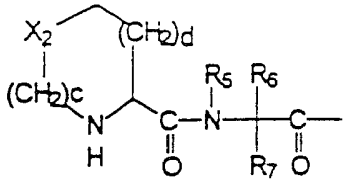
(m) 

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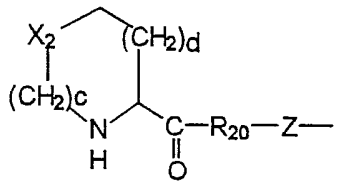
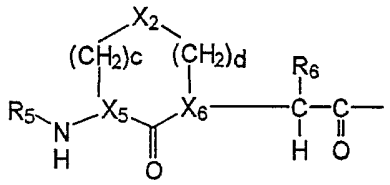
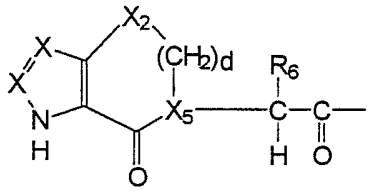
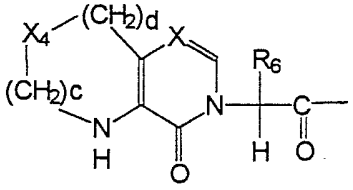
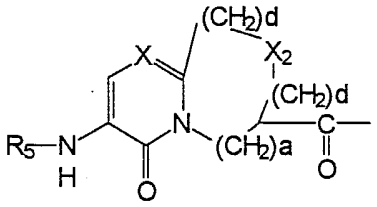
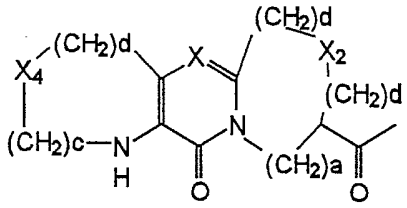
(n)  ;

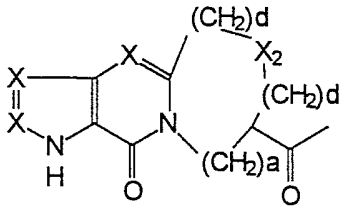
(o)  ;

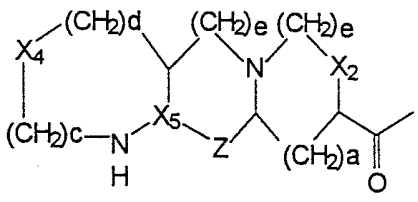
(p)  ;

(q)  ;

(r)  ;

(s)  ;

(t)  ; and

(v)  ;

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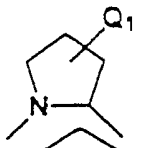
(aa1) 

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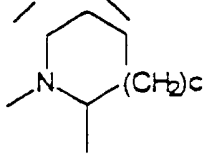
(aa2) 

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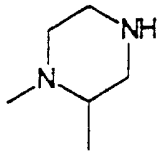
(aa3) 

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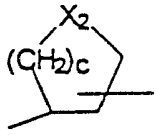
(aa4) 

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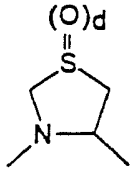
(aa5) 

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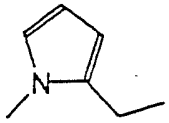
(bb) 

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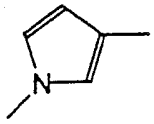
(cc) 

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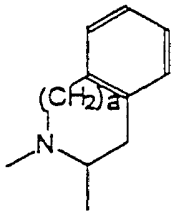
(dd) 

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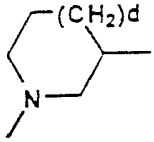
(ee) 

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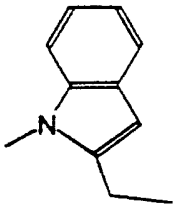
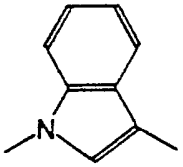
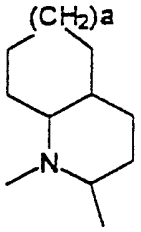
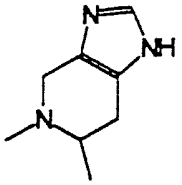
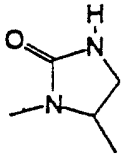
(ff)  ;

(gg)  ;

(gga)  ;

(ggb)  ; and

(ggc)  ;

wherein each ring C is independently chosen from the group consisting of benzo, pyrido, thieno, pyrrolo, furano, thiazolo, isothiazolo, oxazolo, isoxazolo, pyrimido, imidazolo, cyclopentyl, and cyclohexyl;

R_3 is

-CN,

$-CH=CH-R_9$,

$-CH=N-O-R_9$,

$-(CH_2)_{1-3}-T_1-R_9$,

$-CJ_2-R_9$,

$-CO-R_{13}$, or

$$-CO-CO-N\begin{matrix}/R_5\\ \backslash R_{10};\end{matrix}$$

each R_4 is independently selected from the group consisting of:

$-H$,

$-Ar_1$,

$-R_9$,

$-T_1-R_9$, and

$-(CH_2)_{1,2,3}-T_1-R_9$,

each T_1 is independently selected from the group consisting of:

$-CH=CH-$,

$-O-$,

$-S-$,

$-SO-$,

$-SO_2-$,

$-NR_{10}-$,

$-NR_{10}-CO-$,

$-CO-$,

$-O-CO-$,

$-CO-O-$,

$-CO-NR_{10}-$,

$-O-CO-NR_{10}-$,

$-NR_{10}-CO-O-$,

$-NR_{10}-CO-NR_{10}-$,

$-SO_2-NR_{10}-$,

$-NR_{10}-SO_2-$, and

$-NR_{10}-SO_2-NR_{10}-$,

each R_5 is independently selected from the group consisting of:

$-H$,

$-Ar_1$,

$-CO-Ar_1$,

$-SO_2-Ar_1$,

$-R_9$,

$-CO-R_9$,

$-CO-O-R_9$,

$-SO_2-R_9$,

$-CO-N(Ar_1)(R_{10})$,

$-SO_2-N(Ar_1)(R_{10})$,

$-CO-N(R_9)(R_{10})$, and

$-SO_2-N(R_9)(R_{10})$,

R_6 and R_7 taken together form a saturated 4-8 member carbocyclic ring or heterocyclic ring containing -O-, -S-, or -NH-, or

R_7 is -H and R_6 is

-H

$-Ar_1$,

$-R_9$, or

$-(CH_2)_{1,2,3}-T_1-R_9$;

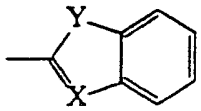
each R_9 is a C_{1-6} straight or branched alkyl group optionally singly or multiply substituted by -OH, -F, or =O and optionally substituted with one or two Ar_1 groups;

each R_{10} is independently selected from the group consisting of -H or a C_{1-6} straight or branched alkyl group;

each R_{13} is independently selected from the group consisting of $-Ar_2$ and $-R_4$;

each Ar_1 is a cyclic group independently selected from the set consisting of an aryl group which contains 6, 10, 12, or 14 carbon atoms and between 1 and 3 rings, a cycloalkyl group which contains between 3 and 15 carbon atoms and between 1 and 3 rings, said cycloalkyl group being optionally benzofused, and a heterocycle group containing between 5 and 15 ring atoms and between 1 and 3 rings, said heterocycle group containing at least one heteroatom group selected from -O-, -S-, -SO-, $-SO_2-$, =N-, and -NH-, said heterocycle group optionally containing one or more double bonds, said heterocycle group optionally comprising one or more aromatic rings, and said cyclic group optionally being singly or multiply substituted by =O, -OH, perfluoro C_{1-3} alkyl, or $-Q_1$;

each Ar_2 is independently selected from the following group, in which any ring may optionally be substituted by $-Q_1$:

(hh) 

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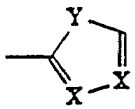
(ii) 

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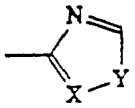
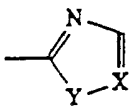
(jj) 

; and

(kk) 

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