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(54) **Peptides and related molecules that bind to TALL - 1**

(57) The present invention concerns therapeutic agents that modulate the activity of TALL-1. In accordance with the present invention, modulators of TALL-1 may comprise an amino acid sequence Dz²Lz⁴ wherein the z² is an amino acid residue and z⁴ is threonyl or isoleucyl. Exemplary molecules comprise a sequence of the formulae a¹a²a³Cd⁶La⁸a⁹a¹⁰Ca¹²a¹³a¹⁴ (SEQ.ID.NO: 100), b¹b²b³Cb⁵b⁶Db⁸Lb¹⁰b¹¹b¹²b¹³b¹⁴Cb¹⁶b¹⁷b¹⁸ (SEQ.ID.NO:104), c¹c²c³Cc⁵Dc⁷Lc⁹c¹⁰c¹¹c¹²c¹³c¹⁴Cc¹⁶c¹⁷c¹⁸ (SEQ.ID.NO:105), d¹d²d³Cd⁵d⁶d⁷Wd¹⁰Ld¹³d¹⁴d¹⁵Cd¹⁶d¹⁷d¹⁸ (SEQ.ID.NO:106),

e¹e²e³Ce⁵e⁶e⁷De⁹Le¹¹Ke¹³Ce¹⁵e¹⁶e¹⁷e¹⁹ (SEQ.ID.NO:107), f¹f²f³Kf⁵Df⁵Lf⁹f¹⁰Qf¹²f¹³f¹⁴ (SEQ.ID.NO:109) wherein the substituents are defined in the specification. The invention further comprises compositions of matter of the formula (X¹)_a-V¹-(X²)_b wherein V¹ is a vehicle that is covalently attached to one or more of the above TALL-1 modulating compositions of matter. The vehicle and the TALL-1 modulating composition of matter may be linked through the N- or C-terminus of the TALL-1 modulating portion. The preferred vehicle is an Fc domain, and the preferred Fc domain is an IgG Fc domain.

EP 2 845 864 A2

Description

[0001] This application is related to U.S. provisional application no. 60/290,196, filed May 11, 2041, which is hereby incorporated by reference.

Background of the Invention

[0002] After years of study in necrosis of tumors, tumor necrosis factors (TNFs) α and β were finally cloned in 1984. The ensuing years witnessed the emergence of a superfamily of TNF cytokines, including fas ligand (FasL), CD27 ligand (CD27L), CD30 ligand (CD30L), CD40 ligand (CD40L), TNF-related apoptosis-inducing ligand (TRAIL, also designated AGP-1), osteoprotegerin binding protein (OPG-BP or OPG ligand), 4-1BB ligand, LIGHT, APRIL, and TALL-1. Smith et al. (1994), *Cell* 76: 959-962; Lacey et al. (1998), *Cell* 93:165-176; Chichepotiche et al. (1997), *I. Biol. Chem.* 272: 32401-32410; Mauri et al. (1998), *Immunity* 8:21-30; Hahne et al. (1998), *I. Exp. Med.* 188:1185-90; Shu et al. (1999), *I. Leukocyte Biology* 65: 680-3. This family is unified by its structure, particularly at the C-terminus. In addition, most members known to date are expressed in immune compartments, although some members are also expressed in other tissues or organs, as well. Smith et al. (1994), *Cell* 76: 959-62. All ligand members, with the exception of LT- α , are type II transmembrane proteins, characterized by a conserved 150 amino acid region within C-terminal extracellular domain. Though restricted to only 20-25% identity, the conserved 150 amino acid domain folds into a characteristic β -pleated sheet sandwich and trimerizes. This conserved region can be proteolytically released, thus generating a soluble functional form. Banner et al. (1993), *Cell* 73:431-445.

[0003] Many members within this ligand family are expressed in lymphoid enriched tissues and play important roles in the immune system development and modulation. Smith et al. (1994). For example, TNF α is mainly synthesized by macrophages and is an important mediator for inflammatory responses and immune defenses. Tracey & Cerami (1994), *Ann. Rev. Med.* 45:491-503. Fas-L, predominantly expressed in activated T cell, modulates TCR-mediated apoptosis of thymocytes. Nagata, S. & Suda, T. (1995) *Immunology Today* 16:39-43; Castrim et al. (1996), *Immunity* 5: 617-27. CD40L, also expressed by activated T cells, provides an essential signal for B cell survival, proliferation and immunoglobulin isotype switching. Noelle (1996), *Immunity* 4:415-9.

[0004] The cognate receptors for most of the TNF ligand family members have been identified. These receptors share characteristic multiple cysteine-rich repeats within their extracellular domains, and do not possess catalytic motifs within cytoplasmic regions. Smith et al. (1994). The receptors signal through direct interactions with death domain proteins (e.g. TRADD, FADD, and RIP) or with the TRAF proteins (e.g. TRAF2, TRAF3, TRAF5, and TRAF6), triggering divergent and overlapping signaling pathways, e.g. apoptosis, NF- κ B activation, or JNK activation. Wallach et al. (1999), *Annual Review of Immunology* 17: 331-67. These signaling events lead to cell death, proliferation, activation or differentiation. The expression profile of each receptor member varies. For example, TNFR1 is expressed on a broad spectrum of tissues and cells, whereas the cell surface receptor of OPGL is mainly restricted to the osteoclasts. Hsu et al. (1999) *Proc. Natl. Acad. Sci. USA* 96:3540-5.

[0005] A number of research groups have recently identified TNF family ligands with the same or substantially similar sequence. The ligand has been variously named neutrokin α (WO 98/18921, published May 7, 1998), 63954 (WO 98/27114, published June 25, 1998), TL5 (EP 869180, published October 7, 1998), NTN-2 (WO 98/55620 and WO 98/55621, published December 10, 1998), TNRL1-alpha (WO 9911791, published March 11, 1999), kay ligand (WO99/12964, published March 18, 1999), and AGP-3 (U.S. Prov. App. Nos. 60/119,906, filed February 12, 1999 and 60/166,271, filed November 18, 1999, respectively); and TALL-1 (WO 00/68378, published Nov. 16, 2000). Each of these references is hereby incorporated by reference. Hereinafter, the ligands reported therein are collectively referred to as TALL-1.

[0006] TALL-1 is a member of the TNF ligand superfamily that is functionally involved in B cell survival and proliferation. Transgenic mice overexpressing TALL-1 had severe B cell hyperplasia and lupus-like autoimmune disease. Khare et al. (2000) *PNAS* 97(7):3370-3375). Both TACI and BCMA serve as cell surface receptors for TALL-1. Gross et al. (2000), *Nature* 404: 995-999; Ware (2000), *I. Exp. Med.* 192(11): F35-F37; Ware (2000), *Nature* 404:949-950; Xia et al. (2000), *J. Exp. Med.* 192(1):137-143; Yu et al. (2000), *Nature Immunology* 1(3):252-256; Marsters et al. (2000), *Current Biology* 10:785-788; Hatzoglou et al. (2000) *I. of Immunology* 165:1322-1330; Shu et al. (2000) *PNAS* 97(16):9156-9161; Thompson et al. (2000) *I. Exp. Med.* 192(1):129-135; Mukhopadhyay et al. (1999) *J. Biol. Chem.* 274(23):15978-81; Shu et al. (1999) *I. Leukocyte Biol.* 65:680-683; Gruss et al. (1995) *Blood* 85(12):3378-3404; Smith et al. (1994), *Cell* 76: 959-962; U.S. Pat. No. 5,969,102, issued October 19, 1999; WO 00/67034, published November 9, 2000; WO 00/40716, published July 13, 2000; WO 99/35170, published July 15, 1999. Both receptors are expressed on B cells and signal through interaction with TRAF proteins. In addition, both TACI and BCMA also bind to another TNF ligand family member, APRIL. Yu et al. (2000), *Nature Immunology* 1(3) :252-256. APRIL has also been demonstrated to induce B cell proliferation.

[0007] To date, no recombinant or modified proteins employing peptide modulators of TALL-1 have been disclosed. Recombinant and modified proteins are an emerging class of therapeutic agents. Useful modifications of protein thera-

peutic agents include combination with the "Fc" domain of an antibody and linkage to polymers such as polyethylene glycol (PEG) and dextran. Such modifications are discussed in detail in a patent application entitled, "Modified Peptides as Therapeutic Agents," published WO 00/24782, which is hereby incorporated by reference in its entirety.

[0008] A much different approach to development of therapeutic agents is peptide library screening. The interaction of a protein ligand with its receptor often takes place at a relatively large interface. However, as demonstrated for human growth hormone and its receptor, only a few key residues at the interface contribute to most of the binding energy. Clackson et al. (1995), *Science* 267:383-6. The bulk of the protein ligand merely displays the binding epitopes in the right topology or serves functions unrelated to binding. Thus, molecules of only "peptide" length (2 to 40 amino acids) can bind to the receptor protein of a given large protein ligand. Such peptides may mimic the bioactivity of the large protein ligand ("peptide agonists") or, through competitive binding, inhibit the bioactivity of the large protein ligand ("peptide antagonists").

[0009] Phage display peptide libraries have emerged as a powerful method in identifying such peptide agonists and antagonists. See, for example, Scott et al. (1990), *Science* 249:386; Devlin et al. (1990), *Science* 249:404; U.S. Pat. No. 5,223,409, issued June 29, 1993; U.S. Pat. No. 5,733,731, issued March 31, 1998; U.S. Pat. No. 5,498,530, issued March 12, 1996; U.S. Pat. No. 5,432,018, issued July 11, 1995; U.S. Pat. No. 5,338,665, issued August 16, 1994; U.S. Pat. No. 5,922,545, issued July 13, 1999; WO 96/40987, published December 19, 1996; and WO 98/15833, published April 16, 1998 (each of which is incorporated by reference in its entirety). In such libraries, random peptide sequences are displayed by fusion with coat proteins of filamentous phage. Typically, the displayed peptides are affinity-eluted against an immobilized target protein. The retained phages may be enriched by successive rounds of affinity purification and repropagation. The best binding peptides may be sequenced to identify key residues within one or more structurally related families of peptides. See, e.g., Cwirla et al. (1997), *Science* 276:1696-9, in which two distinct families were identified. The peptide sequences may also suggest which residues may be safely replaced by alanine scanning or by mutagenesis at the DNA level. Mutagenesis libraries may be created and screened to further optimize the sequence of the best binders. Lowman (1997), *Ann. Rev. Biophys. Biomol. Struct.* 26:401-24.

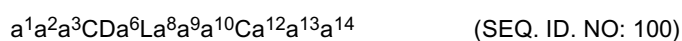
[0010] Structural analysis of protein-protein interaction may also be used to suggest peptides that mimic the binding activity of large protein ligands. In such an analysis, the crystal structure may suggest the identity and relative orientation of critical residues of the large protein ligand, from which a peptide may be designed. See, e.g., Takasaki et al. (1997), *Nature Biotech.* 15:1266-70. These analytical methods may also be used to investigate the interaction between a receptor protein and peptides selected by phage display, which may suggest further modification of the peptides to increase binding affinity.

[0011] Other methods compete with phage display in peptide research. A peptide library can be fused to the carboxyl terminus of the *lac* repressor and expressed in *E. coli*. Another *E. coli*-based method allows display on the cell's outer membrane by fusion with a peptidoglycan-associated lipoprotein (PAL). Hereinafter, these and related methods are collectively referred to as "*E. coli* display." In another method, translation of random RNA is halted prior to ribosome release, resulting in a library of polypeptides with their associated RNA still attached. Hereinafter, this and related methods are collectively referred to as "ribosome display." Other methods employ peptides linked to RNA; for example, PROfusion technology, Phyllos, Inc. See, for example, Roberts & Szostak (1997), *Proc. Natl. Acad. Sci. USA*, 94:12297-303. Hereinafter, this and related methods are collectively referred to as "RNA-peptide screening." Chemically derived peptide libraries have been developed in which peptides are immobilized on stable, non-biological materials, such as polyethylene rods or solvent-permeable resins. Another chemically derived peptide library uses photolithography to scan peptides immobilized on glass slides. Hereinafter, these and related methods are collectively referred to as "chemical-peptide screening." Chemical-peptide screening may be advantageous in that it allows use of D-amino acids and other unnatural analogues, as well as non-peptide elements. Both biological and chemical methods are reviewed in Wells & Lowman (1992), *Curr. Opin. Biotechnol.*, 3: 355-62. Conceptually, one may discover peptide mimetics of any protein using phage display, RNA-peptide screening, and the other methods mentioned above.

Summary of the Invention

[0012] The present invention concerns therapeutic agents that modulate the activity of TALL-1. In accordance with the present invention, modulators of TALL-1 may comprise an amino acid sequence Dz²Lz⁴ (SEQ ID NO:108) wherein z² is an amino acid residue and z⁴ is threonyl or isoleucyl. Such modulators of TALL-1 comprise molecules of the following formulae:

I(a)



wherein:

EP 2 845 864 A2

a¹, a², a³ are each independently absent or amino acid residues;
a⁶ is an amino acid residue;
a⁹ is a basic or hydrophobic residue;
a⁸ is threonyl or isoleucyl;
a¹² is a neutral polar residue; and
a¹³ and a¹⁴ are each independently absent or amino acid residues.

I(b)

b¹b²b³Cb⁵b⁶Db⁸Lb¹⁰b¹¹b¹²b¹³b¹⁴Cb¹⁶b¹⁷b¹⁸ (SEQ. ID. NO: 104)

wherein:

b¹ and b² are each independently absent or amino acid residues;
b³ is an acidic or amide residue;
b⁵ is an amino acid residue;
b⁶ is an aromatic residue;
b⁸ is an amino acid residue;
b¹⁰ is T or I;
b¹¹ is a basic residue;
b¹² and b¹³ are each independently amino acid residues;
b¹⁴ is a neutral polar residue; and
b¹⁶, b¹⁷, and b¹⁸ are each independently absent or amino acid residues.

I(c)

c¹c²c³Cc⁵Dc⁷Lc⁹c¹⁰c¹¹c¹²c¹³C¹⁴Cc¹⁶C¹⁷C¹⁸ (SEQ. ID. NO:105)

wherein:

c¹, c², and c³ are each independently absent or amino acid residues;
c⁵ is an amino acid residue;
c⁷ is an amino acid residue;
c⁹ is T or I;
c¹⁰ is a basic residue;
c¹¹ and c¹² are each independently amino acid residues;
c¹³ is a neutral polar residue;
c¹⁴ is an amino acid residue;
c¹⁶ is an amino acid residue;
c¹⁷ is a neutral polar residue; and
c¹⁸ is an amino acid residue or is absent.

I(d)

d¹d²d³Cd⁵d⁶d⁷WDd¹⁰Ld¹²d¹³d¹⁴Cd¹⁵d¹⁶d¹⁷ (SEQ. ID. NO:106)

wherein:

d¹, d², and d³ are each independently absent or amino acid residues;
d⁵, d⁶, and d⁷ are each independently amino acid residues;
d¹⁰ is an amino acid residue;
d¹³ is T or I;
d¹⁴ is an amino acid residue; and
d¹⁶, d¹⁷, and d¹⁸ are each independently absent or amino acid residues.

I(e)

e¹e²e³Ce⁵e⁶e⁷De⁹Le¹¹Ke¹³Ce¹⁵e¹⁶e¹⁷e¹⁸ (SEQ. ID. NO: 107)

wherein:

5 e¹, e², and e³ are each independently absent or amino acid residues;
 e⁵, e⁶, e⁷, e⁹, and e¹³ are each independently amino acid residues;
 e¹¹ is T or I; and
 e¹⁵, e¹⁶, and e¹⁷ are each independently absent or amino acid residues.

10 I(f)

f¹f²f³Kf⁵Df⁷Lf⁹f¹⁰Qf¹²f¹³f¹⁴ (SEQ. ID NO: 109)

wherein:

15 f¹, f², and f³ are absent or are amino acid residues (with one of f¹, f², and f³ preferred to be C when one of f¹², f¹³, and f¹⁴ is C);
 f⁵ is W, Y, or F (W preferred);
 f⁷ is an amino acid residue (L preferred);
 f⁹ is T or I (T preferred);
 20 f¹⁰ is K, R, or H (K preferred);
 f¹² is C, a neutral polar residue, or a basic residue (W, C, or R preferred);
 f¹³ is C, a neutral polar residue or is absent (V preferred); and
 f¹⁴ is any amino acid residue or is absent;
 25 provided that only one of f¹, f², and f³ may be C, and only one of f¹², f¹³, and f¹⁴ may be C.

[0013] Compounds of formulae I(a) through I(f) above incorporate Dz²Lz⁴, as well as SEQ ID NO: 63 hereinafter. The sequence of I(f) was derived as a consensus sequence as described in Example 1 hereinbelow. Of SIcompounds within formula I(f), those within the formula

30 I(f')

f¹f²f³KWDF⁷Lf⁹KQf¹²f¹³f¹⁴ (SEQ ID NO: 125)

are preferred. Compounds falling within formula I(f) include SEQ ID NOS: 32, 58, 60, 62, 63, 66, 67, 69, 70, 114, 115, 122, 123, 124, 147-150, 152-177, 179, 180, 187.

35 **[0014]** Also in accordance with the present invention are compounds having the consensus motif:

PFPE (SEQ ID NO: 110)

which also bind TALL-1.

40 **[0015]** Further in accordance with the present invention are compounds of the formulae:

I(g)

g¹g²g³Cg⁵PFg⁸Wg¹⁰Cg¹¹g¹²g¹³ (SEQ. ID. NO.101)

45 wherein:

g¹, g² and g³ are each independently absent or amino acid residues;
 g⁵ is a neutral polar residue;
 g⁸ is a neutral polar residue;
 50 g¹⁰ is an acidic residue;
 g¹² and g¹³ are each independently amino acid residues; and
 g¹⁴ is absent or is an amino acid residue.

I(h)

55 h¹h²h³CWh⁶h⁷Wgh¹⁰Ch¹²h¹³h¹⁴ (SEQ. ID. NO: 102)

wherein:

h¹, h², and h³ are each independently absent or amino acid residues;
 h⁶ is a hydrophobic residue;
 h⁷ is a hydrophobic residue;
 h¹⁰ is an acidic or polar hydrophobic residue; and
 h¹², h¹³, and h¹⁴ are each independently absent or amino acid residues.

I(i)

i¹i²i³C_i⁵i⁶i⁷i⁸i⁹i¹⁰C_i¹²i¹³i¹⁴ (SEQ. ID. NO: 103)

wherein:

i¹ is absent or is an amino acid residue;
 i² is a neutral polar residue;
 i³ is an amino acid residue;
 i⁵, i⁶, i⁷, and i⁸ are each independently amino acid residues;
 i⁹ is an acidic residue;
 i¹⁰ is an amino acid residue;
 i¹² and i¹³ are each independently amino acid residues; and i¹⁴ is a neutral polar residue.

[0016] The compounds defined by formulae I(g) through I(i) also bind TALL-1.

[0017] Further in accordance with the present invention, modulators of TALL-1 comprise:

- a) a TALL-1 modulating domain (e.g., an amino acid sequence of Formulae I(a) through I(i)), preferably the amino acid sequence Dz²Lz⁴, or sequences derived therefrom by phage display, RNA-peptide screening, or the other techniques mentioned above; and
- b) a vehicle, such as a polymer (e.g., PEG or dextran) or an Fc domain, which is preferred;

wherein the vehicle is covalently attached to the TALL-1 modulating domain. The vehicle and the TALL-1 modulating domain may be linked through the N- or C-terminus of the TALL-1 modulating domain, as described further below. The preferred vehicle is an Fc domain, and the preferred Fc domain is an IgG Fc domain. Such Fc-linked peptides are referred to herein as "peptibodies." Preferred TALL-1 modulating domains comprise the amino acid sequences described hereinafter in Tables 1 and 2. Other TALL-1 modulating domains can be generated by phage display, RNA-peptide screening and the other techniques mentioned herein.

[0018] Further in accordance with the present invention is a process for making TALL-1 modulators, which comprises:

- a. selecting at least one peptide that binds to TALL-1; and
- b. covalently linking said peptide to a vehicle.

The preferred vehicle is an Fc domain. Step (a) is preferably carried out by selection from the peptide sequences in Table 2 hereinafter or from phage display, RNA-peptide screening, or the other techniques mentioned herein.

[0019] The compounds of this invention may be prepared by standard synthetic methods, recombinant DNA techniques, or any other methods of preparing peptides and fusion proteins. Compounds of this invention that encompass non-peptide portions may be synthesized by standard organic chemistry reactions, in addition to standard peptide chemistry reactions when applicable.

[0020] The primary use contemplated for the compounds of this invention is as therapeutic or prophylactic agents. The vehicle-linked peptide may have activity comparable to- or even greater than- the natural ligand mimicked by the peptide.

[0021] The compounds of this invention may be used for therapeutic or prophylactic purposes by formulating them with appropriate pharmaceutical carrier materials and administering an effective amount to a patient, such as a human (or other mammal) in need thereof. Other related aspects are also included in the instant invention.

[0022] Numerous additional aspects and advantages of the present invention will become apparent upon consideration of the figures and detailed description of the invention.

Brief Description of the Figures

[0023]

EP 2 845 864 A2

Figure 1 shows exemplary Fc dimers that may be derived from an IgG1 antibody. "Fc" in the figure represents any of the Fc variants within the meaning of "Fc domain" herein. "X¹" and "X²" represent peptides or linker-peptide combinations as defined hereinafter. The specific dimers are as follows:

5 A, D: Single disulfide-bonded dimers. IgG1 antibodies typically have two disulfide bonds at the hinge region of the antibody. The Fc domain in Figures 1A and 1D may be formed by truncation between the two disulfide bond sites or by substitution of a cysteinyl residue with an unreactive residue (e.g., alanyl). In Figure 1A, the Fc domain is linked at the amino terminus of the peptides; in 1D, at the carboxyl terminus.

10 B, E: Doubly disulfide-bonded dimers. This Fc domain may be formed by truncation of the parent antibody to retain both cysteinyl residues in the Fc domain chains or by expression from a construct including a sequence encoding such an Fc domain. In Figure 1B, the Fc domain is linked at the amino terminus of the peptides; in 1E, at the carboxyl terminus.

15 C, F: Noncovalent dimers. This Fc domain may be formed by elimination of the cysteinyl residues by either truncation or substitution. One may desire to eliminate the cysteinyl residues to avoid impurities formed by reaction of the cysteinyl residue with cysteinyl residues of other proteins present in the host cell. The noncovalent bonding of the Fc domains is sufficient to hold together the dimer.

Other dimers may be formed by using Fc domains derived from different types of antibodies (e.g., IgG2, IgM).

20 Figure 2 shows the structure of preferred compounds of the invention that feature tandem repeats of the pharmacologically active peptide. Figure 2A shows a single chain molecule and may also represent the DNA construct for the molecule. Figure 2B shows a dimer in which the linker-peptide portion is present on only one chain of the dimer. Figure 2C shows a dimer having the peptide portion on both chains. The dimer of Figure 2C will form spontaneously in certain host cells upon expression of a DNA construct encoding the single chain shown in Figure 3A. In other host cells, the cells could be placed in conditions favoring formation of dimers or the dimers can be formed *in vitro*.

25 Figure 3 shows exemplary nucleic acid and amino acid sequences (SEQ ID NOS: 1 and 2, respectively) of human IgG1 Fc that may be used in this invention. Figures 4A through 4F show the nucleotide and amino acid sequences (SEQ ID NOS: 3-27) S of NdeI to Sall fragments encoding peptide and linker.

30 Figures 5A through 5M show the nucleotide sequence (SEQ ID NO: 28) of pAMG21-RANK-Fc vector, which was used to construct Fc-linked molecules of the present invention. These figures identify a number of features of the nucleic acid, including:

- promoter regions PcopB, PrepA, RNAI, APHII, luxPR, and luxPL;
- mRNA for APHII, luxR;
- 35 • coding sequences and amino acid sequences for the proteins copB protein, copT, repAI, repA4, APHII, luxR, RANK, and Fc;
- binding sites for the proteins copB, CRP;
- hairpins T1, T2, T7, and toop;
- operator site for lux protein;
- 40 • enzyme restriction sites for PfIII08I, RgIII, Scal, BmnI, DrdII, DraIII, BstBI, AceIII, AfII, PfIMI, BgII, SfiI, BstEII, BspLullI, NspV, BpII, EagI, Bcgl, Nsil, BsaI, Psp1406I, AatII, BsmI, NruI, NdeI, AnaLI, Acc65I, KpnI, Sall, AccI, BspEI, AhdI, BspHI, EconI, BsrGI, BmaI, Smal, SexAI, BamHI, and BlpI.

45 Figures 6A and 6B show the DNA sequence (SEQ ID NO: 97) inserted into pCFM1656 between the unique AatII (position #4364 in pCFM1656) and SacII (position #4585 in pCFM1656) restriction sites to form expression plasmid pAMG21 (ATCC accession no. 98113).

50 Figure 7 shows that the TALL-1 peptibody (SEQ ID NO: 70) inhibits TALL-1-mediated B cell proliferation. Purified B cells (10⁵) from B6 mice were cultured in triplicates in 96-well plated with the indicated amounts of TALL-1 consensus peptibody in the presence of 10 ng/ml TALL-1 plus 2 μg/ml anti-IgM antibody. Proliferation was measured by radioactive [³H]thymidine uptake in the last 18h of pulse. Data shown represent mean ± SD triplicate wells.

55 Figure 8 shows that a TALL-1 N-terminal tandem dimer peptibodies (SEQ ID NO: 123, 124 in Table 5B hereinafter) are preferable for inhibition of TALL-1-mediated B cell proliferation. Purified B cells (10⁵) from B6 mice were cultured in triplicates in 96-well plated with the indicated amounts of TALL-1 12-3 peptibody and TALL-1 consensus peptibody (SEQ ID NOS: 115 and 122 of Table 5B) or the related dimer peptibodies (SEQ ID NOS: 123, 124) in the presence of 10 ng/ml TALL-1 plus 2 μg/ml anti-IgM antibody. Proliferation was measured by radioactive [³H]thymidine uptake in the last 18h of pulse. Data shown represent mean ± SD triplicate wells.

Figure 9. AGP3 peptibody binds to AGP3 with high affinity. Dissociation equilibrium constant (K_D) was obtained from nonlinear regression of the competition curves using a dual-curve one-site homogeneous binding model (Kin-

Ex™ software). K_D is about 4 pM for AGP3 peptibody binding with human AGP3 (SEQ ID NO: 123).

Figures 10A and 10B. AGP3 peptibody blocks both human and murine AGP3 in the Biacore competition assay. Soluble human TACI protein was immobilized to B1 chip. 1 nM of recombinant human AGP3 protein (upper panel) or 5 nM of recombinant murine AGP3 protein (lower panel) was incubated with indicated amount of AGP3 peptibody before injected over the surface of receptor. Relative human AGP3 and murine AGP3 (binding response was shown (SEQ ID NO: 123).

Figures 11A and 11B. AGP3 peptibody blocked AGP3 binding to all three receptors TACI, BCMA and BAFFR in Biacore competition assay. Recombinant soluble receptor TACI, BCMA and BAFFR proteins were immobilized to CM5 chip. 1 nM of recombinant human AGP3 (upper panel) were incubated with indicated amount of AGP3 peptibody before injected over each receptor surface. Relative binding of AGP3 was measured. Similarly, 1 nM of recombinant APRIL protein was incubated with indicated amount of AGP3 peptibody before injected over each receptor surface. AGP3 peptibody didn't inhibit APRIL binding to all three receptors (SEQ ID NO: 123).

Figures 12A and 12B. AGP3 peptibody inhibits mouse serum immunoglobulin level increase induced by human AGP3 challenge. Balb/c mice received 7 daily intraperitoneal injections of 1 mg/Kg human AGP3 protein along with saline, human Fc, or AGP3 peptibody at indicated doses, and were bled on day 8. Serum total IgM and IgA level were measured by ELISA (SEQ ID NO: 123).

Figure 13. AGP3 peptibody treatment reduced arthritis severity in the mouse CIA model. Eight to 12 weeks old DBA/1 male mice were immunized with bovine collagen type II (bCII) emulsified in complete freunds adjuvant intradermally at the base of tail, and were boosted 3 weeks after the initial immunization with bCII emulsified in incomplete freunds adjuvant. Treatment with indicated dosage of AGP3 peptibody was begun from the day of booster immunization for 4 weeks. As described before (Khare et al., J. Immunol. 155: 3653-9, 1995), all four paws were individually scored from 0-3 for arthritis severity (SEQ ID NO: 123).

Figure 14. AGP3 peptibody treatment inhibited anti-collagen antibody generation in the mouse CIA model. Serum samples were taken one week after final treatment (day 35) as described above. Serum anti-collagen II antibody level was determined by ELISA analysis (SEQ ID NO: 123).

Figures 15A and 15B. AGP3 peptibody treatment delayed proteinuria onset and improved survival in NZB/NZW lupus mice. Five-month-old lupus prone NZBx NZBWF1 mice were treated i.p. 3X/week for 8 weeks with PBS or indicated doses of AGP3 peptibody (SEQ ID NO: 123) or human Fc proteins. Protein in the urine was evaluated monthly throughout the life of the experiment with Albustix reagent strips (Bayer AG).

Figures 16A and 16B show the nucleic acid and amino acid sequences of a preferred TALL-1-binding peptibody (SEQ ID NOS:189 and 123)

Detailed Description of the Invention

Definition of Terms

[0024] The terms used throughout this specification are defined as follows, unless otherwise limited in specific instances.

General definitions

[0025] The term "comprising" means that a compound may include additional amino acids on either or both of the N- or C- termini of the given sequence. Of course, these additional amino acids should not significantly interfere with the activity of the compound.

[0026] Additionally, physiologically acceptable salts of the compounds of this invention are also encompassed herein. The term "physiologically acceptable salts" refers to any salts that are known or later discovered to be pharmaceutically acceptable. Some specific examples are: acetate; trifluoroacetate; hydrohalides, such as hydrochloride and hydrobromide; sulfate; citrate; tartrate; glycolate; and oxalate.

Amino acids

[0027] The term "acidic residue" refers to amino acid residues in D- or L-form having sidechains comprising acidic groups. Exemplary acidic residues include D and E.

[0028] The term "amide residue" refers to amino acids in D- or L-form having sidechains comprising amide derivatives of acidic groups. Exemplary residues include N and Q.

[0029] The term "aromatic residue" refers to amino acid residues in D- or L-form having sidechains comprising aromatic groups. Exemplary aromatic residues include F, Y, and W.

[0030] The term "basic residue" refers to amino acid residues in D- or L-form having sidechains comprising basic

groups. Exemplary basic residues include H, K, and R.

[0031] The term "hydrophilic residue" refers to amino acid residues in D- or L-form having sidechains comprising polar groups. Exemplary hydrophilic residues include C, S, T, N, and Q.

[0032] The term "nonfunctional residue" refers to amino acid residues in D- or L-form having sidechains that lack acidic, basic, or aromatic groups. Exemplary nonfunctional amino acid residues include M, G, A, V, I, L and norleucine (Nle).

[0033] The term "neutral polar residue" refers to amino acid residues in D- or L-form having sidechains that lack basic, acidic, or polar groups. Exemplary neutral polar amino acid residues include A, V, L, I, P, W, M, and F.

[0034] The term "polar hydrophobic residue" refers to amino acid residues in D- or L-form having sidechains comprising polar groups. Exemplary polar hydrophobic amino acid residues include T, G, S, Y, C, Q, and N.

[0035] The term "hydrophobic residue" refers to amino acid residues in D- or L-form having sidechains that lack basic or acidic groups. Exemplary hydrophobic amino acid residues include A, V, L, I, P, W, M, F, T, G, S, Y, C, Q, and N.

Peptides

[0036] The term "peptide" refers to molecules of 1 to 40 amino acids, with molecules of 5 to 20 amino acids preferred. Exemplary peptides may comprise the TALL-1 modulating domain of a naturally occurring molecule or comprise randomized sequences.

[0037] The term "randomized" as used to refer to peptide sequences refers to fully random sequences (e.g., selected by phage display methods or RNA-peptide screening) and sequences in which one or more residues of a naturally occurring molecule is replaced by an amino acid residue not appearing in that position in the naturally occurring molecule. Exemplary methods for identifying peptide sequences include phage display, *E. coli* display, ribosome display, RNA-peptide screening, chemical screening, and the like.

[0038] The term "TALL-1 modulating domain" refers to any amino acid sequence that binds to the TALL-1 and comprises naturally occurring sequences or randomized sequences. Exemplary TALL-1 modulating domains can be identified or derived by phage display or other methods mentioned herein.

[0039] The term "TALL-1 antagonist" refers to a molecule that binds to the TALL-1 and increases or decreases one or more assay parameters opposite from the effect on those parameters by full length native TALL-1. Such activity can be determined, for example, by such assays as described in the subsection entitled "Biological activity of AGP-3" in the Materials & Methods section of the patent application entitled, "TNF-RELATED PROTEINS", WO 00/47740, published August 17, 2000.

Vehicles and peptibodies

[0040] The term "vehicle" refers to a molecule that prevents degradation and/or increases half-life, reduces toxicity, reduces immunogenicity, or increases biological activity of a therapeutic protein. Exemplary vehicles include an Fc domain (which is preferred) as well as a linear polymer (e.g., polyethylene glycol (PEG), polylysine, dextran, *etc.*); a branched-chain polymer (see, for example, U.S. Patent No. 4,289,872 to Denkenwalter et al., issued September 15, 1981; 5,229,490 to Tam, issued July 20, 1993; WO 93/21259 by Frechet et al., published 28 October 1993); a lipid; a cholesterol group (such as a steroid); a carbohydrate or oligosaccharide (e.g., dextran); any natural or synthetic protein, polypeptide or peptide that binds to a salvage receptor; albumin, including human serum albumin (HSA), leucine zipper domain, and other such proteins and protein fragments. Vehicles are further described hereinafter.

[0041] The term "native Fc" refers to molecule or sequence comprising the sequence of a non-antigen-binding fragment resulting from digestion of whole antibody, whether in monomeric or multimeric form. The original immunoglobulin source of the native Fc is preferably of human origin and may be any of the immunoglobulins, although IgG1 and IgG2 are preferred. Native Fc's are made up of monomeric polypeptides that may be linked into dimeric or multimeric forms by covalent (i.e., disulfide bonds) and non-covalent association. The number of intermolecular disulfide bonds between monomeric subunits of native Fc molecules ranges from 1 to 4 depending on class (e.g., IgG, IgA, IgE) or subclass (e.g., IgG1, IgG2, IgG3, IgA1, IgGA2). One example of a native Fc is a disulfide-bonded dimer resulting from papain digestion of an IgG (see Ellison et al. (1982), *Nucleic Acids Res.* 10:4071-9). The term "native Fc" as used herein is generic to the monomeric, dimeric, and multimeric forms.

[0042] The term "Fc variant" refers to a molecule or sequence that is modified from a native Fc but still comprises a binding site for the salvage receptor, FcRn. International applications WO 97/34631 (published 25 September 1997) and WO 96/32478 describe exemplary Fc variants, as well as interaction with the salvage receptor, and are hereby incorporated by reference in their entirety. Thus, the term "Fc variant" comprises a molecule or sequence that is humanized from a non-human native Fc. Furthermore, a native Fc comprises sites that may be removed because they provide structural features or biological activity that are not required for the fusion molecules of the present invention. Thus, the term "Fc variant" comprises a molecule or sequence that lacks one or more native Fc sites or residues that affect or are

involved in (1) disulfide bond formation, (2) incompatibility with a selected host cell (3) N-terminal heterogeneity upon expression in a selected host cell, (4) glycosylation, (5) interaction with complement, (6) binding to an Fc receptor other than a salvage receptor, or (7) antibody-dependent cellular cytotoxicity (ADCC). Fc variants are described in further detail hereinafter.

[0043] The term "Fc domain" encompasses native Fc and Fc variant molecules and sequences as defined above. As with Fc variants and native Fc's, the term "Fc domain" includes molecules in monomeric or multimeric form, whether digested from whole antibody or produced by other means.

[0044] The term "multimer" as applied to Fc domains or molecules comprising Fc domains refers to molecules having two or more polypeptide chains associated covalently, noncovalently, or by both covalent and non-covalent interactions. IgG molecules typically form dimers; IgM, pentamers; IgD, dimers; and IgA, monomers, dimers, trimers, or tetramers. Multimers may be formed by exploiting the sequence and resulting activity of the native Ig source of the Fc or by derivatizing (as defined below) such a native Fc.

[0045] The term "dimer" as applied to Fc domains or molecules comprising Fc domains refers to molecules having two polypeptide chains associated covalently or non-covalently. Thus, exemplary dimers within the scope of this invention are as shown in Figure 1.

[0046] The terms "derivatizing" and "derivative" or "derivatized" comprise processes and resulting compounds respectively in which (1) the compound has a cyclic portion; for example, cross-linking between cysteinyl residues within the compound; (2) the compound is cross-linked or has a cross-linking site; for example, the compound has a cysteinyl residue and thus forms cross-linked dimers in culture or *in vivo*; (3) one or more peptidyl linkage is replaced by a non-peptidyl linkage; (4) the N-terminus is replaced by -NRR¹, -NRC(O)R¹, -NRC(O)OR¹, -NRS(O)₂R¹, -NHC(O)NHR, a succinimide group, or substituted or unsubstituted benzyloxycarbonyl-NH-, wherein R and R¹ and the ring substituents are as defined hereinafter; (5) the C-terminus is replaced by -C(O)R² or -NR³R⁴ wherein R², R³ and R⁴ are as defined hereinafter; and (6) compounds in which individual amino acid moieties are modified through treatment with agents capable of reacting with selected side chains or terminal residues. Derivatives are further described hereinafter.

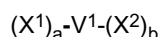
[0047] The terms "peptibody" and "peptibodies" refer to molecules comprising an Fc domain and at least one peptide. Such peptibodies may be multimers or dimers or fragments thereof, and they may be derivatized. In the present invention, the molecules of formulae II through VI hereinafter are peptibodies when V¹ is an Fc domain.

Structure of compounds

[0048] In General. The present inventors identified sequences capable of binding to and modulating the biological activity of TALL-1. These sequences can be modified through the techniques mentioned above by which one or more amino acids may be changed while maintaining or even improving the binding affinity of the peptide.

[0049] In the compositions of matter prepared in accordance with this invention, the peptide(s) may be attached to the vehicle through the peptide's N-terminus or C-terminus. Any of these peptides may be linked in tandem (i.e., sequentially), with or without linkers. Thus, the vehicle-peptide molecules of this invention may be described by the following formula:

II



wherein:

V¹ is a vehicle (preferably an Fc domain);

X¹ and X² are each independently selected from -(L¹)_c-P¹, -(L¹)_c-P¹-(L²)_d-P², -(L¹)_c-P¹-(L²)_d-P²-(L³)_e-P³, and -(L¹)_c-P¹-(L²)_d-P²-(L³)_e-P³-(L⁴)_f-P⁴

P¹, P², P³, and P⁴ are each independently sequences of TALL-1 modulating domains, such as those of Formulae I(a) through I(i);

L¹, L², L³, and L⁴ are each independently linkers; and

a, b, c, d, e, and f are each independently 0 or 1, provided that at least one of a and b is 1.

[0050] Thus, compound II comprises preferred compounds of the formulae

III

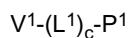


and multimers thereof wherein V¹ is an Fc domain and is attached at the C-terminus of A¹;

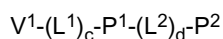
IV



and multimers thereof wherein V^1 is an Fc domain and is attached at the N-terminus of A^2 ;
 V



and multimers thereof wherein V^1 is an Fc domain and is attached at the N-terminus of $-(L^1)_c-P^1$; and
 VI



and multimers thereof wherein V^1 is an Fc domain and is attached at the N-terminus of $-L^1-P^1-L^2-P^2$.

[0051] Peptides. The peptides of this invention are useful as TALL-1 modulating peptides or as TALL-1 modulating domains in the molecules of formulae II through VI. Molecules of this invention comprising these peptide sequences may be prepared by methods known in the art.

[0052] Preferred peptide sequences are those of the foregoing formulae I(a) having the substituents identified below.

Table 1-Preferred peptide substituents

Formula I(a)	a^8 is T; a^9 is a basic residue (K most preferred); and a^{12} is a neutral polar residue (F most preferred).
Formula I(b)	b^3 is D, Q, or E; b^6 is W or Y; b^{10} is T; b^{11} is K or R; and b^{14} is V or L.
Formula I(c)	c^9 is T; c^{10} is K or R; c^{13} is a I, L, or V; and c^{17} is A or L.
Formula I(d)	d^{13} is T.
Formula I(e)	e^{11} is T.
Formula I(f)	f^6 is T; f^7 is K; and f^{10} is V.
Formula I(g)	g^5 is W; g^8 is P; g^{10} is E; and g^{13} is a basic residue.
Formula I(h)	h^1 is G; h^6 is A; h^7 is a neutral polar residue; and h^{10} is an acidic residue.
Formula I(i)	i^2 is W; and i^{14} is W.

[0053] Preferred peptide sequences appear in Table 2 below.

EP 2 845 864 A2

Table 2-Preferred TALL-1 modulating domains

	Sequence	SEQ ID NO:
5	PGTCFFPPWECTHA	29
	WGACWFPFWECFKE	30
	VPFCDLLTKHCFEA	31
	GSRCKYKWDVLTKQCFHH	32
10	LPGCKWDLLIKQWVCDPL	33
	SADCYFDILTKSDVCTSS	34
	SDDCMYDQLTRMFICSNL	35
15	DLNCKYDELTYKEWCQFN	36
	FHDCKYDLLTRQMVCHGL	37
	RNHCFWDHLLKQDICPSP	38
	ANQCWWDSLTKKNVCEFF	39
20	YKGRQMWDILTRSWVSL	126
	QDVGLWWDILTRAWMPNI	127
	QNAQRVWDLIRTWVYPQ	128
25	GWNEAWWDELTKI WVLEQ	129
	RITCDTWDSLTKKCPQS	130
	GAIMQFWDSLTKTWLRQS	131
	WLHSGWWDPLTKHWLQKV	132
30	SEWFFWFDPLTRAQLKFR	133
	GVWFWWFDPLTKQWTQAG	134
	MQCKGYDILTKWCVTNG	135
35	LWSKEVWDILTKSWVSQA	136
	KAAGWWFDWLTKVWVPAP	137
	AYQTFWFDLTRLWLSTT	138
	SGQHFWDLLTRSWTPST	139
40	LGVGQKWDPLTKQWVSRG	140
	VGKMCQWDPLIKRTVCVG	141
	CRQGAKFDLLTKQCLLGR	142
45	GQAIRHWDVLTKQWVDSQ	143
	RGPCGSWDLTKHCLDSQ	144
	WQWKQQWDLLTKQMVWVG	145
	PITICRKDLLTKQVVCLD	146
50	KTCNGKWDLLTKQCLQQA	147
	KCLKGKWDLLTKQCVTEV	148
	RCWNGKWDLLTKQCIHPW	149
55	NRDMRKWDPLIKQWIVRP	150
	QAAAATWDLLTKQWLVPV	151
	PEGGPKWDPLTKQFLPPV	152

EP 2 845 864 A2

(continued)

	Sequence	SEQ ID NO:
5	QTPQKKWDLTKQWFTRN	153
	IGSPCKWDLTKQMICQT	154
	CTAAGKWDLTKQCIQEK	155
	VSQCMKWDLTKQCLQGW	156
10	VWGTWKWDLTKQYLPPQ	157
	GWWEMKWDLTKQWYRPQ	158
	TAQVSKWDLTKQWLPLA	159
15	QLWGTKWDLTKQYIQIM	160
	WATSQKWDLTKQWVQNM	161
	QRQCAKWDLTKQCVLFY	162
	KTTDCKWDLTKQRICQV	163
20	LLCQGKWDLTKQCLKLR	164
	LMWFWKWDLTKQLVPTF	165
	QTWAWKWDLTKQWIGPM	166
25	NKELLKWDLTKQCRGRS	167
	GQKDLKWDLTKQYVRQS	168
	PKPCQKWDLTKQCLGSV	169
	GQIGWKWDLTKQWIQTR	170
30	VWLDWKWDLTKQWIHPQ	171
	QEWEYKWDLTKQWGWLR	172
	HWDSWKWDLTKQWVVQA	173
35	TRPLQKWDLTKQWLRVG	174
	SDQWQKWDLTKQWFWDV	175
	QQTFMKWDLTKQWIRRH	176
	QGECKWDLTKQCFPGQ	177
40	GQMGWRWDPLIKMCLGPS	178
	QLDGCKWDLTKQKVCIP	179
	HGYWQKWDLTKQWVSSE	180
45	HQGQCGWDLTRIYLPCH	181
	LHKACKWDLTKQCWPMQ	182
	GPPGSVWDLTKIWIQTG	183
	ITQDWRFDLTRLWLPLR	184
50	QGGFAAWDVLTKMWITVP	185
	GHGTPWWDALTRIWLGV	186
	VWPWQKWDLTKQVFQD	187
55	WQWSWKWDLTRQYISSS	188
	NQTLWKWDLTKQFITYM	60
	PVYQGWWDTLTKLYIWDG	61

EP 2 845 864 A2

(continued)

5
10
15

Sequence	SEQ ID NO:
WLDGGWRDPLIKRSVQLG	62
GHQQFKWDLTKQWVQSN	63
QRVGQFWDVLTVMFITGS	64
QAQGWSYDALIKTWIRWP	65
GWMHWKWDPLTKQALPMM	66
GHPTYKWDLTKQWILQM	67
WNNWSLWDPLTKLWLQQN	68
WQWGWKWDLTKQWVQQQ	69
GQMGWRWDPLTKMWLGTS	70

[0054] It is noted that the known receptors for TALL-1 bear some sequence homology with preferred peptides:

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12-3 LPGCKWDLLIKQWCDPL
BAFFR MRRGPRSLRGRDAPVPTPCVPTECYDLLVRKCVDCRLL
TACI TICNHQSQRTCAAFCSRSLSCRKEQGKFYDHLRDCISCASI
BCMA FVSPSQEIRGRFRMLQMGQCSQNEYFDSLHACIPQLRC

(SEQ ID NOS: 33,195,196, and 197, respectively).

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[0055] Any peptide containing a cysteinyl residue may be cross-linked with another Cys-containing peptide, either or both of which may be linked to a vehicle. Any peptide having more than one Cys residue may form an intrapeptide disulfide bond, as well. Any of these peptides may be derivatized as described hereinafter.

[0056] Additional useful peptide sequences may result from conservative and/or non-conservative modifications of the amino acid sequences of the sequences in Table 2.

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[0057] Conservative modifications will produce peptides having functional and chemical characteristics similar to those of the peptide from which such modifications are made. In contrast, substantial modifications in the functional and/or chemical characteristics of the peptides may be accomplished by selecting substitutions in the amino acid sequence that differ significantly in their effect on maintaining (a) the structure of the molecular backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the size of the molecule.

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[0058] For example, a "conservative amino acid substitution" may involve a substitution of a native amino acid residue with a nonnative residue such that there is little or no effect on the polarity or charge of the amino acid residue at that position. Furthermore, any native residue in the polypeptide may also be substituted with alanine, as has been previously described for "alanine scanning mutagenesis" (see, for example, MacLennan et al., 1998, Acta Physiol. Scand. Suppl. 643:55-67; Sasaki et al., 1998, Adv. Biophys. 35:1-24, which discuss alanine scanning mutagenesis).

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[0059] Desired amino acid substitutions (whether conservative or non-conservative) can be determined by those skilled in the art at the time such substitutions are desired. For example, amino acid substitutions can be used to identify important residues of the peptide sequence, or to increase or decrease the affinity of the peptide or vehicle-peptide molecules (see preceding formulae) described herein. Exemplary amino acid substitutions are set forth in Table 3.

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Table 3-Amino Acid Substitutions

Original Residues	Exemplary Substitutions	Preferred Substitutions
Ala (A)	Val, Leu, Ile	Val
Arg (R)	Lys, Gln, Asn	Lys
Asn (N)	Gln	Gln
Asp (D)	Glu	Glu
Cys (C)	Ser, Ala	Ser

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EP 2 845 864 A2

(continued)

Original Residues	Exemplary Substitutions	Preferred Substitutions
Gln (Q)	Asn	Asn
Glu (E)	Asp	Asp
Gly (G)	Pro, Ala	Ala
His (H)	Asn, Gln, Lys, Arg	Arg
Ile (I)	Leu, Val, Met, Ala, Phe, Norleucine	Leu
Leu (L)	Norleucine, Ile, Val, Met, Ala, Phe	Ile
Lys (K)	Arg, 1,4 Diamino-butyric Acid, Gln, Asn	Arg
Met (M)	Leu, Phe, Ile	Leu
Phe (F)	Leu, Val, Ile, Ala, Tyr	Leu
Pro (P)	Ala	Gly
Ser (S)	Thr, Ala, Cys	Thr
Thr (T)	Ser	Ser
Trp (W)	Tyr, Phe	Tyr
Tyr (Y)	Trp, Phe, Thr, Ser	Phe
Val (V)	Ile, Met, Leu, Phe, Ala, Norleucine	Leu

[0060] In certain embodiments, conservative amino acid substitutions also encompass non-naturally occurring amino acid residues which are typically incorporated by chemical peptide synthesis rather than by synthesis in biological systems.

[0061] As noted in the foregoing section "Definition of Terms," naturally occurring residues may be divided into classes based on common sidechain properties that may be useful for modifications of sequence. For example, non-conservative substitutions may involve the exchange of a member of one of these classes for a member from another class. Such substituted residues may be introduced into regions of the peptide that are homologous with non-human orthologs, or into the non-homologous regions of the molecule. In addition, one may also make modifications using P or G for the purpose of influencing chain orientation.

[0062] In making such modifications, the hydropathic index of amino acids may be considered. Each amino acid has been assigned a hydropathic index on the basis of their hydrophobicity and charge characteristics, these are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (-0.4); threonine (-0.7); serine (-0.8); tryptophan (-0.9); tyrosine (-1.3); proline (-1.6); histidine (-3.2); glutamate (-3.5); glutamine (-3.5); aspartate (-3.5); asparagine (-3.5); lysine (-3.9); and arginine (-4.5).

[0063] The importance of the hydropathic amino acid index in conferring interactive biological function on a protein is understood in the art. Kyte et al., *J. Mol. Biol.*, 157:105-131 (1982). It is known that certain amino acids may be substituted for other amino acids having a similar hydropathic index or score and still retain a similar biological activity. In making changes based upon the hydropathic index, the substitution of amino acids whose hydropathic indices are within ± 2 is preferred, those which are within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred.

[0064] It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. The greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with its immunogenicity and antigenicity, *i.e.*, with a biological property of the protein.

[0065] The following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0 \pm 1); glutamate (+3.0 \pm 1); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (-0.4); proline (-0.5 \pm 1); alanine (-0.5); histidine (-0.5); cysteine (-1.0); methionine (-1.3); valine (-1.5); leucine (-1.8); isoleucine (-1.8); tyrosine (-2.3); phenylalanine (-2.5); tryptophan (-3.4). In making changes based upon similar hydrophilicity values, the substitution of amino acids whose hydrophilicity values are within ± 2 is preferred, those which

are within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred. One may also identify epitopes from primary amino acid sequences on the basis of hydrophilicity. These regions are also referred to as "epitopic core regions."

[0066] A skilled artisan will be able to determine suitable variants of the polypeptide as set forth in the foregoing sequences using well known techniques. For identifying suitable areas of the molecule that maybe changed without destroying activity, one skilled in the art may target areas not believed to be important for activity. For example, when similar polypeptides with similar activities from the same species or from other species are known, one skilled in the art may compare the amino acid sequence of a peptide to similar peptides. With such a comparison, one can identify residues and portions of the molecules that are conserved among similar polypeptides. It will be appreciated that changes in areas of a peptide that are not conserved relative to such similar peptides would be less likely to adversely affect the biological activity and/or structure of the peptide. One skilled in the art would also know that, even in relatively conserved regions, one may substitute chemically similar amino acids for the naturally occurring residues while retaining activity (conservative amino acid residue substitutions). Therefore, even areas that may be important for biological activity or for structure may be subject to conservative amino acid substitutions without destroying the biological activity or without adversely affecting the peptide structure.

[0067] Additionally, one skilled in the art can review structure-function studies identifying residues in similar peptides that are important for activity or structure. In view of such a comparison, one can predict the importance of amino acid residues in a peptide that correspond to amino acid residues that are important for activity or structure in similar peptides. One skilled in the art may opt for chemically similar amino acid substitutions for such predicted important amino acid residues of the peptides.

[0068] One skilled in the art can also analyze the three-dimensional structure and amino acid sequence in relation to that structure in similar polypeptides. In view of that information, one skilled in the art may predict the alignment of amino acid residues of a peptide with respect to its three dimensional structure. One skilled in the art may choose not to make radical changes to amino acid residues predicted to be on the surface of the protein, since such residues may be involved in important interactions with other molecules. Moreover, one skilled in the art may generate test variants containing a single amino acid substitution at each desired amino acid residue. The variants can then be screened using activity assays known to those skilled in the art. Such data could be used to gather information about suitable variants. For example, if one discovered that a change to a particular amino acid residue resulted in destroyed, undesirably reduced, or unsuitable activity, variants with such a change would be avoided. In other words, based on information gathered from such routine experiments, one skilled in the art can readily determine the amino acids where further substitutions should be avoided either alone or in combination with other mutations.

[0069] A number of scientific publications have been devoted to the prediction of secondary structure. See Moulton J., *Curr. Op. in Biotech.*, 7(4): 422-427 (1996), Chou et al., *Biochemistry*, 13(2): 222-245 (1974); Chou et al., *Biochemistry*, 113(2): 211-222 (1974); Chou et al., *Adv. Enzymol. Relat. Areas Mol. Biol.*, 47: 45-148 (1978); Chou et al., *Ann. Rev. Biochem.*, 47: 251-276 and Chou et al., *Biophys. J.*, 26:367-384 (1979). Moreover, computer programs are currently available to assist with predicting secondary structure. One method of predicting secondary structure is based upon homology modeling. For example, two polypeptides or proteins which have a sequence identity of greater than 30%, or similarity greater than 40% often have similar structural topologies. The recent growth of the protein structural data base (PDB) has provided enhanced predictability of secondary structure, including the potential number of folds within a polypeptide's or protein's structure. See Holm et al., *Nucl. Acid. Res.*, 27(1): 244-247 (1999). It has been suggested (Brenner et al., *Curr. Op. Struct. Biol.*, 7(3): 369-376 (1997)) that there are a limited number of folds in a given polypeptide or protein and that once a critical number of structures have been resolved, structural prediction will gain dramatically in accuracy.

[0070] Additional methods of predicting secondary structure include "threading" (Jones, D., *Curr. Opin. Struct. Biol.*, 7(3): 377-87 (1997); Sippl et al., *Structure*, 4(1): 15-9 (1996)), "profile analysis" (Bowie et al., *Science*, 253: 164-170 (1991); Gribskov et al., *Meth. Enzym.*, 183: 146-159 (1990); Gribskov et al., *Proc. Nat. Acad. Sci.*, 84(13): 4355-8 (1987)), and "evolutionary linkage" (See Home, *supra*, and Brenner, *supra*).

[0071] Vehicles. This invention requires the presence of at least one vehicle (V^1) attached to a peptide through the N-terminus, C-terminus or a sidechain of one of the amino acid residues. Multiple vehicles may also be used; e.g., Fc's at each terminus or an Fc at a terminus and a PEG group at the other terminus or a sidechain. Exemplary vehicles include:

- an Fc domain;
- other proteins, polypeptides, or peptides capable of binding to a salvage receptor;
- human serum albumin (HSA);
- a leucine zipper (LZ) domain;
- polyethylene glycol (PEG), including 5 kD, 20 kD, and 30 kD PEG, as well as other polymers;
- dextran;

and other molecules known in the art to provide extended half-life and/or protection from proteolytic degradation or clearance.

[0072] An Fc domain is the preferred vehicle. The Fc domain may be fused to the N or C termini of the peptides or at both the N and C termini. Fusion to the N terminus is preferred.

[0073] As noted above, Fc variants are suitable vehicles within the scope of this invention. A native Fc may be extensively modified to form an Fc variant in accordance with this invention, provided binding to the salvage receptor is maintained; see, for example WO 97/34631 and WO 96/32478. In such Fc variants, one may remove one or more sites of a native Fc that provide structural features or functional activity not required by the fusion molecules of this invention. One may remove these sites by, for example, substituting or deleting residues, inserting residues into the site, or truncating portions containing the site. The inserted or substituted residues may also be altered amino acids, such as peptidomimetics or D-amino acids. Fc variants may be desirable for a number of reasons, several of which are described below. Exemplary Fc variants include molecules and sequences in which:

1. Sites involved in disulfide bond formation are removed. Such removal may avoid reaction with other cysteine-containing proteins present in the host cell used to produce the molecules of the invention. For this purpose, the cysteine-containing segment at the N-terminus may be truncated or cysteine residues may be deleted or substituted with other amino acids (e.g., alanyl, seryl). In particular, one may truncate the N-terminal 20-amino acid segment of SEQ ID NO: 2 or delete or substitute the cysteine residues at positions 7 and 10 of SEQ ID NO: 2. Even when cysteine residues are removed, the single chain Fc domains can still form a dimeric Fc domain that is held together non-covalently.

2. A native Fc is modified to make it more compatible with a selected host cell. For example, one may remove the PA sequence near the N-terminus of a typical native Fc, which may be recognized by a digestive enzyme in *E. coli* such as proline iminopeptidase. One may also add an N-terminal methionine residue, especially when the molecule is expressed recombinantly in a bacterial cell such as *E. coli*. The Fc domain of SEQ ID NO: 2 is one such Fc variant.

3. A portion of the N-terminus of a native Fc is removed to prevent N-terminal heterogeneity when expressed in a selected host cell. For this purpose, one may delete any of the first 20 amino acid residues at the N-terminus, particularly those at positions 1, 2, 3, 4 and 5.

4. One or more glycosylation sites are removed. Residues that are typically glycosylated (e.g., asparagine) may confer cytolytic response. Such residues may be deleted or substituted with unglycosylated residues (e.g., alanine).

5. Sites involved in interaction with complement, such as the C1q binding site, are removed. For example, one may delete or substitute the EKK sequence of human IgG1. Complement recruitment may not be advantageous for the molecules of this invention and so may be avoided with such an Fc variant.

6. Sites are removed that affect binding to Fc receptors other than a salvage receptor. A native Fc may have sites for interaction with certain white blood cells that are not required for the fusion molecules of the present invention and so may be removed.

7. The ADCC site is removed. ADCC sites are known in the art; see, for example, Molec. Immunol. 29 (5): 633-9 (1992) with regard to ADCC sites in IgG1. These sites, as well, are not required for the fusion molecules of the present invention and so may be removed.

8. When the native Fc is derived from a non-human antibody, the native Fc may be humanized. Typically, to humanize a native Fc, one will substitute selected residues in the non-human native Fc with residues that are normally found in human native Fc. Techniques for antibody humanization are well known in the art.

[0074] Preferred Fc variants include the following. In SEQ ID NO: 2 (Figure 3), the leucine at position 15 may be substituted with glutamate; the glutamate at position 99, with alanine; and the lysines at positions 101 and 103, with alanines. In addition, one or more tyrosine residues can be replaced by phenylalanine residues.

[0075] An alternative vehicle would be a protein, polypeptide, peptide, antibody, antibody fragment, or small molecule (e.g., a peptidomimetic compound) capable of binding to a salvage receptor. For example, one could use as a vehicle a polypeptide as described in U.S. Pat. No. 5,739,277, issued April 14, 1998 to Presta et al. Peptides could also be selected by phage display or RNA-peptide screening for binding to the FcRn salvage receptor. Such salvage receptor-binding compounds are also included within the meaning of "vehicle" and are within the scope of this invention. Such vehicles should be selected for increased half-life (e.g., by avoiding sequences recognized by proteases) and decreased immunogenicity (e.g., by favoring non-immunogenic sequences, as discovered in antibody humanization).

[0076] As noted above, polymer vehicles may also be used for V¹. Various means for attaching chemical moieties useful as vehicles are currently available, see, e.g., Patent Cooperation Treaty ("PCT") International Publication No. WO 96/11953, entitled "N-Terminally Chemically Modified Protein Compositions and Methods," herein incorporated by reference in its entirety. This PCT publication discloses, among other things, the selective attachment of water soluble polymers to the N-terminus of proteins.

[0077] A preferred polymer vehicle is polyethylene glycol (PEG). The PEG group may be of any convenient molecular

weight and may be linear or branched. The average molecular weight of the PEG will preferably range from about 2 kiloDalton ("kD") to about 100 kD, more preferably from about 5 kD to about 50 kD, most preferably from about 5 kD to about 10 kD. The PEG groups will generally be attached to the compounds of the invention via acylation or reductive alkylation through a reactive group on the PEG moiety (e.g., an aldehyde, amino, thiol, or ester group) to a reactive group on the inventive compound (e.g., an aldehyde, amino, or ester group).

[0078] A useful strategy for the PEGylation of synthetic peptides consists of combining, through forming a conjugate linkage in solution, a peptide and a PEG moiety, each bearing a special functionality that is mutually reactive toward the other. The peptides can be easily prepared with conventional solid phase synthesis. The peptides are "preactivated" with an appropriate functional group at a specific site. The precursors are purified and fully characterized prior to reacting with the PEG moiety. Ligation of the peptide with PEG usually takes place in aqueous phase and can be easily monitored by reverse phase analytical HPLC. The PEGylated peptides can be easily purified by preparative HPLC and characterized by analytical HPLC, amino acid analysis and laser desorption mass spectrometry.

[0079] Polysaccharide polymers are another type of water soluble polymer which may be used for protein modification. Dextran is a polysaccharide polymer comprised of individual subunits of glucose predominantly linked by α 1-6 linkages. The dextran itself is available in many molecular weight ranges, and is readily available in molecular weights from about 1 kD to about 70 kD. Dextran is a suitable water soluble polymer for use in the present invention as a vehicle by itself or in combination with another vehicle (e.g., Fc). See, for example, WO 96/11953 and WO 96/05309. The use of dextran conjugated to therapeutic or diagnostic immunoglobulins has been reported; see, for example, European Patent Publication No. 0 315 456, which is hereby incorporated by reference in its entirety. Dextran of about 1 kD to about 20 kD is preferred when dextran is used as a vehicle in accordance with the present invention.

[0080] Linkers. Any "linker" group is optional. When present, its chemical structure is not critical, since it serves primarily as a spacer. The linker is preferably made up of amino acids linked together by peptide bonds. Thus, in preferred embodiments, the linker is made up of from 1 to 30 amino acids linked by peptide bonds, wherein the amino acids are selected from the 20 naturally occurring amino acids. Some of these amino acids may be glycosylated, as is well understood by those in the art. In a more preferred embodiment, the 1 to 20 amino acids are selected from glycine, alanine, proline, asparagine, glutamine, and lysine. Even more preferably, a linker is made up of a majority of amino acids that are sterically unhindered, such as glycine and alanine. Thus, preferred linkers are polyglycines (particularly (Gly)₄, (Gly)₅), poly(Gly-Ala), and polyalanines. Other specific examples of linkers are:

(Gly)₃Lys(Gly)₄ (SEQ ID NO: 40);
 (Gly)₃AsnGlySer(Gly)₂ (SEQ ID NO: 41);
 (Gly)₃Cys(Gly)₄ (SEQ ID NO: 42); and
 GlyProAsnGlyGly (SEQ ID NO: 43).

To explain the above nomenclature, for example, (Gly)₃Lys(Gly)₄ means Gly-Gly-Gly-Lys-Gly-Gly-Gly-Gly (SEQ ID NO: 40). Combinations of Gly and Ala are also preferred. The linkers shown here are exemplary; linkers within the scope of this invention may be much longer and may include other residues.

[0081] Preferred linkers are amino acid linkers comprising greater than 5 amino acids, with suitable linkers having up to about 500 amino acids selected from glycine, alanine, proline, asparagine, glutamine, lysine, threonine, serine or aspartate. Linkers of about 20 to 50 amino acids are most preferred. One group of preferred linkers are those of the formulae

GSGSATGGSGSTASSGSGSA Tx¹x² (SEQ ID NO: 193)

and

GSGSATGGSGSTASSGSGSATx¹x²GSGSATGGSGSTASSGSGSATx³x⁴ (SEQ ID NO: 194)

wherein x¹ and x³ are each independently basic or hydrophobic residues and x² and x⁴ are each independently hydrophobic residues. Specific preferred linkers are:

GSGSATGGSGSTASSGSGSATHM (SEQ ID NO: 59)

GSGSATGGSGSTASSGSGSATGM (SEQ ID NO: 190)

GSGSATGGSGSTASSGSGSATGS (SEQ ID NO:191),

and

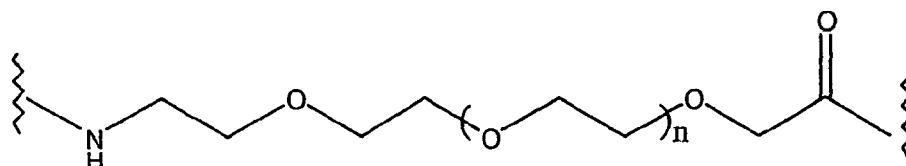
GSGSATGGSGSTASSGSGSATHMGSATGGSGSTASSGSGSATHM

(SEQ ID NO:

192).

[0082] Non-peptide linkers are also possible. For example, alkyl linkers such as $-\text{NH}-(\text{CH}_2)_s-\text{C}(\text{O})-$, wherein $s = 2-20$ could be used. These alkyl linkers may further be substituted by any non-sterically hindering group such as lower alkyl (e.g., C_1-C_6) lower acyl, halogen (e.g., Cl, Br), CN, NH_2 , phenyl, etc. An exemplary non-peptide linker is a PEG linker,

VII

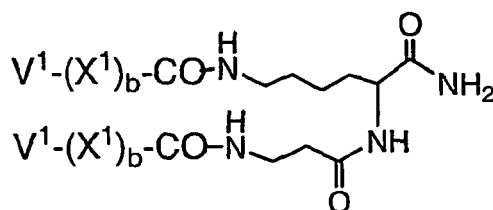


wherein n is such that the linker has a molecular weight of 100 to 5000 kD, preferably 100 to 500 kD. The peptide linkers may be altered to form derivatives in the same manner as described above.

[0083] Derivatives. The inventors also contemplate derivatizing the peptide and/or vehicle portion of the compounds. Such derivatives may improve the solubility, absorption, biological half life, and the like of the compounds. The moieties may alternatively eliminate or attenuate any undesirable side-effect of the compounds and the like. Exemplary derivatives include compounds in which:

1. The compound or some portion thereof is cyclic. For example, the peptide portion may be modified to contain two or more Cys residues (e.g., in the linker), which could cyclize by disulfide bond formation.
2. The compound is cross-linked or is rendered capable of cross-linking between molecules. For example, the peptide portion may be modified to contain one Cys residue and thereby be able to form an intermolecular disulfide bond with a like molecule. The compound may also be cross-linked through its C-terminus, as in the molecule shown below.

VIII



In Formula VIII, each "V¹" may represent typically one strand of the Fc domain.

3. One or more peptidyl [-C(O)NR-] linkages (bonds) is replaced by a non-peptidyl linkage. Exemplary non-peptidyl linkages are $-\text{CH}_2$ -carbamate [$-\text{CH}_2-\text{OC}(\text{O})\text{NR}-$], phosphonate, $-\text{CH}_2$ -sulfonamide [$-\text{CH}_2-\text{S}(\text{O})_2\text{NR}-$], urea [$-\text{NHC}(\text{O})\text{NH}-$], $-\text{CH}_2$ -secondary amine, and alkylated peptide [-C(O)NR⁶- wherein R⁶ is lower alkyl].

4. The N-terminus is derivatized. Typically, the N-terminus may be acylated or modified to a substituted amine. Exemplary N-terminal derivative groups include -NRR¹ (other than -NH₂, -NRC(O)R¹, -NRC(O)OR¹, -NRS(O)₂R¹, -NHC(O)NHR¹, succinimide, or benzyloxycarbonyl-NH- (CBZ-NH-), wherein R and R¹ are each independently hydrogen or lower alkyl and wherein the phenyl ring may be substituted with 1 to 3 substituents selected from the group consisting of C_1-C_4 alkyl, C_1-C_4 alkoxy, chloro, and bromo.

5. The free C-terminus is derivatized. Typically, the C-terminus is esterified or amidated. Exemplary C-terminal derivative groups include, for example, -C(O)R² wherein R² is lower alkoxy or -NR³R⁴ wherein R³ and R⁴ are independently hydrogen or C_1-C_8 alkyl (preferably C_1-C_4 alkyl).

6. A disulfide bond is replaced with another, preferably more stable, cross-linking moiety (e.g., an alkylene). See, e.g., Bhatnagar et al. (1996), J. Med. Chem. 39:3814-9; Alberts et al. (1993) Thirteenth Am. Pep. Symp., 357-9.

7. One or more individual amino acid residues is modified. Various derivatizing agents are known to react specifically with selected sidechains or terminal residues, as described in detail below.

[0084] Lysinyl residues and amino terminal residues may be reacted with succinic or other carboxylic acid anhydrides, which reverse the charge of the lysinyl residues. Other suitable reagents for derivatizing alpha-amino-containing residues include imidoesters such as methyl picolinimidate; pyridoxal phosphate; pyridoxal; chloroborohydride; trinitrobenzenesulfonic acid; O-methylisourea; 2,4 pentanedione; and transaminase-catalyzed reaction with glyoxylate.

[0085] Arginyl residues may be modified by reaction with any one or combination of several conventional reagents, including phenylglyoxal, 2,3-butanedione, 1,2-cyclohexanedione, and ninhydrin. Derivatization of arginyl residues requires that the reaction be performed in alkaline conditions because of the high pKa of the guanidine functional group. Furthermore, these reagents may react with the groups of lysine as well as the arginine epsilon-amino group.

[0086] Specific modification of tyrosyl residues has been studied extensively, with particular interest in introducing spectral labels into tyrosyl residues by reaction with aromatic diazonium compounds or tetranitromethane. Most commonly, N-acetylimidazole and tetranitromethane are used to form O-acetyl tyrosyl species and 3-nitro derivatives, respectively.

[0087] Carboxyl sidechain groups (aspartyl or glutamyl) may be selectively modified by reaction with carbodiimides (R'-N=C=N-R') such as 1-cyclohexyl-3-(2-morpholinyl-(4-ethyl) carbodiimide or 1-ethyl-3-(4-azonia-4,4-dimethylpentyl) carbodiimide. Furthermore, aspartyl and glutamyl residues may be converted to asparaginyl and glutaminyl residues by reaction with ammonium ions.

[0088] Glutaminyl and asparaginyl residues may be deamidated to the corresponding glutamyl and aspartyl residues. Alternatively, these residues are deamidated under mildly acidic conditions. Either form of these residues falls within the scope of this invention.

[0089] Cysteinyl residues can be replaced by amino acid residues or other moieties either to eliminate disulfide bonding or, conversely, to stabilize cross-linking. See, e.g., Bhatnagar et al. (1996), J. Med. Chem. 39: 3814-9.

[0090] Derivatization with bifunctional agents is useful for cross-linking the peptides or their functional derivatives to a water-insoluble support matrix or to other macromolecular vehicles. Commonly used cross-linking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), and bifunctional maleimides such as bis-N-maleimido-1,8-octane. Derivatizing agents such as methyl-3-[(p-azidophenyl)dithio]propionimidate yield photoactivatable intermediates that are capable of forming cross-links in the presence of light. Alternatively, reactive water-insoluble matrices such as cyanogen bromide-activated carbohydrates and the reactive substrates described in U.S. Pat. Nos. 3,969,287; 3,691,016; 4,195,128; 4,247,642; 4,229,537; and 4,330,440 are employed for protein immobilization.

[0091] Carbohydrate (oligosaccharide) groups may conveniently be attached to sites that are known to be glycosylation sites in proteins. Generally, O-linked oligosaccharides are attached to serine (Ser) or threonine (Thr) residues while N-linked oligosaccharides are attached to asparagine (Asn) residues when they are part of the sequence Asn-X-Ser/Thr, where X can be any amino acid except proline. X is preferably one of the 19 naturally occurring amino acids other than proline. The structures of N-linked and O-linked oligosaccharides and the sugar residues found in each type are different. One type of sugar that is commonly found on both is N-acetylneuraminic acid (referred to as sialic acid). Sialic acid is usually the terminal residue of both N-linked and O-linked oligosaccharides and, by virtue of its negative charge, may confer acidic properties to the glycosylated compound. Such site(s) may be incorporated in the linker of the compounds of this invention and are preferably glycosylated by a cell during recombinant production of the polypeptide compounds (e.g., in mammalian cells such as CHO, BHK, COS). However, such sites may further be glycosylated by synthetic or semi-synthetic procedures known in the art.

[0092] Other possible modifications include hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, oxidation of the sulfur atom in Cys, methylation of the alpha-amino groups of lysine, arginine, and histidine side chains. Creighton, Proteins: Structure and Molecule Properties (W. H. Freeman & Co., San Francisco), pp. 79-86 (1983).

[0093] Compounds of the present invention may be changed at the DNA level, as well. The DNA sequence of any portion of the compound may be changed to codons more compatible with the chosen host cell. For *E. coli*, which is the preferred host cell, optimized codons are known in the art. Codons may be substituted to eliminate restriction sites or to include silent restriction sites, which may aid in processing of the DNA in the selected host cell. The vehicle, linker and peptide DNA sequences may be modified to include any of the foregoing sequence changes.

Methods of Making

[0094] The compounds of this invention largely may be made in transformed host cells using recombinant DNA techniques. To do so, a recombinant DNA molecule coding for the peptide is prepared. Methods of preparing such DNA molecules are well known in the art. For instance, sequences coding for the peptides could be excised from DNA using suitable restriction enzymes. Alternatively, the DNA molecule could be synthesized using chemical synthesis techniques, such as the phosphoramidate method. Also, a combination of these techniques could be used.

[0095] The invention also includes a vector capable of expressing the peptides in an appropriate host. The vector comprises the DNA molecule that codes for the peptides operatively linked to appropriate expression control sequences. Methods of effecting this operative linking, either before or after the DNA molecule is inserted into the vector, are well known. Expression control sequences include promoters, activators, enhancers, operators, ribosomal binding sites, start signals, stop signals, cap signals, polyadenylation signals, and other signals involved with the control of transcription or translation.

[0096] The resulting vector having the DNA molecule thereon is used to transform an appropriate host. This transformation may be performed using methods well known in the art.

[0097] Any of a large number of available and well-known host cells may be used in the practice of this invention. The selection of a particular host is dependent upon a number of factors recognized by the art. These include, for example, compatibility with the chosen expression vector, toxicity of the peptides encoded by the DNA molecule, rate of transformation, ease of recovery of the peptides, expression characteristics, bio-safety and costs. A balance of these factors must be struck with the understanding that not all hosts may be equally effective for the expression of a particular DNA sequence. Within these general guidelines, useful microbial hosts include bacteria (such as *E. coli* sp.), yeast (such as *Saccharomyces* sp.) and other fungi, insects, plants, mammalian (including human) cells in culture, or other hosts known in the art.

[0098] Next, the transformed host is cultured and purified. Host cells may be cultured under conventional fermentation conditions so that the desired compounds are expressed. Such fermentation conditions are well known in the art. Finally, the peptides are purified from culture by methods well known in the art.

[0099] The compounds may also be made by synthetic methods. For example, solid phase synthesis techniques may be used. Suitable techniques are well known in the art, and include those described in Merrifield (1973), *Chem. Polypeptides*, pp. 335-61 (Katsoyannis and Panayotis eds.); Merrifield (1963), *J. Am. Chem. Soc.* 85: 2149; Davis et al. (1985), *Biochem. Intl.* 10: 394-414; Stewart and Young (1969), *Solid Phase Peptide Synthesis*; U.S. Pat. No. 3,941,763; Finn et al. (1976), *The Proteins* (3rd ed.) 2:105-253; and Erickson et al. (1976), *The Proteins* (3rd ed.) 2: 257-527. Solid phase synthesis is the preferred technique of making individual peptides since it is the most cost-effective method of making small peptides.

[0100] Compounds that contain derivatized peptides or which contain non-peptide groups may be synthesized by well-known organic chemistry techniques.

Uses of the Compounds

[0101] Compounds of this invention may be particularly useful in treatment of B-cell mediated autoimmune diseases. In particular, the compounds of this invention may be useful in treating, preventing, ameliorating, diagnosing or prognosing lupus, including systemic lupus erythematosus (SLE), and lupus-associated diseases and conditions. Other preferred indications include B-cell mediated cancers, including B-cell lymphoma.

[0102] The compounds of this invention can also be used to treat inflammatory conditions of the joints. Inflammatory conditions of a joint are chronic joint diseases that afflict and disable, to varying degrees, millions of people worldwide. Rheumatoid arthritis is a disease of articular joints in which the cartilage and bone are slowly eroded away by a proliferative, invasive connective tissue called pannus, which is derived from the synovial membrane. The disease may involve peri-articular structures such as bursae, tendon sheaths and tendons as well as extra-articular tissues such as the subcutis, cardiovascular system, lungs, spleen, lymph nodes, skeletal muscles, nervous system (central and peripheral) and eyes (Silberberg (1985), *Anderson's Pathology*, Kissane (ed.), II:1828). Osteoarthritis is a common joint disease characterized by degenerative changes in articular cartilage and reactive proliferation of bone and cartilage around the joint. Osteoarthritis is a cell-mediated active process that may result from the inappropriate response of chondrocytes to catabolic and anabolic stimuli. Changes in some matrix molecules of articular cartilage reportedly occur in early osteoarthritis (Thonar et al. (1993), *Rheumatic disease clinics of North America*, Moskowitz (ed.), 19:635-657 and Shinmei et al. (1992), *Arthritis Rheum.*, 35:1304-1308). TALL-1, TALL-1R and modulators thereof are believed to be useful in the treatment of these and related conditions.

[0103] Compounds of this invention may also be useful in treatment of a number of additional diseases and disorders, including:

- acute pancreatitis;
- ALS;
- Alzheimer's disease;
- asthma;
- atherosclerosis;
- autoimmune hemolytic anemia;
- cancer, particularly cancers related to B cells;

- cachexia/anorexia;
- chronic fatigue syndrome;
- cirrhosis (e.g., primary biliary cirrhosis);
- diabetes (e.g., insulin diabetes);
- 5 • fever;
- glomerulonephritis, including IgA glomerulonephritis and primary glomerulonephritis;
- Goodpasture's syndrome;
- Guillain-Barre syndrome;
- graft versus host disease;
- 10 • Hashimoto's thyroiditis;
- hemorrhagic shock;
- hyperalgesia;
- inflammatory bowel disease;
- inflammatory conditions of a joint, including osteoarthritis, psoriatic arthritis and rheumatoid arthritis;
- 15 • inflammatory conditions resulting from strain, sprain, cartilage damage, trauma, orthopedic surgery, infection or other disease processes;
- insulin-dependent diabetes mellitus;
- ischemic injury, including cerebral ischemia (e.g., brain injury as a result of trauma, epilepsy, hemorrhage or stroke, each of which may lead to neurodegeneration);
- 20 • learning impairment;
- lung diseases (e.g., ARDS);
- multiple myeloma;
- multiple sclerosis;
- Myasthenia gravis;
- 25 • myelogenous (e.g., AML and CML) and other leukemias;
- myopathies (e.g., muscle protein metabolism, esp. in sepsis);
- neurotoxicity (e.g., as induced by HIV);
- osteoporosis;
- pain;
- 30 • Parkinson's disease;
- Pemphigus;
- polymyositis/dermatomyositis;
- pulmonary inflammation, including autoimmune pulmonary inflammation;
- pre-term labor;
- 35 • psoriasis;
- Reiter's disease;
- reperfusion injury;
- septic shock;
- side effects from radiation therapy;
- 40 • Sjogren's syndrome;
- sleep disturbance;
- temporal mandibular joint disease;
- thrombocytopenia, including idiopathic thrombocytopenia and autoimmune neonatal thrombocytopenia;
- tumor metastasis;
- 45 • uveitis; and
- vasculitis.

[0104] Compounds of this invention may be administered alone or in combination with a therapeutically effective amount of other drugs, including analgesic agents, disease-modifying anti-rheumatic drugs (DMARDs), non-steroidal anti-inflammatory drugs (NSAIDs), and any immune and/or inflammatory modulators. Thus, compounds of this invention may be administered with:

- Modulators of other members of the TNF/TNF receptor family, including TNF antagonists, such as etanercept (Enbrel™), sTNF-RI, oncept, D2E7, and Remicade™.
- 55 • Nerve growth factor (NGF) modulators.
- IL-1 inhibitors, including IL-1ra molecules such as anakinra and more recently discovered IL-1ra-like molecules such as IL-1Hy1 and IL-1Hy2; IL-1 "trap" molecules as described in U.S. Pat. No. 5,844,099, issued December 1, 1998; IL-1 antibodies; solubilized IL-1 receptor, and the like.

- IL-6 inhibitors (e.g., antibodies to IL-6).
- IL-8 inhibitors (e.g., antibodies to IL-8).
- IL-18 inhibitors (e.g., IL-18 binding protein, solubilized IL-18 receptor, or IL-18 antibodies).
- Interleukin-1 converting enzyme (ICE) modulators.
- 5 • insulin-like growth factors (IGF-1, IGF-2) and modulators thereof.
- Transforming growth factor- β (TGF- β), TGF- β family members, and TGF- β modulators.
- Fibroblast growth factors FGF-1 to FGF-10, and FGF modulators.
- Osteoprotegerin (OPG), OPG analogues, osteoprotective agents, and antibodies to OPG-ligand (OPG-L).
- 10 • bone anabolic agents, such as parathyroid hormone (PTH), PTH fragments, and molecules incorporating PTH fragments (e.g., PTH (1-34)-Fc).
- PAF antagonists.
- Keratinocyte growth factor (KGF), KGF-related molecules (e.g., KGF-2), and KGF modulators.
- COX-2 inhibitors, such as Celebrex™ and Vioxx™.
- Prostaglandin analogs (e.g., E series prostaglandins).
- 15 • Matrix metalloproteinase (MMP) modulators.
- Nitric oxide synthase (NOS) modulators, including modulators of inducible NOS.
- Modulators of glucocorticoid receptor.
- Modulators of glutamate receptor.
- Modulators of lipopolysaccharide (LPS) levels.
- 20 • Anti-cancer agents, including inhibitors of oncogenes (e.g., fos, jun) and interferons.
- Noradrenaline and modulators and mimetics thereof.

Pharmaceutical Compositions

25 **[0105]** In General. The present invention also provides methods of using pharmaceutical compositions of the inventive compounds. Such pharmaceutical compositions may be for administration for injection, or for oral, pulmonary, nasal, transdermal or other forms of administration. In general, the invention encompasses pharmaceutical compositions comprising effective amounts of a compound of the invention together with pharmaceutically acceptable diluents, preservatives, solubilizers, emulsifiers, adjuvants and/or carriers. Such compositions include diluents of various buffer content
30 (e.g., Tris-HCl, acetate, phosphate), pH and ionic strength; additives such as detergents and solubilizing agents (e.g., Tween 80, Polysorbate 80), anti-oxidants (e.g., ascorbic acid, sodium metabisulfite), preservatives (e.g., Thimersol, benzyl alcohol) and bulking substances (e.g., lactose, mannitol); incorporation of the material into particulate preparations of polymeric compounds such as polylactic acid, polyglycolic acid, etc. or into liposomes. Hyaluronic acid may also be used, and this may have the effect of promoting sustained duration in the circulation. Such compositions may influence
35 the physical state, stability, rate of in vivo release, and rate of in vivo clearance of the present proteins and derivatives. See, e.g., Remington's Pharmaceutical Sciences, 18th Ed. (1990, Mack Publishing Co., Easton, PA 18042) pages 1435-1712 which are herein incorporated by reference in their entirety. The compositions may be prepared in liquid form, or may be in dried powder, such as lyophilized form. Implantable sustained release formulations are also contemplated, as are transdermal formulations.

40 **[0106]** Oral dosage forms. Contemplated for use herein are oral solid dosage forms, which are described generally in Chapter 89 of Remington's Pharmaceutical Sciences (1990), 18th Ed., Mack Publishing Co. Easton PA 18042, which is herein incorporated by reference in its entirety. Solid dosage forms include tablets, capsules, pills, troches or lozenges, cachets or pellets. Also, liposomal or proteinoid encapsulation may be used to formulate the present compositions (as, for example, proteinoid microspheres reported in U.S. Patent No. 4,925,673). Liposomal encapsulation may be used
45 and the liposomes may be derivatized with various polymers (e.g., U.S. Patent No. 5,013,556). A description of possible solid dosage forms for the therapeutic is given in Chapter 10 of Marshall, K., Modern Pharmaceutics (1979), edited by G. S. Banker and C. T. Rhodes, herein incorporated by reference in its entirety. In general, the formulation will include the inventive compound, and inert ingredients which allow for protection against the stomach environment, and release of the biologically active material in the intestine.

50 **[0107]** Also specifically contemplated are oral dosage forms of the above inventive compounds. If necessary, the compounds may be chemically modified so that oral delivery is efficacious. Generally, the chemical modification contemplated is the attachment of at least one moiety to the compound molecule itself, where said moiety permits (a) inhibition of proteolysis; and (b) uptake into the blood stream from the stomach or intestine. Also desired is the increase in overall stability of the compound and increase in circulation time in the body. Moieties useful as covalently attached
55 vehicles in this invention may also be used for this purpose. Examples of such moieties include: PEG, copolymers of ethylene glycol and propylene glycol, carboxymethyl cellulose, dextran, polyvinyl alcohol, polyvinyl pyrrolidone and polyproline. See, for example, Abuchowski and Davis, Soluble Polymer-Enzyme Adducts, Enzymes as Drugs (1981), Hochenberg and Roberts, eds., Wiley-Interscience, New York, NY., pp. 367-83; Newmark, et al. (1982), J. Appl. Biochem.

4:185-9. Other polymers that could be used are poly-1,3-dioxolane and poly-1,3,6-tioxocane. Preferred for pharmaceutical usage, as indicated above, are PEG moieties.

5 [0108] For oral delivery dosage forms, it is also possible to use a salt of a modified aliphatic amino acid, such as sodium N-(8-[2-hydroxybenzoyl] amino) caprylate (SNAC), as a carrier to enhance absorption of the therapeutic compounds of this invention. The clinical efficacy of a heparin formulation using SNAC has been demonstrated in a Phase II trial conducted by Emisphere Technologies. See US Patent No. 5,792,451, "Oral drug delivery composition and methods".

10 [0109] The compounds of this invention can be included in the formulation as fine multiparticulates in the form of granules or pellets of particle size about 1 mm. The formulation of the material for capsule administration could also be as a powder, lightly compressed plugs or even as tablets. The therapeutic could be prepared by compression.

[0110] Colorants and flavoring agents may all be included. For example, the protein (or derivative) may be formulated (such as by liposome or microsphere encapsulation) and then further contained within an edible product, such as a refrigerated beverage containing colorants and flavoring agents.

15 [0111] One may dilute or increase the volume of the compound of the invention with an inert material. These diluents could include carbohydrates, especially mannitol, α -lactose, anhydrous lactose, cellulose, sucrose, modified dextrans and starch. Certain inorganic salts may also be used as fillers including calcium triphosphate, magnesium carbonate and sodium chloride. Some commercially available diluents are Fast-Flo, Emdex, STA-Rx 1500, Emcompress and Avicell.

20 [0112] Disintegrants may be included in the formulation of the therapeutic into a solid dosage form. Materials used as disintegrants include but are not limited to starch including the commercial disintegrant based on starch, Explotab. Sodium starch glycolate, Amberlite, sodium carboxymethylcellulose, ultramylopectin, sodium alginate, gelatin, orange peel, acid carboxymethyl cellulose, natural sponge and bentonite may all be used. Another form of the disintegrants are the insoluble cationic exchange resins. Powdered gums may be used as disintegrants and as binders and these can include powdered gums such as agar, Karaya or tragacanth. Alginic acid and its sodium salt are also useful as disintegrants.

25 [0113] Binders may be used to hold the therapeutic agent together to form a hard tablet and include materials from natural products such as acacia, tragacanth, starch and gelatin. Others include methyl cellulose (MC), ethyl cellulose (EC) and carboxymethyl cellulose (CMC). Polyvinyl pyrrolidone (PVP) and hydroxypropylmethyl cellulose (HPMC) could both be used in alcoholic solutions to granulate the therapeutic.

30 [0114] An antifrictional agent may be included in the formulation of the therapeutic to prevent sticking during the formulation process. Lubricants may be used as a layer between the therapeutic and the die wall, and these can include but are not limited to; stearic acid including its magnesium and calcium salts, polytetrafluoroethylene (PTFE), liquid paraffin, vegetable oils and waxes. Soluble lubricants may also be used such as sodium lauryl sulfate, magnesium lauryl sulfate, polyethylene glycol of various molecular weights, Carbowax 4000 and 6000.

35 [0115] Glidants that might improve the flow properties of the drug during formulation and to aid rearrangement during compression might be added. The glidants may include starch, talc, pyrogenic silica and hydrated silicoaluminate.

40 [0116] To aid dissolution of the compound of this invention into the aqueous environment a surfactant might be added as a wetting agent. Surfactants may include anionic detergents such as sodium lauryl sulfate, dioctyl sodium sulfosuccinate and dioctyl sodium sulfonate. Cationic detergents might be used and could include benzalkonium chloride or benzethonium chloride. The list of potential nonionic detergents that could be included in the formulation as surfactants are lauromacrogol 400, polyoxyl 40 stearate, polyoxyethylene hydrogenated castor oil 10, 50 and 60, glycerol monostearate, polysorbate 40, 60, 65 and 80, sucrose fatty acid ester, methyl cellulose and carboxymethyl cellulose. These surfactants could be present in the formulation of the protein or derivative either alone or as a mixture in different ratios.

[0117] Additives may also be included in the formulation to enhance uptake of the compound. Additives potentially having this property are for instance the fatty acids oleic acid, linoleic acid and linolenic acid.

45 [0118] Controlled release formulation may be desirable. The compound of this invention could be incorporated into an inert matrix which permits release by either diffusion or leaching mechanisms; e.g., gums. Slowly degenerating matrices may also be incorporated into the formulation, e.g., alginates, polysaccharides. Another form of a controlled release of the compounds of this invention is by a method based on the Oros therapeutic system (Alza Corp.), i.e., the drug is enclosed in a semipermeable membrane which allows water to enter and push drug out through a single small opening due to osmotic effects. Some enteric coatings also have a delayed release effect.

50 [0119] Other coatings may be used for the formulation. These include a variety of sugars which could be applied in a coating pan. The therapeutic agent could also be given in a film coated tablet and the materials used in this instance are divided into 2 groups. The first are the nonenteric materials and include methyl cellulose, ethyl cellulose, hydroxyethyl cellulose, methylhydroxy-ethyl cellulose, hydroxypropyl cellulose, hydroxypropyl-methyl cellulose, sodium carboxymethyl cellulose, providone and the polyethylene glycols. The second group consists of the enteric materials that are commonly esters of phthalic acid.

55 [0120] A mix of materials might be used to provide the optimum film coating. Film coating may be carried out in a pan coater or in a fluidized bed or by compression coating.

[0121] Pulmonary delivery forms. Also contemplated herein is pulmonary delivery of the present protein (or derivatives thereof). The protein (or derivative) is delivered to the lungs of a mammal while inhaling and traverses across the lung epithelial lining to the blood stream. (Other reports of this include Adjei et al., *Pharma. Res.* (1990) 7: 565-9; Adjei et al. (1990), *Internatl. J. Pharmaceutics* 63:135-44 (leuprolide acetate); Braquet et al. (1989), *J. Cardiovasc. Pharmacol.* 13 (suppl.5): s.143-146 (endothelin-1); Hubbard et al. (1989), *Annals Int. Med.* 3:206-12 (α 1-antitrypsin); Smith et al. (1989), *J. Clin. Invest.* 84: 1145-6 (α 1-proteinase); Oswein et al. (March 1990), "Aerosolization of Proteins", *Proc. Symp. Resp. Drug Delivery II*, Keystone, Colorado (recombinant human growth hormone); Debs et al. (1988), *J. Immunol.* 140: 3482-8 (interferon- γ and tumor necrosis factor α) and Platz et al., U.S. Patent No. 5,284,656 (granulocyte colony stimulating factor).

[0122] Contemplated for use in the practice of this invention are a wide range of mechanical devices designed for pulmonary delivery of therapeutic products, including but not limited to nebulizers, metered dose inhalers, and powder inhalers, all of which are familiar to those skilled in the art. Some specific examples of commercially available devices suitable for the practice of this invention are the Ultravent nebulizer, manufactured by Mallinckrodt, Inc., St. Louis, Missouri; the Acorn II nebulizer, manufactured by Marquest Medical Products, Englewood, Colorado; the Ventolin metered dose inhaler, manufactured by Glaxo Inc., Research Triangle Park, North Carolina; and the Spinhaler powder inhaler, manufactured by Fisons Corp., Bedford, Massachusetts.

[0123] All such devices require the use of formulations suitable for the dispensing of the inventive compound. Typically, each formulation is specific to the type of device employed and may involve the use of an appropriate propellant material, in addition to diluents, adjuvants and/or carriers useful in therapy.

[0124] The inventive compound should most advantageously be prepared in particulate form with an average particle size of less than 10 μ m (or microns), most preferably 0.5 to 5 μ m, for most effective delivery to the distal lung.

[0125] Pharmaceutically acceptable carriers include carbohydrates such as trehalose, mannitol, xylitol, sucrose, lactose, and sorbitol. Other ingredients for use in formulations may include DPPC, DOPE, DSPC and DOPC. Natural or synthetic surfactants may be used. PEG may be used (even apart from its use in derivatizing the protein or analog). Dextran, such as cyclodextran, may be used. Bile salts and other related enhancers may be used. Cellulose and cellulose derivatives may be used. Amino acids may be used, such as use in a buffer formulation.

[0126] Also, the use of liposomes, microcapsules or microspheres, inclusion complexes, or other types of carriers is contemplated.

[0127] Formulations suitable for use with a nebulizer, either jet or ultrasonic, will typically comprise the inventive compound dissolved in water at a concentration of about 0.1 to 25 mg of biologically active protein per mL of solution. The formulation may also include a buffer and a simple sugar (e.g., for protein stabilization and regulation of osmotic pressure). The nebulizer formulation may also contain a surfactant, to reduce or prevent surface induced aggregation of the protein caused by atomization of the solution in forming the aerosol.

[0128] Formulations for use with a metered-dose inhaler device will generally comprise a finely divided powder containing the inventive compound suspended in a propellant with the aid of a surfactant. The propellant may be any conventional material employed for this purpose, such as a chlorofluorocarbon, a hydrochlorofluorocarbon, a hydrofluorocarbon, or a hydrocarbon, including trichlorofluoromethane, dichlorodifluoromethane, dichlorotetrafluoroethanol, and 1,1,1,2-tetrafluoroethane, or combinations thereof. Suitable surfactants include sorbitan trioleate and soya lecithin. Oleic acid may also be useful as a surfactant.

[0129] Formulations for dispensing from a powder inhaler device will comprise a finely divided dry powder containing the inventive compound and may also include a bulking agent, such as lactose, sorbitol, sucrose, mannitol, trehalose, or xylitol in amounts which facilitate dispersal of the powder from the device, e.g., 50 to 90% by weight of the formulation.

[0130] Nasal delivery forms. Nasal delivery of the inventive compound is also contemplated. Nasal delivery allows the passage of the protein to the blood stream directly after administering the therapeutic product to the nose, without the necessity for deposition of the product in the lung. Formulations for nasal delivery include those with dextran or cyclodextran. Delivery via transport across other mucous membranes is also contemplated.

[0131] Dosages. The dosage regimen involved in a method for treating the above-described conditions will be determined by the attending physician, considering various factors which modify the action of drugs, e.g. the age, condition, body weight, sex and diet of the patient, the severity of any infection, time of administration and other clinical factors. Generally, the daily regimen should be in the range of 0.1-1000 micrograms of the inventive compound per kilogram of body weight, preferably 0.1-150 micrograms per kilogram.

Specific preferred embodiments

[0132] The inventors have determined preferred structures for the preferred peptides listed in Table 4 below. The symbol "A" may be any of the linkers described herein or may simply represent a normal peptide bond (i.e., so that no linker is present). Tandem repeats and linkers are shown separated by dashes for clarity.

Table 4-Preferred embodiments

Sequence/structure	SEQ ID NO:
LPGCKWDLLIKQWVCDPL- Λ -V ¹	44
V ¹ - Λ -LPGCKWDLLIKQWVCDPL	45
LPGCKWDLLIKQWVCDPL - Λ - LPGCKWDLLIKQWVCDPL - Λ -V ¹	46
V ¹ - Λ - LPGCKWDLLIKQWVCDPL - Λ - LPGCKWDLLIKQWVCDPL	47
SADCYFDILTKSDVCTSS- Λ -V ¹	48
V ¹ - Λ -SADCYFDILTKSDVCTSS	49
SADCYFDILTKSDVTSS- Λ - SADCYFDILTKSDVTSS - Λ -V ¹	50
V ¹ - Λ - SADCYFDILTKSDVTSS - Λ - SADCYFDILTKSDVTSS	51
FHDCKWDLTKQWVCHGL- Λ -V ¹	52
V ¹ - Λ - FHDCKWDLTKQWVCHGL	53
FHDCKWDLTKQWVCHGL - Λ - FHDCKWDLTKQWVCHGL - Λ -V ¹	54
V ¹ - Λ - FHDCKWDLTKQWVCHGL - Λ - FHDCKWDLTKQWVCHGL	55

"V¹" is an Fc domain as defined previously herein. In addition to those listed in Table 4, the inventors further contemplate heterodimers in which each strand of an Fc dimer is linked to a different peptide sequence; for example, wherein each Fc is linked to a different sequence selected from Table 2.

[0133] All of the compounds of this invention can be prepared by methods described in PCT appl. no. WO 99/25044.

[0134] The invention will now be further described by the following working examples, which are illustrative rather than limiting.

EXAMPLE 1

Peptides

Peptide Phage Display

1. Magnetic bead preparation

[0135] A. Fc-TALL-1 immobilization on magnetic beads

[0136] The recombinant Fc-TALL-1 protein was immobilized on the Protein A Dynabeads (Dyna) at a concentration of 8 μ g of Fc-TALL-1 per 100 μ l of the bead stock from the manufacturer. By drawing the beads to one side of a tube using a magnet and pipetting away the liquid, the beads were washed twice with the phosphate buffer saline (PBS) and resuspended in PBS. The Fc-TALL-1 protein was added to the washed beads at the above concentration and incubated with rotation for 1 hour at room temperature. The Fc-TALL-1 coated beads were then blocked by adding bovine serum albumin (BSA) to 1% final concentration and incubating overnight at 4 °C with rotation. The resulting Fc-TALL-1 coated beads were then washed twice with PBST (PBS with 0.05% Tween-20) before being subjected to the selection procedures.

B. Negative selection bead preparation

5 [0137] Additional beads were also prepared for negative selections. For each panning condition, 250 μ l of the bead stock from the manufacturer was subjected to the above procedure (section 1A) except that the incubation step with Fc-TALL-1 was omitted. In the last washing step, the beads were divided into five 50 μ l aliquots.

2. Selection of TALL-1 binding phage

10 A. Overall strategy

[0138] Two filamentous phage libraries, TN8-IX (5×10^9 independent transformants) and TN12-I (1.4×10^9 independent transformants) (Dyax Corp.), were used to select for TALL-1 binding phage. Each library was subjected to either pH 2 elution or 'bead elution' (section 2E). Therefore, four different panning conditions were carried out for the TALL-1 project (TN8-IX using the pH2 elution method, TN8-IX using the bead elution method, TN12-I the using pH2 elution method, and TN12-I using the bead elution method). Three rounds of selection were performed for each condition.

B. Negative selection

20 [0139] For each panning condition, about 100 random library equivalent (5×10^{11} pfu for TN8-IX and 1.4×10^{11} pfu for TN12-I) was aliquoted from the library stock and diluted to 300 μ l with PBST. After the last washing liquid was drawn out from the first 50 μ l aliquot of the beads prepared for negative selections (section 1B), the 300 μ l diluted library stock was added to the beads. The resulting mixture was incubated for 10 minutes at room temperature with rotation. The phage supernatant was drawn out using the magnet and added to the second 50 μ l aliquot for another negative selection step. In this way, five negative selection steps were performed.

25 C. Selection using the Fc-TALL-1 protein coated beads

[0140] The phage supernatant after the last negative selection step (section 1B) was added to the Fc-TALL-1 coated beads after the last washing step (section 1A). This mixture was incubated with rotation for two hours at room temperature, allowing specific phage to bind to the target protein. After the supernatant is discarded, the beads were washed seven times with PBST.

D. pH2 elution of bound phage

35 [0141] After the last washing step (section 2C), the bound phages were eluted from the magnetic beads by adding 200 μ l of CBST (50 mM sodium citrate, 150 mM sodium chloride, 0.05% Tween-20, pH2). After 5 minute incubation at room temperature, the liquid containing the eluted phage were drawn out and transferred to another tube. The elution step was repeated again by adding 200 μ l of CBST and incubating for 5 minutes. The liquids from two elution steps were added together, and 100 μ l of 2 M Tris solution (pH 8) was added to neutralize the pH. 500 μ l of Min A Salts solution (60 mM K_2HPO_4 , 33 mM KH_2PO_4 , 7.6 mM $(NH_4)SO_4$, and 1.7 mM sodium citrate) was added to make the final volume to 1 ml.

E. 'bead elution'

45 [0142] After the final washing liquid was drawn out (section 2C), 1 ml of Min A salts solution was added to the beads. This bead mixture was added directly to a concentrated bacteria sample for infection (section 3A and 3B).

3. Amplification

50 A. Preparation of plating cells

[0143] Fresh E. Coli. (XL-1 Blue MRF) culture was grown to $OD_{600} = 0.5$ in LB media containing 12.5 μ g/ml tetracycline. For each panning condition, 20 ml of this culture was chilled on ice and centrifuged. The bacteria pellet was resuspended in 1 ml of the Min A Salts solution.

55 B. Transduction

[0144] Each mixture from different elution methods (section 2D and 2E) was added to a concentrated bacteria sample

EP 2 845 864 A2

(section 3A) and incubated at 37 °C for 15 minutes. 2 ml of NZCYM media (2XNZCYM, 50 µg/ml ampicillin) was added to each mixture and incubated at room temperature for 15 minutes. The resulting 4 ml solution was plated on a large NZCYM agar plate containing 50 µg/ml ampicillin and incubated overnight at 37 °C.

5 C. Phage Harvesting

[0145] Each of the bacteria/phage mixture that was grown overnight on a large NZCYM agar plate (section 3B) was scraped off in 35 ml of LB media, and the agar plate was further rinsed with additional 35 ml of LB media. The resulting bacteria/phage mixture in LB media was centrifuged to pellet the bacteria away. 50 ml of the phage supernatant was transferred to a fresh tube, and 12.5 ml of PEG solution (20% PEG8000, 3.5M ammonium acetate) was added and incubated on ice for 2 hours to precipitate phages. Precipitated phages were centrifuged down and resuspended in 6 ml of the phage resuspension buffer (250 mM NaCl, 100 mM Tris pH8, 1 mM EDTA). This phage solution was further purified by centrifuging away the remaining bacteria and precipitating the phage for the second time by adding 1.5 ml of the PEG solution. After a centrifugation step, the phage pellet was resuspended in 400 µl of PBS. This solution was subjected to a final centrifugation to rid of remaining bacteria debris. The resulting phage preparation was titered by a standard plaque formation assay (Molecular Cloning, Maniatis et al 3rd Edition).

4. Two more rounds of selection and amplification.

[0146] In the second round, the amplified phage (10^{10} pfu) from the first round (section 3C) was used as the input phage to perform the selection and amplification steps (sections 2 and 3). The amplified phage (10^{10} pfu) from the 2nd round in turn was used as the input phage to perform 3rd round of selection and amplification (sections 2 and 3). After the elution steps (sections 2D and 2E) of the 3rd round, a small fraction of the eluted phage was plated out as in the plaque formation assay (section 3C). Individual plaques were picked and placed into 96 well microtiter plates containing 100 µl of TE buffer in each well. These master plates were incubated in a 37 °C incubator for 1 hour to allow phages to elute into the TE buffer.

5. Clonal analysis (Phage ELISA and sequencing)

[0147] The phage clones were analyzed by phage ELISA and sequencing methods. The sequences were ranked based on the combined results from these two assays.

A. Phage ELISA

[0148] An XL-1 Blue MRF⁺ culture was grown until OD₆₀₀ reaches 0.5. 30 µl of this culture was aliquoted into each well of a 96 well microtiter plate. 10 µl of eluted phage (section 4) was added to each well and allowed to infect bacteria for 15 min at room temperature. 130 µl of LB media containing 12.5 µg/ml of tetracycline and 50 µg/ml of ampicillin was added to each well. The microtiter plate was then incubated overnight at 37 °C. The recombinant TALL-1 protein (1 µg/ml in PBS) was allowed to coat onto the 96-well Maxisorp plates (NUNC) overnight and 4°C. As a control, the recombinant Fc-Trail protein was coated onto a separate Maxisorp plate at the same molar concentration as the TALL-1 protein.

[0149] On the following day, liquids in the protein coated Maxisorp plates were discarded, and each well was blocked with 300 µl of 2% BSA solution at 37 °C for one hour. The BSA solution was discarded, and the wells were washed three times with the PBST solution. After the last washing step, 50 µl of PBST was added to each well of the protein coated Maxisorp plates. Each of the 50 µl overnight cultures in the 96 well microtiter plate was transferred to the corresponding wells of the TALL-1 coated plates as well as the control Fc-Trail coated plates. The 100 µl mixtures in the two kinds of plates were incubated for 1 hour at room temperature. The liquid was discarded from the Maxisorp plates, and the wells were washed five times with PBST. The HRP-conjugated anti-M13 antibody (Pharmacia) was diluted to 1:7,500, and 100 µl of the diluted solution was added to each well of the Maxisorp plates for 1 hour incubation at room temperature. The liquid was again discarded and the wells were washed seven times with PBST. 100 µl of tetramethylbenzidine (TMB) substrate (Sigma) was added to each well for the color reaction to develop, and the reaction was stopped with 50 µl of the 5 N H₂SO₄ solution. The OD₄₅₀ was read on a plate reader (Molecular Devices).

[0150] B. Sequencing of the phage clones.

[0151] For each phage clone, the sequencing template was prepared by a PCR method. The following oligonucleotide pair was used to amplify about 500 nucleotide fragment:
primer #1 (5'-CGGCGCAACTATCGGTATCAAGCTG-3') (SEQ ID NO: 56) and primer #2 (5'-CATGTACCGTAACACT-GAGTTTCGTC-3'). (SEQ ID NO: 57) The following mixture was prepared for each clone.

EP 2 845 864 A2

Reagents	volume (μ L) / tube
dH ₂ O	26.25
50% glycerol	10
10B PCR Buffer (w/o MgCl ₂)	5
25 mM MgCl ₂	4
10 mM dNTP mix	1
100 μ M primer 1	0.25
100 μ M primer 2	0.25
Taq polymerase	0.25
Phage in TE (section 4)	3
Final reaction volume	50

[0152] The thermocycler (GeneAmp PCR System 9700, Applied Biosystems) was used to run the following program: 94°C for 5 min; [94°C for 30 sec, 55°C for 30 sec, 72°C for 45 sec.]x30 cycles; 72°C for 7 min; cool to 4°C. The PCR product was checked by running 5 μ l of each PCR reaction on a 1% agarose gel. The PCR product in the remaining 45 μ l from each reaction was cleaned up using the QIAquick Multiwell PCR Purification kit (Qiagen), following the manufacturer's protocol. The resulting product was then sequenced using the ABI 377 Sequencer (Perkin-Elmer) following the manufacturer recommended protocol.

6. Sequence ranking and consensus sequence determination

A. Sequence ranking

[0153] The peptide sequences that were translated from variable nucleotide sequences (section 5B) were correlated to ELISA data. The clones that showed high OD₄₅₀ in the TALL-1 coated wells and low OD₄₅₀ in the Fc-Trail coated wells were considered more important. The sequences that occur multiple times were also considered important. Candidate sequences were chosen based on these criteria for further analysis as peptides or peptibodies. Five and nine candidate peptide sequences were selected from the TN8-IX and TN12-I libraries, respectively.

B. Consensus sequence determination

[0154] The majority of sequences selected from the TN12-I library contained a very conserved DBL motif. This motif was also observed in sequences selected from the TN8-IB library as well. Another motif, PFPWE (SEQ ID NO: 110) was also observed in sequences obtained from the TN8-IB library.

[0155] A consensus peptide, FHDCKWDL~~L~~TKOW~~V~~CHGL (SEQ ID NO: 58), was designed based on the DBL motif. Since peptides derived from the TN12-I library were the most active ones, the top 26 peptide sequences based on the above ranking criteria (section 5A) were aligned by the DBL motif. The underlined "core amino acid sequence" was obtained by determining the amino acid that occur the most in each position. The two cysteines adjacent to the core sequences were fixed amino acids in the TN12-I library. The rest of the amino acid sequence in the consensus peptide is taken from one of the candidate peptides, TALL-1-12-10 (Table 2, SEQ ID NO: 37). The peptide and peptibody that was derived from this consensus sequence were most active in the B cell proliferation assay.

EXAMPLE 2

Peptibodies

[0156] A set of 12 TALL-1 inhibitory peptibodies (Table 5) was constructed in which a monomer of each peptide was fused in-frame to the Fc region of human IgG1. Each TALL-1 inhibitory peptibody was constructed by annealing the pairs of oligonucleotides shown in Table 6 to generate a duplex encoding the peptide and a linker comprised of 5 glycine residues and one valine residue as an NdeI to SalI fragment. These duplex molecules were ligated into a vector (pAMG21-RANK-Fc, described herein) containing the human Fc gene, also digested with NdeI and SalI. The resulting ligation

mixtures were transformed by electroporation into *E. coli* strain 2596 cells (GM221, described herein). Clones were screened for the ability to produce the recombinant protein product and to possess the gene fusion having the correct nucleotide sequence. A single such clone was selected for each of the peptibodies. The nucleotide and amino acid sequences of the fusion proteins are shown in Figure 4A through 4F.

Table 5. Peptide sequences and oligonucleotides used to generate TALL-1 inhibitory peptibodies.

Peptibody	Peptibody SEQ ID NO	Peptide Sequence	Sense oligonucleotide	Antisense oligonucleotide
TALL-1-8-1-a	29	PGTCFPPWECTHA	2517-24	2517-25
TALL-1-8-2-a	30	WGACWFPWECFKE	2517-26	2517-27
TALL-1-8-4-a	31	VPFCDLLTKHCFEA	2517-28	2517-29
TALL-1-12-4-a	32	GSRCKYKWDVLTKQCFHH	2517-30	2517-31
TALL-1-12-3-a	33	LPGCKWDLLIKQWVCDPL	2517-32	2517-33
TALL-1-12-5-a	34	SADCYFDILTKSDVCTSS	2517-34	2517-35
TALL-1-12-8-a	35	SDDCMYDQLTRMFICSNL	2517-36	2517-37
TALL-1-12-9-a	36	DLNCKYDELTYKEWCQFN	2521-92	2521-93
TALL-1-12-10-a	37	FHDCKYDLLTRQMVCHGL	2521-94	2521-95
TALL-1-12-11-a	38	RNHCFWDHLLKQDICPSP	2521-96	2521-97
TALL-1-12-14-a	39	ANQCWWDSLTKKNVCEFF	2521-98	2521-99
TALL-1-consensus	58	FHDCKWDLTKQWVCHGL	2551-48	2551-49

Table 5B TALL-1 inhibitory peptibodies.

Peptibody	Peptibody SEQ ID NO	Peptide Sequence
TALL-1-8-1-a	111	MPGTCFPPFW ECTHAGGGGG VDKTHTCPPC PAPELLGGPS VFLFPPKPKD TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY TLPSPRDELDT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTTPVLD SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPGK
TALL-1-8-2-a	112	MWGACWFPFW ECFKEGGGGG VDKTHTCPPC PAPELLGGPS VFLFPPKPKD TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY TLPSPRDELDT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTTPVLD SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPGK
TALL-1-8-4-a	113	MVPFCDLLTK HCFEAGGGGG VDKTHTCPPC PAPELLGGPS VFLFPPKPKD TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY TLPSPRDELDT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTTPVLD SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPGK
TALL-1-12-4-a	114	MGSRCKYKWD VLTKQCFHHG GGGGVDKTHT CPPCPAPELL GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR DELTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTTP PVLDSGDSFF LYSKLTVDKS RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GK

EP 2 845 864 A2

(continued)

Peptibody	PeptibodySEQ ID NO	Peptide Sequence			
5 TALL-1-12-3-a	115	MLPGCKWDDL GGPSVFLFPP NWXVDGVEVH GKEYKCKVSN DELTKNQVSL PVLDSGGSFF YTQKSLSLSP	IKQWVCDPLG KPKDTLMISR NAKTKPREEQ KALPAPIEKT TCLVKGFYPS LYSKLTVDKS GK	GGGGVDKTHT TPEVTCVVVD YNSTYRVVSV ISKAKGQPRE DIAVEWESNG RWQQGNVFSC GK	CPPCPAPELL VSHEDPEVKF LTVLHQDWLN PQVYTLPPSR QPENNYKTPP SVMHEALHNN GK
10 TALL-1-12-5-a	116	MSADCYFDIL GGPSVFLFPP NWXVDGVEVH GKEYKCKVSN DELTKNQVSL PVLDSGGSFF YTQKSLSLSP	TKSDVCTSSG KPKDTLMISR NAKTKPREEQ KALPAPIEKT TCLVKGFYPS LYSKLTVDKS GK	GGGG VDKTHT TPEVTCVVVD YNSTYRVVSV ISKAKGQPRE DIAVEWESNG RWQQGNVFSC GK	CPPCPAPELL VSHEDPEVKF LTVLHQDWLN PQVYTLPPSR QPENNYKTPP SVMHEALHNN GK
15 TALL-1-12-8-a	117	MSDDCMYDQL GGPSVFLFPP NWXVDGVEVH GKEYKCKVSN DELTKNQVSL PVLDSGGSFF YTQKSLSLSP	TRMFICSNLG KPKDTLMISR NAKTKPREEQ KALPAPIEKT TCLVKGFYPS LYSKLTVDKS GK	GGGGVDKTHT TPEVTCVVVD YNSTYRVVSV ISKAKGQPRE DIAVEWESNG RWQQGNVFSC GK	CPPCPAPELL VSHEDPEVKF LTVLHQDWLN PQVYTLPPSR QPENNYKTPP SVMHEALHNN GK
20 TALL-1-12-9-a	118	MDLNCKYDEL GGPSVFLFPP NWXVDGVEVH GKEYKCKVSN DELTKNQVSL PVLDSGGSFF YTQKSLSLSP	TYKEWCQFNG KPKDTLMISR NAKTKPREEQ KALPAPIEKT TCLVKGFYPS LYSKLTVDKS GK	GGGGVDKTHT TPEVTCVVVD YNSTYRVVSV ISKAKGQPRE DIAVEWESNG RWQQGNVFSC GK	CPPCPAPELL VSHEDPEVKF LTVLHQDWLN PQVYTLPPSR QPENNYKTPP SVMHEALHNN GK
25 TALL-1-12-10-a	119	MFHDCKYDLL GGPSVFLFPP NWXVDGVEVH GKEYKCKVSN DELTKNQVSL PVLDSGGSFF YTQKSLSLSP	TRQMVCHGLG KPKDTLMISR NAKTKPREEQ KALPAPIEKT TCLVKGFYPS LYSKLTVDKS GK	GGGGVDKTHT TPEVTCVVVD YNSTYRVVSV ISKAKGQPRE DIAVEWESNG RWQQGNVFSC GK	CPPCPAPELL VSHEDPEVKF LTVLHQDWLN PQVYTLPPSR QPENNYKTPP SVMHEALHNN GK
30 TALL-1-12-11-a	120	MRNHCFWDHL GGPSVFLFPP NWXVDGVEVH GKEYKCKVSN DELTKNQVSL PVLDSGGSFF YTQKSLSLSP	LKQDICPSPG KPKDTLMISR NAKTKPREEQ KALPAPIEKT TCLVKGFYPS LYSKLTVDKS GK	GGGGVDKTHT TPEVTCVVVD YNSTYRVVSV ISKAKGQPRE DIAVEWESNG RWQQGNVFSC GK	CPPCPAPELL VSHEDPEVKF LTVLHQDWLN PQVYTLPPSR QPENNYKTPP SVMHEALHNN GK
35 TALL-1-12-14-a	121	MANQCWWDLS GGPSVFLFPP NWXVDGVEVH GKEYKCKVSN DELTKNQVSL PVLDSGGSFF YTQKSLSLSP	TKKNVCEFFG KPKDTLMISR NAKTKPREEQ KALPAPIEKT TCLVKGFYPS LYSKLTVDKS GK	GGGGVDKTHT TPEVTCVVVD YNSTYRVVSV ISKAKGQPRE DIAVEWESNG RWQQGNVFSC GK	CPPCPAPELL VSHEDPEVKF LTVLHQDWLN PQVYTLPPSR QPENNYKTPP SVMHEALHNN GK
40 TALL-1-consensus	122	MFHDCKWDDL GGPSVFLFPP NWXVDGVEVH GKEYKCKVSN DELTKNQVSL PVLDSGGSFF YTQKSLSLSP	TKQWVCHGLG KPKDTLMISR NAKTKPREEQ KALPAPIEKT TCLVKGFYPS LYSKLTVDKS GK	GGGGVDKTHT TPEVTCVVVD YNSTYRVVSV ISKAKGQPRE DIAVEWESNG RWQQGNVFSC GK	CPPCPAPELL VSHEDPEVKF LTVLHQDWLN PQVYTLPPSR QPENNYKTPP SVMHEALHNN GK
45					
50					
55					

(continued)

Peptibody	Peptibody SEQ ID NO	Peptide Sequence
TALL-1 12-3 tandem dimer	123	MLPGCKWDDL IKQWVCDPLG SGSATGGSGS TASSGSGSAT HMLPGCKWDL LIKQWVCDPL GGGGGVDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR EPQVYTLPPS RDELTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT PPVLSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLG PGK
TALL-1 consensus tandem dimer	124	MFHDCKWDDL TKQWVCHGLG SGSATGGSGS TASSGSGSAT HMFHDCKWDL LTKQWVCHGL GGGGGVDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR EPQVYTLPPS RDELTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT PPVLSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLG PGK

Table 6. Sequences of oligonucleotides used in peptibody construction.

Oligonucleotide ID number	SEQ ID NO	Sequence
2517-24	71	TAT GCC GGG TAC TTG TTT CCC GTT CCC GTG GGA ATG CAC TCA CGC TGG TGG AGG CGG TGG GG
2517-25	72	TCG ACC CCA CCG CCT CCT GGA GCG TGA GTG CAT TCC CAC GGG AAG CCG AAA CAA GTA CCC GGC A
2517-26	73	TAT GTG GGG TGC TTG TTG GCC GTT CCC GTG GGA ATG TTT CAA AGA AGG TGG AGG CGG TGG GG
2517-27	74	TCG ACC CCA CCG CCT CCA CCT TCT TTG AAA CAT TCC CACGGG AAC GGC CAA CAAGCA CCC CAC A
2517-28	75	TAT GGT TCC GTT CTG TGA CCT GCT GAC TAA ACA CTG TTT CGA AGC TGG TGG AGG CGG TGG GG
2517-29	76	TCG ACC CCA CCG CCT CCA CCA GCT TCG AAA CAG TGT TTA GTC AGC AGG TCA CAGAAC GGA ACC A
2517-30	77	TAT GGG TTC TCG TTG TAA ATA CAA ATG GGA CGT TCT GAC TAA ACA GTG TTT CCA CCA CGG TGG AGG CGG TGG GG
2517-31	78	TCG ACC CCA CCG CCT CCA CCG TGG TGG AAA CAC TGT TTA GTC AGA ACG TCC CAT TTG TAT TTA CAA CGA GAA CCC A
2517-32	79	TAT GCT GCC GGG TTG TAA ATG GGA CCT GCT GAT CAA ACA GTG GGT TTG TGA CCC GCT GGG TGG AGG CGG TGG GG
2517-33	80	TCG ACC CCA CCG CCT CCA CCC AGC GGG TCA CAA ACC CAC TGT TTG ATC AGC AGG TCC CAT TTA CAA CCC GGC AGC A
2517-34	81	TAT GTC TGC TGA CTG TTA CTT CGA CAT CCT GAC TAA ATC TGA CGT TTG TAC TTC TTC TGG TGG AGG CGG TGG GG
2517-35	82	TCG ACC CCA CCG CCT CCA CCA GAA GAA GTA CAA ACG TCA GAT TTA GTC AGG ATG TCG AAG TAA CAG TCA GCA GAC A
2517-36	83	TAT GTC TGA CGA CTG TAT GTA CGA CCA GCT GAC TCG TAT GTT CAT CTG TTC TAA CCT GGG TGG AGG CGG TGG GG

EP 2 845 864 A2

(continued)

Oligonucleotide ID number	SEQ ID NO	Sequence
2517-37	84	TCG ACC CCA CCG CCT CCA CCC AGG TTA GAA CAG ATG AAC ATA CGA GTC AGC TGG TCG TAC ATA CAG TCG TCA GAC A
2521-92	85	TAT GGA CCT GAA CTG TAA ATA CGA CGA ACT GAC TTA CAA AGA ATG GTG TCA GTT CAA CGG TGG AGG CGG TGG GG
25221-93	86	TCG ACC CCA CCG CCT CCA CCG TTG AAC TGA CAC CAT TCT TTG TAA GTC AGTTCG TCG TAT TTA CAG TTC AGG TCC A
2521-94	87	TAT GTT CCA CGA CTG TAA ATA CGA CCT GCT GAC TCG TCA GAT GGT TTG TCA CGG TCT GGG TGG AGG CGG TGG GG
2521-95	88	TCG ACC CCA CCG CCT CCA CCC AGA CCG TGA CAA ACC ATC TGA CGA GTC AGC AGG TCG TAT TTA CAG TCG TGG AAC A
2521-96	89	TAT GCG TAA CCA CTG TTT CTG GGA CCA CCT GCT GAA ACA GGA CAT CTG TCC GTC TCC GGG TGG AGG CGG TGG GG
2521-97	90	TCG ACC CCA CCG CCT CCA CCC GGA GAC GGA CAG ATG TCC TGT TTC AGC AGG TGG TCC CAG AAA CAG TGG TTA CGC A
2521-98	91	TAT GGC TAA CCA GTG TTG GTG GGA CTC TCT GCT GAA AAA AAA CGT TTG TGA ATT CTT CGG TGG AGG CGG TGG GG
2521-99	92	TCG ACC CCA CCG CCT CCA CCG AAG AAT TCA CAA ACG TTT TTT TTC AGC AGA GAG TCC CAC CAA CAC TGG TTA GCC A
2551-48	93	TAT GTT CCA CGA CTG CAA ATG GGA CCT GCT GAC CAA ACA GTG GGT TTG CCA CGG TCT GGG TGG AGG CGG TGG GG
2551-49	94	TCG ACC CCA CCG CCT CCA CCC AGA CCG TGG CAA ACC CAC TGT TTG GTC AGC AGG TCC CAT TTG CAG TCG TGG AAC A

pAMG21-RANK-Fc vector

[0157] pAMG21. The expression plasmid pAMG21 (ATCC accession no. 98113) can be derived from the Amgen expression vector pCFM1656 (ATCC #69576) which in turn be derived from the Amgen expression vector system described in US Patent No. 4,710,473. The pCFM1656 plasmid can be derived from the described pCFM836 plasmid (U.S. Patent No. 4,710,473) by:

- destroying the two endogenous NdeI restriction sites by end filling with T4 polymerase enzyme followed by blunt end ligation;
- replacing the DNA sequence between the unique AatII and ClaI restriction sites containing the synthetic P_L promoter with a similar fragment obtained from pCFM636 (patent No. 4,710,473) containing the P_L promoter (see SEQ ID NO: 95 below); and
- substituting the small DNA sequence between the unique ClaI and KpnI restriction sites with the oligonucleotide having the sequence of SEQ ID NO: 96.
SEQ ID NO: 95:

EP 2 845 864 A2

AatII

5' CTAATTCGGCTCTCACCTACCAAACAATGCCCCCTGCAAAAAATAAATTCATAT-
 3' TGCAGATTAAGGCGAGAGTGGATGGTTTGTACGGGGGGACGTTTTTTATTTAAGTATA-

5 -AAAAAACATACAGATAACCATCTGCGGTGATAAATTATCTCTGGCGGTGTTGACATAAAA-
 -TTTTTGTATGTCTATTGGTAGACGCCACTATTTAATAGAGACCGCCACAACGTATTT-

-TACCACTGGCGGTGATACTGAGCACAT 3'
 -ATGGTGACCGCCACTATGACTCGTGTAGC 5'

ClaI

10 SEQ ID NO: 96:

15 5' CGATTTGATTCTAGAAGGAGGAATAACATATGGTTAACGCGTTGGAATTCGGTAC
 3'

3' TAAACTAAGATCTTCCCTCCTTATTGTATACCAATTGCGCAACCTTAAGC 5'
ClaI KpnI

20 **[0158]** The expression plasmid pAMG21 can then be derived from pCFM1656 by making a series of site-directed base changes by PCR overlapping oligonucleotide mutagenesis and DNA sequence substitutions. Starting with the BglII site (plasmid bp # 180) immediately 5' to the plasmid replication promoter P_{copB} and proceeding toward the plasmid replication genes, the base pair changes are as shown in Table 7 below.

Table 7-Base pair changes resulting in pAMG21

pAMG21 bp #	bp in pCFM1656	bp changed to in pAMG21
# 204	T/A	C/G
# 428	A/T	G/C
# 509	G/C	A/T
# 617	--	insert two G/C bp
# 679	G/C	T/A
# 980	T/A	C/G
# 994	G/C	A/T
# 1004	A/T	C/G
# 1007	C/G	T/A
# 1028	A/T	T/A
# 1047	C/G	T/A
# 1178	G/C	T/A
# 1466	G/C	T/A
# 2028	G/C	bp deletion
# 2187	C/G	T/A
# 2480	A/T	T/A
# 2499-2502	<u>AGTG</u> TCAC	<u>GTCA</u> CAGT
# 2642	<u>TCCGAGC</u> AGGCTCG	7 bp deletion
# 3435	G/C	A/T
# 3446	G/C	A/T
# 3643	A/T	T/A

55 **[0159]** The DNA sequence between the unique AatII (position #4364 in pCFM1656) and SacII (position #4585 in pCFM1656) restriction sites is substituted with the DNA sequence below (SEQ ID NO: 97):.

EP 2 845 864 A2

[AatII sticky end] 5' GCGTAACGTATGCATGGTCTCC-
(position #4358 in pAMG21) 3' TGCACGCATTGCATACGTACCAGAGG-

5 -CCATGCGAGAGTAGGGAAC TGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACT-
-GGTACGCTCTCATCCCTTGACGGTCCGTAGTTTATTTTGGCTTTCCGAGTCAGCTTTCTGA-

-GGGCCTTTTCGTTTTATCTGTTGTTTGTCCGGTGAACGCTCTCCTGAGTAGGACAAATCCGC-
-CCCGAAAGCAAAATAGACAACAACAGCCACTTGCGAGAGGACTCATCTGT'TTAGGCG-

10 -CGGGAGCGGATTTGAACGTTGCCGAAGCAACGGCCCCGGAGGGTGGCGGGCAGGACGCCCGC-
-GCCCTCGCCTAAACTTGCAACGCTTCGTTGCCGGGCTCCCACCGCCCGTCC'TGCGGGCG-

-CATAAACTGCCAGGCATCAAATTAAGCAGAAGGCCATCCTGACGGATGGCC'TTTTTGCGT-
-GTATTTGACGGTCCGTAGTTTAAATCGTCTTCCGGTAGGACTGCCTACCGGAAAAACGCA-

AatII

15 -TTCTACAAACTCTTTTGT'TTATTTTCTAAATACATTCAAATATGGACGTCGTACTTAAAC-
-AAGATGTTTGAGAAAACAAATAAAAAGATTTATGTAAGTTTATACCTGCAGCATGAAT'TG-

-TTTTAAAGTATGGGCAATCAAT'TGCTCCTGTTAAAATTGCTTTAGAAATAC'TTTGGCAGC-
-AAAATTTTCATACCCGTTAGTTAACGAGACAATTTAACGAAATCTTTATGAAACCGTCG-

20 -GGTTTGTGTTATGAGTTTTCATTTGCCATTTGGTTAAATGGAAAGTGACCGTGCGCTTAC-
-CCAAACAACATAACTCAAAGTAAACGCGTAACCAATTTACC'TTTCAC'TGGCACGCCGAATG-

-TACAGCCTAATATTTTTGAAATATCCCAAGAGCTTTTTCC'TTCGCATGCCACGCCTAAAC-
-ATGTCGGATTATAAAAAC'TTATAGGGTCTCGAAAAAGGAAGCGTACGGGTGCCGATTTG-

25 -ATTCTTTTTCTCTTTTGGTTAAATCGTTGTTTATTTATTTGCTATATTTATTTTTC-
-TAAGAAAAGAGAAAACCAATTTAGCAACAACTAAATAATAAACGATATAAATAAAAAG-

-GATAATTATCAACTAGAGAAGGAACAATTAATGGTATGTTTCATACACGCATGTAAAAATA-
-CTATTAATAGTTGATCTCTTCC'TTGTAAATTAACATACAAGTATGTGCGTACATTTTAT-

30 -AACTATCTATATAGTTGCTTTCTCTGAATGTGCAAAACTAAGCATTCGGAAGCCATTAT-
-TTGATAGATATATCAACAGAAAGAGACTTACACGTTTTGATTCGTAAGGCTTCGGTAATA-

-TAGCAGTATGAATAGGGAAACTAAACCCAGTGATAAGACCTGATGATTTTCGCTTCTTTAA-
-ATCGTCATACTTATCCCTTTGATTTGGGTCACTATTCTGGACTACTAAAGCGAAGAAAT-

35 -TTACATTTGGAGATTTTTTATTTACAGCATTGTTTTCAAATATAT'TCCAATTAATCGGTG-
-AATGTAAACCTCTAAAAATAAATGTCGTAACAAAAGTTTATATAAGGTTAATTAGCCAC-

-AATGATTGGAGTTAGAATAATCTACTATAGGATCATATTTTATTAATTAGCGTCATCAT-
-TTACTAACCTCAATCTTATTAGATGATATCCTAGTATAAAATAATTTAATCGCAGTAGTA-

40 -AATATTGCCTCCATTTTTTAGGGTAATTATCCAGAATTGAAATATCAGATTTAACCATAG-
-TTATAACGGAGGTAAAAATCCCATTAATAGGTCTTAAC'TTATAGTCTAAATTTGGTATC-

-AATGAGGATAAATGATCGCGAGTAAATAATATTCACAATGTACCATTTTAGTCATATCAG-
-TTACTCCTATTTACTAGCGCTCATTTATTATAAGTGTACATGGTAAAATCAGTATAGTC-

45 -ATAAGCATTGATTAATATCATTATTGCTTCTACAGGCTTTAATTTTATTAATTAATTTCTGT-
-TATTCGTAACTAAT'TATAGTAATAACGAAGATGTCCGAAATTAATAAATTAATAAGACA-

-AAGTGTGTCGGCAFTTATGTC'TTTCATACCCATCTCTTTATCC'TTACCTATTTGTTGTC-
-TTCACAGCAGCCGTAAATACAGAAAGTATGGGTAGAGAAATAGGAATGGATAACAAACAG-

50 -GCAAGTTTTGCGTGTATATATCATTAAAAACGGTAATAGATTGACATTTGATTC'TAATAA-
-CGTTCAAACGCACAATATATAGTAATTTGCCATTATCTAAC'TGTAAACTAAGATTATT-

-ATTGGATTTTTGTCACACTATTTATATCGCTTGAATACAATGTTTAAACATAAGTACCTG-
-TAACCTAAAAACAGTGTGATAATATAGCGAACTTTATGTTAACAAATGTTATTCATGGAC-

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EP 2 845 864 A2

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-TAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTATAGTCGATTAATCGATTTGATT-
-ATCCTAGCATGTCCAAATGCGTTCTTTTACCAAACAATATCAGCTAATTAGCTAAACTAA-

-CTAGATTTGTTTTAAC TAATTAAGGAGGAATAACATATGGTTAACGCGTTGGAATTCGA-
-5 GATCTAAACAAAATTGATTAATTTCTCTTATTGTATACCAATTGCGCAACCTTAAGCT-

                                     SacII
-GCTCACTAGTGTGACCTGCAGGTTACCATGGAAGCTTACTCGAGGATCCGCGGAAAGAA-
-10 CGAGTGATCACAGCTGGACGTCCCATGGTACCTTCGAATGAGCTCCTAGGCGCCTTTCTT-

-GAAGAAGAAGAAGAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATA-
-15 CTTCTTCTTCTTCTTTCGGGCTTTCCTTCGACTCAACCGACGACGGTGGCGACTCGTTAT-

-ACTAGCATAACCCCTTGGGGCTCTAAACGGGTCTTGAGGGGTTTTTTGCTGAAAGGAGG-
-TGATCGTATTGGGGAACCCCGAGATTTGCCAGAACTCCCCAAAAACGACTTTCCTCC-

-AACCGCTCTTCACGCTCTTCACGC 3'           [SacII sticky end]
-15 -TTGGCGAGAAGTGCAGAAAGTG 5'           (position #5904 in pAMG21)

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[0160] During the ligation of the sticky ends of this substitution DNA sequence, the outside AatII and SacII sites are destroyed. There are unique AatII and SacII sites in the substituted DNA.

[0161] A gene encoding human RANK fused to the N-terminus of Fc was ligated into pAMG21 as an NdeI to BamHI fragment to generate Amgen Strain #4125. This construct was modified to insert a valine codon at the junction of RANK and Fc. The adjacent valine and aspartate codons create a unique Sall site. This allows for the fusion of peptides at the N-terminus of Fc3 between the unique NdeI and Sall sites. The RANK sequence is deleted upon insertion of a new NdeI-Sall fragment. The sequence of the vector is given in Figure 5A through 5M.

[0162] GM221 (Amgen #2596). The Amgen host strain #2596 is an E. coli K-12 strain derived from Amgen strain #393, which is a derivative of E. coli W1485, obtained from the E. coli Genetic Stock Center, Yale University, New Haven, Connecticut (CGSC strain 6159). It has been modified to contain both the temperature sensitive lambda repressor cl857s7 in the early ebg region and the lacI^Q repressor in the late ebg region (68 minutes). The presence of these two repressor genes allows the use of this host with a variety of expression systems, however both of these repressors are irrelevant to the expression from luxP_R. The untransformed host has no antibiotic resistances.

[0163] The ribosome binding site of the cl857s7 gene has been modified to include an enhanced RBS. It has been inserted into the ebg operon between nucleotide position 1170 and 1411 as numbered in Genbank accession number M64441Gb_Ba with deletion of the intervening ebg sequence. The sequence of the insert is shown below with lower case letters representing the ebg sequences flanking the insert shown below (SEQ ID NO: 98):

```

ttatitcgtGCGGCCGCACCAATTATCACCGCCAGAGGTAACACTAGTCAACACGCACGGTGTAGATAT
TTATCCCTTGC GG TGATAGATTGAGCACATCGATTGATTTCTAGAAGGAGGGATAATATATGAG
CACAAAAAAGAAACCATTAAACACAAGAGCAGCTTGAGGACGCACGTCGCCTTAAAGCAATTTA
TGAAAAAAGAAAAATGAACTTGGCTTATCCAGGAATCTGTGCGCAGACAAGATGGGGATGGG
GCAGTCAGGCGTTGGTGTCTTATTTAATGGCATCAATGCATTAAATGCTTATAACGCCGATTGC
40 TTACAAAAATTCTCAAAGTTAGCGTTGAAGAATTTAGCCCTTCAATCGCCAGAGAATCTACGAG
ATGTATGAAGCGGTTAGTATGCAGCCGTCACCTAGAAAGTGAGTATGAGTACCCTGTTTTTCTCA
TGTTTCAGGCAGGGATGTTCTCACCTAAGCTTAGAACCTTTACCAAAGGTGATGCGGAGAGATGG
GTAAGCACAAACCAAAAAAGCCAGTGATTCTGCATTCTGGCTTGAGGTTGAAGGTAATTCATGA
CCGCACCAACAGGCTCCAAGCCAAGCTTTCCTGACGGAATGTTAATTCTCGTTGACCTGAGCA
GGCTGTTGAGCCAGGTGATTTCTGCATAGCCAGACTTGGGGGTGATGAGTTTACCTCAAGAAA
45 CTGATCAGGGATAGCGGTCAGGTGTTTTTACAACCACTAAACCCACAGTACCCAATGATCCCAT
GCAATGAGAGTTGTTCCGTTGTGGGGAAAGTTATCGCTAGTCAGTGGCCTGAAGAGACGTTTGG
CTGATAGACTAGTGGATCCACTAGTgittctgccc

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[0164] The construct was delivered to the chromosome using a recombinant phage called MMeBg-cl857s7enhanced RBS #4 into F'tet/393. After recombination and resolution only the chromosomal insert described above remains in the cell. It was renamed F'tet/GM101. F'tet/GM101 was then modified by the delivery of a lacI^Q construct into the ebg operon between nucleotide position 2493 and 2937 as numbered in the Genbank accession number M64441Gb_Ba with the deletion of the intervening ebg sequence. The sequence of the insert is shown below with the lower case letters representing the ebg sequences flanking the insert (SEQ ID NO: 99) shown below:

ggcggaaccGACGTCCATCGAATGGTGAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGA
 GAGTCAATTCAGGGTGGTGAATGTGAAACCAGTAACGTTATACGATGTGCGCAGAGTATGCCGGT
 GTCTCTTATCAGACCGTTTCCCGCGTGGTGAACCAGGCCAGCCACGTTTCTGCGAAAAACGCGGG
 5 AAAAAAGTCGAAGCGGCGATGGCGGAGCTGAATTACATFCCAACCGCGTGGCACAACAACCTGG
 CGGGCAAAACAGTCGCTCCTGATTGGCGTTGCCACCTCCAGTCTGGCCCTGCACGCGCCGTCCGA
 AATTGTGCGGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCGTGGTGGTGTGCGATGGTA
 GAACGAAGCGGCGTCGAAGCCTGTAAAGCGGCGGTGCACAATCTTCTCGCGCAACCGCTCAGTG
 GGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCATTGCTGTGGAAGCTGCCTGCACTAA
 10 TGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGACACCCATCAACAGTATTAATTTCTCCCATGA
 AGACGGTACCGACTGGGCGTGGAGCATCTGGTCCGATTGGGTCACCAAGCAAAATCGCGCTGTTA
 GCGGGCCCATTAAGTTCTGTCTCGGCGCGTCTGCGTCTGGCTGGCTGGCATAAAATATCTCACTCG
 CAATCAAATTCAGCCGATAGCGGAACGGGAAGGCGACTGGAGTGCCATGTCCGGTTTTCAACAA
 ACCATGCAAATGCTGAATGAGGGCATCGTTCCTCACTGCGATGCTGGTTGCCAACGATCAGATGG
 CGCTGGGCGCAATGCGCGCCATTACCGAGTCCGGGCTGCGCGTTGGTGC GGATATCTCGGTAGT
 15 GGGATACGACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACACCATCAAACAGGAT
 TTTCCGCTGTGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA

AGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAGAAAAACCACCCTGGCGCCAATACGCA
 AACCGCCTCTCCCGCGCGTGGCCGATTCAATTAATGCAGCTGCCACGACAGGTTTCCCGACTGG
 20 AAAGCGGACAGTAAGGTACCATAGGATCCaggcacagga

[0165] The construct was delivered to the chromosome using a recombinant phage called AGebg-LacIQ#5 into F'tet/GM101. After recombination and resolution only the chromosomal insert described above remains in the cell. It was renamed F'tet/GM221. The F'tet episome was cured from the strain using acridine orange at a concentration of 25 $\mu\text{g/ml}$ in LB. The cured strain was identified as tetracycline sensitive and was stored as GM221.

[0166] Expression in E. coli. Cultures of each of the pAMG21-Fc-fusion constructs in *E. coli* GM221 were grown at 37 °C in Luria Broth medium. Induction of gene product expression from the luxPR promoter was achieved following the addition of the synthetic autoinducer N-(3-oxohexanoyl)-DL-homoserine lactone to the culture media to a final concentration of 20 ng/ml. Cultures were incubated at 37 °C for a further 3 hours. After 3 hours, the bacterial cultures were examined by microscopy for the presence of inclusion bodies and were then collected by centrifugation. Refractile inclusion bodies were observed in induced cultures indicating that the Fc-fusions were most likely produced in the insoluble fraction in *E. coli*. Cell pellets were lysed directly by resuspension in Laemmli sample buffer containing 10% β -mercaptoethanol and were analyzed by SDS-PAGE. In each case, an intense Coomassie-stained band of the appropriate molecular weight was observed on an SDS-PAGE gel.

EXAMPLE 3

TALL-1 peptibody inhibits TALL-1 mediated B cell proliferation

[0167] Mouse B lymphocytes were isolated from C57BL/6 spleens by negative selection. (MACS CD43 (Ly-48) Microbeads, Miltenyi Biotech, Auburn, CA). Purified (10^5) B cells were cultured in MEM, 10% heat inactivated FCS, $5 \times 10^{-5}\text{M}$ 2-mercaptoethanol, 100 U/ml penicillin, 100 $\mu\text{g/ml}$ streptomycin) in triplicate in 96-well flat bottom tissue culture plates with 10 ng/ml TALL-1 protein and 2 $\mu\text{g/ml}$ of Goat F(ab')₂ anti-mouse IgM (Jackson ImmunoResearch Laboratory, West Grove, Pennsylvania) with the indicated amount of recombinant TALL-1 peptibody for a period of 4 days at 37 °C, 5%CO₂. Proliferation was measured by the uptake of radioactive ³[H] thymidine after an 18-hour incubation period.

EXAMPLE 4

TALL-1 peptibody blocks TALL-1 binding to its receptors

[0168] Reacti-Gel 6x (Pierce) were pre-coated with human AGP3 (also known as TALL-1, Khare et al., Proc. Natl. Acad. Sci. 97:3370-3375,2000) and blocked with BSA. 100 pM and 40 pM of AGP3 peptibody samples were incubated with indicated various concentrations of human AGP3 at room temperature for 8 hours before run through the human AGP3-coated beads. The amount of the bead-bound peptibody was quantified by fluorescent (Cy5) labeled goat anti-human-Fc antibody (Jackson Immuno Research). The binding signal is proportional to the concentration of free peptibody at binding equilibrium. Dissociation equilibrium constant (K_D) was obtained from nonlinear regression of the competition curves using a dual-curve one-site homogeneous binding model (KinEx™ software). K_D is about 4 pM for AGP3 peptibody (SEQ ID NO: 123) binding with human AGP3 (Figure 10).

[0169] To determine if this AGP3 peptibody can neutralize murine AGP3 binding as well as human AGP3, a BIAcore

neutralizing assay was utilized. All experiments were performed on a BIAcore 3000 at room temperature. Human TACI-Fc protein (Xia et al, J. Exp. Med. 192, 137-144, 2000) was immobilized to a B1 chip using 10 mM Acetate pH 4.0 to a level of 2900RU. A blank flow cell was used as a background control. Using a running buffer of PBS (without calcium or magnesium) containing 0.005% P20, 1 nM recombinant human AGP3 (in running buffer plus, 0.1 mg/ml BSA) was incubated without and with indicated various amount of AGP3 peptibody (x axis) before injected over the surface of the receptor. Regeneration was performed using 8 mM glycine pH 1.5 for 1 minute, 25 mM 3-[cyclohexylamino]-1-propanesulfonic acid (CAPS) pH 10.5, 1 M NaCl for 1 minute. For determination of murine AGP3 binding, human his-tagged TACI was immobilized to 1000 RU in the above buffer. 5 nM recombinant murine AGP3 (in running buffer plus, 0.1 mg/ml BSA) was incubated without and with the various amounts indicated in Figure 11 of AGP3 peptibody (x axis) before injected over the surface of the receptor. Regeneration was performed with 10 mM HCl pH2, twice for 30 seconds. Relative binding of both human and murine AGP3 at presence vs absence of AGP3 peptibody (SEQ ID NO: 123) was measured (y axis). Relative binding response was determined as (RU-RU blank/ RUo-RU blank). The AGP3 peptibody (SEQ ID NO: 123) inhibited both human and murine AGP3 binding to its receptor TACI (Figures 11A and 11B).

[0170] To examine if this AGP3 peptibody blocks AGP3 binding to all three receptors (TACI, BCMA and BAFFR), recombinant soluble receptor TACI, BCMA and BAFFR proteins were immobilized to CM5 chip. Using 10 mM acetate, pH4, human TACI-Fc was immobilized to 6300 RU, human BCMA-Fc to 5000 RU, and BAFFR-Fc to 6000 RU. 1 nM of recombinant human AGP3 (in running buffer containing 0.1 mg/ml BSA and 0.1 mg/ml Heparin) or 1 nM recombinant APRIL protein (Yu, et al., Nat. Immunol., 1:252-256, 2000) were incubated with indicated amount of AGP3 peptibody before injection over each receptor surface. Regeneration for the AGP3 experiment was done with 8 mM glycine, pH 1.5, for 1 minute, followed by 25 mM CAPS, pH 10.5, 1M NaCl for 1 minute. Regeneration for the APRIL experiment was performed with 8 mM glycine, pH 2, for one minute, followed by 25 mM CAPS, pH 10.5, 1 M NaCl for one minute. Relative binding of AGP3 or APRIL was measured. AGP3 peptibody (SEQ ID NO: 123) blocked AGP3 binding to all three receptors (Figure 12A). AGP3 peptibody didn't affect APRIL binding to the receptors (Figure 12B).

EXAMPLE 5

AGP3 peptibody blocks AGP3 mediated B cell proliferation

[0171] Mouse B lymphocytes were isolated from C57BL/6 spleens by negative selection. (MACS CD43 (Ly-48) Microbeads, Miltenyi Biotech, Auburn, CA). Purified (10^5) B cells were cultured in minimal essential medium (MEM), 10% heat inactivated fetal calf serum (FCS), 5×10^{-5} M 2-mercaptoethanol, 100 U/ml penicillin, 100 μ g/ml streptomycin) in triplicate in 96-well flat bottom tissue culture plates with 10 ng/ml AGP3 (TALL-1) protein and 2 μ g/ml of Goat F(ab')₂ anti-mouse IgM (Jackson ImmunoResearch Laboratory, West Grove, Pennsylvania) with the indicated amount of recombinant AGP3 peptibody (SEQ ID NO: 123) for a period of 4 days at 37 °C, 5% CO₂. Proliferation was measured by the uptake of radioactive ³[H] thymidine after an 18-hour incubation period.

EXAMPLE 6

AGP3 peptibody on AGP3-stimulated Ig production in mice

[0172] Mice (Balb/c females of 9-14 weeks of age and 19-21 g of weight) were purchased from Charles River Laboratories, Wilmington, MA. Mice (n = 10) were treated i.p. with 1 mg/Kg of human AGP3 once a day for five consecutive days followed by 5 mg/Kg or 0.5 mg/Kg of AGP3 peptibody (SEQ ID NO: 123) or by saline or by 5 mg/Kg of human Fc. Other mice were left untreated. Mice were sacrificed on the sixth day to measure serum IgM and IgA, which were measured by ELISA. Briefly, plates were coated with capture antibodies specific for IgM or IgA (Southern Biotechnology Associates, Birmingham, AL), blocked, and added with dilutions of standard (IgM from Calbiochem, San Diego, CA and IgA from Southern Biotechnology Associates) or test samples. Captured Ig were revealed using biotinylated antibodies specific for IgM or IgA (Southern Biotechnology Associates), neutravidin-conjugated peroxidase (Pierce, Rockford, IL), and tetramethylbenzidine (TMB) microwell peroxidase substrate (KPL, Gaithersburg, MD). Optical densities were quantitated in a Thermomax ELISA reader (Molecular Devices, Menlo Park, CA).

[0173] Human AGP3-stimulated increase in serum levels of IgM and IgA was blocked by 5 mg/Kg of the anti-AGP3 peptibody (SEQ ID NO: 123) and not by 0.5 mg/Kg (Figures 14A and 14B).

EXAMPLE 7

AGP3 peptibody reduced spleen B cell number in mice

[0174] Mice (as above, n = 7) were treated i.p. for seven consecutive days with 5 mg/Kg or 1.5 mg/Kg or 0.5 mg/Kg

EP 2 845 864 A2

of AGP3 peptibody (SEQ ID NO: 123) or with saline or with 5 mg/Kg of human Fc. Mice were sacrificed on the eighth day to count spleen B cell number. Spleens were collected in saline and gently disrupted by manual homogenization to yield a cell suspension. The total cell number was obtained with a H1E counter (Technicon, Tarrytown, NY). Percentages of B cells were derived by immunofluorescence double staining and flow cytometry using fluorescein isothiocyanate (FITC)-conjugated and phycoerythrin (PE)-conjugated Ab against CD3 and B220, respectively (PharMingen, San Diego, CA) and a FACScan analyser (Becton and Dickinson, Mountain View, CA). B cells were identified for being CD3-B220+. At all doses, the AGP3 peptibody (SEQ ID NO: 123) decreased spleen B cell number in a dose-response fashion (Figure 14) (SEQ ID NO: 123).

EXAMPLE 8

AGP3 peptibody reduced arthritis severity in mouse CIA model

[0175] Eight to 12 week old DBA/1 mice (obtained from Jackson Laboratories, Bar Harbor, ME) were immunized with bovine collagen type II (bCII) (purchased from University of Utah), emulsified in complete Freund's adjuvant (Difco) intradermally at the base of tail. Each injection was 100 μ l containing 100 μ g of bCII. Mice were boosted 3 weeks after the initial immunization with bCII emulsified in incomplete Freund's adjuvant. Treatment was begun from the day of booster immunization for 4 weeks. Mice were examined for the development of arthritis. As described before (Khare et al., J. Immunol. 155: 3653-9, 1995), all four paws were individually scored from 0-3. Therefore arthritis severity could vary from 0 to 12 for each animal. AGP3 (SEQ ID NO: 123) peptibody treatment significantly reduced the severity of arthritic scores (Figure 15).

[0176] Serum samples were taken one week after final treatment (day 35) for the analysis of anti-collagen antibody level. High binding ELISA plates (Immulon, Nunc) were coated with 50 μ l of 4 μ g/ml solution of bovine CII in carbonate buffer and plated were kept in cold overnight in the refrigerator. Plates were washed three times with cold water. 75 μ l of blocking solution made up of PBS/.05% tween 20/1% BSA was used to block non-specific binding for an hour. Samples were diluted (in blocking buffer) in dilution plates at 1:25, 1:100, 1:400, and 1:1600 and 25 μ l of these samples were added to each well of the ELISA plate for a final dilution of 100, 400, 1600, and 6400 with a final volume of 100 μ l/well. After incubation at room temperature for 3 hours, plates were washed three times again. 100 μ l of secondary antibody diluted in blocking buffer (rat anti-mouse IgM, IgG2a, IgG2b, IgG1, IgG3-HRP) was added to each well and plates were incubated for at least 2 hours. Plates were washed four times. 100 μ l of TMB solution (Sigma) was added to each well and the reaction was stopped using 50 μ l of 25% sulfuric acid. Plates were read using an ELISA plate reader at 450 nm. OD was compared with a standard pool representing units/ml. AGP3 peptibody (SEQ ID NO: 123) treatment reduced serum anti-collagen II IgG1, IgG3, IgG2a, and IgG2b levels compared to PBS or Fc control treatment groups (Figure 16).

EXAMPLE 9

Treatment of AGP3 peptibody in NZB/NZW lupus mice

[0177] Five month old lupus prone NZBx NZBWF1 mice were treated i.p. 3X/week for 8 weeks with PBS or indicated doses of AGP3 peptibody or human Fc proteins. Prior to the treatment, animals were pre-screened for protein in the urine with Albustix reagents strips (Bayer AG). Mice having greater than 100 mg/dl of protein in the urine were not included in the study. Protein in the urine was evaluated monthly throughout the life of the experiment. AGP3 peptibody (SEQ ID NO: 123) treatment led to delay of proteinuria onset and improved survival (Figure 17).

[0178] AGP3 peptibody treatment reduced B cell number in mice. Balb/c mice received 7 daily intraperitoneal injections of indicated amount of AGP3 peptibody (SEQ ID NO: 123) or human Fc protein. On day 8, spleens were collected, and subject to FACS analysis for B220+ B cells as set for in Table 8.

Table 8

AGP3 Pb Reduces B Cell Number in Normal Mice				
n=7	dose (1/dayx7)	spleen B cell (1x10e6)	SD	t test
saline		51.3	9.6	
Fc	5mg/Kg	45.5	7.1	
Peptibody	5mg/Kg	20.1	3.8	1.37856E-05
	1.5mg/Kg	22.6	6.9	5.10194E-05

(continued)

AGP3 Pb Reduces B Cell Number in Normal Mice				
n=7	dose (1/dayx7)	spleen B cell (1x10e6)	SD	t test
	0.5mg/Kg	25.8	3.6	0.000111409

[0179] The invention now being fully described, it will be apparent to one of ordinary skill in the art that many changes and modifications can be made thereto, without departing from the spirit and scope of the invention as set forth herein.

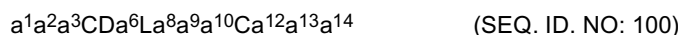
[0180] The invention will now be defined by the following clauses

1. A TALL-1-binding composition of matter comprising an amino acid sequence Dz²Lz⁴, wherein z² is an amino acid residue and z⁴ is T or I, and wherein the composition of matter does not comprise a fragment of TACI, BCMA, or BAFFR (SEQ ID NOS: 195, 196, and 197).

2. The composition of matter of clause 1, wherein z⁴ is T.

3. A TALL-1-binding composition of matter comprising an amino acid sequence Dz²LI, wherein z² is an amino acid residue.

4. The composition of matter of clause 1 comprising an amino acid sequence of the formula



wherein:

a¹, a², a³ are each independently absent or amino acid residues;

a⁶ is an amino acid residue;

a⁸ is T or I;

a⁹ is a basic or hydrophobic residue;

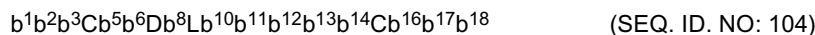
a¹² is a neutral polar residue; and

a¹³ and a¹⁴ are each independently absent or amino acid residues.

5. The composition of matter of clause 4 wherein a⁸ is T and a⁹ is a basic residue.

6. The composition of matter of clause 4 wherein a⁹ is K and a¹² is F.

7. The composition of matter of clause 1 comprising an amino acid sequence of the formula



wherein:

b¹ and b² are each independently absent or amino acid residues;

b³ is an acidic or amide residue;

b⁵ is an amino acid residue;

b⁶ is an aromatic residue;

b⁸ is an amino acid residue;

b¹⁰ is T or I;

b¹¹ is a basic residue;

b¹² and b¹³ are each independently amino acid residues;

b¹⁴ is a neutral polar residue; and

b¹⁶, b¹⁷, and b¹⁸ are each independently absent or amino acid residues.

8. The composition of matter of clause 7 wherein:

b³ is D, Q, or E;

b⁶ is W or Y;

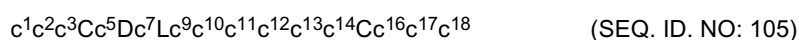
b¹⁰ is T;

b¹¹ is K or R; and

b¹⁴ is V or L.

EP 2 845 864 A2

9. The composition of matter of clause 1 comprising an amino acid sequence of the formula



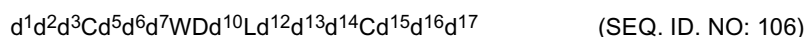
5 wherein:

c^1 , c^2 , and c^3 are each independently absent or amino acid residues;
 c^5 is an amino acid residue;
 c^7 is an amino acid residue;
10 c^9 is T or I;
 c^{10} is a basic residue;
 c^{11} and c^{12} are each independently amino acid residues;
 c^{13} is a neutral polar residue;
 c^{14} is an amino acid residue;
15 c^{16} is an amino acid residue;
 c^{17} is a neutral polar residue; and
 c^{18} is an amino acid residue or is absent.

20 10. The composition of matter of Claim 9 wherein:

c^9 is T;
 c^{10} is K or R;
 c^{13} is a I, L, or V; and
25 c^{17} is A or L.

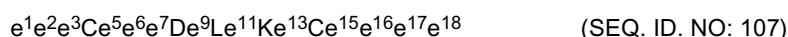
11. The composition of matter of clause 1 comprising an amino acid sequence of the formula



30 wherein:

d^1 , d^2 , and d^3 are each independently absent or amino acid residues;
 d^5 , d^6 , and d^7 are each independently amino acid residues;
35 d^{10} is an amino acid residue;
 d^{13} is T or I;
 d^{14} is an amino acid residue; and
 d^{16} , d^{17} , and d^{18} are each independently absent or amino acid residues.

40 12. The composition of matter of clause 1 comprising an amino acid sequence of the formula



wherein:

45 e^1 , e^2 , and e^3 are each independently absent or amino acid residues;
 e^5 , e^6 , e^7 , e^9 , and e^{13} are each independently amino acid residues;
 e^{11} is T or I; and
 e^{15} , e^{16} , and e^{17} are each independently absent or amino acid residues.

50 13. The composition of matter of clause 1 comprising an amino acid sequence of the formula



55 wherein:

f^1 , f^2 , and f^3 are absent or are amino add residues;
 f^5 is W, Y, or F;
 f^7 is an amino acid residue;

EP 2 845 864 A2

f⁹ is T or I;
f¹⁰ is K, R, or H;
f¹² is C, a neutral polar residue, or a basic residue (W, C, or R preferred);
f¹³ is C, a neutral polar residue or is absent; and
5 f¹⁴ is any amino acid residue or is absent;
provided that only one of f¹, f², and f³ may be C, and only one of f¹², f¹³, and f¹⁴ may be C.

14. The composition of matter of clause 13, wherein f⁵ is W.
15. The composition of matter of clause 13, wherein f⁷ is L.
16. The composition of matter of clause 13, wherein f⁹ is T.
17. The composition of matter of clause 13, wherein f¹⁰ is K.
18. The composition of matter of clause 13, wherein f¹² is C and one of f¹, f², and f³ is C.
19. The composition of matter of clause 13, wherein f¹³ is V.
20. The composition of matter of clause 13 comprising an amino acid sequence of the formula

f¹f²f³KWDF⁷Lf⁹KQf¹²f¹³f¹⁴ (SEQ ID NO: 125).

21. The composition of matter of clause 20 comprising an amino acid sequence selected from the group consisting of SEQ ID NOS: 32, 33, 58, 60, 63, 66, 67, 69, 114, 115, 122, 123, 124, 147-150, 152-177, 179, 180, and 187.

22. The composition of matter of clause 20 comprising an amino acid sequence of the formula

LPGCKWDLLIKQWVCDPL (SEQ ID NO: 33).

23. A composition of matter comprising an amino acid sequence of the formula

g¹g²g³Cg⁵PFg⁸Wg¹⁰Cg¹¹g¹²g¹³ (SEQ. ID. NO: 101)

wherein:

g¹, g² and g³ are each independently absent or amino acid residues;
g⁵ is a neutral polar residue;
g⁸ is a neutral polar residue;
g¹⁰ is an acidic residue;
g¹² and g¹³ are each independently amino acid residues; and
g¹⁴ is absent or is an amino acid residue.

24. The composition of matter of clause 23 wherein:

g² is G;
g⁵ is W;
g⁸ is P;
g¹⁰ is E; and
g¹³ is a basic residue.

25. A composition of matter comprising an amino acid sequence of the formula

h¹h²h³CWh⁶h⁷Wgh¹⁰Ch¹²h¹³h¹⁴ (SEQ. ID. NO: 102)

wherein:

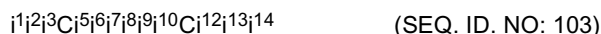
h¹, h², and h³ are each independently absent or amino acid residues;
h⁶ is a hydrophobic residue;
h⁷ is a hydrophobic residue;
h¹⁰ is an acidic or polar hydrophobic residue; and
h¹², h¹³, and h¹⁴ are each independently absent or amino acid residues.

26. The composition of matter of clause 25 wherein:

h¹ is G;
 h⁶ is A;
 h⁷ is a neutral polar residue; and
 h¹⁰ is an acidic residue.

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27. A composition of matter comprising an amino acid sequence of the formula



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wherein:

i¹ is absent or is an amino acid residue;
 i² is a neutral polar residue;
 i³ is an amino acid residue;
 i⁵, i⁶, i⁷, and i⁸ are each independently amino acid residues;
 i⁹ is an acidic residue;
 i¹⁰ is an amino acid residue;
 i¹² and i¹³ are each independently amino acid residues; and
 i¹⁴ is a neutral polar residue.

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28. The composition of matter of clause 27 wherein:

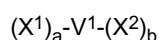
i² is W; and
 i¹⁴ is W.

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29. A TALL-1 binding composition of matter comprising an amino acid sequence of the formula PFPWE (SEQ ID NO: 110). :

30. The composition of matter of clause 1 having the formula

30



and multimers thereof, wherein:

V¹ is a vehicle;
 X¹ and X² are each independently selected from -(L¹)_c-P¹, -(L¹)_c-P¹-(L²)_d-P², -(L¹)_c-P¹-(L²)_d-P²-(L³)_e-P³, and -(L¹)_c-P¹-(L²)_d-P²-(L³)_e-P³-(L⁴)_f-P⁴
 one or more of P¹, P², P³, and P⁴ each independently comprise Dz²Lz⁴;
 L¹, L², L³, and L⁴ are each independently linkers; and
 a, b, c, d, e, and f are each independently 0 or 1, provided that at least one of a and b is 1.

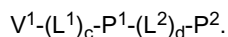
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31. The composition of matter of clause 30 of the formula P¹-(L¹)_c-P²-(L²)_d-V¹.

32. The composition of matter of clause 30 of the formula

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33. The composition of matter of clause: 30, wherein V¹ is an Fc domain.

34. The composition of matter of clause 30 wherein V¹ is an IgG Fc domain.

35. The composition of matter of clause 30 wherein V¹ is an IgG1 Fc domain.

36. The composition of matter of clause 30 wherein V¹ comprises the sequence of SEQ ID NO: 2.

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37. The composition of matter of clause 30 wherein one or more of P¹, P², P³, and P⁴ each independently comprises a sequence selected from:

a¹a²a³CdA⁶La⁸a⁹a¹⁰Ca¹²a¹³a¹⁴ (SEQ. ID. NO: 100)
 b¹b²b³Cb⁵b⁶Db⁸Lb¹⁰b¹¹b¹²b¹³b¹⁴Cb¹⁶b¹⁷b¹⁸ (SEQ. ID. NO: 104)
 c¹c²c³Cc⁵Dc⁷Lc⁹c¹⁰c¹¹c¹²c¹³c¹⁴Cc¹⁶c¹⁷c¹⁸ (SEQ. ID. NO: 105)
 d¹d²d³Cd⁵d⁶d⁷Wd¹⁰Ld¹³d¹⁴d¹⁵Cd¹⁶d¹⁷d¹⁸ (SEQ. ID. NO: 106)
 e¹e²e³Ce⁵e⁶e⁷De⁹Le¹¹Ke¹³Ce¹⁵e¹⁶e¹⁷e¹⁸ (SEQ. ID. NO: 107)
 f¹f²f³Kf⁵Df⁷Lf⁹f¹⁰Qf¹²f¹³f¹⁴ (SEQ. ID. NO: 109)

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EP 2 845 864 A2

$g^1g^2g^3Cg^5PFg^8Wg^{10}Cg^{11}g^{12}g^{13}$ (SEQ ID NO: 101), $h^1h^2h^3CWh^6h^7Wgh^{10}Ch^{12}h^{13}h^{14}$ (SEQ ID NO: 102), and $i^1i^2i^3Ci^5i^6i^7i^8i^9i^{10}Ci^{12}i^{13}i^{14}$ (SEQ ID NO: 103)

wherein:

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a^1 , a^2 , a^3 are each independently absent or amino acid residues;

a^6 is an amino acid residue;

a^9 is a basic or hydrophobic residue;

a^8 is threonyl or isoleucyl;

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a^{12} is a neutral polar residue;

a^{13} and a^{14} are each independently absent or amino acid residues;

b^1 and b^2 are each independently absent or amino acid residues;

b^3 is an acidic or amide residue;

b^5 is an amino acid residue;

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b^6 is an aromatic residue; .

b^8 is an amino acid residue;

b^{10} is T or I;

b^{11} is a basic residue;

b^{12} and b^{13} are each independently amino acid residues;

20

b^{14} is a neutral polar residue;

b^{16} , b^{17} , and b^{18} are each independently absent or amino acid residues;

c^1 , c^2 , and c^3 are each independently absent or amino acid residues;

c^5 is an amino acid residue;

c^7 is an amino acid residue;

25

c^9 is T or I;

c^{10} is a basic residue;

c^{11} and c^{12} are each independently amino acid residues;

c^{13} is a neutral polar residue;

c^{14} is an amino acid residue;

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c^{16} is an amino acid residue;

c^{17} is a neutral polar residue; and

c^{18} is an amino acid residue or is absent;

d^1 , d^2 , and d^3 are each independently absent or amino acid residues;

d^5 , d^6 , and d^7 are each independently amino acid residues;

35

d^{10} is an amino acid residue;

d^{12} is T or I;

d^{13} is an amino acid residue; and

d^{13} , d^{16} , and d^{17} are each independently absent or amino acid residues;

e^1 , e^2 , and e^3 are each independently absent or amino acid residues;

40

e^5 , e^6 , e^7 , e^9 , and e^{13} are each independently amino acid residues;

e^{11} is T or I; and

e^{15} , e^{16} , and e^{17} are each independently absent or amino acid residues;

f^1 , f^2 , and f^3 are absent or are amino acid residues;

f^5 is W, Y, or F;

45

f^7 is an amino acid residue;

f^9 is T or I;

f^{10} is K, R, or H;

f^{12} is C, a neutral polar residue, or a basic residue;

f^{13} is C, a neutral polar residue or is absent; and

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f^{14} is any amino acid residue or is absent;

provided that only one of f^1 , f^2 , and f^3 may be C, and only one of f^{12} , f^{13} , and f^{14} may be C;

g^1 , g^2 and g^3 are each independently absent or amino acid residues;

g^5 is a neutral polar residue;

g^8 is a neutral polar residue;

55

g^{10} is an acidic residue;

g^{12} and g^{13} are each independently amino acid residues; and

g^{14} is absent or is an amino acid residue;

h^1 , h^2 , and h^3 are each independently absent or amino acid residues;

h⁶ is a hydrophobic residue;
 h⁷ is a hydrophobic residue;
 h¹⁰ is an acidic or polar hydrophobic residue; and
 h¹², h¹³, and h¹⁴ are each independently absent or amino acid residues;
 i¹ is absent or is an amino acid residue;
 i² is a neutral polar residue;
 i³ is an amino acid residue;
 i⁵, i⁶, i⁷, and i⁸ are each independently amino acid residues;
 i⁹ is an acidic residue;
 i¹⁰ is an amino acid residue;
 i¹² and i¹³ are each independently amino acid residues; and
 i¹⁴ is a neutral polar residue.

38. The composition of matter of clause 37, wherein:

a⁹ is a basic residue.
 b³ is D, Q, or E;
 b⁶ is W or Y;
 b¹¹ is K or R; and
 b¹⁴ is V or L.
 c¹⁰ is K or R;
 c¹³ is a I, L, or V;
 c¹⁷ is A or L;
 f⁵ is W;
 f⁷ is L; f⁷ is K; and
 f¹⁰ is V.

39. The composition of matter of clause 37, wherein one or more of P¹, P², P³, and P⁴ each independently comprises

f¹f²f³KWdf⁷Lf⁹KQf¹²f¹³f¹⁴ (SEQ ID NO: 125).

40. The composition of matter of Claim 39 of the formula

P¹-(L¹)_c-P²-(L²)_d-V¹.

41. The composition of matter of clause 39 of the formula

V¹-(L¹)_c-P¹-(L²)_d-P².

42. The composition of matter of clause 39 having an amino acid sequence selected from SEQ ID NOS: 122,123, and 124.

43. The composition of matter of clause 40 wherein L² is greater than 5 amino acids.

44. The composition of matter of clause 43 wherein L² is selected from

GSGSATGGSGSTASSGSGSATx¹x² (SEQ ID NO: 193)

and

GSGSATGGSGSTASSGSGSATx¹x²GSGSATGGSGSTASSGSGSATx³x⁴ (SEQ ID

NO: 194)

wherein x¹ and x³ are each independently basic or hydrophobic residues and x² and x⁴ are each independently hydrophobic residues.

45. The composition of matter of Claim 41 wherein L² is selected from

GSGSATGGSGSTASSGSGSATH (SEQ ID NO: 59),

GSGSATGGSGSTASSGSGSATGM (SEQ ID NO: 190)

GSGSATGGSGSTASSGSGSATGS

(SEQ ID NO: 191),

and

5

GSGSATGGSGSTASSGSGSATHMGSGSATGGSGSTASSGSGSATHM

(SEQ ID

NO: 192).

10

46. The composition of matter of clause 28 comprising a sequence selected from Table 2 (SEQ ID NOS: 29-39,60-70, and 126-188).

47. The composition of matter of clause 30 comprising a sequence selected from Table 4 (SEQ ID NOS: 44-55).

48. The composition of matter of clause 46, wherein V¹ is an Fc domain.

49. The composition of matter of clause 46, wherein V¹ is an IgG Fc domain.

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50. The composition of matter of clause 46, wherein V¹ is an IgG1 Fc domain.

51. A DNA encoding a composition of matter of clause. 34.

52. An expression vector comprising the DNA of clause 51.

53. A host cell comprising the expression vector of clause 52.

54. The cell of clause 53, wherein the cell is an E. coli cell.

20

55. A method of treating a B-cell mediated autoimmune disease, which comprises administering a composition of matter of clause 1.

56. A method of treating a B-cell mediated autoimmune disease, which comprises administering a composition of matter of clause 13.

57. A method of treating lupus, which comprises administering a composition of matter of clause 1.

58. A method of treating lupus, which comprises administering a composition of matter of clause 13.

25

59. A method of treating a B-cell mediated cancer, which comprises administering a composition of matter of clause 1.

60. A method of treating a B-cell mediated cancer, which comprises administering a composition of matter of clause 13.

61. A method of treating B-cell lymphoma, which comprises administering a composition of matter of clause 1.

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62. A method of treating B-cell lymphoma, which comprises administering a composition of matter of clause 13.

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EP 2 845 864 A2

SEQUENCE LISTING

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10 <141> 2002-05-13

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Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn	
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EP 2 845 864 A2

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EP 2 845 864 A2

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EP 2 845 864 A2

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EP 2 845 864 A2

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EP 2 845 864 A2

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EP 2 845 864 A2

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EP 2 845 864 A2

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EP 2 845 864 A2

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EP 2 845 864 A2

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EP 2 845 864 A2

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EP 2 845 864 A2

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EP 2 845 864 A2

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EP 2 845 864 A2

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EP 2 845 864 A2

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EP 2 845 864 A2

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EP 2 845 864 A2

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EP 2 845 864 A2

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EP 2 845 864 A2

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	1775						1780					1785			
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	1790						1795					1800			
75	Gly	Gly	Cys	Cys	Cys	Cys	Cys	Cys	Cys	Thr	Gly	Thr	Thr	Thr	Thr

EP 2 845 864 A2

	1805		1810		1815										
5	Cys Gly	Ala Thr	Ala Cys	Ala Ala	Cys Ala	Ala Ala	Ala Ala	Cys Ala	Cys Gly	Cys					
	1820				1825			1830							
10	Cys Thr	Cys Ala	Cys Ala	Gly	Ala Cys	Gly Gly	Gly	Gly Ala	Ala						
	1835			1840			1845								
15	Thr Thr	Thr Thr	Gly Cys	Thr	Thr Ala	Thr Cys	Cys	Ala Cys	Ala						
	1850			1855			1860								
20	Thr Thr	Ala Ala	Ala Cys	Thr	Gly Cys	Ala Ala	Gly	Gly Gly	Ala						
	1865			1870			1875								
25	Cys Thr	Thr Cys	Cys Cys	Cys Cys	Gly	Ala Thr	Ala Ala	Gly	Gly Thr	Thr					
	1880				1885			1890							
30	Ala Cys	Ala Ala	Cys Cys	Gly	Thr	Thr Cys	Ala Thr	Gly	Gly Thr	Cys					
	1895			1900			1905								
35	Ala Thr	Ala Ala	Ala Gly	Cys	Gly Cys	Cys Ala	Thr	Cys Cys	Gly	Cys Cys	Gly				
	1910			1915			1920								
40	Cys Cys	Ala Gly	Cys Gly	Thr	Thr	Ala Cys	Ala Gly	Gly Gly	Thr						
	1925			1930			1935								
45	Gly Cys	Ala Ala	Thr Gly	Thr	Ala Thr	Cys Thr	Thr	Thr Thr	Ala	Thr Thr	Ala				
	1940			1945			1950								
50	Ala Ala	Cys Ala	Cys Cys	Thr	Gly Thr	Thr Thr	Ala Thr	Ala Thr	Ala Thr	Ala Thr					
	1955			1960			1965								
55	Cys Thr	Cys Cys	Thr Thr	Thr	Ala Ala	Ala Cys	Thr	Ala Cys	Thr	Ala Cys	Thr				
	1970			1975			1980								
60	Thr Ala	Ala Thr	Thr Ala	Cys	Ala Thr	Thr Cys	Ala Thr	Thr Thr	Ala Thr	Thr Thr					
	1985			1990			1995								
65	Ala Ala	Ala Ala	Ala Gly	Ala	Ala Ala	Ala Cys	Cys Thr	Ala Thr	Ala Thr						
	2000			2005			2010								
70	Thr Cys	Ala Cys	Thr Gly	Cys	Cys Thr	Gly Thr	Cys Cys	Thr Thr	Thr Thr						
	2015			2020			2025								
75	Gly Gly	Ala Cys	Ala Gly	Ala	Cys Ala	Gly Ala	Thr	Ala Thr	Gly						
	2030			2035			2040								

EP 2 845 864 A2

	Cys	Ala	Cys	Cys	Thr	Cys	Cys	Cys	Ala	Cys	Cys	Gly	Cys	Ala	Ala
	2045						2050					2055			
5	Gly	Cys	Gly	Gly	Cys	Gly	Gly	Gly	Cys	Cys	Cys	Cys	Thr	Ala	Cys
	2060						2065					2070			
10	Cys	Gly	Gly	Ala	Gly	Cys	Cys	Gly	Cys	Thr	Thr	Thr	Ala	Gly	Thr
	2075						2080					2085			
15	Thr	Ala	Cys	Ala	Ala	Cys	Ala	Cys	Thr	Cys	Ala	Gly	Ala	Cys	Ala
	2090						2095					2100			
20	Cys	Ala	Ala	Cys	Cys	Ala	Cys	Cys	Ala	Gly	Ala	Ala	Ala	Ala	Ala
	2105						2110					2115			
25	Cys	Cys	Cys	Cys	Gly	Gly	Thr	Cys	Cys	Ala	Gly	Cys	Gly	Cys	Ala
	2120						2125					2130			
30	Gly	Ala	Ala	Cys	Thr	Gly	Ala	Ala	Ala	Cys	Cys	Ala	Cys	Ala	Ala
	2135						2140					2145			
35	Ala	Gly	Cys	Cys	Cys	Cys	Thr	Cys	Cys	Cys	Thr	Cys	Ala	Thr	Ala
	2150						2155					2160			
40	Ala	Cys	Thr	Gly	Ala	Ala	Ala	Ala	Gly	Cys	Gly	Gly	Cys	Cys	Cys
	2165						2170					2175			
45	Cys	Gly	Cys	Cys	Cys	Cys	Gly	Gly	Thr	Cys	Cys	Gly	Ala	Ala	Gly
	2180						2185					2190			
50	Gly	Gly	Cys	Cys	Gly	Gly	Ala	Ala	Cys	Ala	Gly	Ala	Gly	Thr	Cys
	2195						2200					2205			
55	Gly	Cys	Thr	Thr	Thr	Thr	Ala	Ala	Thr	Thr	Ala	Thr	Gly	Ala	Ala
	2210						2215					2220			
60	Thr	Gly	Thr	Thr	Gly	Thr	Ala	Ala	Cys	Thr	Ala	Cys	Thr	Thr	Cys
	2225						2230					2235			
65	Ala	Thr	Cys	Ala	Thr	Cys	Gly	Cys	Thr	Gly	Thr	Cys	Ala	Gly	Thr
	2240						2245					2250			
70	Cys	Thr	Thr	Cys	Thr	Cys	Gly	Cys	Thr	Gly	Gly	Ala	Ala	Gly	Thr
	2255						2260					2265			
75	Thr	Cys	Thr	Cys	Ala	Gly	Thr	Ala	Cys	Ala	Cys	Gly	Cys	Thr	Cys
	2270						2275					2280			

EP 2 845 864 A2

	Gly	Thr	Ala	Ala	Gly	Cys	Gly	Gly	Cys	Cys	Cys	Thr	Gly	Ala	Cys
	2285						2290					2295			
5	Gly	Gly	Cys	Cys	Cys	Gly	Cys	Thr	Ala	Ala	Cys	Gly	Cys	Gly	Gly
	2300						2305					2310			
10	Ala	Gly	Ala	Thr	Ala	Cys	Gly	Cys	Cys	Cys	Cys	Gly	Ala	Cys	Thr
	2315						2320					2325			
15	Thr	Cys	Gly	Gly	Gly	Thr	Ala	Ala	Ala	Cys	Cys	Cys	Thr	Cys	Gly
	2330						2335					2340			
20	Thr	Cys	Gly	Gly	Gly	Ala	Cys	Cys	Ala	Cys	Thr	Cys	Cys	Gly	Ala
	2345						2350					2355			
25	Cys	Cys	Gly	Cys	Gly	Cys	Ala	Cys	Ala	Gly	Ala	Ala	Gly	Cys	Thr
	2360						2365					2370			
30	Cys	Thr	Cys	Thr	Cys	Ala	Thr	Gly	Gly	Cys	Thr	Gly	Ala	Ala	Ala
	2375						2380					2385			
35	Gly	Cys	Gly	Gly	Gly	Thr	Ala	Thr	Gly	Gly	Thr	Cys	Thr	Gly	Gly
	2390						2395					2400			
40	Cys	Ala	Gly	Gly	Gly	Cys	Thr	Gly	Gly	Gly	Gly	Ala	Thr	Gly	Gly
	2405						2410					2415			
45	Gly	Thr	Ala	Ala	Gly	Gly	Thr	Gly	Ala	Ala	Ala	Thr	Cys	Thr	Ala
	2420						2425					2430			
50	Thr	Cys	Ala	Ala	Thr	Cys	Ala	Gly	Thr	Ala	Cys	Cys	Gly	Gly	Cys
	2435						2440					2445			
55	Thr	Thr	Ala	Cys	Gly	Cys	Cys	Gly	Gly	Gly	Cys	Thr	Thr	Cys	Gly
	2450						2455					2460			
60	Gly	Cys	Gly	Gly	Thr	Thr	Thr	Thr	Ala	Cys	Thr	Cys	Cys	Thr	Gly
	2465						2470					2475			
65	Thr	Thr	Thr	Cys	Ala	Thr	Ala	Thr	Ala	Thr	Gly	Ala	Ala	Ala	Cys
	2480						2485					2490			
70	Ala	Ala	Cys	Ala	Gly	Gly	Thr	Cys	Ala	Cys	Cys	Gly	Cys	Cys	Thr
	2495						2500					2505			
75	Thr	Cys	Cys	Ala	Thr	Gly	Cys	Cys	Gly	Cys	Thr	Gly	Ala	Thr	Gly
	2510						2515					2520			

EP 2 845 864 A2

	Cys	Gly	Gly	Cys	Ala	Thr	Ala	Thr	Cys	Cys	Thr	Gly	Gly	Thr	Ala
	2525						2530					2535			
5	Ala	Cys	Gly	Ala	Thr	Ala	Thr	Cys	Thr	Gly	Ala	Ala	Thr	Thr	Gly
	2540						2545					2550			
10	Thr	Thr	Ala	Thr	Ala	Cys	Ala	Thr	Gly	Thr	Gly	Thr	Ala	Thr	Ala
	2555						2560					2565			
15	Thr	Ala	Cys	Gly	Thr	Gly	Gly	Thr	Ala	Ala	Thr	Gly	Ala	Cys	Ala
	2570						2575					2580			
20	Ala	Ala	Ala	Ala	Thr	Ala	Gly	Gly	Ala	Cys	Ala	Ala	Gly	Thr	Thr
	2585						2590					2595			
25	Ala	Ala	Ala	Ala	Ala	Thr	Thr	Thr	Ala	Cys	Ala	Gly	Gly	Cys	Gly
	2600						2605					2610			
30	Ala	Thr	Gly	Cys	Ala	Ala	Thr	Gly	Ala	Thr	Thr	Cys	Ala	Ala	Ala
	2615						2620					2625			
35	Cys	Ala	Cys	Gly	Thr	Ala	Ala	Thr	Cys	Ala	Ala	Thr	Ala	Thr	Cys
	2630						2635					2640			
40	Gly	Gly	Gly	Gly	Gly	Thr	Gly	Gly	Gly	Cys	Gly	Ala	Ala	Gly	Ala
	2645						2650					2655			
45	Ala	Cys	Thr	Cys	Cys	Ala	Gly	Cys	Ala	Thr	Gly	Ala	Gly	Ala	Thr
	2660						2665					2670			
50	Cys	Cys	Cys	Cys	Gly	Cys	Gly	Cys	Thr	Gly	Gly	Ala	Gly	Gly	Ala
	2675						2680					2685			
55	Thr	Cys	Ala	Thr	Cys	Cys	Ala	Gly	Cys	Cys	Gly	Gly	Cys	Gly	Thr
	2690						2695					2700			
60	Cys	Cys	Cys	Gly	Gly	Ala	Ala	Ala	Ala	Cys	Gly	Ala	Thr	Thr	Cys
	2705						2710					2715			
65	Cys	Gly	Ala	Ala	Gly	Cys	Cys	Cys	Ala	Ala	Cys	Cys	Thr	Thr	Thr
	2720						2725					2730			
70	Cys	Ala	Thr	Ala	Gly	Ala	Ala	Gly	Gly	Cys	Gly	Gly	Cys	Gly	Gly
	2735						2740					2745			
75	Thr	Gly	Gly	Ala	Ala	Thr	Cys	Gly	Ala	Ala	Ala	Thr	Cys	Thr	Cys

EP 2 845 864 A2

	2750		2755		2760									
5	Gly Thr 2765	Gly Ala Thr	Gly Gly 2770	Cys Ala Gly Gly	Thr Thr Gly Gly	Thr Thr Gly Gly								
10	Gly Cys 2780	Gly Thr Cys	Gly Cys 2785	Thr Thr Gly Gly	Thr Thr Gly Gly									
15	Thr Cys 2795	Ala Thr Thr	Thr Cys 2800	Gly Ala Ala Cys	Cys Cys Cys Ala	Cys Cys Ala								
20	Gly Ala 2810	Gly Thr Cys	Cys Cys 2815	Gly Cys Thr Cys	Ala Gly Ala Ala									
25	Gly Cys 2840	Gly Ala Thr	Ala Gly 2845	Ala Ala Gly Gly	Cys Gly Ala Thr									
30	Gly Cys 2855	Gly Cys Thr	Gly Cys 2860	Gly Ala Ala Thr	Cys Gly Gly Gly									
35	Ala Gly 2870	Cys Gly Gly	Cys Gly 2875	Ala Thr Ala Cys	Cys Gly Thr Ala									
40	Ala Ala 2885	Gly Cys Ala	Cys Gly 2890	Ala Gly Gly Ala	Ala Gly Cys Gly									
45	Gly Thr 2900	Cys Ala Gly	Cys Cys 2905	Cys Ala Thr Thr	Cys Gly Thr Thr									
50	Gly Cys 2915	Cys Ala Ala	Gly Cys 2920	Thr Cys Thr Thr	Cys Ala Gly Cys									
55	Ala Ala 2930	Thr Ala Thr	Cys Ala 2935	Cys Gly Gly Gly	Thr Ala Gly Cys									
	Cys Ala 2945	Ala Cys Gly	Cys Thr 2950	Ala Thr Gly Thr	Cys Cys Thr Gly									
	Ala Thr 2960	Ala Gly Cys	Gly Gly 2965	Thr Cys Cys Gly	Cys Cys Ala Cys									
	Ala Cys 2975	Cys Cys Ala	Gly Cys 2980	Cys Gly Gly Cys	Cys Ala Cys Ala									

EP 2 845 864 A2

	Gly	Thr	Cys	Gly	Ala	Thr	Gly	Ala	Ala	Thr	Cys	Cys	Ala	Gly	Ala
	2990						2995					3000			
5	Ala	Ala	Ala	Gly	Cys	Gly	Gly	Cys	Cys	Ala	Thr	Thr	Thr	Thr	Cys
	3005						3010					3015			
10	Cys	Ala	Cys	Cys	Ala	Thr	Gly	Ala	Thr	Ala	Thr	Thr	Cys	Gly	Gly
	3020						3025					3030			
15	Cys	Ala	Ala	Gly	Cys	Ala	Gly	Gly	Cys	Ala	Thr	Cys	Gly	Cys	Cys
	3035						3040					3045			
20	Ala	Thr	Gly	Ala	Gly	Thr	Cys	Ala	Cys	Gly	Ala	Cys	Gly	Ala	Gly
	3050						3055					3060			
25	Ala	Thr	Cys	Cys	Thr	Cys	Gly	Cys	Cys	Gly	Thr	Cys	Gly	Gly	Gly
	3065						3070					3075			
30	Cys	Ala	Thr	Gly	Cys	Gly	Cys	Gly	Cys	Cys	Thr	Thr	Gly	Ala	Gly
	3080						3085					3090			
35	Cys	Cys	Thr	Gly	Gly	Cys	Gly	Ala	Ala	Cys	Ala	Gly	Thr	Thr	Cys
	3095						3100					3105			
40	Gly	Gly	Cys	Thr	Gly	Gly	Cys	Gly	Cys	Gly	Ala	Gly	Cys	Cys	Cys
	3110						3115					3120			
45	Cys	Thr	Gly	Ala	Thr	Gly	Cys	Thr	Cys	Thr	Thr	Cys	Gly	Thr	Cys
	3125						3130					3135			
50	Cys	Ala	Gly	Ala	Thr	Cys	Ala	Thr	Cys	Cys	Thr	Gly	Ala	Thr	Cys
	3140						3145					3150			
55	Gly	Ala	Cys	Ala	Ala	Gly	Ala	Cys	Cys	Gly	Gly	Cys	Thr	Thr	Cys
	3155						3160					3165			
60	Cys	Ala	Thr	Cys	Cys	Gly	Ala	Gly	Thr	Ala	Cys	Gly	Thr	Gly	Cys
	3170						3175					3180			
65	Thr	Cys	Gly	Cys	Thr	Cys	Gly	Ala	Thr	Gly	Cys	Gly	Ala	Thr	Gly
	3185						3190					3195			
70	Thr	Thr	Thr	Cys	Gly	Cys	Thr	Thr	Gly	Gly	Thr	Gly	Gly	Thr	Cys
	3200						3205					3210			
75	Gly	Ala	Ala	Thr	Gly	Gly	Gly	Cys	Ala	Gly	Gly	Thr	Ala	Gly	Cys
	3215						3220					3225			

EP 2 845 864 A2

Cys Gly Gly Ala Thr Cys Ala Ala Gly Cys Gly Thr Ala Thr Gly
 3230 3235 3240
 5
 Cys Ala Gly Cys Cys Gly Cys Cys Gly Cys Ala Thr Thr Gly Cys
 3245 3250 3255
 10
 Ala Thr Cys Ala Gly Cys Cys Ala Thr Gly Ala Thr Gly Gly Ala
 3260 3265 3270
 Thr Ala Cys Thr Thr Thr Cys Thr Cys Gly Gly Cys Ala Gly Gly
 3275 3280 3285
 15
 Ala Gly Cys Ala Ala Gly Gly Thr Gly Ala Gly Ala Thr Gly Ala
 3290 3295 3300
 20
 Cys Ala Gly Gly Ala Gly Ala Thr Cys Cys Thr Gly Cys Cys Cys
 3305 3310 3315
 Cys Gly Gly Cys Ala Cys Thr Thr Cys Gly Cys Cys Cys Ala Ala
 3320 3325 3330
 25
 Thr Ala Gly Cys Ala Gly Cys Cys Ala Gly Thr Cys Cys Cys Thr
 3335 3340 3345
 30
 Thr Cys Cys Cys Gly Cys Thr Thr Cys Ala Gly Thr Gly Ala Cys
 3350 3355 3360
 35
 Ala Ala Cys Gly Thr Cys Gly Ala Gly Cys Ala Cys Ala Gly Cys
 3365 3370 3375
 Thr Gly Cys Gly Cys Ala Ala Gly Gly Ala Ala Cys Gly Cys Cys
 3380 3385 3390
 40
 Cys Gly Thr Cys Gly Thr Gly Gly Cys Cys Ala Gly Cys Cys Ala
 3395 3400 3405
 45
 Cys Gly Ala Thr Ala Gly Cys Cys Gly Cys Gly Cys Thr Gly Cys
 3410 3415 3420
 Cys Thr Cys Gly Thr Cys Cys Thr Gly Cys Ala Ala Thr Thr Cys
 3425 3430 3435
 50
 Ala Thr Thr Cys Ala Gly Gly Ala Cys Ala Cys Cys Gly Gly Ala
 3440 3445 3450
 55
 Cys Ala Gly Gly Thr Cys Gly Gly Thr Cys Thr Thr Gly Ala Cys
 3455 3460 3465

EP 2 845 864 A2

Ala Ala Ala Ala Ala Gly Ala Ala Cys Cys Gly Gly Gly Cys Gly
 3470 3475 3480

5 Cys Cys Cys Cys Thr Gly Cys Gly Cys Thr Gly Ala Cys Ala Gly
 3485 3490 3495

10 Cys Cys Gly Gly Ala Ala Cys Ala Cys Gly Gly Cys Gly Gly Cys
 3500 3505 3510

15 Ala Thr Cys Ala Gly Ala Gly Cys Ala Gly Cys Cys Gly Ala Thr
 3515 3520 3525

Thr Gly Thr Cys Thr Gly Thr Thr Gly Thr Gly Cys Cys Cys Ala
 3530 3535 3540

20 Gly Thr Cys Ala Thr Ala Gly Cys Cys Gly Ala Ala Thr Ala Gly
 3545 3550 3555

25 Cys Cys Thr Cys Thr Cys Cys Ala Cys Cys Cys Ala Ala Gly Cys
 3560 3565 3570

Gly Gly Cys Cys Gly Gly Ala Gly Ala Ala Cys Cys Thr Gly Cys
 3575 3580 3585

30 Gly Thr Gly Cys Ala Ala Thr Cys Cys Ala Thr Cys Thr Thr Gly
 3590 3595 3600

35 Thr Thr Cys Ala Ala Thr Cys Ala Thr Gly Cys Gly Ala Ala Ala
 3605 3610 3615

Cys Gly Ala Thr Cys Cys Thr Cys Ala Thr Cys Cys Thr Gly Thr
 3620 3625 3630

40 Cys Thr Cys Thr Thr Gly Ala Thr Cys Thr Thr Gly Ala Thr Cys Thr
 3635 3640 3645

45 Thr Gly Ala Thr Cys Cys Cys Cys Thr Gly Cys Gly Cys Cys Ala
 3650 3655 3660

50 Thr Cys Ala Gly Ala Thr Cys Cys Thr Thr Gly Gly Cys Gly Gly
 3665 3670 3675

Cys Ala Ala Gly Ala Ala Ala Gly Cys Cys Ala Thr Cys Cys Ala
 3680 3685 3690

55 Gly Thr Thr Thr Ala Cys Thr Thr Thr Gly Cys Ala Gly Gly Gly

EP 2 845 864 A2

	3695		3700		3705														
5	Cys Thr	Thr Cys	Cys Cys	Cys Ala	Ala Cys	Cys Thr	Thr Thr	Ala Cys	Cys Cys										
	3710				3715						3720								
10	Ala Gly	Ala Gly	Gly Gly	Gly Cys	Gly Cys	Cys Cys	Cys Cys	Ala Gly	Cys Cys										
	3725				3730						3735								
15	Thr Gly	Gly Cys	Ala Ala	Thr Thr	Cys Cys	Gly Gly	Thr Thr	Cys Cys	Gly Gly										
	3740				3745						3750								
20	Gly Cys	Thr Thr	Gly Cys	Thr Thr	Cys Cys	Gly Thr	Cys Cys	Ala Thr	Ala Ala										
	3755				3760						3765								
25	Ala Ala	Cys Cys	Gly Cys	Cys Cys	Cys Ala	Gly Thr	Cys Thr	Ala Gly	Thr Cys										
	3770				3775						3780								
30	Cys Thr	Ala Thr	Cys Gly	Cys Cys	Cys Ala	Thr Gly	Thr Thr	Ala Thr	Gly Thr										
	3785				3790						3795								
35	Cys Cys	Cys Ala	Cys Thr	Gly Thr	Cys Ala	Ala Gly	Cys Thr	Ala Ala	Gly Cys										
	3800				3805						3810								
40	Cys Thr	Gly Cys	Thr Thr	Thr Thr	Thr Thr	Thr Thr	Cys Thr	Cys Thr	Thr Thr										
	3815				3820						3825								
45	Gly Cys	Thr Thr	Gly Cys	Gly Thr	Thr Thr	Thr Thr	Thr Thr	Thr Thr	Thr Thr										
	3830				3835						3840								
50	Thr Gly	Thr Cys	Cys Ala	Gly Thr	Ala Thr	Ala Thr	Ala Thr	Ala Thr	Gly Cys										
	3845				3850						3855								
55	Gly Thr	Ala Gly	Cys Thr	Gly Thr	Ala Thr	Ala Thr	Cys Thr	Ala Thr	Thr Thr										
	3860				3865						3870								
60	Cys Cys	Gly Gly	Gly Gly	Gly Thr	Cys Ala	Gly Cys	Ala Thr	Gly Cys	Ala Thr										
	3875				3880						3885								
65	Thr Thr	Thr Cys	Thr Gly	Cys Thr	Gly Thr	Gly Thr	Gly Thr	Ala Thr	Cys Thr										
	3890				3895						3900								
70	Thr Thr	Thr Cys	Thr Ala	Cys Thr	Gly Thr	Gly Thr	Gly Thr	Ala Thr	Thr Thr										
	3905				3910						3915								
75	Cys Thr	Thr Cys	Cys Thr	Thr Thr	Thr Thr	Ala Thr	Ala Thr	Gly Thr	Cys Thr										
	3920				3925						3930								

EP 2 845 864 A2

Cys Thr Thr Gly Cys Gly Cys Cys Cys Thr Gly Ala Gly Thr Gly
 3935 3940 3945
 5
 Cys Thr Thr Gly Cys Gly Gly Cys Ala Gly Cys Gly Thr Gly Ala
 3950 3955 3960
 10
 Ala Gly Cys Thr Ala Cys Ala Thr Ala Thr Ala Thr Gly Thr Gly
 3965 3970 3975
 Ala Thr Cys Cys Gly Gly Gly Cys Ala Ala Ala Thr Cys Gly Cys
 3980 3985 3990
 15
 Thr Gly Ala Ala Thr Ala Thr Thr Cys Cys Thr Thr Thr Thr Gly
 3995 4000 4005
 20
 Thr Cys Thr Cys Cys Gly Ala Cys Cys Ala Thr Cys Ala Gly Gly
 4010 4015 4020
 Cys Ala Cys Cys Thr Gly Ala Gly Thr Cys Gly Cys Thr Gly Thr
 4025 4030 4035
 25
 Cys Thr Thr Thr Thr Thr Cys Gly Thr Gly Ala Cys Ala Thr Thr
 4040 4045 4050
 30
 Cys Ala Gly Thr Thr Cys Gly Cys Thr Gly Cys Gly Cys Thr Cys
 4055 4060 4065
 35
 Ala Cys Gly Gly Cys Thr Cys Thr Gly Gly Cys Ala Gly Thr Gly
 4070 4075 4080
 Ala Ala Thr Gly Gly Gly Gly Gly Thr Ala Ala Ala Thr Gly Gly
 4085 4090 4095
 40
 Cys Ala Cys Thr Ala Cys Ala Gly Gly Cys Gly Cys Cys Thr Thr
 4100 4105 4110
 45
 Thr Thr Ala Thr Gly Gly Ala Thr Thr Cys Ala Thr Gly Cys Ala
 4115 4120 4125
 Ala Gly Gly Ala Ala Ala Cys Thr Ala Cys Cys Cys Ala Thr Ala
 4130 4135 4140
 50
 Ala Thr Ala Cys Ala Ala Gly Ala Ala Ala Ala Gly Cys Cys Cys
 4145 4150 4155
 55
 Gly Thr Cys Ala Cys Gly Gly Gly Cys Thr Thr Cys Thr Cys Ala
 4160 4165 4170

EP 2 845 864 A2

Gly Gly Gly Cys Gly Thr Thr Thr Thr Ala Thr Gly Gly Cys Gly
 4175 4180 4185
 5 Gly Gly Thr Cys Thr Gly Cys Thr Ala Thr Gly Thr Gly Gly Thr
 4190 4195 4200
 10 Gly Cys Thr Ala Thr Cys Thr Gly Ala Cys Thr Thr Thr Thr Thr
 4205 4210 4215
 15 Gly Cys Thr Gly Thr Thr Cys Ala Gly Cys Ala Gly Thr Thr Cys
 4220 4225 4230
 20 Cys Thr Gly Cys Cys Cys Thr Cys Thr Gly Ala Thr Thr Thr Thr
 4235 4240 4245
 25 Cys Cys Ala Gly Thr Cys Thr Gly Ala Cys Cys Ala Cys Thr Thr
 4250 4255 4260
 30 Cys Gly Gly Ala Thr Thr Ala Thr Cys Cys Cys Gly Thr Gly Ala
 4265 4270 4275
 35 Cys Ala Gly Gly Thr Cys Ala Thr Thr Cys Ala Gly Ala Cys Thr
 4280 4285 4290
 40 Gly Gly Cys Thr Ala Ala Thr Gly Cys Ala Cys Cys Cys Ala Gly
 4295 4300 4305
 45 Thr Ala Ala Gly Gly Cys Ala Gly Cys Gly Gly Thr Ala Thr Cys
 4310 4315 4320
 50 Ala Thr Cys Ala Ala Cys Ala Gly Gly Cys Thr Thr Ala Cys Cys
 4325 4330 4335
 55 Cys Gly Thr Cys Thr Thr Ala Cys Thr Gly Thr Cys Gly Ala Ala
 4340 4345 4350
 60 Gly Ala Cys Gly Thr Gly Cys Gly Thr Ala Ala Cys Gly Thr Ala
 4355 4360 4365
 65 Thr Gly Cys Ala Thr Gly Gly Thr Cys Thr Cys Cys Cys Cys Ala
 4370 4375 4380
 70 Thr Gly Cys Gly Ala Gly Ala Gly Thr Ala Gly Gly Gly Ala Ala
 4385 4390 4395
 75 Cys Thr Gly Cys Cys Ala Gly Gly Cys Ala Thr Cys Ala Ala Ala
 4400 4405 4410

EP 2 845 864 A2

Thr Ala Ala Ala Ala Cys Gly Ala Ala Ala Gly Gly Cys Thr Cys
 4415 4420 4425
 5
 Ala Gly Thr Cys Gly Ala Ala Ala Gly Ala Cys Thr Gly Gly Gly
 4430 4435 4440
 10
 Cys Cys Thr Thr Thr Cys Gly Thr Thr Thr Thr Ala Thr Cys Thr
 4445 4450 4455
 15
 Gly Thr Thr Gly Thr Thr Thr Gly Thr Cys Gly Gly Thr Gly Ala
 4460 4465 4470
 20
 Ala Cys Gly Cys Thr Cys Thr Cys Cys Thr Gly Ala Gly Thr Ala
 4475 4480 4485
 25
 Gly Gly Ala Cys Ala Ala Ala Thr Cys Cys Gly Cys Cys Gly Gly
 4490 4495 4500
 30
 Gly Ala Gly Cys Gly Gly Ala Thr Thr Thr Gly Ala Ala Cys Gly
 4505 4510 4515
 35
 Thr Thr Gly Cys Gly Ala Ala Gly Cys Ala Ala Cys Gly Gly Cys
 4520 4525 4530
 40
 Cys Cys Gly Gly Ala Gly Gly Gly Thr Gly Gly Cys Gly Gly Gly
 4535 4540 4545
 45
 Cys Ala Gly Gly Ala Cys Gly Cys Cys Cys Gly Cys Cys Ala Thr
 4550 4555 4560
 50
 Ala Ala Ala Cys Thr Gly Cys Cys Ala Gly Gly Cys Ala Thr Cys
 4565 4570 4575
 55
 Ala Ala Ala Thr Thr Ala Ala Gly Cys Ala Gly Ala Ala Gly Gly
 4580 4585 4590
 60
 Cys Cys Ala Thr Cys Cys Thr Gly Ala Cys Gly Gly Ala Thr Gly
 4595 4600 4605
 65
 Gly Cys Cys Thr Thr Thr Thr Thr Gly Cys Gly Thr Thr Thr Cys
 4610 4615 4620
 70
 Thr Ala Cys Ala Ala Ala Cys Thr Cys Thr Thr Thr Thr Gly Thr
 4625 4630 4635
 75
 Thr Thr Ala Thr Thr Thr Thr Thr Thr Cys Thr Ala Ala Ala Thr Ala

EP 2 845 864 A2

	4640		4645		4650										
5	Cys	Ala	Thr	Thr	Cys	Ala	Ala	Ala	Thr	Ala	Thr	Gly	Gly	Ala	Cys
	4655						4660					4665			
10	Gly	Thr	Cys	Gly	Thr	Ala	Cys	Thr	Thr	Ala	Ala	Cys	Thr	Thr	Thr
	4670						4675					4680			
15	Thr	Ala	Ala	Ala	Gly	Thr	Ala	Thr	Gly	Gly	Gly	Cys	Ala	Ala	Thr
	4685						4690					4695			
20	Cys	Ala	Ala	Thr	Thr	Gly	Cys	Thr	Cys	Cys	Thr	Gly	Thr	Thr	Ala
	4700						4705					4710			
25	Ala	Ala	Ala	Thr	Thr	Gly	Cys	Thr	Thr	Thr	Ala	Gly	Ala	Ala	Ala
	4715						4720					4725			
30	Thr	Ala	Cys	Thr	Thr	Thr	Gly	Gly	Cys	Ala	Gly	Cys	Gly	Gly	Thr
	4730						4735					4740			
35	Thr	Thr	Gly	Thr	Thr	Gly	Thr	Ala	Thr	Thr	Gly	Ala	Gly	Thr	Thr
	4745						4750					4755			
40	Thr	Cys	Ala	Thr	Thr	Thr	Gly	Cys	Gly	Cys	Ala	Thr	Thr	Gly	Gly
	4760						4765					4770			
45	Thr	Thr	Ala	Ala	Ala	Thr	Gly	Gly	Ala	Ala	Ala	Gly	Thr	Gly	Ala
	4775						4780					4785			
50	Cys	Cys	Gly	Thr	Gly	Cys	Gly	Cys	Thr	Thr	Ala	Cys	Thr	Ala	Cys
	4790						4795					4800			
55	Ala	Gly	Cys	Cys	Thr	Ala	Ala	Thr	Ala	Thr	Thr	Thr	Thr	Thr	Gly
	4805						4810					4815			
60	Ala	Ala	Ala	Thr	Ala	Thr	Cys	Cys	Cys	Ala	Ala	Gly	Ala	Gly	Cys
	4820						4825					4830			
65	Thr	Thr	Thr	Thr	Thr	Cys	Cys	Thr	Thr	Cys	Gly	Cys	Ala	Thr	Gly
	4835						4840					4845			
70	Cys	Cys	Cys	Ala	Cys	Gly	Cys	Thr	Ala	Ala	Ala	Cys	Ala	Thr	Thr
	4850						4855					4860			
75	Cys	Thr	Thr	Thr	Thr	Thr	Cys	Thr	Cys	Thr	Thr	Thr	Thr	Gly	Gly
	4865						4870					4875			

EP 2 845 864 A2

	Thr Thr	Ala Ala Ala	Thr Cys	Gly Thr Thr	Gly Thr	Thr Thr Gly								
	4880		4885			4890								
5	Ala Thr	Thr Thr Ala	Thr Thr	Ala Thr	Thr Thr	Ala Thr Thr	Thr Thr	Gly Thr	Cys Thr	Ala Thr				
	4895					4900		4905						
10	Thr Ala	Thr Thr Thr	Ala Thr	Thr Thr	Thr Thr	Thr Thr	Thr Thr	Cys Thr	Gly Ala	Thr Thr				
	4910					4915		4920						
15	Ala Ala	Thr Thr Ala	Thr Thr	Ala Thr	Cys Thr	Ala Ala	Cys Thr	Ala Thr	Gly Ala	Ala Thr	Gly Thr			
	4925					4930		4935						
20	Ala Ala	Gly Gly Ala	Ala Thr	Cys Thr	Ala Thr	Ala Thr	Thr Thr	Ala Thr	Ala Thr	Gly Thr				
	4940					4945		4950						
25	Gly Thr	Ala Thr Gly	Thr Thr	Ala Thr	Thr Thr	Cys Thr	Ala Thr	Ala Thr	Ala Thr	Cys Thr	Ala Thr	Cys Thr	Gly Thr	
	4955					4960		4965						
30	Cys Ala	Thr Gly Thr	Ala Thr	Ala Thr	Ala Thr	Ala Thr	Ala Thr	Ala Thr	Ala Thr	Ala Thr	Ala Thr	Ala Thr	Cys Thr	
	4970					4975		4980						
35	Thr Ala	Thr Cys Thr	Ala Thr	Ala Thr	Ala Thr	Ala Thr	Ala Thr	Gly Thr	Thr Thr	Thr Thr	Gly Thr	Thr Thr		
	4985					4990		4995						
40	Cys Thr	Thr Thr Cys	Thr Thr	Cys Thr	Cys Thr	Thr Thr	Gly Thr	Ala Thr	Ala Thr	Thr Thr	Gly Thr	Thr Thr	Gly Thr	
	5000					5005		5010						
45	Cys Ala	Ala Ala Ala	Cys Thr	Ala Thr	Ala Thr	Ala Thr	Ala Thr	Gly Thr	Cys Thr	Ala Thr	Thr Thr	Thr Thr	Cys Thr	
	5015					5020		5025						
50	Cys Gly	Ala Ala Gly	Cys Thr	Cys Thr	Cys Thr	Ala Thr	Thr Thr	Thr Thr	Ala Thr	Thr Thr	Thr Thr	Ala Thr	Gly Thr	
	5030					5035		5040						
55	Cys Ala	Gly Thr Ala	Thr Thr	Gly Thr	Gly Thr	Ala Thr	Ala Thr	Thr Thr	Ala Thr	Gly Thr	Gly Thr	Gly Thr	Ala Thr	
	5045					5050		5055						
60	Ala Ala	Cys Thr Ala	Ala Thr	Ala Thr	Ala Thr	Cys Thr	Cys Thr	Cys Thr	Ala Thr	Gly Thr	Thr Thr	Gly Thr	Ala Thr	
	5060					5065		5070						
65	Thr Ala	Ala Gly Ala	Cys Thr	Cys Thr	Cys Thr	Thr Thr	Gly Thr	Ala Thr	Thr Thr	Gly Thr	Ala Thr	Thr Thr	Thr Thr	
	5075					5080		5085						
70	Thr Cys	Gly Cys Thr	Thr Thr	Cys Thr	Cys Thr	Thr Thr	Thr Thr	Thr Thr	Ala Thr	Ala Thr	Thr Thr	Thr Thr	Ala Thr	
	5090					5095		5100						
75	Cys Ala	Thr Thr Thr	Gly Thr	Gly Thr	Ala Thr	Gly Thr	Ala Thr	Ala Thr	Thr Thr	Thr Thr	Thr Thr	Thr Thr	Thr Thr	
	5105					5110		5115						

EP 2 845 864 A2

	Thr	Ala	Thr	Thr	Thr	Ala	Cys	Ala	Gly	Cys	Ala	Thr	Thr	Gly	Thr
	5120						5125					5130			
5	Thr	Thr	Thr	Cys	Ala	Ala	Ala	Thr	Ala	Thr	Ala	Thr	Thr	Cys	Cys
	5135						5140					5145			
10	Ala	Ala	Thr	Thr	Ala	Ala	Thr	Cys	Gly	Gly	Thr	Gly	Ala	Ala	Thr
	5150						5155					5160			
15	Gly	Ala	Thr	Thr	Gly	Gly	Ala	Gly	Thr	Thr	Ala	Gly	Ala	Ala	Thr
	5165						5170					5175			
20	Ala	Ala	Thr	Cys	Thr	Ala	Cys	Thr	Ala	Thr	Ala	Gly	Gly	Ala	Thr
	5180						5185					5190			
25	Cys	Ala	Thr	Ala	Thr	Thr	Thr	Thr	Ala	Thr	Thr	Ala	Ala	Ala	Thr
	5195						5200					5205			
30	Thr	Ala	Gly	Cys	Gly	Thr	Cys	Ala	Thr	Cys	Ala	Thr	Ala	Ala	Thr
	5210						5215					5220			
35	Ala	Thr	Thr	Gly	Cys	Cys	Thr	Cys	Cys	Ala	Thr	Thr	Thr	Thr	Thr
	5225						5230					5235			
40	Thr	Ala	Gly	Gly	Gly	Thr	Ala	Ala	Thr	Thr	Ala	Thr	Cys	Cys	Ala
	5240						5245					5250			
45	Gly	Ala	Ala	Thr	Thr	Gly	Ala	Ala	Ala	Thr	Ala	Thr	Cys	Ala	Gly
	5255						5260					5265			
50	Ala	Thr	Thr	Thr	Ala	Ala	Cys	Cys	Ala	Thr	Ala	Gly	Ala	Ala	Thr
	5270						5275					5280			
55	Gly	Ala	Gly	Gly	Ala	Thr	Ala	Ala	Ala	Thr	Gly	Ala	Thr	Cys	Gly
	5285						5290					5295			
60	Cys	Gly	Ala	Gly	Thr	Ala	Ala	Ala	Thr	Ala	Ala	Thr	Ala	Thr	Thr
	5300						5305					5310			
65	Cys	Ala	Cys	Ala	Ala	Thr	Gly	Thr	Ala	Cys	Cys	Ala	Thr	Thr	Thr
	5315						5320					5325			
70	Thr	Ala	Gly	Thr	Cys	Ala	Thr	Ala	Thr	Cys	Ala	Gly	Ala	Thr	Ala
	5330						5335					5340			
75	Ala	Gly	Cys	Ala	Thr	Thr	Gly	Ala	Thr	Thr	Ala	Ala	Thr	Ala	Thr
	5345						5350					5355			

EP 2 845 864 A2

	Cys	Ala	Thr	Thr	Ala	Thr	Thr	Gly	Cys	Thr	Thr	Cys	Thr	Ala	Cys
	5360							5365				5370			
5	Ala	Gly	Gly	Cys	Thr	Thr	Thr	Ala	Ala	Thr	Thr	Thr	Thr	Ala	Thr
	5375							5380				5385			
10	Thr	Ala	Ala	Thr	Thr	Ala	Thr	Thr	Cys	Thr	Gly	Thr	Ala	Ala	Gly
	5390							5395				5400			
15	Thr	Gly	Thr	Cys	Gly	Thr	Cys	Gly	Gly	Cys	Ala	Thr	Thr	Thr	Ala
	5405							5410				5415			
20	Thr	Gly	Thr	Cys	Thr	Thr	Thr	Cys	Ala	Thr	Ala	Cys	Cys	Cys	Ala
	5420							5425				5430			
25	Thr	Cys	Thr	Cys	Thr	Thr	Thr	Ala	Thr	Cys	Cys	Thr	Thr	Ala	Cys
	5435							5440				5445			
30	Cys	Thr	Ala	Thr	Thr	Gly	Thr	Thr	Thr	Gly	Thr	Cys	Gly	Cys	Ala
	5450							5455				5460			
35	Ala	Gly	Thr	Thr	Thr	Thr	Gly	Cys	Gly	Thr	Gly	Thr	Thr	Ala	Thr
	5465							5470				5475			
40	Ala	Thr	Ala	Thr	Cys	Ala	Thr	Thr	Ala	Ala	Ala	Ala	Cys	Gly	Gly
	5480							5485				5490			
45	Thr	Ala	Ala	Thr	Ala	Gly	Ala	Thr	Thr	Gly	Ala	Cys	Ala	Thr	Thr
	5495							5500				5505			
50	Thr	Gly	Ala	Thr	Thr	Cys	Thr	Ala	Ala	Thr	Ala	Ala	Ala	Thr	Thr
	5510							5515				5520			
55	Gly	Gly	Ala	Thr	Thr	Thr	Thr	Thr	Gly	Thr	Cys	Ala	Cys	Ala	Cys
	5525							5530				5535			
60	Thr	Ala	Thr	Thr	Ala	Thr	Ala	Thr	Cys	Gly	Cys	Thr	Thr	Gly	Ala
	5540							5545				5550			
65	Ala	Ala	Thr	Ala	Cys	Ala	Ala	Thr	Thr	Gly	Thr	Thr	Thr	Ala	Ala
	5555							5560				5565			
70	Cys	Ala	Thr	Ala	Ala	Gly	Thr	Ala	Cys	Cys	Thr	Gly	Thr	Ala	Gly
	5570							5575				5580			
75	Gly	Ala	Thr	Cys	Gly	Thr	Ala	Cys	Ala	Gly	Gly	Thr	Thr	Thr	Ala

EP 2 845 864 A2

	5585		5590		5595									
5	Cys Gly 5600	Cys Ala Ala Gly	Ala Ala Ala Thr	Ala 5605	Ala Ala Ala Thr	Gly Gly Thr Thr								
10	Thr Gly 5615	Thr Thr Ala Thr	Ala 5620	Gly Thr Cys Gly	Ala 5625	Thr Thr Ala								
15	Ala Thr 5630	Cys Gly Ala Thr	Thr 5635	Thr Gly Ala Thr	Thr 5640	Cys Thr Ala								
20	Gly Ala 5645	Thr Thr Thr Gly	Thr 5650	Thr Thr Thr Ala	Ala 5655	Cys Thr Ala								
25	Ala Thr 5660	Thr Ala Ala Ala	Gly 5665	Gly Ala Gly Gly	Ala 5670	Ala Thr Ala								
30	Ala Cys 5675	Ala Thr Ala Thr	Gly 5680	Ala Thr Cys Gly	Cys 5685	Thr Cys Cys								
35	Ala Cys 5690	Cys Ala Thr Gly	Cys 5695	Ala Cys Cys Ala	Gly 5700	Thr Gly Ala								
40	Gly Ala 5705	Ala Gly Cys Ala	Thr 5710	Thr Ala Thr Gly	Ala 5715	Gly Cys Ala								
45	Thr Cys 5720	Thr Gly Gly Gly	Ala 5725	Cys Gly Gly Thr	Gly 5730	Cys Thr Gly								
50	Thr Ala 5735	Ala Cys Ala Ala	Ala 5740	Thr Gly Thr Gly	Ala 5745	Ala Cys Cys								
55	Ala Gly 5750	Gly Ala Ala Ala	Gly 5755	Thr Ala Cys Ala	Thr 5760	Gly Thr Cys								
60	Thr Thr 5765	Cys Thr Ala Ala	Ala 5770	Thr Gly Cys Ala	Cys 5775	Thr Ala Cys								
65	Thr Ala 5780	Cys Cys Thr Cys	Thr 5785	Gly Ala Cys Ala	Gly 5790	Thr Gly Thr								
70	Ala Thr 5795	Gly Thr Cys Thr	Gly 5800	Cys Cys Cys Thr	Gly 5805	Thr Gly Gly								
75	Cys Cys 5810	Cys Gly Gly Ala	Thr 5815	Gly Ala Ala Thr	Ala 5820	Cys Thr Thr								

EP 2 845 864 A2

	Gly	Gly	Ala	Thr	Ala	Gly	Cys	Thr	Gly	Gly	Ala	Ala	Thr	Gly	Ala
	5825						5830					5835			
5	Ala	Gly	Ala	Ala	Gly	Ala	Thr	Ala	Ala	Ala	Thr	Gly	Cys	Thr	Thr
	5840						5845					5850			
10	Gly	Cys	Thr	Gly	Cys	Ala	Thr	Ala	Ala	Ala	Gly	Thr	Thr	Thr	Gly
	5855						5860					5865			
15	Thr	Gly	Ala	Thr	Ala	Cys	Ala	Gly	Gly	Cys	Ala	Ala	Gly	Gly	Cys
	5870						5875					5880			
20	Cys	Cys	Thr	Gly	Gly	Thr	Gly	Gly	Cys	Cys	Gly	Thr	Gly	Gly	Thr
	5885						5890					5895			
25	Cys	Gly	Cys	Cys	Gly	Gly	Cys	Ala	Ala	Cys	Ala	Gly	Thr	Ala	Cys
	5900						5905					5910			
30	Gly	Ala	Cys	Cys	Cys	Cys	Cys	Cys	Gly	Gly	Cys	Gly	Cys	Thr	Gly
	5915						5920					5925			
35	Cys	Gly	Cys	Gly	Thr	Gly	Cys	Ala	Cys	Gly	Gly	Cys	Thr	Gly	Gly
	5930						5935					5940			
40	Gly	Thr	Ala	Cys	Cys	Ala	Cys	Thr	Gly	Gly	Ala	Gly	Cys	Cys	Ala
	5945						5950					5955			
45	Gly	Gly	Ala	Cys	Thr	Gly	Cys	Gly	Ala	Gly	Thr	Gly	Cys	Thr	Gly
	5960						5965					5970			
50	Cys	Cys	Gly	Cys	Cys	Gly	Cys	Ala	Ala	Cys	Ala	Cys	Cys	Gly	Ala
	5975						5980					5985			
55	Gly	Thr	Gly	Cys	Gly	Cys	Gly	Cys	Cys	Gly	Gly	Gly	Cys	Cys	Thr
	5990						5995					6000			
60	Gly	Gly	Gly	Cys	Gly	Cys	Cys	Cys	Ala	Gly	Cys	Ala	Cys	Cys	Cys
	6005						6010					6015			
65	Gly	Thr	Thr	Gly	Cys	Ala	Gly	Cys	Thr	Cys	Ala	Ala	Cys	Ala	Ala
	6020						6025					6030			
70	Gly	Gly	Ala	Cys	Ala	Cys	Ala	Gly	Thr	Gly	Thr	Gly	Cys	Ala	Ala
	6035						6040					6045			
75	Ala	Cys	Cys	Thr	Thr	Gly	Cys	Cys	Thr	Thr	Gly	Cys	Ala	Gly	Gly
	6050						6055					6060			

EP 2 845 864 A2

	Cys	Thr	Ala	Cys	Thr	Thr	Cys	Thr	Cys	Thr	Gly	Ala	Thr	Gly	Cys
	6065						6070					6075			
5	Cys	Thr	Thr	Thr	Thr	Cys	Cys	Thr	Cys	Cys	Ala	Cys	Gly	Gly	Ala
	6080						6085					6090			
10	Cys	Ala	Ala	Ala	Thr	Gly	Cys	Ala	Gly	Ala	Cys	Cys	Cys	Thr	Gly
	6095						6100					6105			
15	Gly	Ala	Cys	Cys	Ala	Ala	Cys	Thr	Gly	Thr	Ala	Cys	Cys	Thr	Thr
	6110						6115					6120			
20	Cys	Cys	Thr	Thr	Gly	Gly	Ala	Ala	Ala	Gly	Ala	Gly	Ala	Gly	Thr
	6125						6130					6135			
25	Ala	Gly	Ala	Ala	Cys	Ala	Thr	Cys	Ala	Thr	Gly	Gly	Gly	Ala	Cys
	6140						6145					6150			
30	Ala	Gly	Ala	Gly	Ala	Ala	Ala	Thr	Cys	Cys	Gly	Ala	Thr	Gly	Thr
	6155						6160					6165			
35	Gly	Gly	Thr	Thr	Thr	Gly	Cys	Ala	Gly	Thr	Thr	Cys	Thr	Thr	Cys
	6170						6175					6180			
40	Thr	Cys	Thr	Gly	Cys	Cys	Ala	Gly	Cys	Thr	Ala	Gly	Ala	Ala	Ala
	6185						6190					6195			
45	Ala	Cys	Cys	Ala	Cys	Cys	Ala	Ala	Ala	Thr	Gly	Ala	Ala	Cys	Cys
	6200						6205					6210			
50	Cys	Cys	Ala	Thr	Gly	Thr	Thr	Thr	Ala	Cys	Gly	Thr	Cys	Gly	Ala
	6215						6220					6225			
55	Cys	Ala	Ala	Ala	Ala	Cys	Thr	Cys	Ala	Cys	Ala	Cys	Ala	Thr	Gly
	6230						6235					6240			
60	Thr	Cys	Cys	Ala	Cys	Cys	Thr	Thr	Gly	Thr	Cys	Cys	Ala	Gly	Cys
	6245						6250					6255			
65	Thr	Cys	Cys	Gly	Gly	Ala	Ala	Cys	Thr	Cys	Cys	Thr	Gly	Gly	Gly
	6260						6265					6270			
70	Gly	Gly	Gly	Ala	Cys	Cys	Gly	Thr	Cys	Ala	Gly	Thr	Cys	Thr	Thr
	6275						6280					6285			
75	Cys	Cys	Thr	Cys	Thr	Thr	Cys	Cys	Cys	Cys	Cys	Cys	Ala	Ala	Ala
	6290						6295					6300			

EP 2 845 864 A2

	Ala	Cys	Cys	Cys	Ala	Ala	Gly	Gly	Ala	Cys	Ala	Cys	Cys	Cys	Thr
	6305						6310					6315			
5	Cys	Ala	Thr	Gly	Ala	Thr	Cys	Thr	Cys	Cys	Cys	Gly	Gly	Ala	Cys
	6320						6325					6330			
10	Cys	Cys	Cys	Thr	Gly	Ala	Gly	Gly	Thr	Cys	Ala	Cys	Ala	Thr	Gly
	6335						6340					6345			
15	Cys	Gly	Thr	Gly	Gly	Thr	Gly	Gly	Thr	Gly	Gly	Ala	Cys	Gly	Thr
	6350						6355					6360			
20	Gly	Ala	Gly	Cys	Cys	Ala	Cys	Gly	Ala	Ala	Gly	Ala	Cys	Cys	Cys
	6365						6370					6375			
25	Thr	Gly	Ala	Gly	Gly	Thr	Cys	Ala	Ala	Gly	Thr	Thr	Cys	Ala	Ala
	6380						6385					6390			
30	Cys	Thr	Gly	Gly	Thr	Ala	Cys	Gly	Thr	Gly	Gly	Ala	Cys	Gly	Gly
	6395						6400					6405			
35	Cys	Gly	Thr	Gly	Gly	Ala	Gly	Gly	Thr	Gly	Cys	Ala	Thr	Ala	Ala
	6410						6415					6420			
40	Thr	Gly	Cys	Cys	Ala	Ala	Gly	Ala	Cys	Ala	Ala	Ala	Gly	Cys	Cys
	6425						6430					6435			
45	Gly	Cys	Gly	Gly	Gly	Ala	Gly	Gly	Ala	Gly	Cys	Ala	Gly	Thr	Ala
	6440						6445					6450			
50	Cys	Ala	Ala	Cys	Ala	Gly	Cys	Ala	Cys	Gly	Thr	Ala	Cys	Cys	Gly
	6455						6460					6465			
55	Thr	Gly	Thr	Gly	Gly	Thr	Cys	Ala	Gly	Cys	Gly	Thr	Cys	Cys	Thr
	6470						6475					6480			
60	Cys	Ala	Cys	Cys	Gly	Thr	Cys	Cys	Thr	Gly	Cys	Ala	Cys	Cys	Ala
	6485						6490					6495			
65	Gly	Gly	Ala	Cys	Thr	Gly	Gly	Cys	Thr	Gly	Ala	Ala	Thr	Gly	Gly
	6500						6505					6510			
70	Cys	Ala	Ala	Gly	Gly	Ala	Gly	Thr	Ala	Cys	Ala	Ala	Gly	Thr	Gly
	6515						6520					6525			
75	Cys	Ala	Ala	Gly	Gly	Thr	Cys	Thr	Cys	Cys	Ala	Ala	Cys	Ala	Ala
	6530						6535					6540			

EP 2 845 864 A2

	6530		6535		6540										
5	Ala Gly 6545	Cys Cys Cys	Thr Cys 6550	Cys Cys Ala Gly 6555	Cys Cys Cys										
10	Cys Ala 6560	Thr Cys Gly	Ala Gly 6565	Ala Ala Ala Ala 6570	Cys Cys Ala Thr										
15	Cys Thr 6575	Cys Cys Ala Ala	Ala Ala 6580	Gly Cys Cys Ala 6585	Ala Ala Gly Gly										
20	Gly Cys 6590	Ala Gly Cys Cys	Cys Cys 6595	Cys Gly Ala Gly 6600	Ala Ala Cys Cys										
25	Ala Cys 6605	Ala Gly Gly Thr	Gly Thr 6610	Ala Cys Ala Cys 6615	Cys Cys Thr										
30	Gly Cys 6620	Cys Cys Cys Cys	Ala Thr 6625	Cys Cys Cys Gly 6630	Gly Gly Ala										
35	Thr Gly 6635	Ala Gly Cys Thr	Gly Ala 6640	Cys Cys Ala Ala 6645	Gly Ala Ala										
40	Cys Cys 6650	Ala Gly Gly Thr	Cys Ala 6655	Gly Cys Cys Thr 6660	Gly Ala Cys										
45	Cys Thr 6665	Gly Cys Cys Thr	Gly Gly 6670	Gly Thr Cys Ala 6675	Ala Ala Gly Gly										
50	Cys Thr 6680	Thr Cys Thr Ala	Thr Thr 6685	Cys Cys Cys Ala 6690	Gly Cys Gly Ala										
55	Cys Ala 6695	Thr Cys Gly Cys	Cys Cys 6700	Gly Thr Gly Gly 6705	Ala Gly Thr Gly										
60	Gly Gly 6710	Ala Gly Ala Gly	Cys Cys 6715	Ala Ala Thr Gly 6720	Gly Cys Ala										
65	Gly Cys 6725	Cys Gly Gly Ala	Gly Ala 6730	Ala Ala Cys Ala 6735	Ala Cys Thr Ala										
70	Cys Ala 6740	Ala Gly Ala Cys	Cys Cys 6745	Ala Cys Gly Cys 6750	Cys Thr Cys Cys										
75	Cys Gly 6755	Thr Gly Cys Thr	Gly Gly 6760	Gly Ala Cys Thr 6765	Cys Cys Gly Ala										

EP 2 845 864 A2

	Cys	Gly	Gly	Cys	Thr	Cys	Cys	Thr	Thr	Cys	Thr	Thr	Cys	Cys	Thr
	6770						6775					6780			
5	Cys	Thr	Ala	Cys	Ala	Gly	Cys	Ala	Ala	Gly	Cys	Thr	Cys	Ala	Cys
	6785						6790					6795			
10	Cys	Gly	Thr	Gly	Gly	Ala	Cys	Ala	Ala	Gly	Ala	Gly	Cys	Ala	Gly
	6800						6805					6810			
15	Gly	Thr	Gly	Gly	Cys	Ala	Gly	Cys	Ala	Gly	Gly	Gly	Gly	Ala	Ala
	6815						6820					6825			
20	Cys	Gly	Thr	Cys	Thr	Thr	Cys	Thr	Cys	Ala	Thr	Gly	Cys	Thr	Cys
	6830						6835					6840			
25	Cys	Gly	Thr	Gly	Ala	Thr	Gly	Cys	Ala	Thr	Gly	Ala	Gly	Gly	Cys
	6845						6850					6855			
30	Thr	Cys	Thr	Gly	Cys	Ala	Cys	Ala	Ala	Cys	Cys	Ala	Cys	Thr	Ala
	6860						6865					6870			
35	Cys	Ala	Cys	Gly	Cys	Ala	Gly	Ala	Ala	Gly	Ala	Gly	Cys	Cys	Thr
	6875						6880					6885			
40	Cys	Thr	Cys	Cys	Cys	Thr	Gly	Thr	Cys	Thr	Cys	Cys	Gly	Gly	Gly
	6890						6895					6900			
45	Thr	Ala	Ala	Ala	Thr	Ala	Ala	Thr	Gly	Gly	Ala	Thr	Cys	Cys	Gly
	6905						6910					6915			
50	Cys	Gly	Gly	Ala	Ala	Ala	Gly	Ala	Ala	Gly	Ala	Ala	Gly	Ala	Ala
	6920						6925					6930			
55	Gly	Ala	Ala	Gly	Ala	Ala	Gly	Ala	Ala	Ala	Gly	Cys	Cys	Cys	Gly
	6935						6940					6945			
60	Ala	Ala	Ala	Gly	Gly	Ala	Ala	Gly	Cys	Thr	Gly	Ala	Gly	Thr	Thr
	6950						6955					6960			
65	Gly	Gly	Cys	Thr	Gly	Cys	Thr	Gly	Cys	Cys	Ala	Cys	Cys	Gly	Cys
	6965						6970					6975			
70	Thr	Gly	Ala	Gly	Cys	Ala	Ala	Thr	Ala	Ala	Cys	Thr	Ala	Gly	Cys
	6980						6985					6990			
75	Ala	Thr	Ala	Ala	Cys	Cys	Cys	Cys	Thr	Thr	Gly	Gly	Gly	Gly	Cys
	6995						7000					7005			

EP 2 845 864 A2

	Cys Thr	Cys Thr	Ala Ala	Ala Ala	Cys Gly	Gly Gly	Thr	Cys Thr	Thr				
	7010				7015			7020					
5	Gly Ala	Gly Gly	Gly Gly	Thr	Thr	Thr	Thr	Thr	Gly Cys	Thr			
	7025			7030				7035					
10	Gly Ala	Ala Ala	Gly Gly	Ala	Gly Gly	Ala Ala	Cys	Cys Gly	Cys				
	7040			7045			7050						
	Thr Cys	Thr Thr	Cys Ala	Cys	Gly Cys	Thr Cys	Thr	Thr Cys	Ala				
	7055			7060			7065						
15	Cys Gly	Cys Gly	Gly Ala	Thr	Ala Ala	Ala Thr	Ala	Ala Gly	Thr				
	7070			7075			7080						
20	Ala Ala	Cys Gly	Ala Thr	Cys	Cys Gly	Gly Thr	Cys	Cys Ala	Gly				
	7085			7090			7095						
	Thr Ala	Ala Thr	Gly Ala	Cys	Cys Thr	Cys Ala	Gly	Ala Ala	Cys				
	7100			7105			7110						
25	Thr Cys	Cys Ala	Thr Cys	Thr	Gly Gly	Ala Thr	Thr	Thr Gly	Thr				
	7115			7120			7125						
30	Thr Cys	Ala Gly	Ala Ala	Cys	Gly Cys	Thr Cys	Gly	Gly Thr	Thr				
	7130			7135			7140						
35	Gly Cys	Cys Gly	Cys Cys	Gly	Gly Gly	Cys Gly	Thr	Thr Thr	Thr				
	7145			7150			7155						
	Thr Thr	Ala Thr	Thr Gly	Gly	Thr Gly	Ala Gly	Ala	Ala Thr	Cys				
	7160			7165			7170						
40	Gly Cys	Ala Gly	Cys Ala	Ala	Cys Thr	Thr Gly	Thr	Cys Gly	Cys				
	7175			7180			7185						
45	Gly Cys	Cys Ala	Ala Thr	Cys	Gly Ala	Gly Cys	Cys	Ala Thr	Gly				
	7190			7195			7200						
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	7205			7210			7215						
50	Cys Cys	Cys Cys	Ala Thr	Thr	Cys Ala	Ala Gly	Ala	Ala Cys	Ala				
	7220			7225			7230						
55	Gly Cys	Ala Ala	Gly Cys	Ala	Gly Cys	Ala Thr	Thr	Gly Ala	Gly				
	7235			7240			7245						

EP 2 845 864 A2

Ala Ala Cys Thr Thr Thr Gly Gly Ala Ala Thr Cys Cys Ala Gly
 7250 7255 7260

5 Thr Cys Cys Cys Thr Cys Thr Thr Cys Cys Ala Cys Cys Thr Gly
 7265 7270 7275

10 Cys Thr Gly Ala Cys Cys Gly
 7280 7285

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30 <220>
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40 <210> 31
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<220>
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45 <400> 31

Val Pro Phe Cys Asp Leu Leu Thr Lys His Cys Phe Glu Ala
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50 <210> 32
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EP 2 845 864 A2

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His His

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<400> 33

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 1 5 10 15

Pro Leu

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<210> 34
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<220>
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Ser Ser

45

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<220>
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Asn Leu

EP 2 845 864 A2

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Asp Leu Asn Cys Lys Tyr Asp Glu Leu Thr Tyr Lys Glu Trp Cys Gln
1 5 10 15

Phe Asn

15

<210> 37
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<220>
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<400> 37

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Phe His Asp Cys Lys Tyr Asp Leu Leu Thr Arg Gln Met Val Cys His
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Gly Leu

30

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Arg Asn His Cys Phe Trp Asp His Leu Leu Lys Gln Asp Ile Cys Pro
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45

Ser Pro

<210> 39
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<220>
<223> Preferred TALL-1 Modulating Domains

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EP 2 845 864 A2

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Phe Phe

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<220>
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EP 2 845 864 A2

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5 <210> 44
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10 <220>
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<223> Xaa = a peptide bond

Fc domain attached at Position 19 to C-terminus

20 <400> 44

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25 Pro Leu Xaa

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<212> PRT
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<220>
<223> Peptide bond

35 <220>
<221> misc_feature
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<223> Xaa = a peptide bond

40 Fc domain attached at Position 1 to N-terminus

<400> 45

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1 5 10 15

Asp Pro Leu

50 <210> 46
<211> 38
<212> PRT
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55 <220>
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EP 2 845 864 A2

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 <223> Xaa = a peptide bond
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<220>
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 <222> (38)..(38)
 <223> Xaa = a peptide bond
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Fc domain attached at Position 38 to C-terminus

<400> 46
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Leu Pro Gly Cys Lys Trp Asp Leu Leu Ile Lys Gln Trp Val Cys Asp
 1 5 10 15

Pro Leu Xaa Leu Pro Gly Cys Lys Trp Asp Leu Leu Ile Lys Gln Trp
 20 20 25 30

Val Cys Asp Pro Leu Xaa
 25 35

<210> 47
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 <223> Xaa = a peptide bond
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Fc domain attached at Position 1 to N-terminus
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<400> 47

Xaa Leu Pro Gly Cys Lys Trp Asp Leu Leu Ile Lys Gln Trp Val Cys
 1 5 10 15

Asp Pro Leu Xaa Leu Pro Gly Cys Lys Trp Asp Leu Leu Ile Lys Gln
 20 25 30

Trp Val Cys Asp Pro Leu
 55 35

EP 2 845 864 A2

<210> 48
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 Ser Ser Xaa
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 1 5 10 15
 45
 Thr Ser Ser
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EP 2 845 864 A2

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 5 <221> misc_feature
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 Fc domain attached at Position 36 to C-terminus

 10 <400> 50

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 1 5 10 15

 15 Ser Xaa Ser Ala Asp Cys Tyr Phe Asp Ile Leu Thr Lys Ser Asp Val
 20 25 30

 Thr Ser Ser Xaa
 20 35

 <210> 51
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 30 <220>
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 <223> Xaa = a peptide bond

 35 Fc domain attached at Position 1 to N-terminus

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 <221> misc_feature
 <222> (19)..(19)
 <223> Xaa = a peptide bond

 40 <400> 51

 Xaa Ser Ala Asp Cys Tyr Phe Asp Ile Leu Thr Lys Ser Asp Val Thr
 45 1 5 10 15

 Ser Ser Xaa Ser Ala Asp Cys Tyr Phe Asp Ile Leu Thr Lys Ser Asp
 50 20 25 30

 Val Thr Ser Ser
 55 35

 <210> 52
 <211> 19
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EP 2 845 864 A2

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<223> Peptide bond

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<221> misc_feature
<222> (19)..(19)
<223> Xaa = a peptide bond

10
Fc domain attached at Position 19 to C-terminus

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1 5 10 15

15
Gly Leu Xaa

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Fc domain attached at Position 1 to N-terminus

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1 5 10 15

40
His Gly Leu

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EP 2 845 864 A2

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 Gly Leu Xaa Phe His Asp Cys Lys Trp Asp Leu Leu Thr Lys Gln Trp
 15 20 25 30
 Val Cys His Gly Leu Xaa
 35
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 30 Fc domain attached at Position 1 to N-terminus
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 40 1 5 10 15
 His Gly Leu Xaa Phe His Asp Cys Lys Trp Asp Leu Leu Thr Lys Gln
 45 20 25 30
 Trp Val Cys His Gly Leu
 50 35
 <210> 56
 <211> 25
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EP 2 845 864 A2

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5 <210> 57
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10 <220>
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<400> 57
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15 <210> 58
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20 <220>
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<400> 58

25 Phe His Asp Cys Lys Trp Asp Leu Leu Thr Lys Gln Trp Val Cys His
 1 5 10 15

Gly Leu

30

<210> 59
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40 Gly Ser Gly Ser Ala Thr Gly Gly Ser Gly Ser Thr Ala Ser Ser Gly
 1 5 10 15

Ser Gly Ser Ala Thr His Met
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45

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50 <220>
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EP 2 845 864 A2

1 5 10 15

Tyr Met

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<210> 61
 <211> 18
 <212> PRT
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<220>
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<400> 61

Pro Val Tyr Gln Gly Trp Trp Asp Thr Leu Thr Lys Leu Tyr Ile Trp
 1 5 10 15

20

Asp Gly

<210> 62
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25

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<400> 62

Trp Leu Asp Gly Gly Trp Arg Asp Pro Leu Ile Lys Arg Ser Val Gln
 1 5 10 15

35

Leu Gly

<210> 63
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40

<220>
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45

<400> 63

Gly His Gln Gln Phe Lys Trp Asp Leu Leu Thr Lys Gln Trp Val Gln
 1 5 10 15

50

Ser Asn

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<210> 64
 <211> 18

EP 2 845 864 A2

<212> PRT
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<220>
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<400> 64

Gln Arg Val Gly Gln Phe Trp Asp Val Leu Thr Lys Met Phe Ile Thr
 1 5 10 15

Gly Ser

<210> 65
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Gln Ala Gln Gly Trp Ser Tyr Asp Ala Leu Ile Lys Thr Trp Ile Arg
 1 5 10 15

Trp Pro

<210> 66
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<400> 66

Gly Trp Met His Trp Lys Trp Asp Pro Leu Thr Lys Gln Ala Leu Pro
 1 5 10 15

Trp Met

<210> 67
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<400> 67

Gly His Pro Thr Tyr Lys Trp Asp Leu Leu Thr Lys Gln Trp Ile Leu

EP 2 845 864 A2

1 5 10 15

Gln Met

5

<210> 68
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<220>
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<400> 68
 Trp Asn Asn Trp Ser Leu Trp Asp Pro Leu Thr Lys Leu Trp Leu Gln
 1 5 10 15

20

Gln Asn

<210> 69
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<400> 69
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Gln Gln

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Thr Ser

<210> 71
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EP 2 845 864 A2

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 10 gg 62

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 ggca 64

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 25 <213> Artificial Sequence

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 caca 64

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 55 <223> Oligonucleotides

 <400> 75

EP 2 845 864 A2

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EP 2 845 864 A2

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EP 2 845 864 A2

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EP 2 845 864 A2

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EP 2 845 864 A2

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 ctctgagta ggacaaatcc gccgggagcg gatttgaacg ttgcgaagca acggcccggg 180
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EP 2 845 864 A2

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 5 gctttagaaa tactttggca gcggtttggt gtattgagtt tcatttgogc attggttaaa 420
 tggaaagtga ccgtgcgctt actacagcct aatatttttg aaatatccca agagcttttt 480
 ccttcgcatg cccacgctaa acattctttt tctcttttgg ttaaatoegt gtttgattta 540
 10 ttatttgcta tattttatttt tcgataatta tcaactagag aaggaacaat taatggtatg 600
 ttcatacacg catgtaaaaa taaactatct atatagttgt ctttctctga atgtgcaaaa 660
 ctaagcattc cgaagccatt attagcagta tgaatagggg aactaaacco agtgataaga 720
 15 cctgatgatt tcgcttcttt aattacattt ggagattttt tatttacagc attgttttca 780
 aatatattcc aattaatcgg tgaatgattg gagttagaat aatctactat aggatcatat 840
 20 tttattaaat tagcgtcatc ataatttgc ctccattttt tagggtaatt atccagaatt 900
 gaaatatcag atttaacccat agaatgagga taaatgatcg cgagtaaata atattcacia 960
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 25 ttaattttat taattattct gtaagtgtcg tcggcattta tgtctttcat acccatctct 1080
 ttatccttac ctattgtttg tcgcaagttt tgcgtgttat atatcattaa aacggtaata 1140
 gattgacatt tgattctaataaattggatt tttgtcacac tattatatcg cttgaaatac 1200
 30 aattgtttaa cataagtacc tgtaggatcg tacaggttta cgcaagaaaa tggtttgтта 1260
 tagtcgatta atcgatttga ttctagattt gttttaacta attaaaggag gaataacata 1320
 tggttaacgc gttggaattc gagctcacta gtgtcgacct gcagggtacc atggaagctt 1380
 35 actcgaggat ccgcggaaag aagaagaaga agaagaaagc ccgaaaggaa gctgagttgg 1440
 ctgctgccac cgctgagcaa taactagcat aacccttgg ggctctaaa cgggtcttga 1500
 40 ggggtttttt gctgaaagga ggaaccgctc ttcacgctct tcacgc 1546

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 <211> 872
 <212> DNA
 45 <213> Artificial Sequence

 <220>
 <223> GM221

 50 <400> 98
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 55 gataatatat gagcacaataa aagaaacctat taacacaaga gcagcttgag gacgcacgtc 180
 gccttaaagc aatttatgaa aaaaagaaaa atgaacttgg cttatcccag gaatctgtcg 240

EP 2 845 864 A2

cagacaagat ggggatgggg cagtcaggcg ttggtgcttt atttaatggc atcaatgcat 300
 taaatgctta taacgccgca ttgcttacia aaattctcaa agttagcggt gaagaattta 360
 5 gcccttcaat cgccagagaa tctacgagat gtatgaagcg gttagtatgc agccgtcact 420
 tagaagtgag tatgagtacc ctgttttttc tcatgttcag gcagggatgt tctcacctaa 480
 gcttagaacc tttaccaaag gtgatgcgga gagatgggta agcacaacca aaaaagccag 540
 10 tgattctgca ttctggcttg aggttgaaggt taattocatg accgcaccaa caggctccaa 600
 gccaaagcttt cctgacggaa tgtaattct cgttgaccct gagcaggctg ttgagccagg 660
 tgatttctgc atagccagac ttgggggtga tgagtttacc ttcaagaaac tgatcagggg 720
 15 tagcggtcag gtgtttttac aaccactaaa cccacagtac ccaatgatcc catgcaatga 780
 gagttgttcc gttgtgggga aagttatcgc tagtcagtgg cctgaagaga cgtttggtg 840
 atagactagt ggatccacta gtgtttctgc cc 872
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 agtatgccgg tgtctcttat cagaccgttt cccgcgtggt gaaccaggcc agccacgttt 180
 35 ctgcgaaaac gcgggaaaaa gtcgaagcgg cgatggcgga gctgaattac attcccaacc 240
 gcgtggcaca acaactggcg ggcaaacagt cgctcctgat tggcgttgcc acctccagtc 300
 tggccctgca cgcgccgtcg caaattgtcg cggcgattaa atctcgcgcc gatcaactgg 360
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 45 ctgaccagac acccatcaac agtattattt tctcccatga agacggtagc cgactgggcg 600
 tggagcatct ggtcgcattg ggtcaccagc aaatcgcgct gttagcgggc ccattaagtt 660
 ctgtctcggc gcgtctgcgt ctggctggct ggcataaata tctcactcgc aatcaaattc 720
 50 agccgatagc ggaacgggaa ggcgactgga gtgccatgtc cggttttcaa caaacatgc 780
 aaatgctgaa tgagggcatc gttcccactg cgatgctggt tgccaacgat cagatggcgc 840
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 tgggatacga cgataccgaa gacagctcat gttatatccc gccgtaacc accatcaaac 960

EP 2 845 864 A2

aggattttcg cctgctgggg caaaccagcg tggaccgctt gctgcaactc tctcagggcc 1020
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 5 cgccaatac gcaaaccgcc tctccccgcg cgttggccga ttcattaatg cagctggcac 1140
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10 <210> 100
 <211> 14
 <212> PRT
 <213> Artificial Sequence

15 <220>
 <223> Modulators of TALL-1

<220>
 <221> misc_feature
 20 <222> (1, 2, 3, 13)..(14)
 <223> Xaa (Pos1,2,3,13,14) are each independently absent or amino acid residues;

<220>
 <221> misc_feature
 25 <222> (6)..(6)
 <223> Xaa (Pos6) is an amino acid residue; Xaa (Pos9) is a basic or hydrophobic residue;

<220>
 <221> misc_feature
 30 <222> (12)..(12)
 <223> Xaa (Pos12) is a neutral hydrophobic residue.

<400> 100
 35 Xaa Xaa Xaa Cys Asp Xaa Leu Xaa Xaa Xaa Cys Xaa Xaa Xaa
 1 5 10

40 <210> 101
 <211> 14
 <212> PRT
 <213> Artificial Sequence

45 <220>
 <223> Modulators of TALL-1

<220>
 <221> misc_feature
 50 <222> (1, 2, 3, 12 and)..(13)
 <223> Xaa (Pos1,2,3,12,13) are each independently absent or amino acid residues;

<220>
 <221> misc_feature
 55 <222> (5 and)..(8)
 <223> Xaa (Pos5,8) is a neutral hydrophobic residue; Xaa (Pos 10) is an acidic residue;

EP 2 845 864 A2

<220>
 <221> misc_feature
 <222> (14)..(14)
 <223> Xaa (Pos14) is absent or is an amino acid residue.
 5
 <400> 101

 Xaa Xaa Xaa Cys Xaa Pro Phe Xaa Trp Xaa Cys Xaa Xaa Xaa
 1 5 10
 10
 <210> 102
 <211> 14
 <212> PRT
 <213> Artificial Sequence
 15
 <220>
 <223> Modulator of TALL-1

 <220>
 <221> misc_feature
 <222> (1, 2, 3, 12, 13 and)..(14)
 <223> Xaa (Pos1,2,3,12,13,14) are each independently absent or amino
 acid residues;
 20
 <220>
 <221> misc_feature
 <222> (6 and)..(7)
 <223> Xaa (Pos6,7) is a hydrophobic residue;
 25
 <220>
 <221> misc_feature
 <222> (10)..(10)
 <223> Xaa (Pos10) is an acidic or polar hydrophobic residue.
 30
 <400> 102
 35
 Xaa Xaa Xaa Cys Trp Xaa Xaa Trp Gly Xaa Cys Xaa Xaa Xaa
 1 5 10
 40
 <210> 103
 <211> 14
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Modulator of TALL-1
 45
 <220>
 <221> misc_feature
 <222> (1)..(1)
 <223> Xaa (Pos1) is absent or is an amino acid residue;
 50
 <220>
 <221> misc_feature
 <222> (2 and)..(14)
 <223> Xaa (Pos2,14) is a neutral hydrophobic residue;
 55
 <220>
 <221> misc_feature

EP 2 845 864 A2

<222> (3 and)..(10)
 <223> Xaa (Pos3,10) is an amino acid residue;

 <220>
 5 <221> misc_feature
 <222> (5, 6, 7, 8, 12 and)..(13)
 <223> Xaa (Pos5,6,7,8,12,13) are each independently amino acid
 residues;

 <220>
 10 <221> misc_feature
 <222> (9)..(9)
 <223> Xaa (Pos9) is an acidic residue.

 <400> 103

 15 Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa
 1 5 10

 <210> 104
 20 <211> 18
 <212> PRT
 <213> Artificial Sequence

 <220>
 25 <223> Modulator of TALL-1

 <220>
 <221> misc_feature
 <222> (1, 2, 12, 13, 16, 17 and)..(18)
 30 <223> Xaa (Pos1,2,12,13,16,17,18) are each independently absent or
 amino acid residues;

 <220>
 <221> misc_feature
 <222> (3)..(3)
 35 <223> Xaa (Pos3) is an acidic or amide residue;

 <220>
 <221> misc_feature
 <222> (5 and)..(8)
 40 <223> Xaa (Pos5,8) is an amino acid residue;

 <220>
 <221> misc_feature
 <222> (6)..(6)
 45 <223> Xaa (Pos6) is an aromatic residue;

 <220>
 <221> misc_feature
 <222> (11)..(11)
 <223> Xaa (Pos11) is a basic residue;

 50 <220>
 <221> misc_feature
 <222> (14)..(14)
 <223> Xaa (Pos14) is a neutral hydrophobic residue.

 55 <400> 104

 Xaa Xaa Xaa Cys Xaa Xaa Asp Xaa Leu Xaa Xaa Xaa Xaa Xaa Cys Xaa

EP 2 845 864 A2

1 5 10 15

Xaa Xaa

5

<210> 105
 <211> 18
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Modulator of TALL-1

10

15

<220>
 <221> misc_feature
 <222> (1, 2 and)..(3)
 <223> Xaa (Pos1,2,3) are each independently absent or amino acid residues;

20

<220>
 <221> misc_feature
 <222> (5, 7, 14 and)..(16)
 <223> Xaa (Pos5,7,14,16) is an amino acid residue;

25

<220>
 <221> misc_feature
 <222> (10)..(10)
 <223> Xaa (Pos10) is a basic residue;

30

<220>
 <221> misc_feature
 <222> (11 and)..(12)
 <223> Xaa (Pos11,12) are each independently amino acid residues;

35

<220>
 <221> misc_feature
 <222> (13 and)..(17)
 <223> Xaa (Pos13,17) is a neutral hydrophobic residue;

40

<220>
 <221> misc_feature
 <222> (18)..(18)
 <223> Xaa (Pos18) is an amino acid residue or is absent.

<400> 105

45

Xaa Xaa Xaa Cys Xaa Asp Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa
 1 5 10 15

Xaa Xaa

50

<210> 106
 <211> 18
 <212> PRT
 <213> Artificial Sequence
 <220>

55

EP 2 845 864 A2

<223> Modulator of TALL-1

<220>

<221> misc_feature

<222> (1, 2, 3, 16, 17 and)..(18)

<223> Xaa (Pos1,2,3,16,17,18) are each independently absent or amino acid residues;

<220>

<221> misc_feature

<222> (5, 6, 7, 10 and)..(14)

<223> Xaa (Pos5,6,7,10,14) are each independently amino acid residues.

<400> 106

Xaa Xaa Xaa Cys Xaa Xaa Xaa Trp Asp Xaa Leu Xaa Xaa Xaa Cys Xaa
1 5 10 15

Xaa Xaa

<210> 107

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Modulator of TALL-1

<220>

<221> misc_feature

<222> (1,2,3,15,16,17)..(18)

<223> Xaa (Pos1,2,3,15,16,17,18) are each independently absent or amino acid residues;

<220>

<221> misc_feature

<222> (5, 6, 7, 9 and)..(13)

<223> Xaa (Pos 5,6,7,9 13) are each independently amino acid residues;

<220>

<221> misc_feature

<222> (11)..(11)

<223> Xaa (Pos 11) is T or I; and

<400> 107

Xaa Xaa Xaa Cys Xaa Xaa Xaa Asp Xaa Leu Xaa Lys Xaa Cys Xaa Xaa
1 5 10 15

Xaa Xaa

<210> 108

<211> 4

<212> PRT

<213> Artificial Sequence

<220>
 <223> Modulator of TALL-1

5

<220>
 <221> misc_feature
 <222> (2)..(2)
 <223> X at (Pos 2) is an amino acid residue

10

<220>
 <221> misc_feature
 <222> (4)..(4)
 <223> X at (Pos 4) is threonyl or isoleucyl

<400> 108

15

Asp Xaa Leu Xaa
 1

20

<210> 109
 <211> 14
 <212> PRT
 <213> Artificial Sequence

25

<220>
 <223> Modulator of TALL-1

30

<220>
 <221> misc_feature
 <222> (1, 2 and)..(3)
 <223> X at (Pos 1, 2, 3) are absent or are amino acid residues (with
 one of X1, X2, and X3 preferred to be C when one o:
 X12, X13, and X14 is C);

35

<220>
 <221> misc_feature
 <222> (5)..(5)
 <223> X at (Pos 5) is W, Y, or F (W preferred);

40

<220>
 <221> misc_feature
 <222> (7)..(7)
 <223> X at (Pos 7) is an amino acid residue (L preferred);

45

<220>
 <221> misc_feature
 <222> (9)..(9)
 <223> X at (Pos 9) is T or I (T preferred);

50

<220>
 <221> misc_feature
 <222> (10)..(10)
 <223> X at (Pos 10) is K, R, or H (K preferred).

55

<220>
 <221> misc_feature
 <222> (12)..(12)
 <223> X at (Pos 12) is C, a neutral hydrophobic residue, or a basic
 residue (W, C, or R preferred);

EP 2 845 864 A2

5
 <220>
 <221> misc_feature
 <222> (13)..(13)
 <223> X at (Post 13) is C, a neutral hydrophobic residue or is absent
 (V preferred);

10
 <220>
 <221> misc_feature
 <222> (14)..(14)
 <223> X at (Pos 14) is any amino acid residue or is absent.

<400> 109

Xaa Xaa Xaa Lys Xaa Asp Xaa Leu Xaa Xaa Gln Xaa Xaa Xaa
 1 5 10

15
 <210> 110
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Modulator of TALL-1

<400> 110

25
 Pro Phe Pro Trp Glu
 1 5

30
 <210> 111
 <211> 248
 <212> PRT
 <213> Artificial Sequence

35
 <220>
 <223> TALL-1 inhibitory peptibodies

<400> 111

40
 Met Pro Gly Thr Cys Phe Pro Phe Pro Trp Glu Cys Thr His Ala Gly
 1 5 10 15

Gly Gly Gly Gly Val Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 20 25 30

45
 Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 35 40 45

50
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 50 55 60

55
 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 65 70 75 80

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln

EP 2 845 864 A2

				85					90				95			
5	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
				100					105					110		
10	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala
			115					120					125			
15	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro
		130					135					140				
20	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr
	145					150					155					160
25	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser
				165						170					175	
30	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr
			180						185					190		
35	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr
			195					200					205			
40	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe
		210					215					220				
45	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys
	225				230						235					240
50	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys								
				245												
55	<210>	112														
	<211>	248														
	<212>	PRT														
	<213>	Artificial Sequence														
	<220>															
	<223>	TALL-1 inhibitory peptibodies														
	<400>	112														
60	Met	Trp	Gly	Ala	Cys	Trp	Pro	Phe	Pro	Trp	Glu	Cys	Phe	Lys	Glu	Gly
	1				5					10					15	
65	Gly	Gly	Gly	Gly	Val	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala
				20					25					30		
70	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
			35					40					45			

EP 2 845 864 A2

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 50 55 60
 5 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 65 70 75 80
 10 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 85 90 95
 15 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 100 105 110
 20 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 115 120 125
 25 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 130 135 140
 30 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 145 150 155 160
 35 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 165 170 175
 40 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 180 185 190
 45 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 195 200 205
 50 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 210 215 220
 55 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 225 230 235 240
 60 Ser Leu Ser Leu Ser Pro Gly Lys
 245
 <210> 113
 <211> 248
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> TALL-1 inhibitory peptibodies
 <400> 113

EP 2 845 864 A2

Met Val Pro Phe Cys Asp Leu Leu Thr Lys His Cys Phe Glu Ala Gly
 1 5 10 15
 Gly Gly Gly Gly Val Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 5 20 25 30
 Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 10 35 40 45
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 50 55 60
 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 65 70 75 80
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 20 85 90 95
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 100 105 110
 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 115 120 125
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 130 135 140
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 145 150 155 160
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 165 170 175
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 180 185 190
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 195 200 205
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 210 215 220
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 225 230 235 240
 Ser Leu Ser Leu Ser Pro Gly Lys
 245

EP 2 845 864 A2

<210> 114
 <211> 252
 <212> PRT
 <213> Artificial Sequence

5

<220>
 <223> TALL-1 inhibitory peptibodies

<400> 114

10

Met Gly Ser Arg Cys Lys Tyr Lys Trp Asp Val Leu Thr Lys Gln Cys
 1 5 10 15

15

Phe His His Gly Gly Gly Gly Gly Val Asp Lys Thr His Thr Cys Pro
 20 25 30

20

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 35 40 45

25

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 50 55 60

30

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 65 70 75 80

35

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 85 90 95

40

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 100 105 110

45

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 115 120 125

50

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 130 135 140

55

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 145 150 155 160

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 165 170 175

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 180 185 190

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 195 200 205

EP 2 845 864 A2

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 210 215 220
 5
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 225 230 235 240
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 10 245 250
 <210> 115
 <211> 252
 <212> PRT
 15 <213> Artificial Sequence
 <220>
 <223> TALL-1 inhibitory peptibodies
 20 <400> 115
 Met Leu Pro Gly Cys Lys Trp Asp Leu Leu Ile Lys Gln Trp Val Cys
 1 5 10 15
 25 Asp Pro Leu Gly Gly Gly Gly Gly Val Asp Lys Thr His Thr Cys Pro
 20 25 30
 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 30 35 40 45
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 35 50 55 60
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 65 70 75 80
 40 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 85 90 95
 45 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 100 105 110
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 50 115 120 125
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 130 135 140
 55 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 145 150 155 160

EP 2 845 864 A2

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 165 170 175
 5 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 180 185 190
 10 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 195 200 205
 15 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 210 215 220
 20 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 225 230 235 240
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 245 250
 <210> 116
 <211> 252
 <212> PRT
 25 <213> Artificial Sequence
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 <223> TALL-1 inhibitory peptibodies
 30 <400> 116
 Met Ser Ala Asp Cys Tyr Phe Asp Ile Leu Thr Lys Ser Asp Val Cys
 1 5 10 15
 35 Thr Ser Ser Gly Gly Gly Gly Val Asp Lys Thr His Thr Cys Pro
 20 25 30
 40 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 35 40 45
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 50 55 60
 45 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 65 70 75 80
 50 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 85 90 95
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 100 105 110
 55 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val

EP 2 845 864 A2

	115		120		125														
5	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala			
	130						135					140							
	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg			
10	145					150					155					160			
	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly			
					165					170					175				
15	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro			
				180					185					190					
	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser			
20			195					200					205						
	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln			
	210						215					220							
25	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His			
	225					230					235					240			
	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys							
30					245					250									
	<210>	117																	
	<211>	252																	
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35	<213>	Artificial Sequence																	
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	<223>	TALL-1 inhibitory peptibodies																	
40	<400>	117																	
	Met	Ser	Asp	Asp	Cys	Met	Tyr	Asp	Gln	Leu	Thr	Arg	Met	Phe	Ile	Cys			
	1				5					10					15				
45	Ser	Asn	Leu	Gly	Gly	Gly	Gly	Gly	Val	Asp	Lys	Thr	His	Thr	Cys	Pro			
				20					25					30					
	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe			
50			35					40					45						
	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val			
	50						55					60							
55	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe			
	65					70					75					80			

EP 2 845 864 A2

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 85 90 95
 5 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 100 105 110
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 10 115 120 125
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 130 135 140
 15 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 145 150 155 160
 20 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 165 170 175
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 180 185 190
 25 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 195 200 205
 30 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 210 215 220
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 225 230 235 240
 35 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 245 250
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 <210> 118
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 45 <213> Artificial Sequence
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 <223> TALL-1 inhibitory peptibodies
 50 <400> 118
 Met Asp Leu Asn Cys Lys Tyr Asp Glu Leu Thr Tyr Lys Glu Trp Cys
 1 5 10 15
 55 Gln Phe Asn Gly Gly Gly Gly Gly Val Asp Lys Thr His Thr Cys Pro
 20 25 30

EP 2 845 864 A2

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 35 40 45
 5 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 50 60
 10 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 65 70 75 80
 15 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 85 90 95
 20 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 100 105 110
 25 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 115 120 125
 30 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 130 135 140
 35 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 145 150 155 160
 40 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 165 170 175
 45 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 180 185 190
 50 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 195 200 205
 55 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 210 215 220
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 225 230 235 240
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 245 250
 <210> 119
 <211> 252
 <212> PRT
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EP 2 845 864 A2

<223> TALL-1 inhibitory peptibodies

<400> 119

5 Met Phe His Asp Cys Lys Tyr Asp Leu Leu Thr Arg Gln Met Val Cys
1 5 10 15

10 His Gly Leu Gly Gly Gly Gly Gly Val Asp Lys Thr His Thr Cys Pro
20 25 30

15 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
35 40 45

20 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
50 55 60

25 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
65 70 75 80

30 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
85 90 95

35 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
100 105 110

40 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
115 120 125

45 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
130 135 140

50 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
145 150 155 160

55 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
165 170 175

60 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
180 185 190

65 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
195 200 205

70 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
210 215 220

75 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
225 230 235 240

EP 2 845 864 A2

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 245 250

5 <210> 120
 <211> 252
 <212> PRT
 <213> Artificial Sequence

10 <220>
 <223> TALL-1 inhibitory peptibodies
 <400> 120

15 Met Arg Asn His Cys Phe Trp Asp His Leu Leu Lys Gln Asp Ile Cys
 1 5 10 15

20 Pro Ser Pro Gly Gly Gly Gly Gly Val Asp Lys Thr His Thr Cys Pro
 20 25 30

25 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 35 40 45

30 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 50 55 60

35 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 65 70 75 80

40 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 85 90 95

45 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 100 105 110

50 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 115 120 125

55 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 130 135 140

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 145 150 155 160

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 165 170 175

60 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 180 185 190

EP 2 845 864 A2

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 195 200 205
 5 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 210 215 220
 10 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 225 230 235 240
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 245 250
 15 <210> 121
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 <212> PRT
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 20 <220>
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 <400> 121
 25 Met Ala Asn Gln Cys Trp Trp Asp Ser Leu Thr Lys Lys Asn Val Cys
 1 5 10 15
 30 Glu Phe Phe Gly Gly Gly Gly Gly Val Asp Lys Thr His Thr Cys Pro
 20 25 30
 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 35 35 40 45
 40 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 50 55 60
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 65 70 75 80
 45 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 85 90 95
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 100 105 110
 50 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 115 120 125
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 130 135 140
 55 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg

EP 2 845 864 A2

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 115 120 125

5 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 130 135 140

10 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 145 150 155 160

15 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 165 170 175

20 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 180 185 190

25 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 195 200 205

30 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 210 215 220

35 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 225 230 235 240

40 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 245 250

45 <210> 123
 <211> 293
 <212> PRT
 <213> Artificial Sequence

50 <220>
 <223> TALL-1 inhibitory peptibodies

55 <400> 123

Met Leu Pro Gly Cys Lys Trp Asp Leu Leu Ile Lys Gln Trp Val Cys
 1 5 10 15

Asp Pro Leu Gly Ser Gly Ser Ala Thr Gly Gly Ser Gly Ser Thr Ala
 20 25 30

Ser Ser Gly Ser Gly Ser Ala Thr His Met Leu Pro Gly Cys Lys Trp
 35 40 45

Asp Leu Leu Ile Lys Gln Trp Val Cys Asp Pro Leu Gly Gly Gly Gly
 50 55 60

EP 2 845 864 A2

Gly Val Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
 65 70 75 80
 5 Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 85 90 95
 10 Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 100 105 110
 Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 115 120 125
 15 Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
 130 135 140
 20 Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 145 150 155 160
 Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
 165 170 175
 25 Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 180 185 190
 30 Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
 195 200 205
 35 Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 210 215 220
 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 225 230 235 240
 40 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 245 250 255
 45 Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 260 265 270
 50 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 275 280 285
 Leu Ser Pro Gly Lys
 290
 55 <210> 124
 <211> 293

EP 2 845 864 A2

<212> PRT
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<220>
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<400> 124

5
 10
 15
 20
 25
 30
 35
 40
 45
 50
 55

Met Phe His Asp Cys Lys Trp Asp Leu Leu Thr Lys Gln Trp Val Cys
 1 5 10 15

His Gly Leu Gly Ser Gly Ser Ala Thr Gly Gly Ser Gly Ser Thr Ala
 20 25 30

Ser Ser Gly Ser Gly Ser Ala Thr His Met Phe His Asp Cys Lys Trp
 35 40 45

Asp Leu Leu Thr Lys Gln Trp Val Cys His Gly Leu Gly Gly Gly Gly
 50 55 60

Gly Val Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
 65 70 75 80

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 85 90 95

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 100 105 110

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 115 120 125

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
 130 135 140

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 145 150 155 160

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
 165 170 175

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 180 185 190

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
 195 200 205

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 210 215 220

EP 2 845 864 A2

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 225 230 235 240

5 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 245 250 255

10 Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 260 265 270

15 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 275 280 285

Leu Ser Pro Gly Lys
 290

20 <210> 125
 <211> 14
 <212> PRT
 <213> Artificial Sequence

25 <220>
 <223> Consensus Sequence

30 <220>
 <221> misc_feature
 <222> (1, 2 and)..(3)
 <223> X at (Pos 1, 2, 3) are absent or are amino acid residues (with
 one of X1, X2, and X3 preferred to be C when one of
 X12, X13,
 and X14 is C);

35 <220>
 <221> misc_feature
 <222> (7)..(7)
 <223> X at (Pos 7) is an amino acid residue (L preferred);

40 <220>
 <221> misc_feature
 <222> (9)..(9)
 <223> X at (Pos 9) is T or I (T preferred);

45 <220>
 <221> misc_feature
 <222> (12)..(12)
 <223> X at (Pos 12) is C, a neutral hydrophobic residue, or a basic
 residue (W, C, or R

50 preferred);

55 <220>
 <221> misc_feature
 <222> (13)..(13)
 <223> X at (Pos 13) is C, a neutral hydrophobic residue or is absent (V
 preferred);

<220>

EP 2 845 864 A2

<221> misc_feature
<222> (14)..(14)
<223> X at (Pos 14) is any amino acid residue or is absent.

5

<400> 125

Xaa Xaa Xaa Lys Trp Asp Xaa Leu Xaa Lys Gln Xaa Xaa Xaa
1 5 10

10

<210> 126
<211> 18
<212> PRT
<213> Artificial Sequence

15

<220>
<223> Preferred TALL-1 modulating domains

<400> 126

20

Tyr Lys Gly Arg Gln Met Trp Asp Ile Leu Thr Arg Ser Trp Val Val
1 5 10 15

Ser Leu

25

<210> 127
<211> 18
<212> PRT
<213> Artificial Sequence

30

<220>
<223> Preferred TALL-1 modulating domains

<400> 127

35

Gln Asp Val Gly Leu Trp Trp Asp Ile Leu Thr Arg Ala Trp Met Pro
1 5 10 15

40

Asn Ile

<210> 128
<211> 18
<212> PRT
<213> Artificial Sequence

45

<220>
<223> Preferred TALL-1 modulating domains

50

<400> 128

Gln Asn Ala Gln Arg Val Trp Asp Leu Leu Ile Arg Thr Trp Val Tyr
1 5 10 15

55

Pro Gln

EP 2 845 864 A2

<210> 129
<211> 18
<212> PRT
<213> Artificial Sequence

5

<220>
<223> Preferred TALL-1 modulating domains

<400> 129

10

Gly Trp Asn Glu Ala Trp Trp Asp Glu Leu Thr Lys Ile Trp Val Leu
1 5 10 15

Glu Gln

15

<210> 130
<211> 18
<212> PRT
<213> Artificial Sequence

20

<220>
<223> Preferred TALL-1 modulating domains

<400> 130

25

Arg Ile Thr Cys Asp Thr Trp Asp Ser Leu Ile Lys Lys Cys Val Pro
1 5 10 15

Gln Ser

30

<210> 131
<211> 18
<212> PRT
<213> Artificial Sequence

35

<220>
<223> Preferred TALL-1 modulating domains

<400> 131

40

Gly Ala Ile Met Gln Phe Trp Asp Ser Leu Thr Lys Thr Trp Leu Arg
1 5 10 15

45

Gln Ser

<210> 132
<211> 18
<212> PRT
<213> Artificial Sequence

50

<220>
<223> Preferred TALL-1 modulating domains

55

EP 2 845 864 A2

<400> 132

Trp Leu His Ser Gly Trp Trp Asp Pro Leu Thr Lys His Trp Leu Gln
1 5 10 15

5

Lys Val

10

<210> 133
<211> 18
<212> PRT
<213> Artificial Sequence

15

<220>
<223> Preferred TALL-1 modulating domains

<400> 133

20

Ser Glu Trp Phe Phe Trp Phe Asp Pro Leu Thr Arg Ala Gln Leu Lys
1 5 10 15

Phe Arg

25

<210> 134
<211> 18
<212> PRT
<213> Artificial Sequence

30

<220>
<223> Preferred TALL-1 modulating domains

<400> 134

35

Gly Val Trp Phe Trp Trp Phe Asp Pro Leu Thr Lys Gln Trp Thr Gln
1 5 10 15

Ala Gly

40

<210> 135
<211> 18
<212> PRT
<213> Artificial Sequence

45

<220>
<223> Preferred TALL-1 modulating domains

<400> 135

50

Met Gln Cys Lys Gly Tyr Tyr Asp Ile Leu Thr Lys Trp Cys Val Thr
1 5 10 15

55

Asn Gly

EP 2 845 864 A2

<210> 136
<211> 18
<212> PRT
<213> Artificial Sequence

5

<220>
<223> Preferred TALL-1 modulating domains

<400> 136

10

Leu Trp Ser Lys Glu Val Trp Asp Ile Leu Thr Lys Ser Trp Val Ser
1 5 10 15

Gln Ala

15

<210> 137
<211> 18
<212> PRT
<213> Artificial Sequence

20

<220>
<223> Preferred TALL-1 modulating domains

<400> 137

25

Lys Ala Ala Gly Trp Trp Phe Asp Trp Leu Thr Lys Val Trp Val Pro
1 5 10 15

30

Ala Pro

<210> 138
<211> 18
<212> PRT
<213> Artificial Sequence

35

<220>
<223> Preferred TALL-1 modulating domains

<400> 138

40

Ala Tyr Gln Thr Trp Phe Trp Asp Ser Leu Thr Arg Leu Trp Leu Ser
1 5 10 15

45

Thr Thr

<210> 139
<211> 18
<212> PRT
<213> Artificial Sequence

50

<220>
<223> Preferred TALL-1 modulating domains

55

EP 2 845 864 A2

<400> 139

Ser Gly Gln His Phe Trp Trp Asp Leu Leu Thr Arg Ser Trp Thr Pro
1 5 10 15

5

Ser Thr

10

<210> 140
<211> 18
<212> PRT
<213> Artificial Sequence

15

<220>
<223> Preferred TALL-1 modulating domains

<400> 140

20

Leu Gly Val Gly Gln Lys Trp Asp Pro Leu Thr Lys Gln Trp Val Ser
1 5 10 15

Arg Gly

25

<210> 141
<211> 18
<212> PRT
<213> Artificial Sequence

30

<220>
<223> Preferred TALL-1 modulating domains

<400> 141

35

Val Gly Lys Met Cys Gln Trp Asp Pro Leu Ile Lys Arg Thr Val Cys
1 5 10 15

Val Gly

40

<210> 142
<211> 18
<212> PRT
<213> Artificial Sequence

45

<220>
<223> Preferred TALL-1 modulating domains

50

<400> 142

Cys Arg Gln Gly Ala Lys Phe Asp Leu Leu Thr Lys Gln Cys Leu Leu
1 5 10 15

55

Gly Arg

EP 2 845 864 A2

<210> 143
<211> 18
<212> PRT
<213> Artificial Sequence

5

<220>
<223> Preferred TALL-1 modulating domains

<400> 143

10

Gly Gln Ala Ile Arg His Trp Asp Val Leu Thr Lys Gln Trp Val Asp
1 5 10 15

Ser Gln

15

<210> 144
<211> 18
<212> PRT
<213> Artificial Sequence

20

<220>
<223> Preferred TALL-1 modulating domains

<400> 144

25

Arg Gly Pro Cys Gly Ser Trp Asp Leu Leu Thr Lys His Cys Leu Asp
1 5 10 15

Ser Gln

30

<210> 145
<211> 18
<212> PRT
<213> Artificial Sequence

35

<220>
<223> Preferred TALL-1 modulating domains

<400> 145

40

Trp Gln Trp Lys Gln Gln Trp Asp Leu Leu Thr Lys Gln Met Val Trp
1 5 10 15

45

Val Gly

<210> 146
<211> 18
<212> PRT
<213> Artificial Sequence

50

<220>
<223> Preferred TALL-1 modulating domains

55

EP 2 845 864 A2

<400> 146

Pro Ile Thr Ile Cys Arg Lys Asp Leu Leu Thr Lys Gln Val Val Cys
 1 5 10 15

5

Leu Asp

10

<210> 147
 <211> 18
 <212> PRT
 <213> Artificial Sequence

15

<220>
 <223> Preferred TALL-1 modulating domains

<400> 147

20

Lys Thr Cys Asn Gly Lys Trp Asp Leu Leu Thr Lys Gln Cys Leu Gln
 1 5 10 15

Gln Ala

25

<210> 148
 <211> 18
 <212> PRT
 <213> Artificial Sequence

30

<220>
 <223> Preferred TALL-1 modulating domains

<400> 148

35

Lys Cys Leu Lys Gly Lys Trp Asp Leu Leu Thr Lys Gln Cys Val Thr
 1 5 10 15

40

Glu Val

<210> 149
 <211> 18
 <212> PRT
 <213> Artificial Sequence

45

<220>
 <223> Preferred TALL-1 modulating domains

50

<400> 149

Arg Cys Trp Asn Gly Lys Trp Asp Leu Leu Thr Lys Gln Cys Ile His
 1 5 10 15

55

Pro Trp

EP 2 845 864 A2

<210> 150
<211> 18
<212> PRT
<213> Artificial Sequence

5

<220>
<223> Preferred TALL-1 modulating domains

<400> 150

10

Asn Arg Asp Met Arg Lys Trp Asp Pro Leu Ile Lys Gln Trp Ile Val
1 5 10 15

Arg Pro

15

<210> 151
<211> 18
<212> PRT
<213> Artificial Sequence

20

<220>
<223> Preferred TALL-1 modulating domains

<400> 151

25

Gln Ala Ala Ala Ala Thr Trp Asp Leu Leu Thr Lys Gln Trp Leu Val
1 5 10 15

30

Pro Pro

<210> 152
<211> 18
<212> PRT
<213> Artificial Sequence

35

<220>
<223> Preferred TALL-1 modulating domains

<400> 152

40

Pro Glu Gly Gly Pro Lys Trp Asp Pro Leu Thr Lys Gln Phe Leu Pro
1 5 10 15

45

Pro Val

<210> 153
<211> 18
<212> PRT
<213> Artificial Sequence

50

<220>
<223> Preferred TALL-1 modulating domains

55

EP 2 845 864 A2

<400> 153

Gln Thr Pro Gln Lys Lys Trp Asp Leu Leu Thr Lys Gln Trp Phe Thr
1 5 10 15

5

Arg Asn

10

<210> 154
<211> 18
<212> PRT
<213> Artificial Sequence

15

<220>
<223> Preferred TALL-1 modulating domains

<400> 154

20

Ile Gly Ser Pro Cys Lys Trp Asp Leu Leu Thr Lys Gln Met Ile Cys
1 5 10 15

Gln Thr

25

<210> 155
<211> 18
<212> PRT
<213> Artificial Sequence

30

<220>
<223> Preferred TALL-1 modulating domains

<400> 155

35

Cys Thr Ala Ala Gly Lys Trp Asp Leu Leu Thr Lys Gln Cys Ile Gln
1 5 10 15

Glu Lys

40

<210> 156
<211> 18
<212> PRT
<213> Artificial Sequence

45

<220>
<223> Preferred TALL-1 modulating domains

50

<400> 156

Val Ser Gln Cys Met Lys Trp Asp Leu Leu Thr Lys Gln Cys Leu Gln
1 5 10 15

55

Gly Trp

EP 2 845 864 A2

<210> 157
<211> 18
<212> PRT
<213> Artificial Sequence

5

<220>
<223> Preferred TALL-1 modulating domains

<400> 157

10

Val Trp Gly Thr Trp Lys Trp Asp Leu Leu Thr Lys Gln Tyr Leu Pro
1 5 10 15

Pro Gln

15

<210> 158
<211> 18
<212> PRT
<213> Artificial Sequence

20

<220>
<223> Preferred TALL-1 modulating domains

<400> 158

25

Gly Trp Trp Glu Met Lys Trp Asp Leu Leu Thr Lys Gln Trp Tyr Arg
1 5 10 15

Pro Gln

30

<210> 159
<211> 18
<212> PRT
<213> Artificial Sequence

35

<220>
<223> Preferred TALL-1 modulating domains

<400> 159

40

Thr Ala Gln Val Ser Lys Trp Asp Leu Leu Thr Lys Gln Trp Leu Pro
1 5 10 15

45

Leu Ala

<210> 160
<211> 18
<212> PRT
<213> Artificial Sequence

50

<220>
<223> Preferred TALL-1 modulating domains

55

EP 2 845 864 A2

<400> 160

Gln Leu Trp Gly Thr Lys Trp Asp Leu Leu Thr Lys Gln Tyr Ile Gln
1 5 10 15

5

Ile Met

10

<210> 161
<211> 18
<212> PRT
<213> Artificial Sequence

15

<220>
<223> Preferred TALL-1 modulating domains

<400> 161

20

Trp Ala Thr Ser Gln Lys Trp Asp Leu Leu Thr Lys Gln Trp Val Gln
1 5 10 15

Asn Met

25

<210> 162
<211> 18
<212> PRT
<213> Artificial Sequence

30

<220>
<223> Preferred TALL-1 modulating domains

<400> 162

35

Gln Arg Gln Cys Ala Lys Trp Asp Leu Leu Thr Lys Gln Cys Val Leu
1 5 10 15

40

Phe Tyr

45

<210> 163
<211> 18
<212> PRT
<213> Artificial Sequence

50

<220>
<223> Preferred TALL-1 modulating domains

<400> 163

55

Lys Thr Thr Asp Cys Lys Trp Asp Leu Leu Thr Lys Gln Arg Ile Cys
1 5 10 15

Gln Val

EP 2 845 864 A2

<210> 164
<211> 18
<212> PRT
<213> Artificial Sequence

5

<220>
<223> Preferred TALL-1 modulating domains

<400> 164

10

Leu Leu Cys Gln Gly Lys Trp Asp Leu Leu Thr Lys Gln Cys Leu Lys
1 5 10 15

Leu Arg

15

<210> 165
<211> 18
<212> PRT
<213> Artificial Sequence

20

<220>
<223> Preferred TALL-1 modulating domains

<400> 165

25

Leu Met Trp Phe Trp Lys Trp Asp Leu Leu Thr Lys Gln Leu Val Pro
1 5 10 15

30

Thr Phe

<210> 166
<211> 18
<212> PRT
<213> Artificial Sequence

35

<220>
<223> Preferred TALL-1 modulating domains

<400> 166

40

Gln Thr Trp Ala Trp Lys Trp Asp Leu Leu Thr Lys Gln Trp Ile Gly
1 5 10 15

45

Pro Met

<210> 167
<211> 18
<212> PRT
<213> Artificial Sequence

50

<220>
<223> Preferred TALL-1 modulating domains

55

EP 2 845 864 A2

<400> 167

Asn Lys Glu Leu Leu Lys Trp Asp Leu Leu Thr Lys Gln Cys Arg Gly
1 5 10 15

5

Arg Ser

10

<210> 168
<211> 18
<212> PRT
<213> Artificial Sequence

15

<220>
<223> Preferred TALL-1 modulating domains

<400> 168

20

Gly Gln Lys Asp Leu Lys Trp Asp Leu Leu Thr Lys Gln Tyr Val Arg
1 5 10 15

Gln Ser

25

<210> 169
<211> 18
<212> PRT
<213> Artificial Sequence

30

<220>
<223> Preferred TALL-1 modulating domains

<400> 169

35

Pro Lys Pro Cys Gln Lys Trp Asp Leu Leu Thr Lys Gln Cys Leu Gly
1 5 10 15

Ser Val

40

<210> 170
<211> 18
<212> PRT
<213> Artificial Sequence

45

<220>
<223> Preferred TALL-1 modulating domains

50

<400> 170

Gly Gln Ile Gly Trp Lys Trp Asp Leu Leu Thr Lys Gln Trp Ile Gln
1 5 10 15

55

Thr Arg

EP 2 845 864 A2

<210> 171
<211> 18
<212> PRT
<213> Artificial Sequence

5

<220>
<223> Preferred TALL-1 modulating domains

<400> 171

10

Val Trp Leu Asp Trp Lys Trp Asp Leu Leu Thr Lys Gln Trp Ile His
1 5 10 15

Pro Gln

15

<210> 172
<211> 18
<212> PRT
<213> Artificial Sequence

20

<220>
<223> Preferred TALL-1 modulating domains

<400> 172

25

Gln Glu Trp Glu Tyr Lys Trp Asp Leu Leu Thr Lys Gln Trp Gly Trp
1 5 10 15

30

Leu Arg

<210> 173
<211> 18
<212> PRT
<213> Artificial Sequence

35

<220>
<223> Preferred TALL-1 modulating domains

<400> 173

40

His Trp Asp Ser Trp Lys Trp Asp Leu Leu Thr Lys Gln Trp Val Val
1 5 10 15

45

Gln Ala

<210> 174
<211> 18
<212> PRT
<213> Artificial Sequence

50

<220>
<223> Preferred TALL-1 modulating domains

55

EP 2 845 864 A2

<400> 174

Thr Arg Pro Leu Gln Lys Trp Asp Leu Leu Thr Lys Gln Trp Leu Arg
1 5 10 15

5

Val Gly

10

<210> 175
<211> 18
<212> PRT
<213> Artificial Sequence

15

<220>
<223> Preferred TALL-1 modulating domains

<400> 175

20

Ser Asp Gln Trp Gln Lys Trp Asp Leu Leu Thr Lys Gln Trp Phe Trp
1 5 10 15

Asp Val

25

<210> 176
<211> 18
<212> PRT
<213> Artificial Sequence

30

<220>
<223> Preferred TALL-1 modulating domains

<400> 176

35

Gln Gln Thr Phe Met Lys Trp Asp Leu Leu Thr Lys Gln Trp Ile Arg
1 5 10 15

40

Arg His

45

<210> 177
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Preferred TALL-1 modulating domains

50

<400> 177

Gln Gly Glu Cys Arg Lys Trp Asp Leu Leu Thr Lys Gln Cys Phe Pro
1 5 10 15

55

Gly Gln

EP 2 845 864 A2

<210> 178
<211> 18
<212> PRT
<213> Artificial Sequence

5

<220>
<223> Preferred TALL-1 modulating domains

<400> 178

10

Gly Gln Met Gly Trp Arg Trp Asp Pro Leu Ile Lys Met Cys Leu Gly
1 5 10 15

Pro Ser

15

<210> 179
<211> 18
<212> PRT
<213> Artificial Sequence

20

<220>
<223> Preferred TALL-1 modulating domains

<400> 179

25

Gln Leu Asp Gly Cys Lys Trp Asp Leu Leu Thr Lys Gln Lys Val Cys
1 5 10 15

Ile Pro

30

<210> 180
<211> 18
<212> PRT
<213> Artificial Sequence

35

<220>
<223> Preferred TALL-1 modulating domains

<400> 180

40

His Gly Tyr Trp Gln Lys Trp Asp Leu Leu Thr Lys Gln Trp Val Ser
1 5 10 15

45

Ser Glu

<210> 181
<211> 18
<212> PRT
<213> Artificial Sequence

50

<220>
<223> Preferred TALL-1 modulating domains

55

EP 2 845 864 A2

<400> 181

His Gln Gly Gln Cys Gly Trp Asp Leu Leu Thr Arg Ile Tyr Leu Pro
1 5 10 15

5

Cys His

10

<210> 182
<211> 18
<212> PRT
<213> Artificial Sequence

15

<220>
<223> Preferred TALL-1 modulating domains

<400> 182

20

Leu His Lys Ala Cys Lys Trp Asp Leu Leu Thr Lys Gln Cys Trp Pro
1 5 10 15

Met Gln

25

<210> 183
<211> 18
<212> PRT
<213> Artificial Sequence

30

<220>
<223> Preferred TALL-1 modulating domains

<400> 183

35

Gly Pro Pro Gly Ser Val Trp Asp Leu Leu Thr Lys Ile Trp Ile Gln
1 5 10 15

40

Thr Gly

<210> 184
<211> 18
<212> PRT
<213> Artificial Sequence

45

<220>
<223> Preferred TALL-1 modulating domains

50

<400> 184

Ile Thr Gln Asp Trp Arg Phe Asp Thr Leu Thr Arg Leu Trp Leu Pro
1 5 10 15

55

Leu Arg

EP 2 845 864 A2

<400> 188

Trp Gln Gln Trp Ser Trp Lys Trp Asp Leu Leu Thr Arg Gln Tyr Ile
 1 5 10 15

5

Ser Ser Ser

10

<210> 189
 <211> 882
 <212> DNA
 <213> Artificial Sequence

15

<220>
 <223> TALL-1 12-3 tandem dimer

<400> 189
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 20 tccggttctg ctactggtgg ttccggctcc accgcaagct ctggttcagg cagtgcgact 120
 catatgctgc cgggttgtaa atgggacctg ctgatcaaac agtggggttg tgaccgctg 180
 ggtggaggcg gtggggtcga caaaactcac acatgtccac cttgtccagc tccggaactc 240
 25 ctggggggac cgtcagtctt cctcttcccc caaaaccca aggacaccct catgatctcc 300
 cggacccttg aggtcacatg cgtgggtggg gacgtgagcc acgaagacc tgaggtcaag 360
 30 ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 420
 cagtacaaca gcacgtaccg tgtggtcagc gtctctaccg tcctgcacca ggactggctg 480
 aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 540
 35 accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc 600
 cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tgggtcaaagg cttctatccc 660
 agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccag 720
 40 cctcccgtgc tggactccga cggtctcttc ttctctaca gcaagctcac cgtggacaag 780
 agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcattgggc tctgcacaac 840
 cactacacgc agaagagcct ctccctgtct ccgggtaaat aa 882

45

<210> 190
 <211> 23
 <212> PRT
 <213> Artificial Sequence

50

<220>
 <223> Preferred linker

<400> 190

55

Gly Ser Gly Ser Ala Thr Gly Gly Ser Gly Ser Thr Ala Ser Ser Gly
 1 5 10 15

EP 2 845 864 A2

Ser Gly Ser Ala Thr Gly Met
20

5 <210> 191
<211> 23
<212> PRT
<213> Artificial Sequence

10 <220>
<223> Preferred linker

<400> 191

15 Gly Ser Gly Ser Ala Thr Gly Gly Ser Gly Ser Thr Ala Ser Ser Gly
1 5 10 15

Ser Gly Ser Ala Thr Gly Ser
20

20 <210> 192
<211> 46
<212> PRT
<213> Artificial Sequence

25 <220>
<223> Preferred linker

<400> 192

30 Gly Ser Gly Ser Ala Thr Gly Gly Ser Gly Ser Thr Ala Ser Ser Gly
1 5 10 15

35 Ser Gly Ser Ala Thr His Met Gly Ser Gly Ser Ala Thr Gly Gly Ser
20 25 30

Gly Ser Thr Ala Ser Ser Gly Ser Gly Ser Ala Thr His Met
35 40 45

40 <210> 193
<211> 23
<212> PRT
<213> Artificial Sequence

45 <220>
<223> Preferred linker

50 <220>
<221> misc_feature
<222> (22)..(23)
<223> X at (Pos 22) is independently a basic or hydrophobic residue and
X at (Pos 23) is independently a hydrophobic residue.

<400> 193

55 Gly Ser Gly Ser Ala Thr Gly Gly Ser Gly Ser Thr Ala Ser Ser Gly

EP 2 845 864 A2

Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala Phe Cys Arg
 1 5 10 15

5 Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu
 20 25 30

10 Arg Asp Cys Ile Ser Cys Ala Ser Ile
 35 40

15 <210> 197
 <211> 42
 <212> PRT
 <213> Human

<400> 197

20 Phe Val Ser Pro Ser Gln Glu Ile Arg Gly Arg Phe Arg Arg Met Leu
 1 5 10 15

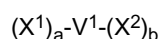
25 Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu Leu
 20 25 30

30 His Ala Cys Ile Pro Cys Gln Leu Arg Cys
 35 40

Claims

1. A TALL-1 binding composition comprising:

- 35 a) the amino acid sequence of SEQ ID NO: 12;
 b) the amino acid sequence of SEQ ID NO:44; or
 c) the structure:



40 wherein
 V¹ is a vehicle (preferably an Fc domain);
 X¹ and X² each independently comprise the structure -(L¹)-P¹-(L²)-P²;
 P¹ and P² are each independently sequences of TALL-1 modulating domains, such as those of Formulae I(a)
 45 through I(i);
 L¹ and L² are each independently linkers;
 a and b are each independently 0 or 1, provided that at least one of a and b is 1; and optionally P¹-(L¹) comprises
 the amino acid sequence of SEQ ID NO: 12 or the amino acid sequence of SEQ ID NO: 44.

- 50 2. The TALL-1 binding composition of claim 1, wherein the composition comprises SEQ ID NO: 193.
 3. The TALL-1 binding composition of claim 2, wherein the composition comprises SEQ ID NO:59.
 4. The TALL-1 binding composition of claim 1, wherein the composition comprises SEQ ID NO: 115.
 55 5. A TALL-1 binding composition of claim 1, wherein
 P¹ comprises the amino acid sequence of SEQ ID NO:33;
 P² comprises the amino acid sequence of SEQ ID NO:125, wherein X¹ is Pro or Met, X² is Gly, X³ is Cys, X⁷ is Leu,

EP 2 845 864 A2

X⁹ is Ile, X¹² is Trp, X¹³ is Val, and X¹⁴ is Cys;
L¹ comprises the amino acid sequence Gly-Gly-Gly-Gly-Gly-Val;
L² comprises the amino acid sequence of SEQ ID NO:59; and
V¹ is an Fc domain, preferably an IgG Fc domain;
wherein said composition optionally comprises an N-terminal Met residue.

5

6. The TALL-1 binding composition of claim 4, wherein P¹-(L¹) comprises the amino acid sequence of SEQ ID NO: 12 or the amino acid sequence of SEQ ID NO:44.

10

7. The TALL-1 binding composition of any of claims 1-6 for use in therapy.

8. The TALL-1 binding composition of any of claims 1-6 for use in treating a B-cell mediated autoimmune disease.

9. The TALL-1 binding composition for the use of claim 8, wherein said B-cell mediated autoimmune disease is lupus.

15

10. The TALL-1 binding composition of any of claims 1-6 for use in treating a B-cell mediated cancer.

11. The TALL-1 binding composition for the use of claim 10, wherein said B-cell mediated cancer is B-cell lymphoma.

20

12. The use of a TALL-1 binding composition of any of claims 1-6 for the manufacture of a medicament for the treatment of a B-cell mediated autoimmune disease.

13. The use of the TALL-1 binding composition of claim 12, wherein said B-cell mediated autoimmune disease is lupus.

25

14. The use of a TALL-1 binding composition of any of claims 1-6 for the manufacture of a medicament for the treatment of a B-cell mediated cancer.

15. The use of the TALL-1 binding composition of claim 14, wherein said B-cell mediated cancer is B-cell lymphoma.

30

35

40

45

50

55

FIG. 1

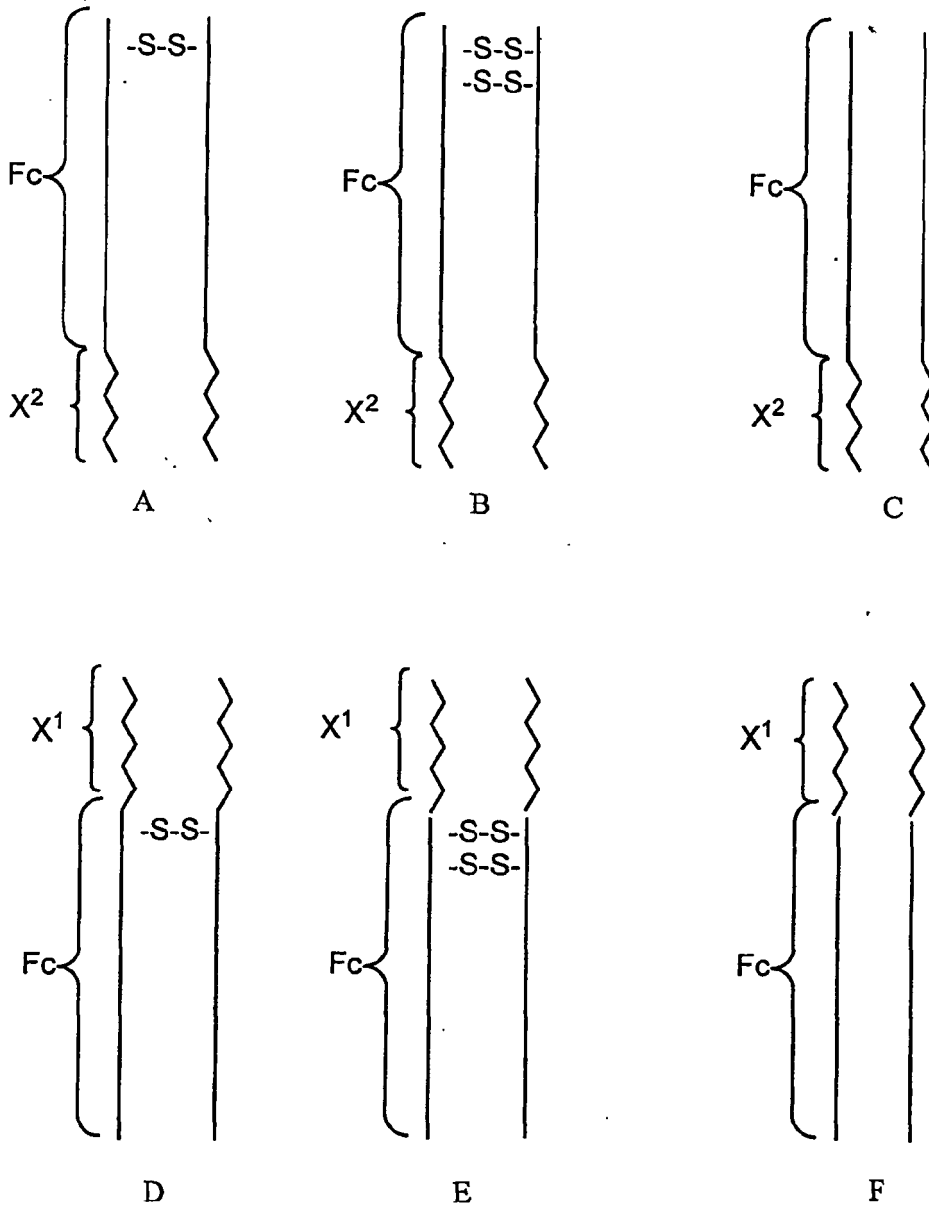


FIG. 2

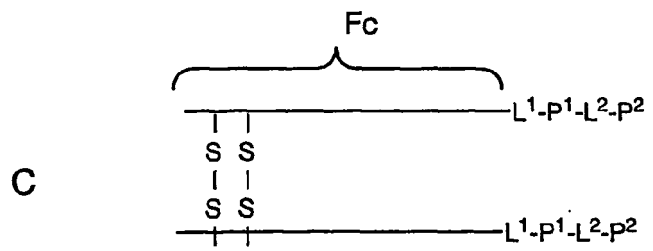
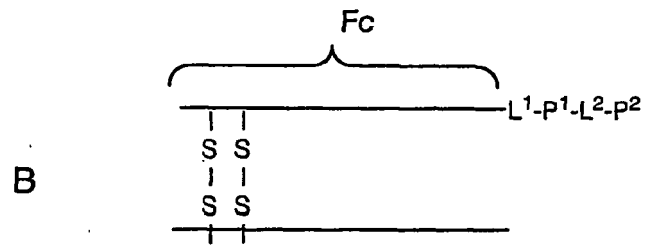
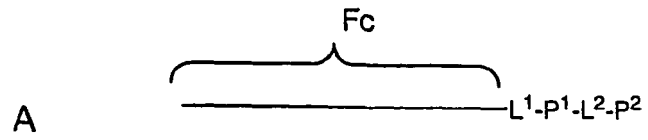


FIG. 3

```

    ATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCTGGGGGGACCGTCA
1  -----+-----+-----+-----+-----+-----+-----+-----+-----+ 60
    TACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGT
a   M D K T H T C P P C P A P E L L G G P S -
    GTCTTCCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC
61  -----+-----+-----+-----+-----+-----+-----+-----+ 120
    CAGAAGGAGAAGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGCCTGGGGACTCCAG
a   V F L F P P K P K D T L M I S R T P E V -
    ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
121 -----+-----+-----+-----+-----+-----+-----+-----+ 180
    TGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCAC
a   T C V V V D V S H E D P E V K F N W Y V -
    GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGGGAGGAGCAGTACAACAGCAGC
181 -----+-----+-----+-----+-----+-----+-----+-----+ 240
    CTGCCGCACCTCCACGTATTACGGTCTGTTCGGCGCCCTCCTCGTCATGTTGTCGTGC
a   D G V E V H N A K T K P R E E Q Y N S T -
    TACCGTGTGGTCAGCGTCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
241 -----+-----+-----+-----+-----+-----+-----+-----+ 300
    ATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCCTTCCTCATG
a   Y R V V S V L T V L H Q D W L N G K E Y -
    AAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGCC
301 -----+-----+-----+-----+-----+-----+-----+-----+ 360
    TTCACGTCCAGAGGTGTTTCGGGAGGGTCGGGGTAGCTCTTTGGTAGAGGTTTCGG
a   K C K V S N K A L P A P I E K T I S K A -
    AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCATCCCGGGATGAGCTGACC
361 -----+-----+-----+-----+-----+-----+-----+-----+ 420
    TTTCCCGTCGGGGCTCTGGGTGTCCACATGTGGGACGGGGTAGGGCCCTACTCGACTGG
a   K G Q P R E P Q V Y T L P P S R D E L T -
    AAGAACCAGGTGACCTGACCTGGTCAAAGGCTTCTATCCAGCGACATCGCCCGTG
421 -----+-----+-----+-----+-----+-----+-----+-----+ 480
    TTCTTGGTCCAGTCGGACTGGACGGACCAGTTCCGAAGATAGGGTCGCTGTAGCGGCAC
a   K N Q V S L T C L V K G F Y P S D I A V -
    GAGTGGGAGAGCAATGGGCAGCCGAGAACTACAAGACCACGCCTCCCGTGTGGAC
481 -----+-----+-----+-----+-----+-----+-----+-----+ 540
    CTCACCCTCTCGTTACCCGTCCGGCCTCTTGTGATGTTCTGGTGGGAGGGCAGCACCTG
a   E W E S N G Q P E N N Y K T T P P V L D -
    TCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
541 -----+-----+-----+-----+-----+-----+-----+-----+ 600
    AGGCTGCCGAGGAAGAAGGAGATGTCGTTCCGAGTGGCACCTGTCTCGTCCACCGTCGTC
a   S D G S F F L Y S K L T V D K S R W Q Q -
    GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG
601 -----+-----+-----+-----+-----+-----+-----+-----+ 660
    CCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTGGTGTGATGTGCGTCTTC
a   G N V F S C S V M H E A L H N H Y T Q K -
    AGCCTCTCCCTGTCTCCGGGTAAA
661 -----+-----+-----+-----+-----+-----+-----+-----+ 684
    TCGGAGAGGGACAGAGGCCATTT
a   S L S L S P G K

```

FIG. 4A

1) AGP3-8-1-a

NdeI

|

TATGCCGGGTACTTGTTCCTCCCGTCCCGTGGGAATGCACTCACGCTGGTGGAGGCGGT

1 -----+-----+-----+-----+-----+-----+ 60

GGCCCATGAACAAAGGGCAAGGGCACCCCTTACGTGAGTGCGACCACCTCCGCCA

a M P G T C F P F P W E C T H A G G G G -

SalI

|

GGGG

61 ----- 69

CCCCAGCT

a G V D -

2) AGP3-8-2-a

NdeI

|

TATGTGGGGTGCTTGTGGCCGTCCCGTGGGAATGTTCAAAGAAGGTGGAGGCGGT

1 -----+-----+-----+-----+-----+-----+ 60

ACACCCACGAACAACCGGCAAGGGCACCCCTTACAAAGTTCTTCCACCTCCGCCA

a M W G A C W P F P W E C F K E G G G G -

SalI

|

GGGG

61 ----- 69

CCCCAGCT

a G V D -

FIG. 4B

3) AGP3-8-4-a

```

NdeI
|
TATGGTTCCGTTCTGTGACCTGCTGACTAAACACTGTTTCGAAGCTGGTGGAGGCGGT
1 -----+-----+-----+-----+-----+ 60
ACCAAGGCAAGACACTGGACGACTGATTTGTGACAAAGCTTCGACCACCTCCGCCA

a      M V P F C D L L T K H C F E A G G G G -
    
```

```

Sali
|
GGGG
61 ----- 69
CCCCAGCT

a      G V D -
    
```

4) AGP3-12-4-a

November 6, 2000 12:53 ..

```

NdeI
|
TATGGGTTCTCGTTGTAATAACAAATGGGACGTTCTGACTAAACAGTGTTCACCAC
1 -----+-----+-----+-----+-----+ 60
ACCAAGAGCAACATTTATGTTTACCCTGCAAGACTGATTTGTCACAAAGGTGGTG

a      M G S R C K Y K W D V L T K Q C F H H -
    
```

```

Sali
|
GGTGGAGGCGGTGGGG
61 -----+-----+ 81
CCACCTCCGCCACCCAGCT

a      G G G G G V D -
    
```

FIG. 4C

5) AGP3-12-3-a

NdeI

|

TATGCTGCCGGGTTGTAAATGGGACCTGCTGATCAAACAGTGGGTTTGTGACCCGCTG

1 -----+-----+-----+-----+-----+-----+ 60

ACGACGGCCCAACATTTACCCTGGACGACTAGTTTGTACCCAAACACTGGGCGAC

a M L P G C K W D L L I K Q W V C D P L -

SalI

|

GGTGGAGGCGGTGGGG

61 -----+-----+ 81

CCACCTCCGCCACCCAGCT

a G G G G G V D -

6) AGP3-12-5-a

NdeI

|

TATGTCTGCTGACTGTTACTTCGACATCCTGACTAAATCTGACGTTTGTACTTCTTCT

1 -----+-----+-----+-----+-----+ 60

ACAGACGACTGACAATGAAGCTGTAGGACTGATTTAGACTGCAAACATGAAGAAGA

a M S A D C Y F D I L T K S D V C T S S -

SalI

|

GGTGGAGGCGGTGGGG

61 -----+-----+ 81

CCACCTCCGCCACCCAGCT

a G G G G G V D -

FIG. 4D

7) AGP3-12-8-a

NdeI

|

TATGTCTGACGACTGTATGTACGACCAGCTGACTCGTATGTTTCATCTGTTCTAACCTG

1 -----+-----+-----+-----+-----+-----+ 60

ACAGACTGCTGACATACATGCTGGTCGACTGAGCATAACAAGTAGACAAGATTGGAC

a M S D D C M Y D Q L T R M F I C S N L -

SalI

|

GGTGGAGCGGTGGGG

61 -----+-----+ 81

CCACCTCCGCCACCCAGCT

a G G G G G V D -

8) AGP3-12-9-a

NdeI

|

TATGGACCTGAACGTAAATACGACGAACTGACTTACAAAGAATGGTGTCAAGTCAAC

1 -----+-----+-----+-----+-----+-----+ 60

ACCTGGACTTGACATTTATGCTGCTGACTGAATGTTTCTTACCACAGTCAAGTTG

a M D L N C K Y D E L T Y K E W C Q F N -

SalI

|

GGTGGAGCGGTGGGG

61 -----+-----+ 81

CCACCTCCGCCACCCAGCT

a G G G G G V D -

FIG. 4E

9) AGP3-12-10-a

NdeI

|

TATGTTCCACGACTGTAAATACGACCTGCTGACTCGTCAGATGGTTTGTACGGTCTG

1 -----+-----+-----+-----+-----+-----+-----+ 60

ACAAGGTGCTGACATTTATGCTGGACGACTGAGCAGTCTACCAAACAGTGCCAGAC

a M F H D C K Y D L L T R Q M V C H G L -

SalI

|

GGTGGAGGCGGTGGGG

61 -----+-----+-----+-----+-----+-----+ 81

CCACCTCCGCCACCCCAGCT -

a G G G G G V D -

10) AGP3-12-11-a

NdeI

|

TATGCGTAACCACTGTTTCTGGGACCACCTGCTGAAACAGGACATCTGTCCGTCTCCG

1 -----+-----+-----+-----+-----+-----+ 60

ACGCATTGGTGACAAAGACCCCTGGTGGACGACTTTGTCTGTAGACAGGCAGAGGC

a M R N H C F W D H L L K Q D I C P S P -

SalI

|

GGTGGAGGCGGTGGGG

61 -----+-----+-----+-----+-----+-----+ 81

CCACCTCCGCCACCCCAGCT

a G G G G G V D -

FIG. 4F

11) AGP3-12-14-a

```

      NdeI
      |
      TATGGCTAACCAGTGTGGTGGGACTCTCTGCTGAAAAAAAAACGTTTGTGAATCTTC
1  -----+-----+-----+-----+-----+-----+-----+ 60
      ACCGATTGGTCACAACCACCCTGAGAGACGACTTTTTTTTGCAAACACTTAAGAAG
a      M A N Q C W W D S L L K K N V C E F F -

```

```

      SalI
      |
      GGTGGAGGCGGTGGGG
61 -----+-----+-----+-----+-----+-----+ 81
      CCACCTCCGCCACCCCAGCT
a      G G G G G V D -

```

12) AGP3 Consensus

```

      NdeI
      |
      TATGTTCCACGACTGCAAATGGGACCTGCTGACCAAACAGTGGGTTTGCCACGGTCTG
1  -----+-----+-----+-----+-----+-----+-----+ 60
      gtATACAAGGTGCTGACGTTTACCCTGGACGACTGGTTTGTACCCAAACGGTGCCAGAC
a      M F H D C K W D L L T R Q W V C H G L -

```

```

      SalI
      |
      GGTGGAGGCGGTGGGG
61 -----+-----+-----+-----+-----+-----+ 81
      CCACCTCCGCCACCCCAGCT
a      G G G G G V D -

```


FIG. 5B

```

                                     -35
                                     -----
                                     ---- Promoter (PrepA) ----->
                                     |-- copB binding site --|
481 TTGAGAAAATCATCAAAGATGAACTGCAAAGACTGGATATACTAAAGTAAAGACTTTACT
-----+-----+-----+-----+-----+-----+-----+
c   AACTCTTTTAGTAGTTTCTACTTGACGTTTCTGACCTATATGATTCATTTCTGAAATGA 540
     E K I I K D E L Q R L D I L K *

                                     -10
                                     -----
541 TTGTGGCGTAGCATGCTAGATTACTGATCGTTTAAAGGAATTTGTGGCTGGCCACGCCGT
-----+-----+-----+-----+-----+-----+-----+
c   AACACCGCATCGTACGATCTAATGACTAGCAAATTCCTTAAAACACCGACCGGTGCGGCA 600
     |-- mRNA -->
     D
     B r
     m d
     n I
     I I
                                     |<-----
601 AAGGTGGCAAGGAACTGGTTCTGATGTGGATTTACAGGAGCCAGAAAAGCAAAAACCCCG
-----+-----+-----+-----+-----+-----+-----+
c   TTCCACCGTTCCTTGACCAAGACTACACCTAAATGTCCTCGGTCTTTTCGTTTTTGGGGC 660
     M W I Y R S Q K S K N P D -
     --- copT (ORF) --->

<----- copA RNAI -----
661 ATAATCTTCTCAACTTTTGGGAGTACGAAAAGATTACCGGGGCCACTTAAACCGTATA
-----+-----+-----+-----+-----+-----+-----+
c   TATTAGAAGAAGTTGAAAACGCTCATGCTTTTCTAATGGCCCCGGGTGAATTTGGCATAT 720
     N L L Q L L R V R K D Y R G P L K P Y S -

                                     <----- Promoter (RNAI) -----
                                     -10           -35
                                     -----
<-----|-----
721 GCCAACAATTCAGCTATGCGGGGAGTATAGTTATATGCCCGGAAAAGTTCAAGACTTCTT
-----+-----+-----+-----+-----+-----+-----+
c   CGGTTGTTAAGTCGATACGCCCTCATATCAATATACGGGCTTTTCAAGTTCTGAAGAA 780
     Q Q F S Y A G S I V I C P E K F K T S F -

781 TCTGTGCTCGCTCCTTCTGCGCATTGTAAGTGCAGGATGGTGTGACTGATCTTACCAAAA
-----+-----+-----+-----+-----+-----+-----+
c   AGACACGAGCGAGGAAGACGCGTAACATTACGTCCTACCACACTGACTAGAAGTGGTTT 840
     C A R S F C A L *           M T D L H Q T -
                                     --- repA1 protein --->
                                     D
                                     r
                                     a
                                     I
                                     I
                                     I
841 CGTATTACCGCCAGGTAAGAACC CGAATCCGGTGTTTACACCCCGTGAAGGTGCAGGAA
-----+-----+-----+-----+-----+-----+-----+
c   GCATAATGGCGGTCCATTTCTPGGGCTTAGGCCACAAATGTGGGGCACTTCCACGTCCTT
     Y Y R Q V K N P N P V F T P R E G A G T -

901 CGCTGAAGTTCTGCGAAAACTGATGGAAAAGCGGTGGGCTTCACTTCCCCTTTTGATT
-----+-----+-----+-----+-----+-----+-----+
c   GCGACTTCAAGACGCTTTTTGACTACCTTTTCCGCCACCCGAAGTGAAGGGCAAACTAA 960
     L K F C E K L M E K A V G F T S R F D F -

```

FIG. 5C

B
S
E
B
I

961 TCGCCATTCATGTGGCGCACGCCCGTTCCGCGTGATCTGCGTCGCCGTATGCCACCAGTGC 1020
 -----+-----+-----+-----+-----+-----+-----+-----+
 AGCGGTAAGTACACCGCGTGC GGGCAAGCGCACTAGACGCAGCGGCATACGGTGGTCACG
 c A I H V A H A R S R D L R R R M P P V L -

1021 TCGCTCGTCGGGCTATTGATGCGCTCTTGCAGGGGCTGTGTTCCACTATGACCCGCTGG 1080
 -----+-----+-----+-----+-----+-----+-----+-----+
 ACGCAGCAGCCCGATAACTACGCGAGAACGTC CCCCACACAAAGGTGATACTGGGCGACC
 c R R R A I D A L L Q G L C F H Y D P L A -

1081 CCAACCGCGTCCAGTGTCCATCACCACGCTGGCCATTGAGTCCGGACTGGCGACGGAGT 1140
 -----+-----+-----+-----+-----+-----+-----+-----+
 GGTGGCGCAGGTCACGAGGTAGTGGTGC GACCGGTAACACGCCTGACCGCTGCCTCA
 c N R V Q C S I T T L A I E C G L A T E S -

A
c
e
I
I
I

1141 CTGCTGCCGAAAACCTCTCCATCACCCGTGCCACCCGTGCCCTGACGTTCCCTGTCAGAGC 1200
 -----+-----+-----+-----+-----+-----+-----+-----+
 GACGACGGCCTTTTGAGAGGTAGTGGGCACGGTGGGCACGGGACTGCAAGGACAGTCTCG
 c A A G K L S I T R A T R A L T F L S E L -

1201 TGGGACTGATTACCTACCAGACGGAATATGACCCGCTTATCGGGTGCTACATTCGGACCG 1260
 -----+-----+-----+-----+-----+-----+-----+-----+
 ACCCTGACTAATGGATGGTCTGCCTTATACTGGGCGAATAGCCACGATGTAAGGCTGGC
 c G L I T Y Q T E Y D P L I G C Y I P T D -

1261 ATATCACGTTACATCTGCACTGTTTGCCTGCCCTCGATGTATCAGAGGAGGCACTGGCCG 1320
 -----+-----+-----+-----+-----+-----+-----+-----+
 TATAGTCAAGTGTAGACGTGACAAACGACGGGAGCTACATAGTCTCCTCCGTCACCGGC
 c I T F T S A L F A A L D V S E E A V A A -

1321 CCGCGCGCCGACCCGTGTGGTATGGGAAAACAACAACGCAAAAAGCAGGGGCTGGATA 1380
 -----+-----+-----+-----+-----+-----+-----+-----+
 GGCGCGCGCGTTCGGCACACCATAACCCTTTGTTGTTGCGTTTTTCGTCCCGACCTAT
 c A R R S R V V W E N K Q R K K Q G L D T -

1381 CCCTGGGCATGGATGAACTGATAGCGAAAGCCTGGCGTTTTGTTTCGTGAGCGTTTTCGCA 1440
 -----+-----+-----+-----+-----+-----+-----+-----+
 GGGACCCGTACCTACTTACTATCGCTTTTCGGACCGCAAAAACAAGCACTCGCAAAAAGCGT
 c L G M D E L I A K A W R F V R E R F R S -

A
f
l
I
I
I

1441 GTTATCAGACAGAGCTTAAGTCCCGTGGAAATAAAGCGTGCCCGTGCGCGTCGTGATGCGG 1500
 -----+-----+-----+-----+-----+-----+-----+-----+
 CAATAGTCTGTCTCGAATTCAGGGCACCTTATTTGCGACGGGCAGCGCAGCACTACGCC
 c Y Q T E L K S R G I K R A R A R R D A D -

FIG. 5D

```

ACAGGGAACGTCAGGATATTGTCACCTGGTGAAACGGCAGCTGACGCGCGAAATCGCGG
1501 -----+-----+-----+-----+-----+-----+-----+ 1560
TGTCCTTGCAGTCTATAACAGTGGGACCACCTTTGCCGTCGACTGCGCGCTTTAGCGCC
c   R E R Q D I V T L V K R Q L T R E I A E -
AAGGGCGCTTCACTGCCAATCGTGAGGCGGTAAAACGCGAAGTTGAGCGTCGTGTGAAGG
1561 -----+-----+-----+-----+-----+-----+-----+ 1620
TTCCCGCGAAGTGACGGTTAGCACTCCGCCATTTTGGCTTCAACTCGCAGCACACTTCC
c   G R F T A N R E A V K R E V E R R V K E -
AGCGCATGATTCTGTCACGTAACCSTAATTACAGCCGGCTGGCCACAGCTTCCCCCTGAA
1621 -----+-----+-----+-----+-----+-----+-----+ 1680
TCGCGTACTAAGCAGTGCATTGGCATTAAATGTCGGCCGACCGGTTCGAAGGGGGACTT
c   R M I L S R N R N Y S R L A T A S P *
AGTGACCTCCTCTGAATAATCCGGCCTGCGCCGGAGGCTTCCGCACGTCTGAAGCCCGAC
1681 -----+-----+-----+-----+-----+-----+-----+ 1740
TCACTGGAGGAGACTTATTAGCCCGACGCGGCCCTCCGAAGGCGTGCAGACTTCCGGGCTG

                                     P
                                     E
                                     l
                                     M
                                     I
AGCGCACAAAAATCAGCACCACATACAAAAACAACCTCATCATCCAGCTTCTGGTGCA
1741 -----+-----+-----+-----+-----+-----+-----+ 1800
TCGCGTGTTTTTTAGTCGTGGTGTATGTTTTTGTGGAGTAGTAGGTCGAAGACCACGT
TCCGGCCCCCCTGTTTTCGATACAAAACACGCCTCACAGACGGGGAATTTTGCCTTATCC
1801 -----+-----+-----+-----+-----+-----+-----+ 1860
AGGCCGGGGGGACAAAAGCTATGTTTTGTGCGGAGTGTCTGCCCTTAAAACGAATAGG

|----- ori -----|
ACATTAACTGCAAGGGACTTCCCCATAAGGTTACAACCGTTCATGTCATAAAGCGCCAT
1861 -----+-----+-----+-----+-----+-----+-----+ 1920
TGTAATTTGACGTTCCCTGAAGGGGTATTCCAATGTTGGCAAGTACAGTATTTCCGGGTA

----- ori -----
CCGCCAGCGTTACAGGGTGAATGTATCTTTTAAACACCTGTTTATATCTCCTTTAAACT
1921 -----+-----+-----+-----+-----+-----+-----+ 1980
GGCGGTGCAATGTCCACGTTACATAGAAAATTTGTGGACAAATATAGAGGAAATTTGA

-----|-----|
ACTTAATTACATTCATTTAAAAGAAAACCTATTCACTGCCTGTCCTTGGACAGACAGAT
1981 -----+-----+-----+-----+-----+-----+-----+ 2040
TGAATTAATGTAAGTAAATTTTCTTTTGGATAAGTGACGGACAGGAACCTGTCTGTCTA

ATGCACCTCCACCGCAAGCGGCGGGCCCTACCGGAGCCGCTTTAGTTACAACACTCAG
2041 -----+-----+-----+-----+-----+-----+-----+ 2100
TACGTGGAGGGTGGCGTTCGCCCGCCGGGATGGCCTCGGCGAAATCAATGTTGTGAGTC
a   M H L P P Q A A G P Y R S R F S Y N T Q -
--- repA4 protein --->
ACACAACCACCAGAAAACCCCGGTCCAGCGCAGAACTGAAACCACAAAGCCCTCCCTC
2101 -----+-----+-----+-----+-----+-----+-----+ 2160
TGTGTTGGTGGTCTTTTTGGGGCCAGGTCGCTCTTGACTTTGGTGTTCGGGGAGGGAG
a   T Q P P E K P R S S A E L K P Q S P S L -
ATAACTGAAAAGCGGCCCGCCCGGTCGGAAGGGCCGGAACAGAGTGCCTTTTAATTAT
2161 -----+-----+-----+-----+-----+-----+-----+ 2220
TATTGACTTTTCGCCGGGGCGGGCCAGGCTTCCGGCCTTGCTCAGCGAAAATTAATA
a   I T E K R P R P G P K G R N R V A F N Y -

```

FIG. 5E

```

2221 GAATGTTGTAAC TACTTCATCATCGCTGTCAGTCTTCTCGCTGGAAGTTCTCAGTACACG 2280
-----+-----+-----+-----+-----+-----+-----+-----+
a   CTTACAACATTGATGAAGTAGTAGCCGACAGTCAGAAGAGCGACCTTCAAGAGTCATGTGC
E . C C N Y F I I A V S L L A G S S Q Y T -

          BS
          gf
          li
          II
          /

2281 CTCGTAAGCGGCCCTGACGGCCCCGCTAACGCGGAGATACGCCCCGACTTCGGGTAAACCC 2340
-----+-----+-----+-----+-----+-----+-----+
a   GAGCATTCCGCCGGGACTGCCGGGCGATTGCGCCTCTATGCGGGGCTGAAGCCCATTGCGG
L V S G P D G P L T R R Y A P T S G K P -

2341 TCGTCGGGACC ACTCCGACCGCGCACAGAAGCTCTCTCATGGCTGAAAGCGGGTATGGTC 2400
-----+-----+-----+-----+-----+-----+-----+
a   AGCAGCCCTGGTGAGGCTGGCGCGTGTCTTCGAGAGAGTACCGACTTTCGCCCATACCAG
S S G P L R P R T E A L S W L K A G M V -

2401 TGGCAGGGCTGGGGATGGGTAAGGTGAAATCTATCAATCAGTACCGGCTTACGCCGGGCT 2460
-----+-----+-----+-----+-----+-----+-----+
a   ACCGTCCCACCCCTACCCATTCCACTTTAGATAGTTAGTCATGGCCGAATGCGGCCCGA
W Q G W G W V R *

          B
          s
          t
          E
          I
          I
          I

2461 TCGGCGGTTTTACTCCTGTTTCATATATGAAACAACAGGTCACCGCCTTCCATGCCGCTG 2520
-----+-----+-----+-----+-----+-----+-----+
AGCCGCCAAAATGAGGACAAAGTATATACTTTGTTGTCCAGTGGCGGAAGGTACGGCGAC

          B
          s
          p
          l
          u
          l
          l
          I

2521 ATGCGGCATATCCTGGTAACGATATCTGAATTGTTATACATGTGTATATACGTGGTAATG 2580
-----+-----+-----+-----+-----+-----+-----+
TACGCCGTATAGGACCATTGCTATAGACTTAACAATATGTACACATATATGCACCATTAC

2581 ACAAAAATAGGACAAGTTAAAAATTTACAGGCGATGCAATGATTCAAACACGTAATCAAT 2640
-----+-----+-----+-----+-----+-----+-----+
TGTTTTTATCCGTTC AATTTTTTAAATGTCCGCTACGTTACTAAGTTTGTGCATTAGTTA

2641 ATCGGGGGTGGGCGAAGAACTCCAGCATGAGATCCCCGCGCTGGAGGATCATCCAGCCGG 2700
-----+-----+-----+-----+-----+-----+-----+
TAGCCCCCACC CGCTTCTTGAGGTCTACTCTAGGGGCGGACCTCCTAGTAGGTCCGGC

2701 CGTCCCCGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCGGTGGAATCGAAAT 2760
-----+-----+-----+-----+-----+-----+-----+
GCAGGGCCTTTTGCTAAGGCTTCGGGTGGAAGTATCTTCCGCCCCACCTTAGCTTTA

```


FIG. 5G

```

f      A E D Q L E N L V G S L D T K V F L V P -
3481  GCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGC
      CGCGGGGACGCGACTGTGGCCCTTGTGCCCGTAGTCTCGTCCGCTAACAGACAACACG
f      R G Q A S L R F V A A D S C G I T Q Q A -
                                     E
                                     a
                                     g
                                     I
3541  CCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGAGAACCCTGCGTGAATCCATC
      GGTCAGTATCGGCTTATCGGAGAGGTGGGTTCCGCCGCCCTCTTGGACGCACGTTAGGTAG
f      W D Y G F L R E V W A A P S G A H . L G D -
3601  TTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCTGATCTTGATCCCCTGCG
      AACAAAGTTAGTACGCTTTGCTAGGAGTAGGACAGAGAAGTACACTAGAAGTACGGGGACGC
f      Q E I M
<--- APHII (kanamycin resistance) protein --)
                                     -10.
                                     <--- mRNA APHII ---|
3661  CCATCAGATCCTTGCGCGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTT
      GGTAGTCTAGGAACCGCCGTTCTTTCGGTAGGTCAAATGAAACGTCGCCAAGGGTTGGAA
                                     -35
                                     -----
<----- Promoter (APHII) -----
3721  ACCAGAGGGCGCCCAGCTGGCAAATCCGGTTCGCTTGCTGTCCATAAAACCGCCAGTC
      TGGTCTCCCGCGGGTCCGACCGTTAAGGCCAAGCGAACGACAGGTATTTTGGCGGGTCAG
3781  TAGCTATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTTTGCGCTTGCGTTTTC
      ATCGATAGCGGTACATTCGGGTGACGTTTCGATGGACGAAAGAGAAACGCGAAGCGAAAAG
3841  CCTTGTCCAGATAGCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGACT
      GGAACAGGTCATCGGGTCATCGACTGTAAGTAGGCCCCAGTCGTGGCAAAGACGCCTGA
3901  GGCTTTCTACGTGTCCGCTTCCCTTTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGCAGCG
      CCGAAAGATGCACAAGGCCAAGGAAATCGTCGGGAACCGGGACTCACGAACGCCGTCGC
                                     |----- par locus -----
3961  TGAAGCTACATATATGTGATCCGGGCAAATCGCTGAATATTCCTTTGTCTCCGACCATC
      ACTTCGATGTATATACACTAGGCCCGTTTAGCGACTTATAAGGAAAACAGAGGCTGGTAG
                                     B
                                     c
                                     g
                                     I
----- par locus -----
4021  AGGCACCTGAGTCGCTGTCTTTTTCGTGACATTCAGTTCGCTGCGCTCACGGCTCTGGCA
      TCCGTGGACTCAGCGACAGAAAAGCACTGTAAGTCAAGCGACGCGAGTCCCGAGACCGT
----- par locus -----

```

FIG. 5H

```

4081 GTGAATGGGGTAAATGGCACTACAGGCGCTTTTATGGATTCATGCAAGGAACTACCC 4140
-----+-----+-----+-----+-----+-----+-----+
CACTTACCCCCATTTACCGTGATGTCCGCGGAAAATACCTAAGTACGTTCCCTTTGATGGG

----- par locus -----
4141 ATAATACAAGAAAAGCCCGTCACGGGCTTCTCAGGGCGTTTTATGGCGGGTCTGCTATGT 4200
-----+-----+-----+-----+-----+-----+-----+
TATTATGTTCTTTTCGGGCAGTGCCCGAAGAGTCCCGCAAAAATACCGCCCAGACGATACA

----- par locus -----
4201 GGTGCTATCTGACTTTTGTGCTGTTTCAGCAGTTCCTGCCCCTCTGATTTTCCAGTCTGACCA 4260
-----+-----+-----+-----+-----+-----+-----+
CCACGATAGACTGAAAAACGACAAGTCTCAAGGACGGGAGACTAAAAGGTCAGACTGGT

----- par locus -----
4261 CTTCGGATTATCCCGTGACAGGTCATTCAGACTGGCTAATGCACCCAGTAAGGCAGCGGT 4320
-----+-----+-----+-----+-----+-----+-----+
GAAGCCTAATAGGGCACTGTCCAGTAAGTCTGACCGATTACGTGGGTTCATCCGTCGCCA

-----+-----+-----+-----+-----+-----+-----+
ATCATCAACAGGCTTACCCGCTTACTGTGCGAAGACGTCGCGTAACGTATGCATGGTCTCC 4380
-----+-----+-----+-----+-----+-----+-----+
TAGTAGTTGTCCGAATGGGCAGAATGACAGCTTCTGCACGCATTGCATACGTACCAGAGG

-----+-----+-----+-----+-----+-----+-----+
CCATGCGAGAGTAGGGAAGTCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTT 4440
-----+-----+-----+-----+-----+-----+-----+
GGTACGCTCTCATCCCTTGACGGTCCGTAGTTTATTTTGGCTTTCGAGTCAGCTTTCTGA

-----+-----+-----+-----+-----+-----+-----+
GGGCCTTTCGTTTTATCTGTTGTTGTCGGTGAACGCTCTCCTGAGTAGGACAAATCCGC 4500
-----+-----+-----+-----+-----+-----+-----+
CCCGGAAAGCAAAATAGACAACAAACAGCCACTTGGCAGAGGACTCATCTGTTTAGGCG
-- T1 stop -->|

P
S
P
1
4
0
6
I
4501 CGGGAGCGGATTTGAACGTTGCGAAGCAACGGCCCGGAGGGTGGCGGGCAGGACGCCCGC 4560
-----+-----+-----+-----+-----+-----+-----+
GCCCTCGCCTAAACTTGCAACGCTTCGTTGCCGGGCCTCCACCGCCCGTCTGCGGGCG

-----+-----+-----+-----+-----+-----+-----+
CATAAACTGCCAGGCATCAAATTAAGCAGAAGGCCATCTGACGGATGGCCTTTTTCGCT 4620
-----+-----+-----+-----+-----+-----+-----+
GTATTTGACGGTCCGTAGTTTAATTCGTTCCGGTAGGACTGCCTACCGGAAAACGCA
----- T2 stop ---->|

```

FIG. 5I

A
a
t
t
I
I

4621 TTCTACAAACTCTTTTGTATTATTTTCTAAATACATTCAAATATGGACGTCGTACTTAAAC 4680
 -----+-----+-----+-----+-----+-----+-----+
 AAGATGTTTGAGAAAACAAATAAAAAGATTTATGTAAGTTTATACCTGCAGCATGAATTG
 * -

4681 TTTTAAAGTATGGGCAATCAATTGCTCCTGTTAAAAATTGCTTTAGAAATACTTTGGCAGC 4740
 -----+-----+-----+-----+-----+-----+-----+
 AAAATTTTCATACCCGTTAGTTAACGAGGACAATTTTAAACGAAATCTTTATGAAACCGTGC
 d * S K F Y P C D I A G T L I A K S I S Q C -
 |<--- luxR protein ---

4741 GGTGTGTTGTATTGAGTTTCATTTGCGCATTGGTTAAATGGAAAGTGACCGTGCCTTAC 4800
 -----+-----+-----+-----+-----+-----+-----+
 CCAAACAACATAACTCAAAGTAAACGCGTAACCAATTTACCTTTCCTGCGCAGCGAATG
 d R N T T N L K M Q A N T L H F T V T R K -

4801 TACAGCCTAATATTTTGAATATCCCAAGAGCTTTTTCCTTCGCATGCCACGCTAAAC 4860
 -----+-----+-----+-----+-----+-----+-----+
 ATGTCGGATTATAAAAACCTTTATAGGGTCTCGAAAAAGGAAGCGTACGGGTGCGATTTG
 d S C G L I K S I D W S S K G E C A W A L -

4861 ATTCTTTTCTCTTTTGGTTAAATCGTTGTTGATTATTATTGCTATATTTATTTTTC 4920
 -----+-----+-----+-----+-----+-----+-----+
 TAAGAAAAAGAGAAAACCAATTTAGCAACAACTAAATAATAAACGATATAAAATAAAAAG
 d C E K E R K T L D N N S K N N A I N I K -

4921 GATAATTATCAACTAGAGAAGGAACAATTAATGGTATGTTTCATACACGCATGTAAAAATA 4980
 -----+-----+-----+-----+-----+-----+-----+
 CTATTAATAGTTGATCTCTTCTTCTTGAATGTTTACCATACAAGTATGTGCGTACATTTTAT
 d R Y N D V L S P V I L P I N M C A H L F -

B
s
m
I

4981 AACTATCTATATAGTTGTCTTTCTCTGAATGTGCAAACTAAGCATTCGGAAGCCATTAT 5040
 -----+-----+-----+-----+-----+-----+-----+
 TTGATAGATATATCAACAGAAAGAGACTTACACGTTTGGATTTCGTAAGGCTTCGGTAATA
 d L S D I Y N D K E S H A F S L M G F G N -

5041 TAGCAGTATGAATAGGAAAACATAACCAGTGATAAGACCTGATGATTTTCGCTTCTTTAA 5100
 -----+-----+-----+-----+-----+-----+-----+
 ATCGTCATACCTTATCCCTTTGATTTGGGTCACTATCTGGACTACTAAAGCGAAGAAATT
 d N A T H I P F S F G T I L G S S K A E K -

5101 TTACATTTGGAGATTTTTTATTTACAGCATTGTTTTCAAATATATCCAATTAATCGGTG 5160
 -----+-----+-----+-----+-----+-----+-----+
 AATGTAACCTCTAAAAATAAATGTCGTAACAAAAGTTTATATAAGGTTAATTAGCCAC
 d I V N P S K K N V A N N E F I N W N I P -

5161 AATGATTGGAGTTAGAATAATCTACTATAGGATCATATTTTATTAATTTAGCGTCATCAT 5220
 -----+-----+-----+-----+-----+-----+-----+
 TTACTAACCTCAATCTTATTAGATGATATCTAGTATAAAATAATTTAATCGCAGTAGTA
 d S H N S N S Y D V I P D Y K I L N A D D -

FIG. 5J

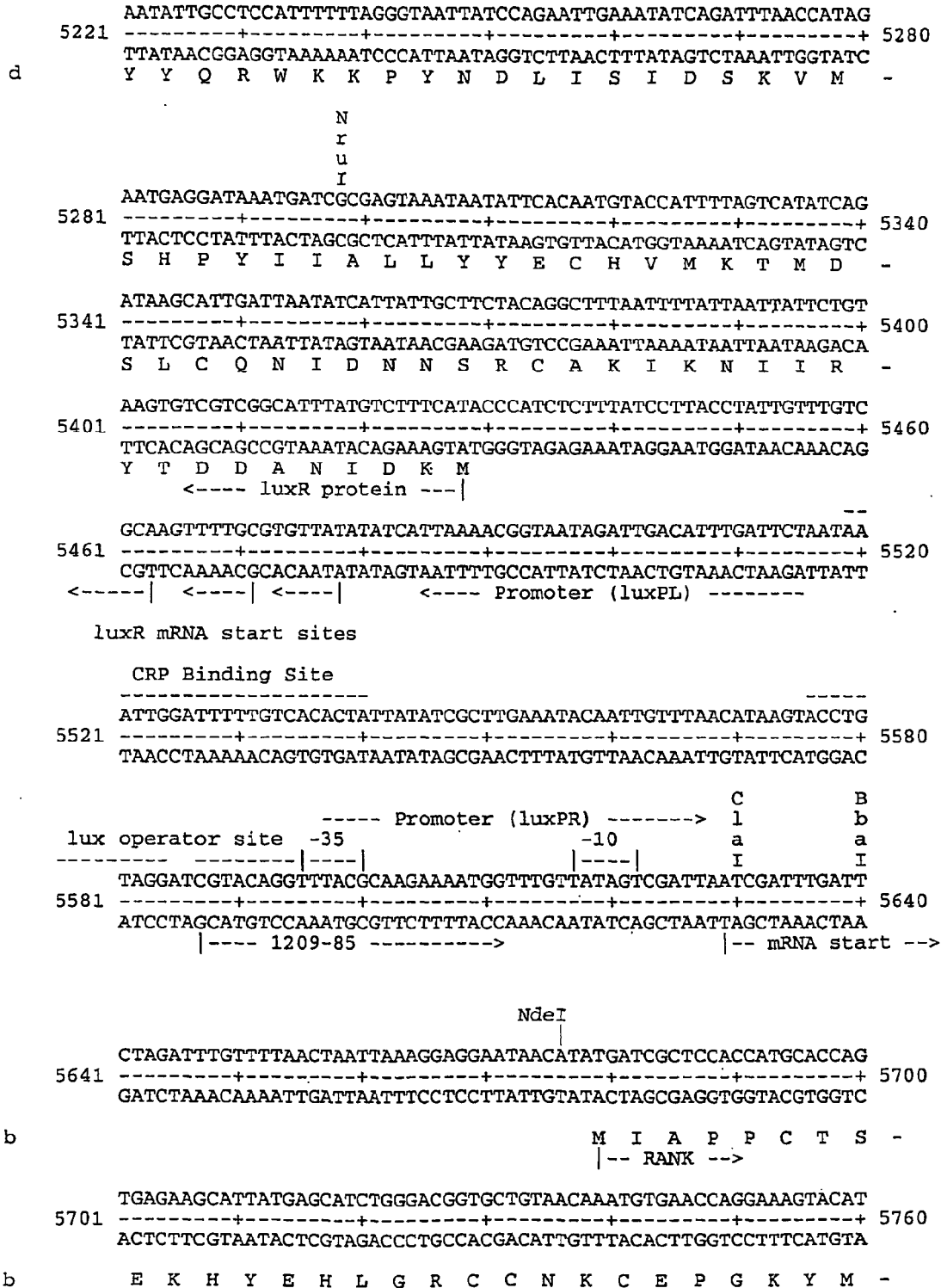


FIG. 5K

```

5761 GTCTTCTAAATGCACTACTACCTCTGACAGTGTATGTCTGCCCTGTGGCCCGGATGAATA 5820
-----+-----+-----+-----+-----+-----+-----+
CAGAAGATTTACGTGATGATGGAGACTGTCACATACAGACGGGACACCGGGCCTACTTAT

b      S S K C T T T S D S V C L P C G P D E Y -

5821 CTTGGATAGCTGGAATGAAGAAGATAAATGC'TTGCTGCATAAAGTTTGTGATACAGCAA
-----+-----+-----+-----+-----+-----+-----+
5880 GAACCTATCGACCTTACTTCTTCTATTTACGAACGACGTATTTCAAACACTATGTCCGTT

b      L D S W N E E D K C L L H K V C D T G K -

                                     ApaLI
                                     |
5881 GGCCCTGGTGGCCGTGGTCGCCGGCAACAGTACGACCCCCCGGCGCTGCGCGTGCACGGC
-----+-----+-----+-----+-----+-----+-----+
5940 CCGGGACCACCGGCACCAGCGGCCGTTGTGCATGCTGGGGGGCCGCGACGCGCACGTCCCG

b      A L V A V V A G N S T T P R R C A C T A -

Acc65I  KpnI
|       |
5941 TGGGTACCACTGGAGCCAGGACTGCGAGTGTCTGCCCGCAACACCGAGTGC CGCCGGG
-----+-----+-----+-----+-----+-----+-----+
6000 ACCCATGGTGACCTCGGTCTGACGCTCACGACGGCGGCGTTGTGGCTCACGCGCGGCC

b      G Y H W S Q D C E C C R R N T E C A P G -

6001 CCTGGGCGCCAGCACCCGTTGCAGCTCAACAAGGACACAGTGTGCAAACCTTGCCTTGC
-----+-----+-----+-----+-----+-----+-----+
6060 GGACCCGCGGGTCTGTTGGCAACGTCGAGTTGTTCTCTGTGTACACGTTTGAACGGAACG

b      L G A Q H P L Q L N K D T V C K P C L A -

6061 AGGCTACTTCTCTGATGCCTTTTCTCCACGGACAAATGCAGACCCTGGACCAACTGTAC
-----+-----+-----+-----+-----+-----+-----+
6120 TCCGATGAAGAGACTACGGAAGGAGGTGCCTGTTTACGTCTGGGACCTGGTTGACATG

b      G Y F S D A F S S T D K C R P W T N C T -

6121 CTTCTTGGAAAAGAGAGTAGAATCATGGGACAGAGAAATCCGATGTGGTTTGCAGTTC
-----+-----+-----+-----+-----+-----+-----+
6180 GAAGGAACCTTCTCTCATCTTGTAGTACCCTGTCTCTTTAGGCTACACCAAACGTC AAG

b      F L G K R V E H H G T E K S D V V C S S -

                                     AccI
                                     SalI
                                     ||
6181 TTCTCTGCCAGCTAGAAAACCACCAAATGAACCCCATGTTTACGTGACAAAACCTCACAC
-----+-----+-----+-----+-----+-----+-----+
6240 AAGAGACGGTTCGATCTTTTGGTGGTTTACTTGGGGTACAAATGCAGCTGTTTGTAGTGTG

b      S L P A R K P P N E P H V Y V D K T H T -
          <-- end RANK --||--start Fc-->

```


FIG. 6B

```

-ATTGÁATTTTTGTACACTATTATATCGCTTGAAATACAATTGTTTAAACATAAGTACCTG-
-TAACCTAAAAACAGTGTGATAATATAGCGAACTTTATGTTAACAAATTGTATTCATGGAC-

-TAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTATAGTCGATTAATCGATTTGATT-
-ATCCTAGCATGTCCAAATGCGTTCCTTTTACCAAACAATATCAGCTAATTAGCTAAACTAA-

-CTAGATTTGTTTTAAC TAATTAAGGAGGAATAACATATGGTTAACGCGTTGGAATTCGA-
-GATCTAAACAAAATTGATTAATTTCTCCTTATTTGTATACCAATTGCGCAACCTTAAGCT-

-GCTCACTAGTGTGACCTGCAGGGTACCATGGAAGCTTACTCGAGGATCCGCGAAAAGAA-
-CGAGTGATCACAGCTGGACGTCCCATGGTACCTTCGAATGAGCTCCTAGGCGCCTTTCTT-

-GAAGAAGAAGAAGAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATA-
-CTTCTTCTTCTTCTTTCGGGCTTTCCTTCGACTCAACCGACGACGGTGGCGACTCGTTAT-

-ACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTTGCTGAAAGGAGG-
-TGATCGTATTGGGGAACCCCGGAGATTTGCCCAGAACTCCCCAAAAACGACTTTCCTCC-

-AACCGCTCTTCACGCTCTTCACGC 3'           [SacII sticky end]
-TTGGCGAGAAGTGCGAGAAGTG 5'           (position #5904 in pAMG21)

```

FIG. 7

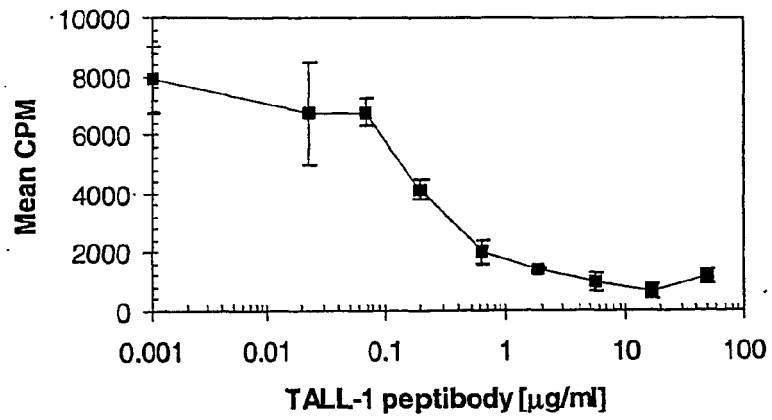


FIG. 8

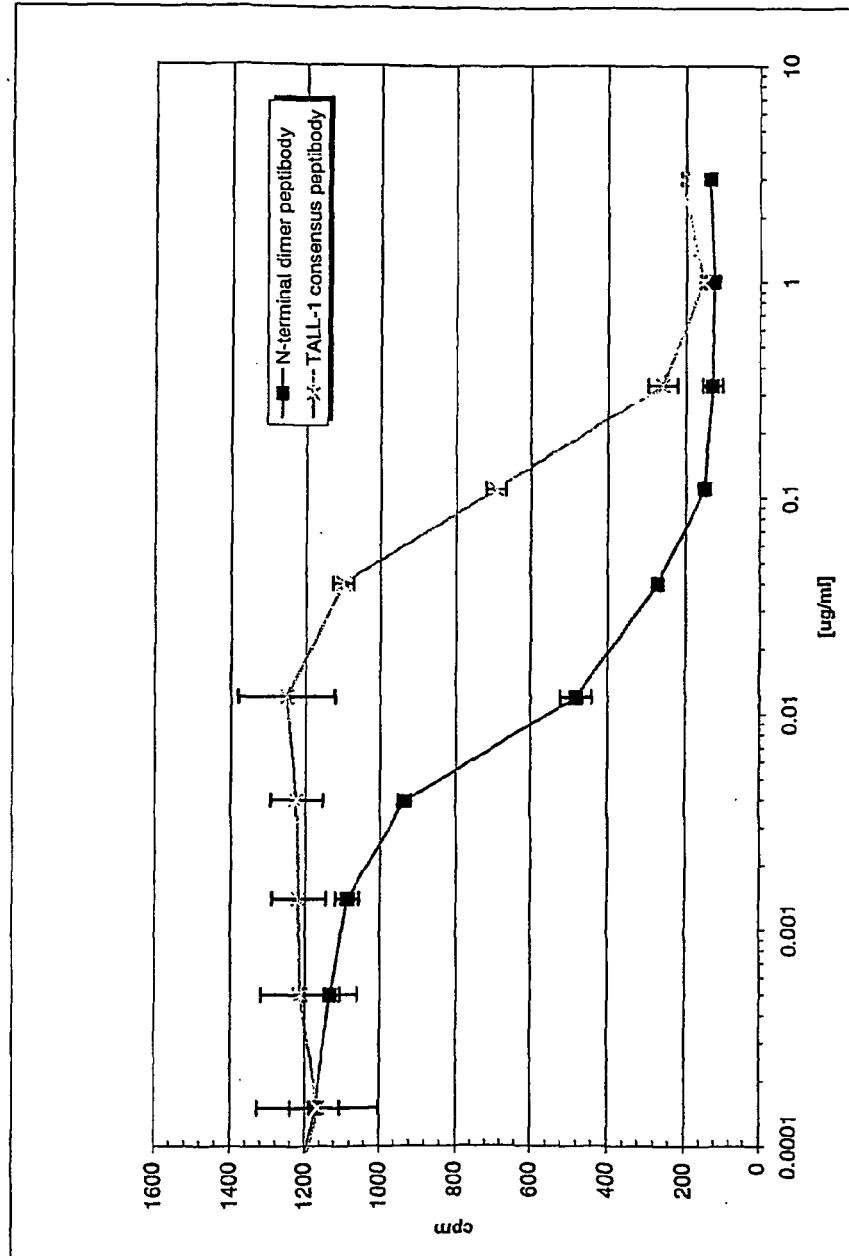


FIG. 9

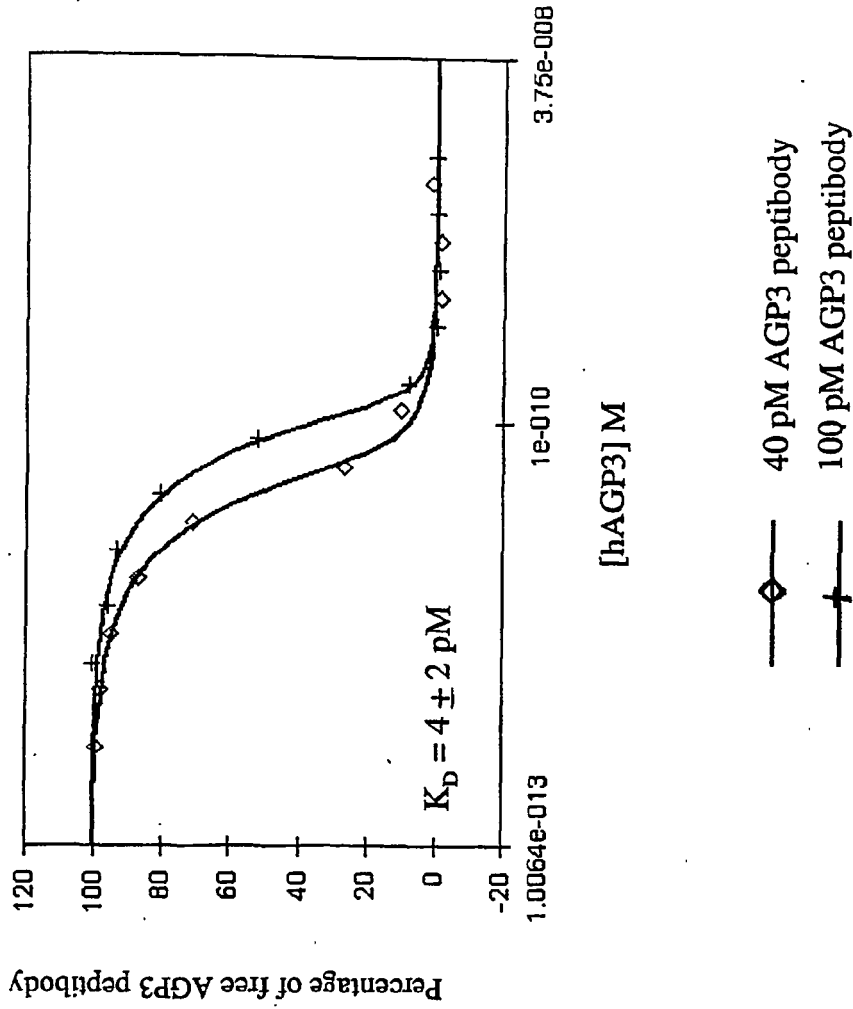


FIG. 10A

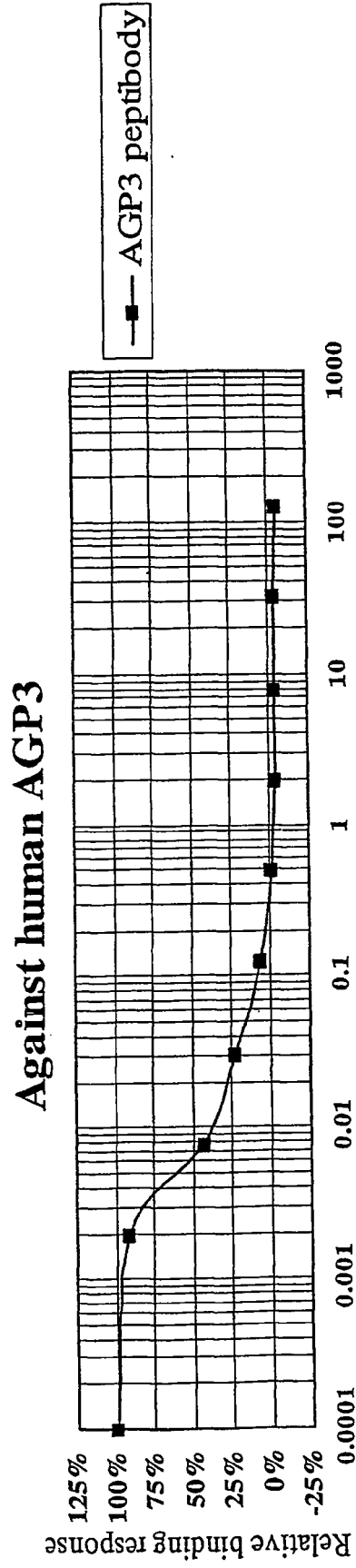


FIG. 10B

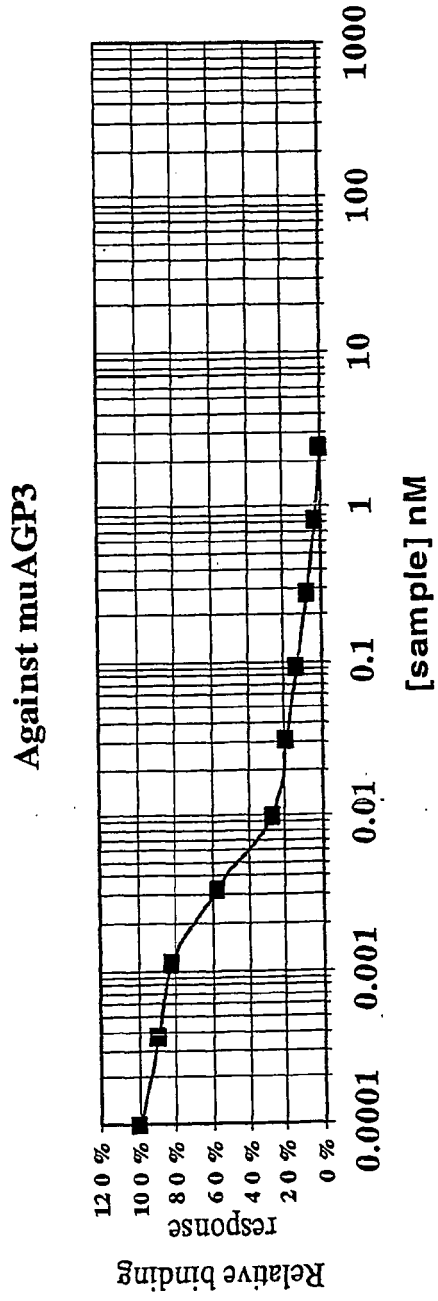


FIG. 11A

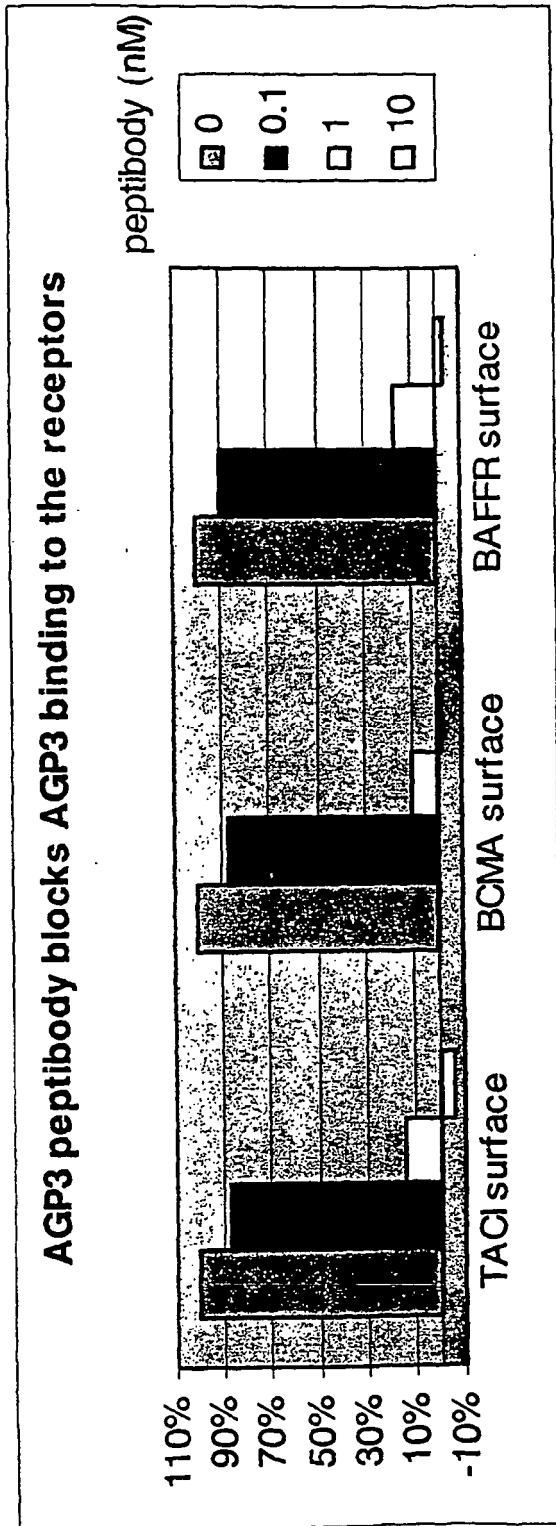


FIG. 11B

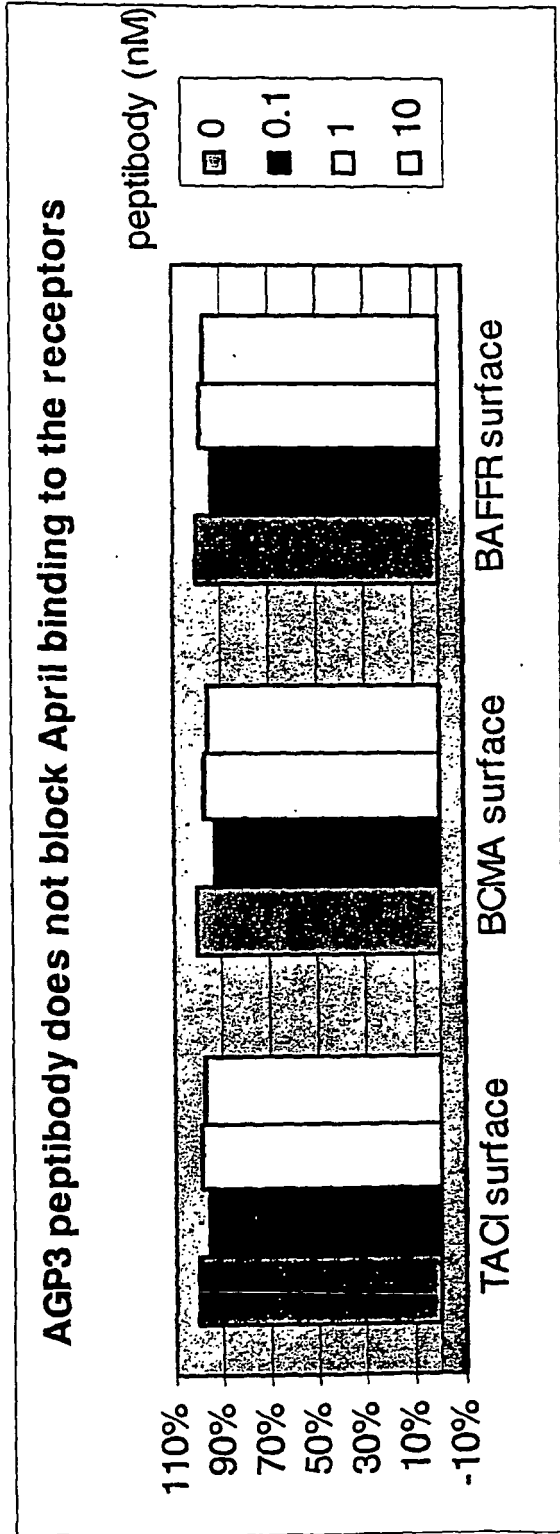


FIG. 12B

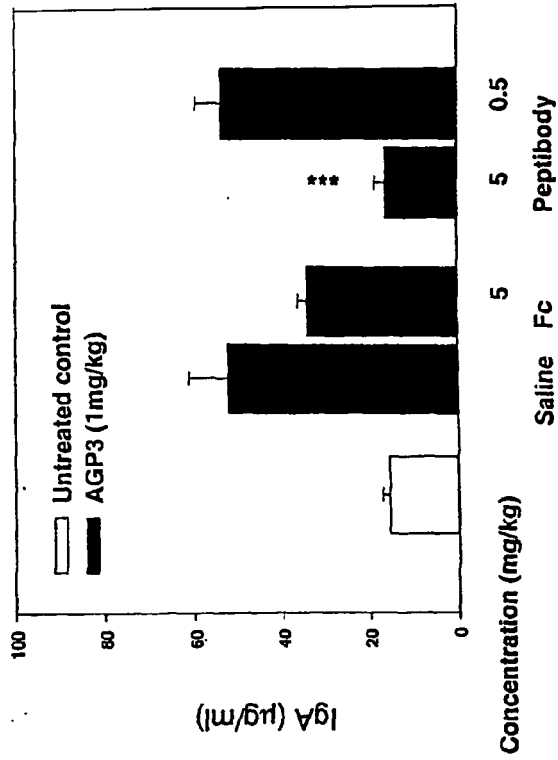


FIG. 12A

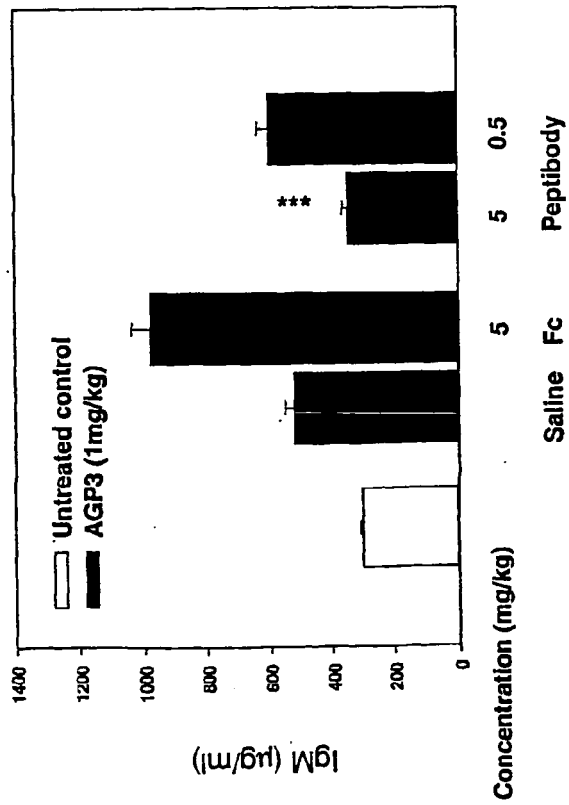
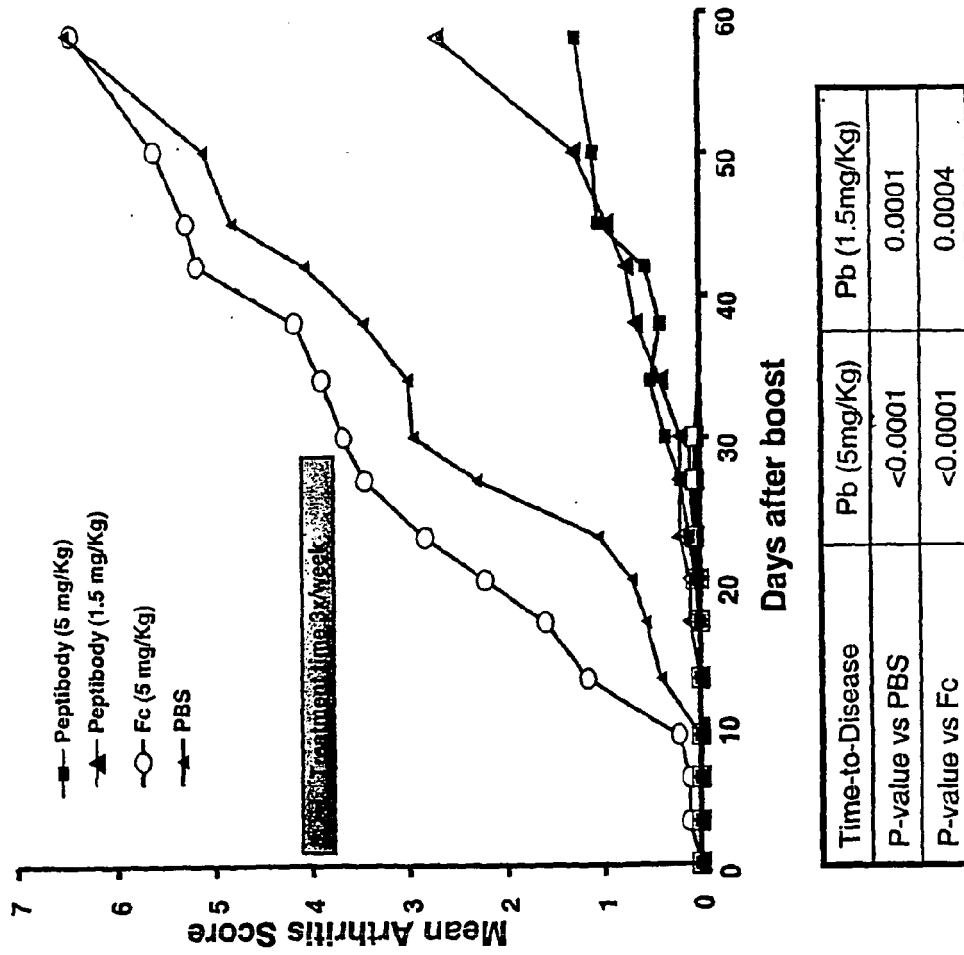


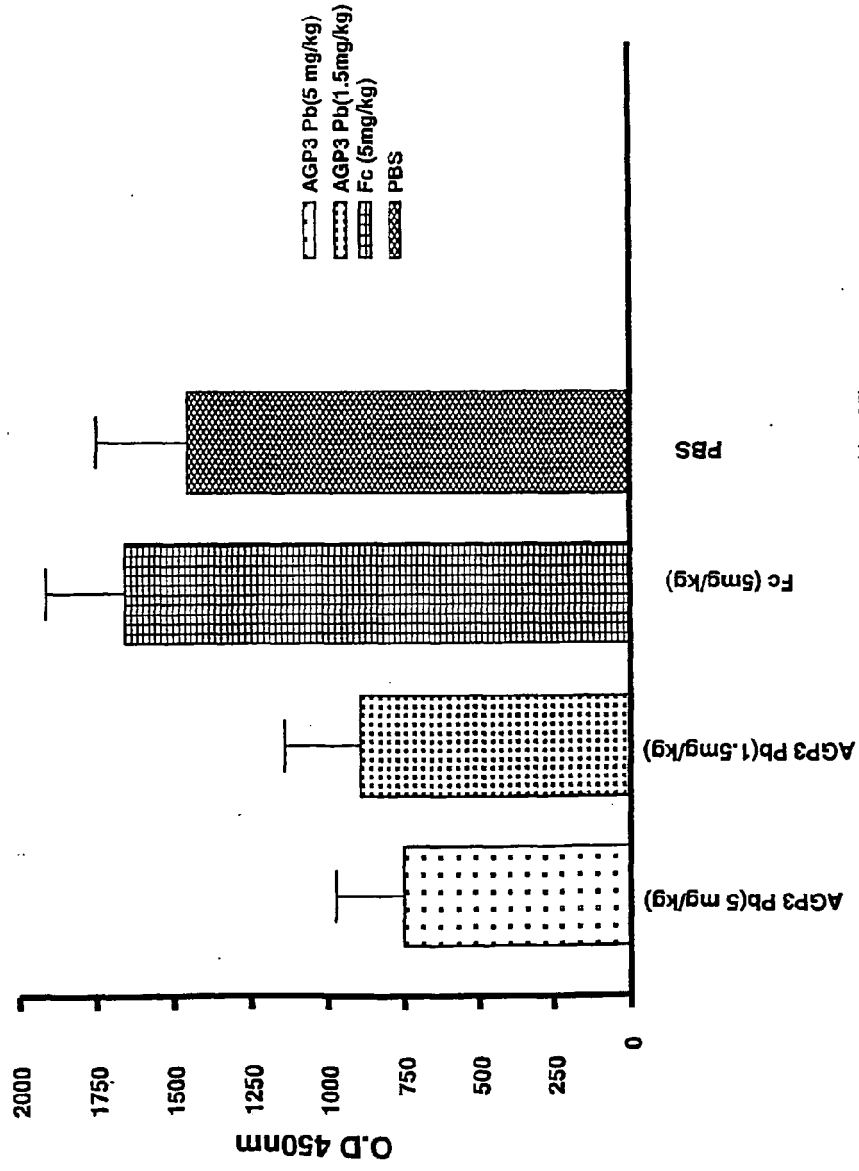
FIG. 13



Note: p-value based on log-rank test

FIG. 14

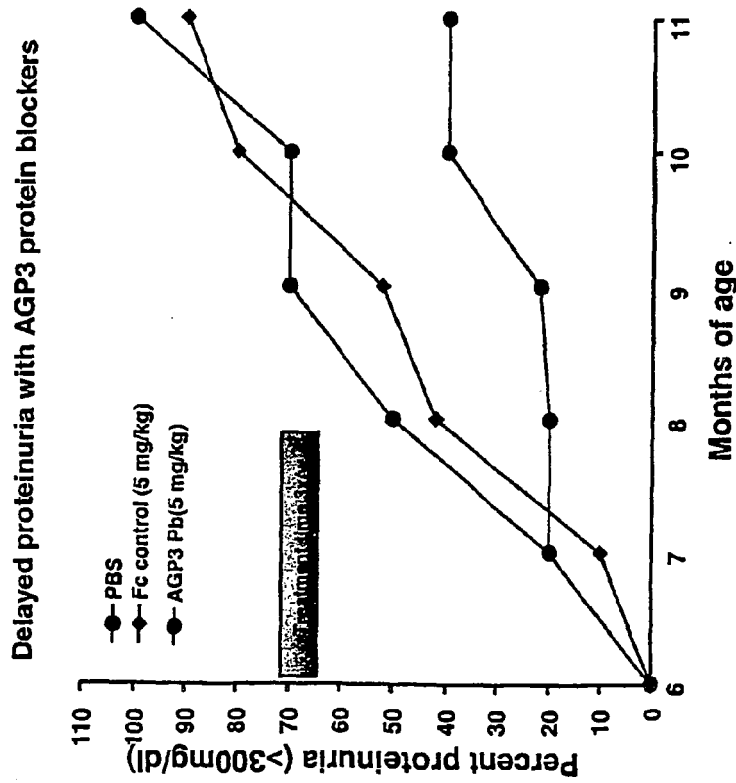
Reduced anti-collagen IgG2b upon treatment with AGP3 peptibody



Serum samples were taken one week after final treatment of reagent (day 35).

The graph above is representative of the IgG1, IgG3, and IgG2a isotypes as well.

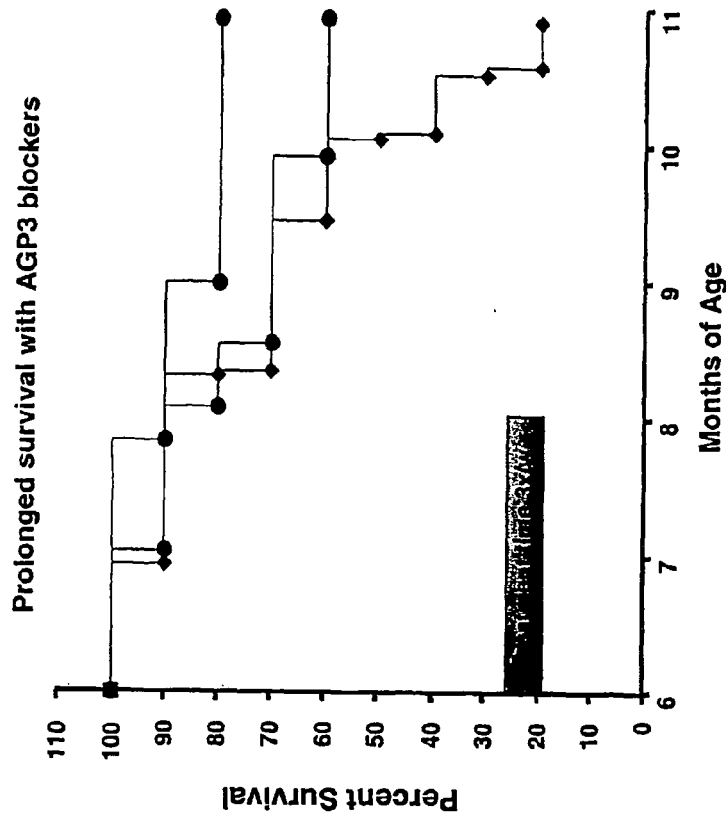
Fig. 15A



Proteinuria Incidence	Pb
p-value vs PBS	0.0108
P-vs Fc	0.0573

P-value based Fisher's Exact test

Fig. 15B



Time-to-Death	Pb
p-value vs PBS	0.3685
p-value vs Fc	0.0159

P-value based log-rank test

FIG. 16A

```

                                                    BamHI
                                                    |
ATGCTTCCAGGCTGCAAGTGGGATCTTCTTATTAAGCAATGGGTATGCGATCCACTTGGA
1 -----+-----+-----+-----+-----+-----+-----+ 60
TACGAAGGTCCGACGTTACCCTAGAAGAATAATTCGTTACCCATACGCTAGGTGAACCT

M L P G C K W D L L I K Q W V C D P L G -

TCCGGTTCTGCTACTGGTGGTTCCGGCTCCACCGCAAGCTCTGGTTCAGGCAGTGGCACT
61 -----+-----+-----+-----+-----+-----+ 120
AGGCCAAGACGATGACCACCAAGGCCGAGGTGGCGTTCGAGACCAAGTCCGTCACGCTGA

S G S A T G G S G S T A S S G S G S A T -

NdeI
|
CATATGCTGCCGGTTGTAAATGGGACCTGCTGATCAAACAGTGGGTTTGTGACCCGCTG
121 -----+-----+-----+-----+-----+-----+ 180
GTATACGACGGCCCAACATTTACCCTGGACGACTAGTTTGTACCCAAACACTGGGCGAC

H M L P G C K W D L L I K Q W V C D P L -

SalI
|
GGTGGAGGCGGTGGGGTCGACAAAACCTCACACATGTCCACCTTGTCCAGCTCCGGAACTC
181 -----+-----+-----+-----+-----+-----+ 240
CCACCTCCGCCACCCAGCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAG

G G G G G V D K T H T C P P C P A P E L -

CTGGGGGACCGTCAGTCTTCCTCTTCCCCCAAACCAAGGACACCCTCATGATCTCC
241 -----+-----+-----+-----+-----+-----+ 300
GACCCCTCCGTCAGTCAGAAGGAGAAGGGGGTTTTGGGTTTCTGTGGGAGTACTAGAGG

L G G P S V F L F P P K P K D T L M I S -

CGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG
301 -----+-----+-----+-----+-----+-----+ 360
GCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTC

R T P E V T C V V V D V S H E D P E V K -

TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG
361 -----+-----+-----+-----+-----+-----+ 420
AAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTC

F N W Y V D G V E V H N A K T K P R E E -

CAGTACAACAGCACGTACCGTGTGGTTCAGCGTCCCTACCGTCCTGCACCAGGACTGGCTG
421 -----+-----+-----+-----+-----+-----+ 480
GTCATGTTGTGTCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTGACCGAC

Q Y N S T Y R V V S V L T V L H Q D W L -

```

FIG. 16B

```

AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAA
481 -----+-----+-----+-----+-----+ 540
TTACCGTTCCATGTTACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGTAGCTCTTT
N G K E Y K C K V S N K A L P A P I E K -
ACCATCTCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCATCC
541 -----+-----+-----+-----+-----+ 600
TGGTAGAGGTTTCGGTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGTAGG
T I S K A K G Q P R E P Q V Y T L P P S -
CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
601 -----+-----+-----+-----+-----+ 660
GCCCTACTCGACTGGTCTTGGTCCAGTCGGACTGGACGGACCAGTTCCGAAGATAGGG
R D E L T K N Q V S L T C L V K G F Y P -
AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCAG
661 -----+-----+-----+-----+-----+ 720
TCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGC
S D I A V E W E S N G Q P E N N Y K T T -
CCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTTCTACAGCAAGCTCACCGTGGACAAG
721 -----+-----+-----+-----+-----+ 780
GGAGGGCAGCACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTT
P P V L D S D G S F F L Y S K L T V D K -
AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC
781 -----+-----+-----+-----+-----+ 840
TCGTCCACCGTCGTTCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTG
S R W Q Q G N V F S C S V M H E A L H N -
CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAA
841 -----+-----+-----+-----+ 882
GTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTATT
H Y T Q K S L S L S P G K * -

```

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摘要

本發明涉及能調節TALL-1活動的治療劑。根據本發明，TALL-1的調節劑可以包括氨基酸序列Dz2Lz4，其中，z2是氨基酸殘基，z4是蘇氨酸或異亮氨酸。典型分子包括具有下式的序列 a1a2a3CDa6La8a9a10Ca12a13a14 (SEQ. ID. NO:100) ， b1b2b3Cb5b6Db8Lb10b11b12b13b14Cb16b17b18 (SEQ. ID. N:104) , c1c2c3Cc5Dc7Lc9c10c11c12c13c14Cc16c17c18 (SEQ. ID. N:105) , d1d2d3Cd5d6d7Wdd10Ld13d14d15Cd16d17d18 (SEQ. ID. N:106) , e1e2e3Ce5e6e7De9Le11Ke13Ce15e16e17e18 (SEQ. ID. NO:107) , f1f2f3Kf5Df7Lf9f10Qf12f13f14 (SEQ. ID NO : 109) ，其中，取代基團如規格中定義的。本發明還包括通式(X1)^a-V1-(X2)^b的組合物，其中，V1是一種媒介物，它與上述一種或多種TALL-1調節組合物進行共價連接。所述媒介物和所述TALL-1調節組合物可以通過TALL-1調節部分的N-或C-末端連接。優選的媒介物是Fc結構域，並且優選的Fc結構域是IgG Fc結構域。