(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification[7]: A61K 47/48

(21) International Application Number: PCT/US00/35325

(22) International Filing Date:
22 December 2000 (22.12.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/173,048 23 December 1999 (23.12.1999) US

(71) Applicant (for all designated States except US): GENENTECH, INC. [US/US]; 1 DNA Way, South San Francisco, CA 94080-4990 (US).

(72) Inventors; and
(75) Inventors/Applicants (for US only): DELANO, Warren, L. [US/US]; 1080 Ralston Ave., #20, Belmont, CA 94002 (US). DENNIS, Mark, S. [US/US]; 120 Plymouth, San Carlos, CA 94070 (US). LOWMAN, Henry, B. [US/US]; 400 San Juan Avenue, P.O. Box 2556, El Granada, CA 94018 (US).

(74) Agents: KUBINEC, Jeffrey, S. et al.; Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080-4990 (US).

(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:
— Without international search report and to be republished upon receipt of that report.

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: METHODS AND COMPOSITIONS FOR PROLONGING ELIMINATION HALF-TIMES OF BIOACTIVE COMPOUNDS

(57) Abstract: Peptide ligands having affinity for IgG or for serum albumin are disclosed. Also disclosed are hybrid molecules comprising a peptide ligand domain and an active domain. The active domain may comprise any molecule having utility as a therapeutic or diagnostic agent. The hybrid molecules of the invention may be prepared using any of a number techniques including production in and purification from recombinant organisms transformed or transfected with an isolated nucleic acid encoding the hybrid molecule, or by chemical synthesis of the hybrid. The hybrid molecules have utility as agents to alter the elimination half-times of active domain molecules. Elimination half-time is altered by generating a hybrid molecule of the present invention wherein the peptide ligand has binding affinity for a plasma protein. In a preferred embodiment, a bioactive molecule having a short elimination half-time is incorporated as or into an active domain of the hybrid molecules of the invention, and the binding affinity of the peptide ligand domain prolongs the elimination half-time of the hybrid as compared to that of the bioactive molecule.

Methods and Compositions for Prolonging Elimination
Half-Times of Bioactive Compounds

Field of the Invention

5   This invention relates to novel compounds termed peptide ligands which bind a predetermined molecule such as a plasma protein. In particular aspects, the invention relates to compositions comprising a hybrid molecule comprising a peptide ligand domain and an active domain such as a biologically active molecule. The active domain may comprise a molecule useful for diagnostic or therapeutic purposes. In preferred embodiments, the hybrid compositions

10   comprising the peptide ligand domain and active domain have improved pharmacokinetic or pharmacological properties. The invention further provides for the research, diagnostic and therapeutic use of the peptide ligand and includes compositions such as pharmaceutical compositions comprising the peptide ligand molecules.

Description of Related Disclosures

15   Phage-display provides a means for generating constrained and unconstrained peptide libraries (Devlin *et al.*, (1990) *Science* **249**:404-406; Cwirla *et al.*, (1990) *Proc. Natl. Acad. Sci. USA* **87**:6378-6382; Lowman (1997) *Ann. Rev. Biophys. Biomol. Struct.* **26**:401-424). These libraries can be used to identify and select peptide ligands that can bind a predetermined target molecule (Lowman (1997), *supra*); Clackson and Wells (1994) *Trends Biotechnol.* **12**:173-184;

20   Devlin *et al.*, (1990) *supra*). The technique has been used to identify peptide motifs that home to a cellular target (Arap *et al.*, (1998) *Science* **279**:377-380); bind the human type I interleukin 1 (IL-1) receptor blocking the binding of IL-α (Yanofsky *et al.*, (1996) *Proc. Natl. Acad. Sci. USA* **93**:7381-7386); bind to and activate the receptor for the cytokine erythropoietin (EPO) (Wrighton *et al.*, (1996) *Science* **273**:458-463); bind the human thrombopoietin receptor and compete with the

25   binding of the natural ligand thrombopoietin (TPO)(Cwirla *et al.*, (1996) *Science* **276**:1696-1699), or to generate affinity improved or matured peptide ligands from native protein binding ligands (Lowman *et al.*, (1991) *Biochemistry* **30**:10832-10838).

        Using structurally constrained peptide libraries generated by monovalent phage display, 14 amino acid peptides that specifically bind to insulin-like growth factor 1 binding proteins (IGFBPs)

30   have been isolated (Lowman *et al.* (1998), *Biochemistry* **37**:8870-8878). The peptides contain a helix structure and bind IGFBPs *in vitro* liberating insulin like growth factor-a (IGF-1) activity (Lowman *et al.*, (1998) *supra*). Utilizing *in vivo* phage selection peptides capable of mediating selective localization to various organs such as brain and kidney (Pasqualini and Ruoslohti (1996) *Nature* **380**:364-366) as well as peptides that home to particular tumor types bearing $\alpha_V\beta_3$ or

35      $\alpha V\beta_5$ integrins have been identified (Arap *et al.* (1998), *Science* **279**:377-380). U.S. Patent

5,627,263 describes peptides that are recognized by and selectively bind the $\alpha_5\beta_1$ integrin. Examples of affinity or specificity improved proteins include human growth hormone, zinc fingers, protease inhibitors, atrial natriuretic factor, and antibodies (Wells, J. and Lowman H. (1992), *Curr. Opin. Struct. Biol.* **2**:597-604; Clackson, T. and Wells, J. (1994), *Trends Biotechnol.* **12**:173-184;

5   Lowman *et al.*, (1991) *Biochemistry* **30**(10):832-838; Lowman and Wells J. (1993), *J. Mol. Biol.* **234**:564-578; Dennis M. and Lazarus R. (1994), *J. Biol. Chem.* **269**(22):137-144).

It has been suggested that the pharmakodynamics of insulin are altered if bound to serum albumin. Acylation of insulin with saturated fatty acids containing 10-16 carbon atoms produces insulin with affinity for albumin (Kurtzhals, P. *et al.* (1995) *Biochem. J.* **312**:725-731).

10 Differences in albumin binding affinity among acylated insulins were correlated with the timing of the blood-glucose lowering effects of the various molecules after subcutaneous injection into rabbits. Tighter binding to albumin was correlated with a delay in blood glucose lowering, possibly due to acylated insulin binding albumin in the subcutaneous tissue, resulting in a lower absorption rate of the acylated insulins when compared with non-acylated insulin.

15   A serum albumin-CD4 conjugate in which the V1 and V2 domains of CD4 were fused with human serum albumin (HSA) has been described (Yeh, P. *et al.* (1992), *Proc. Natl. Acad. Sci. USA* **89**:1904-1908). The conjugate's elimination half-time was 140-fold that of a soluble CD4 (sCD4) in a rabbit experimental model.

Extended *in vivo* half-times of human soluble complement receptor type 1 (sCR1) fused to

20 the albumin binding domains from *Streptococcal* protein G have been reported (Makrides, S. *et al.* (1996) *J. Pharmacol. Exptl. Ther.* **277**:532-541). The constructs contained albumin binding domains of protein G having approximately 80 amino acids (fragment BA), and approximately 155 amino acids (fragment BABA).

The pharmacokinetics of a labeled IgG binding domain derived from the Z domain of

25 protein A having approximately 60 amino acids and of a serum albumin binding domain derived from *Streptococcal* protein G (B-domain) having approximately 200 amino acids have been described (EP 0 486,525).

Summary of the Invention

The present invention provides novel compounds that bind to plasma proteins. The

30 compounds of the present invention (referred to as peptide ligands) are, for example, peptides or peptide derivatives such as peptide mimetics and peptide analogs. According to preferred aspects of the invention, the compounds are non-naturally occurring amino acid sequences that bind plasma proteins such as serum albumin or a portion of an immunoglobulin, as for example, IgG-Fc. Preferably the peptide ligand is a non-naturally occurring amino acid sequence of between

35 about 10 and 20 amino acid residues.

2

Such compounds preferably bind a desired plasma protein with an affinity characterized by a dissociation constant, K_d, that is less than about 100 μM, preferably less than about 100 nM, and preferably do not substantially bind other plasma proteins. Specific examples of such compounds include linear or cyclic, especially cyclic peptides, preferably between about 10 and 20 amino acid residues in length, and combinations thereof, optionally modified at the N-terminus or C-terminus or both, as well as their salts and derivatives, functional analogues thereof and extended peptide chains carrying amino acids or polypeptides at the termini of the sequences.

Preferred peptide ligands bind IgG-Fc and include linear and cyclic peptides, preferably cyclic peptide compounds comprising the following core formula:

Xaa$_i$-Cys-Xaa$_j$-Cys-Xaa$_k$ (SEQ ID NO: 1), wherein Xaa$_i$ is absent or is a peptide of between 1 and 4 amino acids, preferably 4 amino acids; X$_j$ is preferably 9 amino acids having a preferred sequence Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Leu-Val-Trp (SEQ ID NO: 10); or Xaa-Xaa-Xaa-Xaa-Gly-Glu-Leu-Val-Trp (SEQ ID NO: 11); or Xaa$_1$-Xaa$_2$-Xaa$_3$-Xaa$_4$-Gly-Glu-Leu-Val-Trp (SEQ ID NO: 12), wherein Xaa$_1$ preferably is Ala, Ser, or Thr; Xaa$_2$ preferably is Trp or Tyr; Xaa$_3$ preferably is His, or Trp; Xaa$_4$ preferably is Leu or Met, and Xaa$_k$ is absent or between 1 and 5 amino acids, preferably 5 amino acids, so long as the cyclic peptide or analog thereof retains the qualitative biological activity of IgG-Fc binding.

Preferred among this group of compounds are compounds that bind IgG-Fc comprising the sequence:

Xaa-Xaa-Xaa-Xaa-Cys-Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Leu-Val-Trp-Cys-Xaa-Xaa-Xaa-Xaa-Xaa (SEQ ID NO: 13);

Xaa-Xaa-Xaa-Xaa-Cys-Xaa-Xaa-Xaa-Xaa-Gly-Glu-Leu-Val-Trp-Cys-Xaa-Xaa-Xaa-Xaa-Xaa (SEQ ID NO: 14);

Xaa$_1$-Xaa$_2$-Xaa$_3$-Xaa$_4$-Cys-Xaa$_5$-Xaa$_6$-Xaa$_7$-Xaa$_8$-Gly-Glu-Leu-Val-Trp-Cys-Xaa$_9$-Xaa$_{10}$-Xaa$_{11}$-Xaa$_{12}$-Xaa$_{13}$ (SEQ ID NO: 15), wherein Xaa$_5$ is Ala, Ser, or Thr; Xaa$_6$ is Trp or Tyr; Xaa$_7$ is His or Trp; and Xaa$_8$ is Leu or Met; and

Xaa$_1$-Xaa$_2$-Xaa$_3$-Xaa$_4$-Cys-Xaa$_5$-Xaa$_6$-Xaa$_7$-Xaa$_8$-Gly-Glu-Leu-Val-Trp-Cys-Xaa$_9$-Xaa$_{10}$-Xaa$_{11}$-Xaa$_{12}$-Xaa$_{13}$ (SEQ ID NO: 16) wherein Xaa$_4$ is Ser, Arg, or Asp; Xaa$_5$ is Ala, Ser, or Thr; Xaa$_6$ is Trp or Tyr; Xaa$_7$ is His or Trp; Xaa$_8$ is Leu or Met; and Xaa$_9$ is Glu, Ser, Thr or Val.

Preferred peptide ligands that bind serum albumin include linear and cyclic peptides, preferably cyclic peptide compounds comprising the following formulae:

3

$(Xaa)_X$-Xaa-Xaa-Cys-Xaa-Xaa-Xaa-Xaa-Xaa-Cys-Xaa-Xaa-$(Xaa)_z$

$(Xaa)_X$-Phe-Cys-Xaa-Asp-Trp-Pro-Xaa-Xaa-Xaa-Ser-Cys-$(Xaa)_z$

$(Xaa)_X$-Val-Cys-Tyr-Xaa-Xaa-Xaa-Ile-Cys-Phe-$(Xaa)_z$

$(Xaa)_X$-Cys-Tyr-Xaa_1-Pro-Gly-Xaa-Cys-$(Xaa)_z$

and $(Xaa)_X$-Asp-Xaa-Cys-Leu-Pro-Xaa-Trp-Gly-Cys-Leu-Trp-$(Xaa)_z$

Preferred are peptide compounds of the general formulae wherein Xaa is an amino acid and x and z are a whole number greater or equal to 0 (zero), generally less than 100, preferably less than 10 and more preferably 0, 1, 2, 3, 4 or 5 and more preferably 4 or 5 and Xaa_1 is selected from the group consisting of Ile, Phe, Tyr and Val.

In particular aspects the invention is directed to combinations of a peptide ligand with a bioactive compound to form a hybrid molecule that comprises a peptide ligand domain and an active domain. The bioactive compounds of the invention include any compound useful as a therapeutic or diagnostic agent. Non-limiting examples of bioactive compounds include polypeptides such as enzymes, hormones, cytokines, antibodies or antibody fragments, as well as organic compounds such as analgesics, antipyretics, antiinflammatory agents, antibiotics, antiviral agents, anti-fungal drugs, cardiovascular drugs, drugs that affect renal function and electrolyte metabolism, drugs that act on the central nervous system and chemotherapeutic drugs, to name but a few.

In preferred embodiments, the hybrid molecules comprising a peptide ligand domain and an active domain have improved pharmacokinetic or pharmacodynamic properties as compared to the same bioactive molecule comprising the active domain but lacking the peptide ligand domain. The improved pharmacokinetic or pharmacodynamic properties of the hybrids thereby provide for low-dose pharmaceutical formulations and novel pharmaceutical compositions. In certain aspects, the invention provides for methods of using the novel compositions including the therapeutic or diagnostic use of the hybrid molecules.

In particular aspects, the invention is directed to combinations of peptide ligands with bioactive compounds that have relatively short elimination half-times. The combinations are prepared with various objectives in mind, including improving the therapeutic or diagnostic efficacy of the bioactive compound in aspects of the invention involving *in vivo* use of the bioactive compound, by for example, increasing the elimination half-time of the bioactive compound. Fusing or linking (*i.e.*, "conjugating") the peptide ligand directed against a plasma protein such as serum albumin, an immunoglobulin, an apolipoprotein or transferrin to a bioactive compound provides compositions with increased elimination half-times. Such combinations or

fusions are conveniently made in recombinant host cells, or by the use of bifunctional crosslinking agents.

Other aspects of the invention include methods and compositions to purify antibodies using peptide ligands having binding affinity for immunoglobulins, such as, for example, the IgG-Fc peptide ligands disclosed herein.

The present invention further extends to therapeutic and diagnostic applications for the compositions described herein. Therefore, the invention includes pharmaceutical compositions comprising a pharmaceutically acceptable excipient and the hybrid molecules of the invention.

Brief Description of the Drawings

Fig. 1. Phage competitive ELISA assay showing IgG binding of peptide-ligand tagged anti-VEGF Fab-phagemid particles. Four different constructs are shown: pY0192-569 (large filled circles), pY0192-570 (large open circles), PY0317-569 (small filled circles), and pY0317-570 ("x"s).

Fig. 2. BIAcore^{TM} analysis of IgG binding to peptide-ligand tagged anti-VEGF Fab Y0317-570 (tagged; top panel) Y0317 Fab (control; bottom panel). A cartoon illustration at top shows a model for the binding events observed in the tagged Fab experiment.

Fig. 3. Group average serum concentration vs. time data ($\pm$SD) are presented in the figure for Fab-Y0317-570 and Fab-Y0317.

Fig. 4. The peptide sequences displayed by phage clones selected for binding to rabbit, human or rat albumin are shown in Figure 4. Also indicated is the ability of individual phage clones to bind the 3 species of immobilized albumin.

Fig. 5A and 5B. Sequences identified following soft randomization are shown in Figure 5 along with their species specificity as determined by phage ELISA.

Fig. 6. Clones originating from the RB soft randomization library were found by ELISA to bind each of these species of albumin and were specific for albumin based upon their lack of binding to ovalbumin and casein.

Fig. 7. Clones that bind to multiple species of albumin (multi-species binders) are listed in Figure 7.

Fig. 8A, 8B and 8C. Sequences from libraries selected against rat, rabbit and human albumin are shown in Figures 8A, 8B, and 8C respectively.

Fig. 9. Peptides corresponding to identified phage sequences were synthesized and their affinity for rat, rabbit or mouse albumin measured using the SA08b binding assay.

Fig. 10 A peptides corresponding to the SA06 identified phage sequence was synthesized and its affinity for rat, rabbit or mouse albumin measured using the SA08b binding assay.

Fig. 11. The SA06 sequence was added to the carboxy terminus of either the light chain (D3H44-L) or heavy chain (D3H44-Ls) of the Fab. In addition, identical constructs were made with the intra-chain disulfide replaced by alanines (D3H44-Ls and D3H44-Hs, respectively) as depicted in Figure 11.

Fig. 12. Purified D3H44 fusions retained their ability to bind TF as measured using a FX activation assay.

Fig. 13. Purified D3H44 fusions retained their ability to bind TF as measured using a prothrombin time assay that measures prolongation of tissue factor dependent clotting.

Fig. 14 Unlike D3H44 lacking the albumin binding sequence (WT), both D3H44-L and D3H44-Ls are able to bind to albumin as measured in the SA08b binding assay.

Fig. 15 Both D3H44 albumin-binding fusions are capable of binding TF and albumin simultaneously as judged by a biotin-TF binding assay.

Fig. 16 Fusion of the albumin binding peptide to D3H44 results in a protein having improved pharmacokinetic parameters.

Fig. 17. Fusion of the albumin binding peptide to D3H44 results in a protein having improved pharmacokinetic parameters.

Detailed Description of the Preferred Embodiments

I.   Definitions

The term "peptide ligand" within the context of the present invention is meant to refer to non-naturally occurring amino acid sequences that function to bind a particular target molecule. Peptide ligands within the context of the present invention are generally constrained (that is, having some element of structure as, for example, the presence of amino acids which initiate a β turn or β pleated sheet, or for example, cyclized by the presence of disulfide-bonded Cys residues) or unconstrained (linear) amino acid sequences of less than about 50 amino acid residues, and preferably less than about 40 amino acids residues. Of the peptide ligands less than about 40 amino acid residues, preferred are the peptide ligands of between about 10 and about 30 amino acid residues and especially the peptide ligands of about 20 amino acid residues. However, upon reading the instant disclosure, the skilled artisan will recognize that it is not the length of a particular peptide ligand but its ability to bind a particular target molecule that distinguishes the peptide ligand of the present invention. Therefore peptide ligands of 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 and 25 amino acid residues, for example, are equally likely to be peptide ligands within the context of the present invention.

A peptide ligand of the present invention will bind a target molecule with sufficient affinity and specificity if the peptide ligand "homes" to, "binds" or "targets" a target molecule such as a specific cell type bearing the target molecule *in vitro* and preferably *in vivo* (*see*, for example,

the use of the term "homes to," "homing," and "targets" in Pasqualini and Ruoslahti (1996) *Nature*, **380**:364-366 and Arap *et al.*, (1998) *Science,* **279**:377-380). In general, the peptide ligand will bind a target molecule with an affinity characterized by a dissociation constant, K_d, of less than about 1 µM, preferably less than about 100 nM and more preferably less than about 10 nM.

5   However, peptide ligands having an affinity for a target molecule of less than about 1 nM and preferably between about 1 pM and 1 nM are equally likely to be peptide ligands within the context of the present invention. In general a peptide ligand that binds a particular target molecule as described above can be isolated and identified by any of a number of art-standard techniques as described herein.

10   Peptides ligands are amino acid sequences as described above which may contain naturally as well as non-naturally occurring amino acid residues. Therefore, so-called "peptide mimetics" and "peptide analogs" which may include non-amino acid chemical structures that mimic the structure of a particular amino acid or peptide may be peptide ligands within the context of the invention. Such mimetics or analogs are characterized generally as exhibiting similar physical characteristics such as size, charge or hydrophobicity present in the appropriate spacial orientation

15   as found in their peptide counterparts. A specific example of a peptide mimetic compound is a compound in which the amide bond between one or more of the amino acids is replaced by, for example, a carbon-carbon bond or other bond as is well known in the art (*see*, for example Sawyer, in Peptide Based Drug Design pp. 378-422 (ACS, Washington DC 1995)).

20   Therefore, the term "amino acid" within the scope of the present invention is used in its broadest sense and is meant to include naturally occurring L α-amino acids or residues. The commonly used one and three letter abbreviations for naturally occurring amino acids are used herein (Lehninger, A.L., Biochemistry, 2d ed., pp. 71-92, (1975), Worth Publishers, New York). The correspondence between the standard single letter codes and the standard three letter codes is

25   well known to the skilled artisan, and is reproduced here: A = Ala; C = Cys; D = Asp; E = Glu; F = Phe; G = Gly; H = His; I = Ile; K = Lys; L = Leu; M = Met; N = Asn; P = Pro; Q = Gln; R = Arg; S = Ser; T = Thr; V = Val; W = Trp; Y = Tyr. The term includes D-amino acids as well as chemically modified amino acids such as amino acid analogs, naturally occurring amino acids that are not usually incorporated into proteins such as norleucine, and chemically synthesized

30   compounds having properties known in the art to be characteristic of an amino acid. For example, analogs or mimetics of phenylalanine or proline, which allow the same conformational restriction of the peptide compounds as natural Phe or Pro are included within the definition of amino acid. Such analogs and mimetics are referred to herein as "functional equivalents" of an amino acid. Other examples of amino acids are listed by Roberts and Vellaccio The Peptides: Analysis,

Synthesis, Biology, Gross and Meiehofer, eds., Vol. 5 p. 341, Academic Press, Inc., N.Y. 1983, which is incorporated herein by reference.

Peptide ligands synthesized by, for example, standard solid phase synthesis techniques, are not limited to amino acids encoded by genes. Commonly encountered amino acids which are not

5   encoded by the genetic code, include, for example, those described in International Publication No. WO 90/01940 such as, for example, 2-amino adipic acid (Aad) for Glu and Asp; 2-aminopimelic acid (Apm) for Glu and Asp; 2-aminobutyric (Abu) acid for Met, Leu, and other aliphatic amino acids; 2-aminoheptanoic acid (Ahe) for Met, Leu and other aliphatic amino acids; 2-aminoisobutyric acid (Aib) for Gly; cyclohexylalanine (Cha) for Val, and Leu and Ile;

10   homoarginine (Har) for Arg and Lys; 2,3-diaminopropionic acid (Dpr) for Lys, Arg and His; N-ethylglycine (EtGly) for Gly, Pro, and Ala; N-ethylglycine (EtGly) for Gly, Pro, and Ala; N-ethylasparigine (EtAsn) for Asn, and Gln; Hydroxyllysine (Hyl) for Lys; allohydroxyllysine (AHyl) for Lys; 3-(and 4)-hydoxyproline (3Hyp, 4Hyp) for Pro, Ser, and Thr; allo-isoleucine (AIle) for Ile, Leu, and Val; ρ-amidinophenylalanine for Ala; N-methylglycine (MeGly, sarcosine)

15   for Gly, Pro, and Ala; N-methylisoleucine (MeIle) for Ile; Norvaline (Nva) for Met and other aliphatic amino acids; Norleucine (Nle) for Met and other aliphatic amino acids; Ornithine (Orn) for Lys, Arg and His; Citrulline (Cit) and methionine sulfoxide (MSO) for Thr, Asn and Gln; N-methylphenylalanine (MePhe), trimethylphenylalanine, halo (F, Cl, Br, and I) phenylalanine, trifluorylphenylalanine, for Phe.

20   Peptide ligands within the context of the present invention may be "engineered", i.e., they are non-native or non-naturally occurring peptide ligands. By "non-native" or "non-naturally occurring" is meant that the amino acid sequence of the particular peptide ligand is not found in nature. That is to say, amino acid sequences of non-native or non-naturally occurring peptide ligands do not correspond to an amino acid sequence of a naturally occurring protein or

25   polypeptide. Peptide ligands of this variety may be produced or selected using a variety of techniques well known to the skilled artisan. For example, constrained or unconstrained peptide libraries may be randomly generated and displayed on phage utilizing art standard techniques, for example, Lowman et al., (1998) Biochemistry 37:8870-8878.

Peptide ligands, when used within the context of the present invention, may be

30   "conjugated" to a therapeutic or diagnostic substance. The term "conjugated" is used in its broadest sense to encompass all methods of attachment or joining that are known in the art. For example, in a typical embodiment, the therapeutic or diagnostic substance is a protein (referred to herein as a "protein therapeutic"), and the peptide ligand will be an amino acid extension of the C- or N-terminus of the protein therapeutic. In addition, a short amino acid linker sequence may lie

35   between the protein therapeutic and the peptide ligand. In this scenario, the peptide ligand,

optional linker and protein therapeutic will be coded for by a nucleic acid comprising a sequence encoding protein therapeutic operably linked to (in the sense that the DNA sequences are contiguous and in reading frame) an optional linker sequence encoding a short polypeptide as described below, and a sequence encoding the peptide ligand. In this typical scenario, the peptide

5   ligand is considered to be "conjugated" to the protein therapeutic optionally via a linker sequence. In a related embodiment, the peptide ligand amino acid sequence may interrupt or replace a section of the protein therapeutic amino acid sequence, provided, of course, that the insertion of the peptide ligand amino acid sequence does not interfere with the function of the protein therapeutic. In this embodiment, the "conjugate" may be coded for by a nucleic acid comprising a sequence

10   encoding protein therapeutic interrupted by and operably linked to a sequence encoding the peptide ligand. In a further typical embodiment, the peptide will be linked, e.g., by chemical conjugation to the protein therapeutic or other therapeutic optionally via a linker sequence. Typically, according to this embodiment, the peptide ligand will be linked to the protein therapeutic via a side chain of an amino acid somewhere in the middle of the protein therapeutic that doesn't interfere

15   with the therapeutic's activity. Here again, the peptide is considered to be "conjugated" to the therapeutic.

As used within the context of the present invention the term "target molecule" includes, proteins, peptides, glycoproteins, glycopeptides, glycolipids, polysaccharides, oligosaccharides, nucleic acids, and the like. Target molecules include, for example, extracellular molecules such as

20   various serum factors including but not limited to plasma proteins such as serum albumin, immunoglobulins, apolipoproteins or transferrin, or proteins found on the surface of erythrocytes or lymphocytes, provided, of course, that binding of the peptide ligand to the cell surface protein does not substantially interfere with the normal function of the cell.

"Antibodies" and "immunoglobulins" are usually heterotetrameric glycoproteins of about

25   150,000 Daltons, composed of two identical light (L) chains and two identical heavy (H) chains.

Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments or regions, each with a single antigen-binding site, and a residual "Fc" fragment or region. Although the boundaries of the Fc region of an immunoglobulin heavy chain might vary, the human IgG heavy chain Fc region is usually defined to stretch from an amino acid

30   residue at position Cys226, or from Pro230, to the carboxyl-terminus thereof.

Pepsin treatment yields an F(ab')$_2$ fragment that has two antigen-combining sites and is still capable of cross-linking antigen. The Fab' fragment contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain.

"Treatment" refers to both therapeutic treatment and prophylactic or preventative measures. Those in need of treatment include those already with the disorder as well as those in which the disorder is to be prevented.

"Mammal" for purposes of treatment refers to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, horses, cats, cows, *etc.* Preferably, the mammal is human.

A "disorder" is any condition that would benefit from treatment with the compositions comprising the peptide ligands of the invention. This includes chronic and acute disorders or diseases including those pathological conditions which predispose the mammal to the disorder in question.

"Elimination half-time" is used in its ordinary sense, as is described in <u>Goodman and Gillman's The Pharmaceutical Basis of Therapeutics</u> 21-25 (Alfred Goodman Gilman, Louis S. Goodman, and Alfred Gilman, eds., 6th ed. 1980). Briefly, the term is meant to encompass a quantitative measure of the time course of drug elimination. The elimination of most drugs is exponential (*i.e.*, follows first-order kinetics), since drug concentrations usually do not approach those required for saturation of the elimination process. The rate of an exponential process may be expressed by its rate constant, k, which expresses the fractional change per unit of time, or by its half-time, $t_{1/2}$, the time required for 50% completion of the process. The units of these two constants are time^{-1} and time, respectively. A first-order rate constant and the half-time of the reaction are simply related (k x $t_{1/2}$ = 0.693) and may be interchanged accordingly. Since first-order elimination kinetics dictates that a constant fraction of drug is lost per unit time, a plot of the log of drug concentration versus time is linear at all times following the initial distribution phase (*i.e.* after drug absorption and distribution are complete). The half-time for drug elimination can be accurately determined from such a graph.

"Transfection" refers to the taking up of an expression vector by a host cell whether or not any coding sequences are in fact expressed. Numerous methods of transfection are known to the ordinarily skilled artisan, for example, $CaPO_4$ precipitation and electroporation. Successful transfection is generally recognized when any indication of the operation of this vector occurs within the host cell.

"Transformation" means introducing DNA into an organism so that the DNA is replicable, either as an extrachromosomal element or by chromosomal integrant. Depending on the host cell used, transformation is done using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in section 1.82 of Sambrook *et al.*, <u>Molecular Cloning</u> (2nd ed.), Cold Spring Harbor Laboratory, NY (1989), is generally used for prokaryotes or other cells that contain substantial cell-wall barriers. Infection with *Agrobacterium tumefaciens*

is used for transformation of certain plant cells, as described by Shaw *et al.*, (1983) *Gene*, **23**:315 and WO 89/05859 published 29 June 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method described in sections 16.30-16.37 of Sambrook *et al.*, *supra*, is preferred. General aspects of mammalian cell host system transformations have been

5   described by Axel in U.S. Patent No. 4,399,216 issued 16 August 1983. Transformations into yeast are typically carried out according to the method of Van Solingen *et al.*, (1977) *J. Bact.*, **130**:946 and Hsiao *et al.*, (1979) *Proc. Natl. Acad. Sci. (USA)*, **76**:3829. However, other methods for introducing DNA into cells such as by nuclear injection, electroporation, or by protoplast fusion may also be used.

10   As used herein, the term "pulmonary administration" refers to administration of a formulation of the invention through the lungs by inhalation. As used herein, the term "inhalation" refers to intake of air to the alveoli. In specific examples, intake can occur by self-administration of a formulation of the invention while inhaling, or by administration via a respirator, *e.g.*, to an patient on a respirator. The term "inhalation" used with respect to a formulation of the invention is

15   synonymous with "pulmonary administration."

       As used herein, the term "parenteral" refers to introduction of a compound of the invention into the body by other than the intestines, and in particular, intravenous (i.v.), intraarterial (i.a.), intraperitoneal (i.p.), intramuscular (i.m.), intraventricular, and subcutaneous (s.c.) routes.

       As used herein, the term "aerosol" refers to suspension in the air. In particular, aerosol

20   refers to the particlization of a formulation of the invention and its suspension in the air. According to the present invention, an aerosol formulation is a formulation comprising a compound of the present invention that is suitable for aerosolization, *i.e.*, particlization and suspension in the air, for inhalation or pulmonary administration.

II.   **Modes for Carrying out the Invention**

25   A.   **Peptide Ligands**

       Peptide ligands within the context of the present invention bind a target, preferably a serum protein such as serum albumin or an immunoglobulin, and can be identified in a direct binding assay, or by their ability to compete for target binding with a known ligand for the target. Preferred peptide ligands that bind serum albumin include linear and cyclic peptides, preferably

30   cyclic peptide compounds comprising the following formulae or are peptides that compete for binding serum albumin of a particular mammalian species with peptides of the following formulae:

$(Xaa)_X$-Xaa-Xaa-Cys-Xaa-Xaa-Xaa-Xaa-Xaa-Cys-Xaa-Xaa-$(Xaa)_Z$

$(Xaa)_X$-Phe-Cys-Xaa-Asp-Trp-Pro-Xaa-Xaa-Xaa-Ser-Cys-$(Xaa)_Z$ (SEQ ID NO: y)

$(Xaa)_X$-Val-Cys-Tyr-Xaa-Xaa-Xaa-Ile-Cys-Phe-$(Xaa)_Z$ (SEQ ID NO: y2)

(Xaa)$_x$-Cys-Tyr-Xaa$_1$-Pro-Gly-Xaa-Cys-(Xaa)$_z$ (SEQ ID NO: y3)

and (Xaa)$_x$-Asp-Xaa-Cys-Leu-Pro-Xaa-Trp-Gly-Cys-Leu-Trp-(Xaa)$_z$ (SEQ ID NO: z)

Preferred are peptide compounds of the foregoing general formulae wherein Xaa is an amino acid and x and z are a whole number greater or equal to 0 (zero), generally less than 100, preferably

5   less than 10 and more preferably 0, 1, 2, 3, 4 or 5 and more preferably 4 or 5 and wherein Xaa$_1$ is selected from the group consisting of Ile, Phe, Tyr and Val.

Further preferred peptide ligands that bind a serum albumin are identified as described herein in the context of the following general formulae (Xaa)$_x$-Trp-Cys-Asp-Xaa-Xaa-Leu-Xaa-Ala-Xaa-Asp-Leu-Cys-(Xaa)$_z$ and

10   (Xaa)$_x$-Asp-Leu-Val-Xaa-Leu-Gly-Leu-Glu-Cys-Trp-(Xaa)$_z$

wherein Xaa is an amino acid and x and z are a whole number greater or equal to zero, generally less than 100, preferably less than 10 and more preferably 0, 1, 2, 3, 4 or 5 and more preferably 4 or 5.

According to this aspect of the invention reference is made to the Figures and especially

15   Figures 5A and 5B, 8A, 8B and 8C and Figure 9 for exemplary peptides and appropriate amino acids for selecting peptides ligands that bind a mammalian serum albumin. In a preferred aspect, reference is made to Figure 9 for selecting peptide ligands that bind accross several species of serum albumin.

Preferred compounds according to this aspect of the invention include:

20   Asp-Leu-Cys-Leu-Arg-Asp-Trp-Gly-Cys-Leu-Trp   (SEQ ID NO: z1)

Asp-Ile-Cys-Leu-Pro-Arg-Trp-Gly-Cys-Leu-Trp   (SEQ ID NO: z2)

Met-Glu-Asp-Ile-Cys-Leu-Pro-Arg-Trp-Gly-Cys-Leu-Trp-Glu-Asp   (SEQ ID NO: z3)

Gln-Arg-Leu-Met-Glu-Asp-Ile-Cys-Leu-Pro-Arg-Trp-Gly-Cys-Leu-Trp-Glu-Asp-Asp-Phe

(SEQ ID NO: z4)

25   Gln-Gly-Leu-Ile-Gly-Asp-Ile-Cys-Leu-Pro-Arg-Trp-Gly-Cys-Leu-Trp-Gly-Asp-Ser-Val

(SEQ ID NO: z5)

Gln-Gly-Leu-Ile-Gly-Asp-Ile-Cys-Leu-Pro-Arg-Trp-Gly-Cys-Leu-Trp-Gly-Asp-Ser-Val-Lys

(SEQ ID NO: z6)

Glu-Asp-Ile-Cys-Leu-Pro-Arg-Trp-Gly-Cys-Leu-Trp-Glu-Asp-Asp   (SEQ ID NO: z7)

30   Arg-Leu-Met-Glu-Asp-Ile-Cys-Leu-Pro-Arg-Trp-Gly-Cys-Leu-Trp-Glu-Asp-Asp

(SEQ ID NO: z8)

Met-Glu-Asp-Ile-Cys-Leu-Pro-Arg-Trp-Gly-Cys-Leu-Trp-Glu-Asp-Asp (SEQ ID NO: z9)

Met-Glu-Asp-Ile-Cys-Leu-Pro-Arg-Trp-Gly-Cys-Leu-Trp-Glu-Asp   (SEQ ID NO: z10)

Arg-Leu-Met-Glu-Asp-Ile-Cys-Leu-Ala-Arg-Trp-Gly-Cys-Leu-Trp-Glu-Asp-Asp

35   (SEQ ID NO: z11)

12

Glu-Val-Arg-Ser-Phe-Cys-Thr-Asp-Trp-Pro-Ala-Glu-Lys-Ser-Cys-Lys-Pro-Leu-Arg-Gly   (SEQ
ID NO: z12)

Arg-Ala-Pro-Glu-Ser-Phe-Val-Cys-Tyr-Trp-Glu-Thr-Ile-Cys-Phe-Glu-Arg-Ser-Glu-Gln (SEQ ID
NO: z13)

Glu-Met-Cys-Tyr-Phe-Pro-Gly-Ile-Cys-Trp-Met (SEQ ID NO: z14)

In a preferred embodiment, peptide ligands of the present invention bind IgG-Fc and can
be identified by their ability to compete for binding of IgG-Fc in an *in vitro* assay with a peptide
ligand having the general formula:

Xaa$_i$-Cys-Xaa$_j$-Cys-Xaa$_k$ (SEQ ID NO: 1), wherein Xaa$_i$ is absent or is a peptide of
between 1 and 4 amino acids, preferably 4 amino acids; X$_j$ is preferably 9 amino acids having a
preferred sequence Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Leu-Val-Trp (SEQ ID NO: 10); or Xaa-Xaa-Xaa-
Xaa-Gly-Glu-Leu-Val-Trp (SEQ ID NO: 11); or Xaa$_1$-Xaa$_2$-Xaa$_3$-Xaa$_4$-Gly-Glu-Leu-Val-Trp
(SEQ ID NO: 12), wherein Xaa$_1$ is Ala, Ser, or Thr; Xaa$_2$ is Trp or Tyr; Xaa$_3$ is His, or Trp; Xaa$_4$
is Leu or Met, and Xaa$_k$ is absent or between 1 and 5 amino acids, preferably 5 amino acids, so
long as the cyclic peptide or analog thereof retains the qualitative biological activity of binding
IgG-Fc described above.

Preferred among this group of compounds are compounds comprising the sequence:

Xaa-Xaa-Xaa-Xaa-Cys-Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Leu-Val-Trp-Cys-Xaa-Xaa-Xaa-
Xaa-Xaa (SEQ ID NO: 13);

Xaa-Xaa-Xaa-Xaa-Cys-Xaa-Xaa-Xaa-Xaa-Gly-Glu-Leu-Val-Trp-Cys-Xaa-Xaa-Xaa-Xaa-
Xaa (SEQ ID NO: 14);

Xaa$_1$-Xaa$_2$-Xaa$_3$-Xaa$_4$-Cys-Xaa$_5$-Xaa$_6$-Xaa$_7$-Xaa$_8$-Gly-Glu-Leu-Val-Trp-Cys-Xaa$_9$-
Xaa$_{10}$-Xaa$_{11}$-Xaa$_{12}$-Xaa$_{13}$ (SEQ ID NO: 15), wherein Xaa$_5$ is Ala, Ser, or Thr; Xaa$_6$ is Trp or
Tyr; Xaa$_7$ is His, or Trp; and Xaa$_8$ is Leu or Met; and

Xaa$_1$-Xaa$_2$-Xaa$_3$-Xaa$_4$-Cys-Xaa$_5$-Xaa$_6$-Xaa$_7$-Xaa$_8$-Gly-Glu-Leu-Val-Trp-Cys-Xaa$_9$-
Xaa$_{10}$-Xaa$_{11}$-Xaa$_{12}$-Xaa$_{13}$ (SEQ ID NO: 16) wherein Xaa$_4$ is Ser, Arg, or Asp; Xaa$_5$ is Ala, Ser,
or Thr; Xaa$_6$ is Trp, Tyr; Xaa$_7$ is His, or Trp; Xaa$_8$ is Leu or Met; and Xaa$_9$ is Glu, Ser, Thr or
Val. In particular embodiments, the IgG-Fc binding peptide ligands of the present invention will
compete with any of the peptide ligands represented in SEQ ID NO: 3 - SEQ ID NO: 4, SEQ ID
NO: 9; and SEQ ID NO: 13 - SEQ ID NO: 111 described herein and preferably will compete with
SEQ ID NO: 9 for binding IgG-Fc.

In another preferred embodiment, peptide ligands of the present invention bind human
serum albumin and can be identified by their ability to compete for binding of human serum
albumin in an *in vitro* assay with peptide ligands having the general formulae:

(Xaa)$_x$-Asp-Xaa-Cys-Leu-Pro-Xaa-Trp-Gly-Cys-Leu-Trp-(Xaa)$_z$

(Xaa)$_X$-Phe-Cys-Xaa-Asp-Trp-Pro-Xaa-Xaa-Xaa-Ser-Cys-(Xaa)$_z$

(Xaa)$_X$-Val-Cys-Tyr-Xaa-Xaa-Xaa-Ile-Cys-Phe-(Xaa)$_z$ or

(Xaa)$_X$-Cys-Tyr-Xaa$_1$-Pro-Gly-Xaa-Cys-(Xaa)$_z$

wherein Xaa is an amino acid, x and z are preferably 4 or 5 and Xaa$_1$ is selected from the group

consisting of Ile, Phe, Tyr and Val.

In particular embodiments, the human serum albumin binding peptide ligands of the present invention will compete with any of the peptide ligands represented in SEQ ID NO: z2 - z14 described herein above and preferably will compete with SEQ ID NO: z4 for binding human serum albumin.

As will be appreciated from the foregoing, the term "compete" and "ability to compete" are relative terms. Thus the terms, when used to describe the peptide ligands of the present invention, refer to peptide ligands that produce a 50% inhibition of binding of, for example SEQ ID NO: 9 or SEQ ID NO: z4, when present at 50 μM, preferably when present at 1 μM, more preferably 100 nM, and preferably when present at 1 nM or less in a standard competition assay as described herein. Such peptide ligands generally will bind IgG-Fc with an affinity of less than 1 μM, preferably less than about 100 nM and more preferably less than about 10 nM as determined by a standard competition assay such as the one described in the Example sections. However, peptide ligands having an affinity for a serum protein such as serum albumin or IgG-Fc of less than about 1 nM and preferably between about 1 pM and 1 nM are equally likely to be peptide ligands within the context of the present invention.

For *in vitro* assay systems to determine whether a peptide or other compound has the "ability" to compete with a peptide ligand for binding to an IgG-Fc (or other plasma protein such as, *e.g.*, serum albumin) as noted herein, the skilled artisan can employ any of a number of standard competition assays. Competitive binding assays rely on the ability of a labeled standard to compete with the test sample analyte for binding with a limited amount of ligand. The amount of analyte in the test sample is inversely proportional to the amount of standard that becomes bound to the ligand.

Thus, the skilled artisan may determine whether a peptide or other compound has the ability to compete with a peptide ligand for binding to an IgG-Fc (or other target such as a plasma protein) employing procedures which include but are not limited to competitive assay systems using techniques such as radioimmunoassays (RIA), enzyme immunoassays (EIA), preferably the enzyme linked immunosorbent assay (ELISA), "sandwich" immunoassays, immunoradiometric assays, fluorescent immunoassays, and immunoelectrophoresis assays, to name but a few.

For these purposes the selected peptide ligand will be labeled with a detectable moiety (the detectably labeled peptide ligand hereafter called the "tracer") and used in a competition assay with a candidate compound for binding IgG-Fc domain or other target. Numerous detectable labels are available which can be preferably grouped into the following categories:

5   (a) Radioisotopes, such as ^{35}S, ^{14}C, ^{125}I, ^3H, and ^{131}I. The peptide compound can be labeled with the radioisotope using the techniques described in Coligen et al., eds., Current Protocols in Immunology, Volumes 1 and 2 (1991), Wiley-Interscience, New York, N.Y., for example and radioactivity can be measured using scintillation counting.

(b) Fluorescent labels such as rare earth chelates (europium chelates) or fluorescein and its

10   derivatives, rhodamine and its derivatives, dansyl, lissamine, phycoerythrin and Texas Red are available. The fluorescent labels can be conjugated to the peptide compounds using the techniques disclosed in Current Protocols in Immunology, supra, for example. Fluorescence can be quantified using a fluorimeter.

(c) Various enzyme-substrate labels are available and U.S. Patent No. 4,275,149 provides

15   a review of some of these. The enzyme preferably catalyzes a chemical alteration of the chromogenic substrate which can be measured using various techniques. For example, the enzyme may catalyze a color change in a substrate, which can be measured spectrophotometrically. Alternatively, the enzyme may alter the fluorescence or chemiluminescence of the substrate. Techniques for quantifying a change in fluorescence are described above. The chemiluminescent

20   substrate becomes electronically excited by a chemical reaction and may then emit light which can be measured (using a chemiluminometer, for example) or donates energy to a fluorescent acceptor. Examples of enzymatic labels include luciferases (e.g., firefly luciferase and bacterial luciferase; U.S. Patent No. 4,737,456), luciferin, 2,3-dihydrophthalazinediones, malate dehydrogenase, urease, peroxidase such as horseradish peroxidase (HRP), alkaline phosphatase, β-galactosidase,

25   glucoamylase, lysozyme, saccharide oxidases (e.g., glucose oxidase, galactose oxidase, and glucose-6-phosphate dehydrogenase), heterocyclic oxidases (such as uricase and xanthine oxidase), lactoperoxidase, microperoxidase, and the like.

Examples of enzyme-substrate combinations include, for example:

(i) Horseradish peroxidase (HRP) with hydrogen peroxidase as a substrate, wherein the

30   hydrogen peroxidase oxidizes a dye precursor (e.g. ABTS, orthophenylene diamine (OPD) or 3,3',5,5'-tetramethyl benzidine hydrochloride (TMB));

(ii) alkaline phosphatase (AP) with para-nitrophenyl phosphate as chromogenic substrate; and

(iii) β-D-galactosidase (β-D-Gal) with a chromogenic substrate (e.g. p-nitrophenyl-β-D-

35   galactosidase) or fluorogenic substrate 4-methylumbelliferyl-β-D-galactosidase.

15

According to a particular assay, the tracer is incubated with immobilized target in the presence of varying concentrations of unlabeled candidate compound. Increasing concentrations of successful candidate compound effectively compete with binding of the tracer to immobilized target. The concentration of unlabeled candidate compound at which 50% of the maximally-bound

5   tracer is displaced is referred to as the "IC_{50}" and reflects the IgG binding affinity of the candidate compound. Therefore a candidate compound with an IC_{50} of 1 mM displays a substantially weaker interaction with the target than a candidate compound with an IC_{50} of 1 μM.

In some phage display ELISA assays, binding affinity of a mutated ("mut") sequence was directly compared of a control ("con") peptide using methods described in B.C. Cunningham, D.G.

10   Lowe, B. Li, B.D. Bennett, and J.A. Wells, *EMBO J.* **13**:2508 (1994) and characterized by the parameter EC_{50}. Assays were performed under conditions where $EC_{50}(con)/EC_{50}(mut)$ will approximate $K_d(con)/K_d(mut)$.

Accordingly, the invention provides compounds "having the ability to compete" for target molecules such as IgG or human serum albumin binding in an *in vitro* assay as described.

15   Preferably the compound has an IC_{50} for the target such as IgG or human serum albumin of less than 1 μM. Preferred among these compound are compounds having an IC_{50} of less than about 100 nM and preferably less than about 10 nM or less than about 1 nM. In further preferred embodiments according to this aspect of the invention the compounds display an IC_{50} for the target molecule such as IgG or human serum albumin of less than about 100 pM and more

20   preferably less than about 10 pM.

A preferred *in vitro* assay for the determination of a candidate compound's ability to compete with a peptide ligand described herein is as follows and is described more fully in the Examples. In preferred embodiments the candidate compound is a peptide. The ability of a candidate compound to compete with a labeled peptide ligand tracer for binding to IgG or human

25   serum albumin is monitored using an ELISA. Dilutions of a candidate compound in buffer are added to microtiter plates coated with IgG or human serum albumin (as described in the Example Sections) along with tracer for 1 hr. The microtiter plate is washed with wash buffer and the amount of tracer bound to IgG or human serum albumin measured.

B.   Peptide Ligand Combinations

30   According to the present invention, the peptide ligand is optionally linked to a bioactive compound to form a hybrid molecule that comprises a peptide ligand domain and an active domain. The bioactive compounds of the invention include any compound useful as a therapeutic or diagnostic agent. Non-limiting examples of bioactive compounds include polypeptides such as enzymes, hormones, cytokines, antibodies or antibody fragments, as well as organic compounds

35   such as analgesics, antipyretics, antiinflammatory agents, antibiotics, antiviral agents, anti-fungal

16

drugs, cardiovascular drugs, drugs that affect renal function and electrolyte metabolism, drugs that act on the central nervous system, chemotherapeutic drugs, *etc.* According to the present invention the peptide ligand domain is joined to an active domain, optionally via a flexible linker domain.

5   The hybrid molecules of the present invention are constructed by combining a peptide ligand domain with a suitable active domain. Depending on the type of linkage and its method of production, the peptide ligand domain may be joined via its N- or C-terminus to the N- or C-terminus of the active domain. For example, when preparing the hybrid molecules of the present invention via recombinant techniques, nucleic acid encoding a peptide ligand will be operably linked to nucleic acid encoding the active domain sequence, optionally via a linker domain.

10 Typically the construct encodes a fusion protein wherein the C-terminus of the peptide ligand is joined to the N-terminus of the active domain. However, especially when synthetic techniques are employed, fusions where, for example, the N-terminus of the peptide ligand is joined to the N- or C-terminus of the active domain also are possible.   In some instances, the peptide ligand domain may be inserted within the active domain molecule rather than being joined to the active

15 domain at its N-or C-terminus. This configuration may be used to practice the invention so long as the functions of the peptide ligand domain and the active domain are preserved. For example, a peptide ligand may be inserted into a non-binding light chain CDR of an immunoglobulin without interfering with the ability of the immunoglobulin to bind to its target. Regions of active domain molecules that can accommodate peptide ligand domain insertions may be identified empirically

20 (*i.e.*, by selecting an insertion site, randomly, and assaying the resulting conjugate for the function of the active domain), or by sequence comparisons amongst a family of related active domain molecules (*e.g.*, for active domains that are proteins) to locate regions of low sequence homology. Low sequence homology regions are more likely to tolerate insertions of peptide ligands domains than are regions that are well-conserved. For active domain molecules whose three-dimensional

25 structures are known (*e.g.* from X-ray crystallographic or NMR studies), the three-dimensional structure may provide guidance as to peptide ligand insertion sites. For example, loops or regions with high mobility (*i.e.*, large temperature or "B" factors) are more likely to accommodate peptide ligand domain insertions than are highly ordered regions of the structure, or regions involved in ligand binding or catalysis.

30

C.   Linker Domains

        According to the present invention, the peptide ligand domain is optionally linked to the active domain via a linker. The linker component of the hybrid molecule of the invention does not necessarily participate in but may contribute to the function of the hybrid molecule. Therefore,

according to the present invention, the linker domain, is any group of molecules that provides a spatial bridge between the active domain and the peptide ligand domain.

The linker domain can be of variable length and makeup, however, according to the present invention, it is the length of the linker domain and not its structure that is important. The linker domain preferably allows for the peptide ligand domain of the hybrid molecule to bind, substantially free of steric and/or conformational restrictions to the target molecule. Therefore, the length of the linker domain is dependent upon the character of the two "functional" domains of the hybrid molecule, *i.e.*, the peptide ligand domain and the active domain.

One skilled in the art will recognize that various combinations of atoms provide for variable length molecules based upon known distances between various bonds (Morrison, and Boyd, Organic Chemistry, 3rd Ed, Allyn and Bacon, Inc., Boston, MA (1977)). For example, the linker domain may be a polypeptide of variable length. The amino acid composition of the polypeptide determines the character and length of the linker. In a preferred embodiment, the linker molecule comprises a flexible, hydrophilic polypeptide chain. Exemplary, linker domains comprises one or more Gly and or Ser residues, such as those described in the Example sections herein.

D.   Recombinant Synthesis

The present invention encompasses a composition of matter comprising an isolated nucleic acid, preferably DNA, encoding a peptide ligand or a hybrid molecule comprising a peptide ligand domain and a polypeptide active domain as described herein. DNAs encoding the peptides of the invention can be prepared by a variety of methods known in the art. These methods include, but are not limited to, chemical synthesis by any of the methods described in Engels *et al.* (1989), *Agnew. Chem. Int. Ed. Engl.* **28**:716-734, the entire disclosure of which is incorporated herein by reference, such as the triester, phosphite, phosphoramidite and H-phosphonate methods. In one embodiment, codons preferred by the expression host cell are used in the design of the encoding DNA. Alternatively, DNA encoding the peptides of the invention can be altered to encode one or more variants by using recombinant DNA techniques, such as site specific mutagenesis (Kunkel *et al.* (1991), *Methods Enzymol.*, **204**:125-139; Carter *et al.* (1986), *Nucl. Acids Res.* **13**:4331; Zoller *et al.* (1982), *Nucl. Acids Res.* **10**:6487), cassette mutagenesis (Wells *et al.* (1985), *Gene* **34**:315), restriction selection mutagenesis (Carter, Directed Mutagenesis: A Practical Approach (M.J. McPherson, ed.) IRL Press, Oxford, 1991), and the like.

According to preferred aspects described above, the nucleic acid encodes a peptide ligand capable of binding a target molecule. Target molecules include, for example, extracellular molecules such as various serum factors including but not limited to plasma proteins such as serum

albumin, immunoglobulins, apolipoproteins or transferrin, or proteins found on the surface of erythrocytes or lymphocytes, provided, of course, that binding of the peptide ligand to the cell surface protein does not substantially interfere with the normal function of the cell.

5   According to another preferred aspect of the invention, the nucleic acid encodes a hybrid molecule comprising a peptide ligand domain sequence and an active domain. In this aspect of the invention, the active domain may comprise any polypeptide compound useful as a therapeutic or diagnostic agent, e.g., enzymes, hormones, cytokines, antibodies or antibody fragments. The nucleic acid molecule according to this aspect of the present invention encodes a hybrid molecule and the nucleic acid encoding the peptide ligand domain sequence is operably linked to (in the

10   sense that the DNA sequences are contiguous and in reading frame) the nucleic acid encoding the biologically active agent. Optionally these DNA sequences may be linked through a nucleic acid sequence encoding a linker domain amino acid sequence.

        According to this aspect, the invention further comprises an expression control sequence operably linked to the DNA molecule encoding a peptide of the invention, an expression vector,

15   such as a plasmid, comprising the DNA molecule, wherein the control sequence is recognized by a host cell transformed with the vector, and a host cell transformed with the vector. In general, plasmid vectors contain replication and control sequences which are derived from species compatible with the host cell. The vector ordinarily carries a replication site, as well as sequences which encode proteins that are capable of providing phenotypic selection in transformed cells.

20   For expression in prokaryotic hosts, suitable vectors include pBR322 (ATCC No. 37,017), phGH107 (ATCC No. 40,011), pBO475, pS0132, pRIT5, any vector in the pRIT20 or pRIT30 series (Nilsson and Abrahmsen (1990), *Meth. Enzymol.* **185**:144-161), pRIT2T, pKK233-2, pDR540 and pPL-lambda. Prokaryotic host cells containing the expression vectors of the present invention include *E. coli* K12 strain 294 (ATCC NO. 31,446), *E. coli* strain JM101 (Messing *et*

25   *al.*(1981), *Nucl. Acid Res.* **9**:309), *E. coli* strain B, *E. coli* strain _1776 (ATCC No. 31537), *E. coli* c600, *E. coli* W3110 (F-, gamma-, prototrophic, ATCC No. 27,325), *E. coli* strain 27C7 (W3110, tonA, phoA E15, (argF-lac)169, ptr3, degP41, ompT, kan^r) (U.S. Patent No. 5,288,931, ATCC No. 55,244), *Bacillus subtilis*, *Salmonella typhimurium*, *Serratia marcesans*, and *Pseudomonas* species.

30   In addition to prokaryotes, eukaryotic organisms, such as yeasts, or cells derived from multicellular organisms can be used as host cells. For expression in yeast host cells, such as common baker's yeast or *Saccharomyces cerevisiae*, suitable vectors include episomally-replicating vectors based on the 2-micron plasmid, integration vectors, and yeast artificial chromosome (YAC) vectors. For expression in insect host cells, such as Sf9 cells, suitable vectors

35   include baculoviral vectors. For expression in plant host cells, particularly dicotyledonous plant

hosts, such as tobacco, suitable expression vectors include vectors derived from the Ti plasmid of
Agrobacterium tumefaciens.

Examples of useful mammalian host cells include monkey kidney CV1 line transformed
by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned

5   for growth in suspension culture, Graham *et al.* (1977), *J. Gen Virol.* **36**:59); baby hamster kidney
cells (BHK, ATCC CCL 10); Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin
(1980), *Proc. Natl. Acad. Sci. USA* **77**:4216); mouse sertoli cells (TM4, Mather (1980), *Biol.
Reprod.* **23**:243-251); monkey kidney cells (CV1 ATCC CCL 70); African green monkey kidney
cells (VERO-76, ATCC CRL-1587); human cervical carcinoma cells (HELA, ATCC CCL 2);

10   canine kidney cells (MDCK, ATCC CCL 34); buffalo rat liver cells (BRL 3A, ATCC CRL 1442);
human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); mouse
mammary tumor (MMT 060562, ATCC CCL51); TRI cells (Mather *et al.* (1982), *Annals N.Y.
Acad. Sci.* **383**:44-68); MRC 5 cells; FS4 cells; and a human hepatoma cell line (Hep G2). For
expression in mammalian host cells, useful vectors include vectors derived from SV40, vectors

15   derived from cytomegalovirus such as the pRK vectors, including pRK5 and pRK7 (Suva *et al.*
(1987), *Science* **237**:893-896; EP 307,247 (3/15/89), EP 278,776 (8/17/88)) vectors derived from
vaccinia viruses or other pox viruses, and retroviral vectors such as vectors derived from
Moloney's murine leukemia virus (MoMLV).

Optionally, the DNA encoding the peptide of interest is operably linked to a secretory

20   leader sequence resulting in secretion of the expression product by the host cell into the culture
medium. Examples of secretory leader sequences include STII, ecotin, lamB, herpes GD, lpp,
alkaline phosphatase, invertase, and alpha factor. Also suitable for use herein is the 36 amino acid
leader sequence of protein A (Abrahmsen *et al.* (1985), *EMBO J.* **4**:3901).

Host cells are transfected and preferably transformed with the above-described expression

25   or cloning vectors of this invention and cultured in conventional nutrient media modified as
appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the
desired sequences.

Prokaryotic host cells used to produce the present peptides can be cultured as described
generally in Sambrook *et al.*, *supra.*

30   The mammalian host cells used to produce peptides of the invention can be cultured in a
variety of media. Commercially available media such as Ham's F10 (Sigma), Minimal Essential
Medium ((MEM), Sigma), RPMI-1640 (Sigma), and Dulbecco's Modified Eagle's Medium
((DMEM), Sigma) are suitable for culturing the host cells. In addition, any of the media described
in Ham and Wallace (1979), *Meth. in Enz.* **58**:44, Barnes and Sato (1980), *Anal. Biochem.*

35   **102**:255, U.S. Patent Nos. 4,767,704; 4,657,866; 4,927,762; or 4,560,655; WO 90/03430;

WO 87/00195; U.S. Pat. Re. 30,985; or U.S. 5,122,469, the disclosures of all of which are incorporated herein by reference, may be used as culture media for the host cells. Any of these media may be supplemented as necessary with hormones and/or other growth factors (such as insulin, transferrin, or epidermal growth factor), salts (such as sodium chloride, calcium,

5   magnesium, and phosphate), buffers (such as HEPES), nucleosides (such as adenosine and thymidine), antibiotics (such as Gentamycin™ drug), trace elements (defined as inorganic compounds usually present at final concentrations in the micromolar range), and glucose or an equivalent energy source. Any other necessary supplements may also be included at appropriate concentrations that would be known to those skilled in the art. The culture conditions, such as

10   temperature, pH, and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

The host cells referred to in this disclosure encompass cells in *in vitro* culture as well as cells that are within a host animal.

E.   Chemical Synthesis

15   Another method of producing the compounds of the invention involves chemical synthesis. This can be accomplished by using methodologies well known in the art (*see* Kelley, R.F. & Winkler, M.E. in Genetic Engineering Principles and Methods, Setlow, J.K, ed., Plenum Press, N.Y., Vol. 12, pp 1-19 (1990); Stewart, J.M. Young, J.D., Solid Phase Peptide Synthesis, Pierce Chemical Co., Rockford, IL (1984); *see also* U.S. Pat. Nos. 4,105,603; 3,972,859; 3,842,067; and

20   3,862,925).

Peptide ligands of the invention can be prepared conveniently using solid-phase peptide synthesis. Merrifield (1964), *J. Am. Chem. Soc.* **85**:2149; Houghten (1985), *Proc. Natl. Acad. Sci. USA* **82**:5132. Solid-phase peptide synthesis also can be used to prepare the hybrid molecule compositions of the invention if the active domain is or comprises a polypeptide.

25   Solid-phase synthesis begins at the carboxy terminus of the nascent peptide by coupling a protected amino acid to an inert solid support. The inert solid support can be any macromolecule capable of serving as an anchor for the C-terminus of the initial amino acid. Typically, the macromolecular support is a cross-linked polymeric resin (*e.g.*, a polyamide or polystyrene resin) as shown in Figures 1-1 and 1-2, on pages 2 and 4 of Stewart and Young, *supra*. In one

30   embodiment, the C-terminal amino acid is coupled to a polystyrene resin to form a benzyl ester. A macromolecular support is selected such that the peptide anchor link is stable under the conditions used to deprotect the α-amino group of the blocked amino acids in peptide synthesis. If a base-labile α-protecting group is used, then it is desirable to use an acid-labile link between the peptide and the solid support. For example, an acid-labile ether resin is effective for base-labile Fmoc-

35   amino acid peptide synthesis as described on page 16 of Stewart and Young, *supra*. Alternatively,

a peptide anchor link and α-protecting group that are differentially labile to acidolysis can be used. For example, an aminomethyl resin such as the phenylacetamidomethyl (Pam) resin works well in conjunction with Boc-amino acid peptide synthesis as described on pages 11-12 of Stewart and Young, *supra*.

5   After the initial amino acid is coupled to an inert solid support, the α-amino protecting group of the initial amino acid is removed with, for example, trifluoroacetic acid (TFA) in methylene chloride and neutralized in, for example, triethylamine (TEA). Following deprotection of the initial amino acid's α-amino group, the next α-amino and side chain protected amino acid in the synthesis is added. The remaining α-amino and, if necessary, side chain protected amino acids

10   are then coupled sequentially in the desired order by condensation to obtain an intermediate compound connected to the solid support. Alternatively, some amino acids may be coupled to one another to form a fragment of the desired peptide followed by addition of the peptide fragment to the growing solid phase peptide chain.

        The condensation reaction between two amino acids, or an amino acid and a peptide, or a

15   peptide and a peptide can be carried out according to the usual condensation methods such as the axide method, mixed acid anhydride method, DCC (N,N'-dicyclohexylcarbodiimide) or DIC (N,N'-diisopropylcarbodiimide) methods, active ester method, p-nitrophenyl ester method, BOP (benzotriazole-1-yl-oxy-tris [dimethylamino] phosphonium hexafluorophosphate) method, N-hydroxysuccinic acid imido ester method, *etc.*, and Woodward reagent K method.

20   It is common in the chemical synthesis of peptides to protect any reactive side chain groups of the amino acids with suitable protecting groups. Ultimately, these protecting groups are removed after the desired polypeptide chain has been sequentially assembled. Also common is the protection of the α-amino group on an amino acid or peptide fragment while the C-terminal carboxy group of the amino acid or peptide fragment reacts with the free N-terminal amino group

25   of the growing solid phase polypeptide chain, followed by the selective removal of the α-amino group to permit the addition of the next amino acid or peptide fragment to the solid phase polypeptide chain. Accordingly, it is common in polypeptide synthesis that an intermediate compound is produced which contains each of the amino acid residues located in the desired sequence in the peptide chain wherein individual residues still carry side-chain protecting groups.

30   These protecting groups can be removed substantially at the same time to produce the desired polypeptide product following removal from the solid phase.

        α- and ε-amino side chains can be protected with benzyloxycarbonyl (abbreviated Z), isonicotinyloxycarbonyl (iNOC), o-chlorobenzyloxycarbonyl [Z(2Cl)], p-nitrobenzyloxycarbonyl [Z(NO$_2$)], p-methoxybenzyloxycarbonyl [Z(OMe)], t-butoxycarbonyl (Boc), t-amyloxycarbonyl

(Aoc), isobornyloxycarbonyl, adamantyloxycarbonyl, 2-(4-biphenyl)-2-propyloxycarbonyl (Bpoc), 9-fluorenylmethoxycarbonyl (Fmoc), methylsulfonyethoxycarbonyl (Msc), trifluoroacetyl, phthalyl, formyl, 2-nitrophenylsulphenyl (NPS), diphenylphosphinothioyl (Ppt), and dimethylphosphinothioyl (Mpt) groups, and the like.

5   Protective groups for the carboxy functional group are exemplified by benzyl ester (OBzl), cyclohexyl ester (Chx), 4-nitrobenzyl ester (ONb), t-butyl ester (Obut), 4-pyridylmethyl ester (OPic), and the like. It is often desirable that specific amino acids such as arginine, cysteine, and serine possessing a functional group other than amino and carboxyl groups are protected by a suitable protective group. For example, the guanidino group of arginine may be protected with

10   nitro, p-toluenesulfonyl, benzyloxycarbonyl, adamantyloxycarbonyl, p-methoxybenzesulfonyl, 4-methoxy-2,6-dimethylbenzenesulfonyl (Nds), 1,3,5-trimethylphenysulfonyl (Mts), and the like. The thiol group of cysteine can be protected with p-methoxybenzyl, trityl, and the like.

Many of the blocked amino acids described above can be obtained from commercial sources such as Novabiochem (San Diego, CA), Bachem CA (Torrence, CA) or Peninsula Labs

15   (Belmont, CA).

Stewart and Young, *supra*, provides detailed information regarding procedures for preparing peptides. Protection of α-amino groups is described on pages 14-18, and side chain blockage is described on pages 18-28. A table of protecting groups for amine, hydroxyl and sulfhydryl functions is provided on pages 149-151.

20   After the desired amino acid sequence has been completed, the peptide can be cleaved away from the solid support, recovered and purified. The peptide is removed from the solid support by a reagent capable of disrupting the peptide-solid phase link, and optionally deprotects blocked side chain functional groups on the peptide. In one embodiment, the peptide is cleaved away from the solid phase by acidolysis with liquid hydrofluoric acid (HF), which also removes

25   any remaining side chain protective groups. Preferably, in order to avoid alkylation of residues in the peptide (for example, alkylation of methionine, cysteine, and tyrosine residues), the acidolysis reaction mixture contains thio-cresol and cresol scavengers. Following HF cleavage, the resin is washed with ether, and the free peptide is extracted from the solid phase with sequential washes of acetic acid solutions. The combined washes are lyophilized, and the peptide is purified.

30   F.   **Chemical Conjugation of Hybrids**

In certain embodiments of the present invention, the hybrid molecules may comprise active domains that are organic compounds having diagnostic or therapeutic utility, or alternatively, fusions between a peptide ligand domain and a polypeptide active domain in configurations that cannot be encoded in a single nucleic acid. Examples of the latter embodiment

35   include fusions between the amino terminus of a peptide ligand and the amino terminus of the

active domain, or fusions between the carboxy-terminus of a peptide ligand and the carboxy-terminus of the active domain.

Chemical conjugation may be employed to prepare these embodiments of the hybrid molecule, using a variety of bifunctional protein coupling agents such as N-succinimidyl-3-(2-
5   pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCl), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as toluene, 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-
10   dinitrobenzene).

G.   **Disulfide-Linked Peptides**

As described above, some embodiments of the invention include cyclized peptide ligands. Peptide ligands may be cyclized by formation of a disulfide bond between cysteine residues. Such peptides can be made by chemical synthesis as described above and then cyclized by any
15   convenient method used in the formation of disulfide linkages. For example, peptides can be recovered from solid phase synthesis with sulfhydryls in reduced form, dissolved in a dilute solution wherein the intramolecular cysteine concentration exceeds the intermolecular cysteine concentration in order to optimize intramolecular disulfide bond formation, such as a peptide concentration of 25 mM to 1 µM, and preferably 500 µM to 1 µM, and more preferably 25 µM to
20   1 µM, and then oxidized by exposing the free sulfhydryl groups to a mild oxidizing agent that is sufficient to generate intramolecular disulfide bonds, *e.g.*, molecular oxygen with or without catalysts such as metal cations, potassium ferricyanide, sodium tetrathionate, *etc.* Alternatively, the peptides can be cyclized as described in Pelton *et al.* (1986), *J. Med. Chem.* **29**:2370-2375.

Cyclization can be achieved by the formation, for example, of a disulfide bond or a lactam
25   bond between a first Cys and a second Cys. Residues capable of forming a disulfide bond include, for example, Cys, Pen, Mpr, and Mpp and its 2-amino group-containing equivalents. Residues capable of forming a lactam bridge include, for example, Asp Glu, Lys, Orn, αβ-diaminobutyric acid, diaminoacetic acid, aminobenzoic acid and mercaptobenzoic acid. The compounds herein can be cyclized for example via a lactam bond which can utilize the side chain group of a non-
30   adjacent residue to form a covalent attachment to the N-terminus amino group of Cys or other amino acid. Alternative bridge structures also can be used to cyclize the compounds of the invention, including for example, peptides and peptidomimetics, which can cyclize via S-S, CH2-S, CH2-O-CH2, lactam ester or other linkages.

H.   Pharmaceutical Compositions

Pharmaceutical compositions which comprise the hybrid molecules of the invention may be administered in any suitable manner, including parental, topical, oral, or local (such as aerosol or transdermal) or any combination thereof.

5   Other suitable compositions of the present invention comprise any of the above-noted compositions with a pharmaceutically acceptable carrier, the nature of the carrier differing with the mode of administration, for example, in oral administration, usually using a solid carrier and ini.v. administration, a liquid salt solution carrier.

The compositions of the present invention include pharmaceutically acceptable

10   components that are compatible with the subject and the protein of the invention. These generally include suspensions, solutions and elixirs, and most especially biological buffers, such as phosphate buffered saline, saline, Dulbecco's Media, and the like. Aerosols may also be used, or carriers such as starches, sugars, microcrystalline cellulose, diluents, granulating agents, lubricants, binders, disintegrating agents, and the like (in the case of oral solid preparations, such as powders,

15   capsules, and tablets).

As used herein, the term "pharmaceutically acceptable" generally means approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in animals, and more particularly in humans.

The formulation of choice can be accomplished using a variety of the aforementioned

20   buffers, or even excipients including, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharin cellulose, magnesium carbonate, and the like. "PEGylation" of the compositions may be achieved using techniques known to the art (see for example International Patent Publication No. WO92/16555, U.S. Patent No. 5,122,614 to Enzon, and International Patent Publication No. WO92/00748).

25   A preferred route of administration of the present invention is in the aerosol or inhaled form. The compounds of the present invention, combined with a dispersing agent, or dispersant, can be administered in an aerosol formulation as a dry powder or in a solution or suspension with a diluent.

As used herein, the term "dispersant" refers to a agent that assists aerosolization of the

30   compound or absorption of the protein in lung tissue, or both. Preferably the dispersant is pharmaceutically acceptable. Suitable dispersing agents are well known in the art, and include but are not limited to surfactants and the like. For example, surfactants that are generally used in the art to reduce surface induced aggregation of a compound, especially a peptide compound, caused by atomization of the solution forming the liquid aerosol, may be used. Nonlimiting examples of

35   such surfactants are surfactants such as polyoxyethylene fatty acid esters and alcohols, and

polyoxyethylene sorbitan fatty acid esters. Amounts of surfactants used will vary, being generally within the range of from about 0.001% to about 4% by weight of the formulation. In a specific aspect, the surfactant is polyoxyethylene sorbitan monooleate or sorbitan trioleate. Suitable surfactants are well known in the art, and can be selected on the basis of desired properties,

5   depending on the specific formulation, concentration of the compound, diluent (in a liquid formulation) or form of powder (in a dry powder formulation), *etc.*

Moreover, depending on the choice of the peptide ligand, the desired therapeutic effect, the quality of the lung tissue (*e.g.*, diseased or healthy lungs), and numerous other factors, the liquid or dry formulations can comprise additional components, as discussed further below.

10   The liquid aerosol formulations generally contain the peptide ligand/active domain hybrid and a dispersing agent in a physiologically acceptable diluent. The dry powder aerosol formulations of the present invention consist of a finely divided solid form of the peptide ligand/active domain hybrid and a dispersing agent. With either the liquid or dry powder aerosol formulation, the formulation must be aerosolized. That is, it must be broken down into liquid or

15   solid particles in order to ensure that the aerosolized dose actually reaches the alveoli. In general the mass median dynamic diameter will be 5 micrometers or less in order to ensure that the drug particles reach the lung alveoli (Wearley, L.L. (1991), *Crit. Rev. in Ther. Drug Carrier Systems* **8**:333). The term "aerosol particle" is used herein to describe the liquid or solid particle suitable for pulmonary administration, *i.e.*, that will reach the alveoli. Other considerations such as

20   construction of the delivery device, additional components in the formulation and particle characteristics are important. These aspects of pulmonary administration of a drug are well known in the art, and manipulation of formulations, aerosolization means and construction of a delivery device require at most routine experimentation by one of ordinary skill in the art.

With regard to construction of the delivery device, any form of aerosolization known in

25   the art, including but not limited to nebulization, atomization or pump aerosolization of a liquid formulation, and aerosolization of a dry powder formulation, can be used in the practice of the invention. A delivery device that is uniquely designed for administration of solid formulations is envisioned. Often, the aerosolization of a liquid or a dry powder formulation will require a propellant. The propellant may be any propellant generally used in the art. Specific nonlimiting

30   examples of such useful propellants are a chloroflourocarbon, a hydrofluorocarbon, a hydochlorofluorocarbon, or a hydrocarbon, including triflouromethane, dichlorodiflouromethane, dichlorotetrafuoroethanol, and 1,1,1,2-tetraflouroethane, or combinations thereof.

In a preferred aspect of the invention, the device for aerosolization is a metered dose inhaler. A metered dose inhaler provides a specific dosage when administered, rather than a

variable dose depending on administration. Such a metered dose inhaler can be used with either a liquid or a dry powder aerosol formulation. Metered dose inhalers are well known in the art.

Once the peptide ligand/active domain hybrid reaches the lung, a number of formulation-dependent factors affect the drug absorption. It will be appreciated that in treating a disease or
5   disorder that requires circulatory levels of the compound, such factors as aerosol particle size, aerosol particle shape, the presence or absence of infection, lung disease or emboli may affect the absorption of the compounds. For each of the formulations described herein, certain lubricators, absorption enhancers, protein stabilizers or suspending agents may be appropriate. The choice of these additional agents will vary depending on the goal. It will be appreciated that in instances
10   where local delivery of the compounds is desired or sought, such variables as absorption enhancement will be less critical.

I.   Liquid Aerosol Formulations

The liquid aerosol formulations of the present invention will typically be used with a nebulizer. The nebulizer can be either compressed air driven or ultrasonic. Any nebulizer known
15   in the art can be used in conjunction with the present invention such as but not limited to: Ultravent, Mallinckrodt, Inc. (St. Louis, MO); the Acorn II nebulizer (Marquest Medical Products, Englewood CO). Other nebulizers useful in conjunction with the present invention are described in U.S. Patent Nos. 4,624,251 issued November 25, 1986; 3,703,173 issued November 21, 1972; 3,561,444 issued February 9, 1971 and 4,635,627 issued January 13, 1971.

20   The formulation may include a carrier. The carrier is a macromolecule which is soluble in the circulatory system and which is physiologically acceptable where physiological acceptance means that those of skill in the art would accept injection of said carrier into a patient as part of a therapeutic regime. The carrier preferably is relatively stable in the circulatory system with an acceptable elimination half-time. Such macromolecules include but are not limited to soya
25   lecithin, oleic acid and sorbetan trioleate, with sorbitan trioleate preferred.

The formulations of the present embodiment may also include other agents useful for protein stabilization or for the regulation of osmotic pressure. Examples of the agents include but are not limited to salts, such as sodium chloride, or potassium chloride, and carbohydrates, such as glucose, galactose or mannose, and the like.

30   **J.   Aerosol Dry Powder Formulations**

It is also contemplated that the present pharmaceutical formulation will be used as a dry powder inhaler formulation comprising a finely divided powder form of the peptide ligand and a dispersant. The form of the compound will generally be a lyophilized powder. Lyophilized forms of peptide ligand/active domain hybrid compounds can be obtained through standard techniques.

In another embodiment, the dry powder formulation will comprise a finely divided dry powder containing one or more compounds of the present invention, a dispersing agent and also a bulking agent. Bulking agents useful in conjunction with the present formulation include such agents as lactose, sorbitol, sucrose, or mannitol, in amounts that facilitate the dispersal of the powder from the device.

K.   Research, Manufacturing, and Diagnostic Compositions

In a preferred embodiment, the peptide ligands or the hybrid molecules of the invention are non-covalently adsorbed or covalently bound to a macromolecule, such as a solid support. It will be appreciated that the invention encompasses macromolecules complexed with the peptide ligands or hybrid molecules. In a preferred embodiment, the peptide ligands of the invention are directed against an immunoglobulin, such as, e.g., the IgG-Fc peptide ligands disclosed *infra*. Such peptide ligands may be used as affinity purification agents. In this process, the peptide ligands are immobilized on a solid phase support such as a Sephadex resin or filter paper, using methods well known in the art. The immobilized peptide ligand is contacted with a sample containing the immunoglobulin protein (or fragment thereof) to be purified, and thereafter the support is washed with a suitable solvent that will remove substantially all the material in the sample except the immunoglobulin protein, which is bound to the immobilized peptide ligand. Finally, the support is washed with another suitable solvent, such as glycine buffer, pH 5.0, that will release the immunoglobulin protein from the peptide ligand.

In general, the solid support is an inert matrix, such as a polymeric gel, comprising a three-dimensional structure, lattice or network of a material. Almost any macromolecule, synthetic or natural, can form a gel in a suitable liquid when suitably cross-linked with a bifunctional reagent. Preferably, the macromolecule selected is convenient for use in affinity chromatography. Most chromatographic matrices used for affinity chromatography are xerogels. Such gels shrink on drying to a compact solid comprising only the gel matrix. When the dried xerogel is resuspended in the liquid, the gel matrix imbibes liquid, swells and returns to the gel state. Xerogels suitable for use herein include polymeric gels, such as cellulose, cross-linked dextrans (e.g. Sepharose), agarose, cross-linked agarose, polyacrylamide gels, and polyacrylamide-agarose gels.

Alternatively, aerogels can be used for affinity chromatography. These gels do not shrink on drying but merely allow penetration of the surrounding air. When the dry gel is exposed to liquid, the latter displaces the air in the gel. Aerogels suitable for use herein include porous glass and ceramic gels.

Also encompassed herein are the peptide ligands or hybrid molecules of the invention coupled to derivatized gels wherein the derivative moieties facilitate the coupling of the hybrid molecules to the gel matrix and avoid steric hindrance of the peptide ligand-target molecule

interaction in affinity chromatography. Alternatively, spacer arms can be interposed between the gel matrix and the hybrid molecules for similar benefits.

A variation on the above contemplates the use of gene fusions and the use of the peptide ligands as purification reagents. According to this aspect of the invention the gene encoding a peptide ligand is associated, in a vector, with a gene encoding another protein or a fragment of another protein. This results in the peptide ligand being produced by the host cell as a fusion with another protein or peptide. The "other" protein or peptide is often a protein or peptide which can be secreted by the cell, making it possible to isolate and purify the other protein from the culture medium and eliminating the necessity of destroying the host cells which arises when the other protein remains inside the cell. Alternatively, the fusion protein can be expressed intracellularly. It is useful to use fusion proteins that are highly expressed.

The use of gene fusions is analogous to the use of Protein A fusions which are often used because the binding of protein A, or more specifically the Z domain of protein A binds to IgG and provides an "affinity handle" for the purification of the fused protein. According to a preferred aspect of the invention, peptide ligands which bind serum albumin are use as "affinity handles" for the purification of fused proteins on a solid serum albumin support. For example, a DNA sequence encoding the desired peptide ligand can be fused by site directed mutagenesis to the gene for protein. After expression and secretion, the fusion protein can be purified on a matix of serum albumin to which the peptide ligand will bind. After purification the peptide ligand can be enzymatically or chemically cleaved to yield free protein or left intact to aid in increasing the elimination half life of the fused protein. Fusion proteins can be cleaved using chemicals, such as cyanogen bromide, which cleaves at a methionine, or hydroxylamine, which cleaves between an Asn and Gly residue. Using standard recombinant DNA methodology, the nucleotide base pairs encoding these amino acids may be inserted just prior to the 5' end of the gene encoding the desired peptide. Alternatively, one can employ proteolytic cleavage of fusion protein. Carter, in Protein Purification: From Molecular Mechanisms to Large-Scale Processes, Ladisch et al., eds. (American Chemical Society Symposium Series No. 427, 1990), Ch 13, pages 181-193.

The following examples are offered by way of illustration and not by way of limitation. The disclosures of all citations in the specification are expressly incorporated herein by reference.

EXAMPLE 1

IgG-Fc Peptide Ligands

An *in vitro* selection designed to identify peptide ligands which bind the IgG-Fc surface without the constraint that the peptides function *in vivo* was performed. The selection was accomplished using a combination of polyvalent and monovalent phage display which has recently been applied to generate peptides that bind a variety of cellular hormones and receptors. N. C.

Wrighton, *et al.* (1996), *Science* 273:458, O. Livnah, *et al.* (1996), *Science* 273:464. A single -disulfide-constrained peptide library was constructed that consisted of 4×10^9 different peptides of the form Xaa_i-Cys-Xaa_j-Cys-Xaa_k (SEQ ID NO: 1) wherein Xaa is a random amino acid from an NNS codon, i+j+k = 18, and j = 4 through 10. This library was expressed on the surface of M13

5   bacteriophage as an N-terminal fusion to the gene VIII protein with a short linker consisting of glycine and serine residues. H. B. Lowman *et al.* (1998), *Biochemistry* 37: 8870-8878. More particularly, the library construct contained an STII secretion signal peptide, the peptide library of twenty amino acid length, *i.e.*, Xaa_i-Cys-Xaa_j-Cys-Xaa_k (SEQ ID NO: 1) wherein Xaa is a random amino acid from an NNS codon, i+j+k = 18, and j = 4 through 10, a Gly-Gly-Gly-Ser-Gly-Gly-Gly

10   linker (SEQ ID NO: 2) , and the M13 gene VIII starting at the first residue of the mature protein.

In principle, peptides could be selected that bind to potentially any region of the IgG-Fc due to the unbiased nature of this library. However, after several rounds of selection, the library became dominated by a single peptide, Fc-I (Glu-Thr-Gln-Arg-Cys-Thr-Trp-His-Met-Gly-Glu-Leu-Val-Trp-Cys-Glu-Arg-Glu-His-Asn) (SEQ ID NO: 3). Selections were performed as

15   described in H. B. Lowman, *et al.*, *supra,* with the following modifications: microtiter wells were coated using 5 µg/ml IgG-Fc; Casein Blocker Buffer (Pierce) was used in place of 0.1% BSA to better prevent non-specific binding; elution of phage was effected with either 75 mM DTT or 0.2 mM glycine pH 2.0 with equivalent results. IgG-Fc was obtained by papain cleavage of CD4-IgG_1 immunoadhesin protein, Capon *et al.* (1989), *Nature,* 337: 525. Cleaved material was purified

20   over Protein A Sepharose followed by Superdex-75 (Pharmacia) and then quantified by absorbance at 280 nm.

Repetition of the selection experiment again gave Fc-I and also a related peptide, Fc-II (Lys-Glu-Ala-Ser-Cys-Ser-Tyr-Trp-Leu-Gly-Glu-Leu-Val-Trp-Cys-Val-Ala-Gly-Val-Glu) (SEQ ID NO: 4). The Fc-II peptide shared the cysteine spacing and the internal Gly-Glu-Leu-Val-Trp

25   (SEQ ID NO: 134) sequence seen in Fc-I. Apparently, these two peptides bound IgG-Fc with an affinity high enough to be selected over any of the other IgG-Fc binding peptides present in the starting pool. Both peptides were synthesized on solid phase using standard 9-fluorenylmethoxycarbonyl protocols and purified by reversed-phase HPLC. Masses were confirmed by electrospray mass spectrometry, and purified peptides were quantified by UV

30   absorbance at 280 nm.

Competition ELISAs were performed in a manner similar to the method described in H. B. Lowman, *et al., supra.* Briefly, Protein A Z-domain was immobilized on microtiter wells at a concentration of 5 µg/ml, blocked, and washed as described. A matrix of mixtures of biotinylated-IgG-Fc at concentrations from 312 nM to 0.3 nM and peptide at concentrations from 215 µM to

0.8 nM was prepared. These mixtures were incubated with immobilized Protein A Z-domain for 1

hour. Plates were then washed and developed as described using avidin/HRP conjugate.

Inhibition curves were then computed for each concentration of biotin-IgG-Fc, and then the curve

of half-maximal inhibition, "IC_{50}", was extrapolated to zero biotin-IgG-Fc concentration in order

5   to obtain a K_i. The Fc-I and Fc-II peptides both were found to compete with Protein A (Z-

domain) (B. Nilsson *et al.* (1987), *Protein Eng.* 1:107) for binding to IgG-Fc with inhibition

constants (K_i) of about 5 μM. The results imply that these peptides bind to an overlapping site on

IgG-Fc that coincides with the Protein A binding site.

The DNA sequence of the Fc-II peptide was moved to a monovalent phage display format

10   by cassette mutagenesis to give a construct with the STII signal sequence, the Fc-II peptide Lys-

Glu-Ala-Ser-Cys-Ser-Tyr-Trp-Leu-Gly-Glu-Leu-Val-Trp-Cys-Val-Ala-Gly-Val-Glu (SEQ ID NO:

4), a Gly-Gly-Gly-Pro-Gly-Gly-Gly linker (SEQ ID NO: 5), and the M13 gene III protein starting

at residue 253. The Fc-II sequence was affinity-matured by monovalent phage display. Five

residue blocks were randomly mutated in six separate libraries to exhaustively cover the non-

15   cysteine positions in the peptide sequence and then screened against IgG-Fc.

A series of second generation monovalent phage display libraries were constructed based

on the Fc-II sequence Lys-Glu-Ala-Ser-Cys-Ser-Tyr-Trp-Leu-Gly-Glu-Leu-Val-Trp-Cys-Val-Ala-

Gly-Val-Glu (SEQ ID NO: 4) in which five sequential residues were randomized using NNS

codons in each library starting at positions 1, 4, 7,10, 12, and 16, excluding the two cysteines.

20   Each library had a diversity of approximately 1×10^8. These libraries were independently screened

for binding to IgG-Fc for six rounds and then sequenced. Preferred residues from this selection

were then recombined using three additional libraries that spanned the entire peptide sequence.

The three additional libraries were constructed using the degeneracy of the genetic code to

recombine the preferred amino acids at each position into one peptide. The DNA sequences for

25   these libraries contained the following mixtures of bases (IUPAC codes): DRG GWA GMA RRC

TGC KCT TRS CAC MTG GGC GAG CTG GTC TGG TGC RVC RVM BKC GAS KDW (SEQ

ID NO: 6), DRS VWG SVG RRC TGC KCC TRS YRS MTG GGC GAG CTG GTC TGG TGC

RNC VVS NBS GWS KDM (SEQ ID NO: 7), and DNS NNS NNS VNS TGC BVG TDS HRS

MDS GGC GAG STC KKG WRG TGC RNM NNS NNS NNS NNM (SEQ ID NO: 8). These

30   libraries also were sorted against IgG-Fc for six rounds and then sequenced.

After screening against IgG-Fc, the consensus patterns from these libraries suggested a

highly conserved 13-residue core sequence (Asp-Cys-Ala-Trp-His-Leu-Gly-Glu-Leu-Val-Trp-

Cys-Thr) (SEQ ID NO: 9). The corresponding peptide (Fc-III) was synthesized and found to

inhibit binding of Protein A (Z-domain) to Fc with an IC_{50} of 100 nM. Thus, although Fc-III is

seven residues shorter than Fc-II, it binds 50-times more tightly. Despite its smaller size, the binding affinity of Fc-III to Fc was only ten-fold weaker than that of the domains from Protein A and Protein G, which are each about four times larger and bind with K_dS around 10 nM. S. R. Fahnestock, *et al.* in <u>Bacterial Immunoglobulin-Binding Proteins</u> (Academic Press, Inc. 1990) Vol. 1, chap. 11. R. Karlsson, L. Jendeberg, B. Nilsson, J. Nilsson, P. Nygren (1995), *J. Immuno. Methods* **183**:43.

Table I lists the amino acid sequences and IgG-Fc binding affinities of exemplary IgG-Fc peptide ligands that were identified using the procedures described above.

Table I
IgG-Fc Peptide Ligand Sequences and Affinities

Sequence	Sequence ID NO	Binding Affinity
Peptides		
*All peptides have an N-terminal amine and a C-terminal amide		
KEASCSYWLGELVWCVAGVE	SEQ ID NO: 4	5000 nM (K_i)
ETQRCTWHMGELVWCEREHN	SEQ ID NO: 3	5000 nM (K_i)
DLADCSWHMGELVWCSRVEG	SEQ ID NO: 17	50 nM (K_d)
WEADCAWHLGELVWCTPMEF	SEQ ID NO: 18	30 nM (IC_{50})
DCAWHLGELVWCT	SEQ ID NO: 9	100 nM (IC_{50})
Phage Clones (M13/gIII Display)		All phage affinities are $EC_{50}s$

N/A = Not individually assayed. Since they were selected for binding, EC_{50} likely to be < 1 uM or better.

All of the peptides listed bind IgG-Fc.

Focused Libraries		
KEASCSYWLGELVWCDTLTE	SEQ ID NO: 19	N/A
KEASCSYWLGELVWCSPGVE	SEQ ID NO: 20	734 nM
KEASCSYWLGELVWCSGVEG	SEQ ID NO: 21	N/A
KEASCSYWLGELVWCSAGVE	SEQ ID NO: 22	N/A

Sequence	Sequence ID NO	Binding Affinity
ESEDCSYWLGELVWCVAGVE	SEQ ID NO: 23	N/A
EKEDCSYWLGELVWCVAGVE	SEQ ID NO: 24	N/A
EDPDCSYWLGELVWCVAGVE	SEQ ID NO: 25	N/A
EEADCSYWLGELVWCVAGVE	SEQ ID NO: 26	N/A
NADD CSYWLGELVWCVAGVE	SEQ ID NO: 27	N/A
SETTCSYWLGELVWCVAGVE	SEQ ID NO: 28	N/A
AWKTCQWLGELVWCVAGVE	SEQ ID NO: 29	N/A
DLADCSYWLGELVWCSRVEG	SEQ ID NO: 30	776 nM
KEADCAWHLGELVWCVAGVE	SEQ ID NO: 31	138 nM
KEAECSYHLGELVWCVAGVE	SEQ ID NO: 32	N/A
KEARCWYWHGELVWCSDPEE	SEQ ID NO: 33	809 nM
KEASCSYHLGELVWCVAGVE	SEQ ID NO: 34	416 nM
KEASCSWHLGELVWCVAGVE	SEQ ID NO: 35	225 nM
KEASCSYWLGELVWCTEGVE	SEQ ID NO: 36	818 nM
KEASCSYWLGELVWCDDGVE	SEQ ID NO: 37	N/A
KEASCSYWLGELVWCSEGVE	SEQ ID NO: 38	N/A
KEASCSYWLGELVWCSPGVE	SEQ ID NO: 39	N/A
KEASCSYWLGEVWKCKSGVE	SEQ ID NO: 40	N/A
KEASCSYWLGELVWCDNGVE	SEQ ID NO: 41	N/A
KEASCSYWLGELVWCDTFDE	SEQ ID NO: 42	301 nM
KEASCSYWLGELVWCDGLDE	SEQ ID NO: 43	326 nM
KEASCSYWLGELVWCVGLDE	SEQ ID NO: 44	278 nM
KEASCSYWLGELVWCEDTLE	SEQ ID NO: 45	N/A
KEASCSYWLGELVWCEDTME	SEQ ID NO: 46	N/A
KEASCSYWLGELVWCEDMME	SEQ ID NO: 47	N/A
WVEDCSWHMGELVWCDGGEF	SEQ ID NO: 48	139 nM
KEASCSYWLGELVWCDWMNG	SEQ ID NO: 49	N/A
KEASCSYWLGELVWCDDTPV	SEQ ID NO: 50	N/A
KEASCSYWLGELVWCDDYGE	SEQ ID NO: 51	N/A
KEASCSYWLGELVWCSDLWE	SEQ ID NO: 52	N/A
WRGGCSWHMGELVWCEHDME	SEQ ID NO: 53	N/A
AVSKCSFHMGELVWCSDVMN	SEQ ID NO: 54	N/A
NQVSCSYSRGELVWCSKQSQ	SEQ ID NO: 55	N/A
GRMECAWHQGELVWCTPTLE	SEQ ID NO: 56	N/A
GTMECSWHQGELVWCTPTLA	SEQ ID NO: 57	N/A
EMRDCSWHLGELVWCAHMEG	SEQ ID NO: 58	N/A
GSWECAYHLGELVWCETGSG	SEQ ID NO: 59	N/A

Sequence	Sequence ID NO	Binding Affinity
VAEPCAYHLGELVWCEVLKG	SEQ ID NO: 60	N/A
KEAMCSYWLGELVWCESDMP	SEQ ID NO: 61	N/A

Designed Clones

DLADCSWHLGELVWCSRVEG	SEQ ID NO: 62	9 nM
DLADCSWHLGELVWCVGLDE	SEQ ID NO: 63	28 nM
WVEDCSWHLGELVWCVGLDF	SEQ ID NO: 64	31 nM

Secondary Optimization

KVADCAWHMGELVWCTEVEG	SEQ ID NO: 65	23 nM
GEEDCSYHLGELVMCTELDD	SEQ ID NO: 66	69 nM
GVADCAWHLGELVWCTERED	SEQ ID NO: 67	N/A
GEEDCAWHLGELVWCSGGDF	SEQ ID NO: 68	100 nM
WEADCAWHLGELVWCTKVEE	SEQ ID NO: 69	7 nM
GEADCSYHLGELVWCNDFEE	SEQ ID NO: 70	156 nM
WVDCAYHLGELVWCSTFEE	SEQ ID NO: 71	9 nM
WVEDCAWHMGELVWCTKVDE	SEQ ID NO: 72	70 nM
READCAWHLGELVWCSERDL	SEQ ID NO: 73	47 nM
EEASCAYHLGELVWCDAFDV	SEQ ID NO: 74	77 nM
RVASCAWHLGELVWCDGLDG	SEQ ID NO: 75	N/A
GEADCAWHLGELVWCTKVEE	SEQ ID NO: 76	38 nM
GEASCAYHLGELVWCDEGEG	SEQ ID NO: 77	386 nM
RVEDCAYHLGELVWCTEGDE	SEQ ID NO: 78	63 nM
EEPDCSWHLGELVMCTPMEV	SEQ ID NO: 79	14 nM
KEADCAWHMGELVWCSEMEG	SEQ ID NO: 80	66 nM
EQADCAWHLGELVWCTPMVF	SEQ ID NO: 81	8 nM
EEPDCSWHLGELVWCTPIEV	SEQ ID NO: 82	15 nM
GEPDCAWHLGELVWCTPMVF	SEQ ID NO: 83	7 nM
GEQDCSYHMGELVWCTTVDG	SEQ ID NO: 84	210 nM
GVRNCAYHLGELVWCTPMEF	SEQ ID NO: 85	10 nM
RVADCAWHMGELVWCSELEV	SEQ ID NO: 86	44 nM
GEADCAWHLGELVWCTPMDL	SEQ ID NO: 87	N/A
GEQDCSWHLGELVWCTPMEV	SEQ ID NO: 88	N/A
GMRDCSYHLGELVWCSDMEL	SEQ ID NO: 89	N/A

Sequence	Sequence ID NO	Binding Affinity
EVADCSWHLGELVWCTEGEF	SEQ ID NO: 90	54 nM
GEEDCAWHLGELVWCTDVED	SEQ ID NO: 91	52 nM
EVEDCAYHLGELVWCSDLEG	SEQ ID NO: 92	82 nM
WEEDCAWHLGELVWCAEFDE	SEQ ID NO: 93	44 nM
KEASCAWHLGELVWCSEVEE	SEQ ID NO: 94	130 nM

ALA Scan on Phage

Sequence	Sequence ID NO	Binding Affinity
AEADCAWHLGELVWCTKVEE	SEQ ID NO: 95	20 nM
WAADCAWHLGELVWCTKVEE	SEQ ID NO: 96	34 nM
WEPDCAWHLGELVWCTKVEE	SEQ ID NO: 97	36 nM
WEAACAWHLGELVWCTKVEE	SEQ ID NO: 98	55 nM
WEAACSWHLGELVWCTKVEE	SEQ ID NO: 99	10 nM
WEADCAAHLGELVWCTKVEE	SEQ ID NO: 100	798 nM
WEADCAWALGELVWCTKVEE	SEQ ID NO: 101	139 nM
WEADCAWHAGELVWCTKVEE	SEQ ID NO: 102	56 nM
WEADCAWHLAELVWCTKVEE	SEQ ID NO: 103	12 nM
WEADCAWHLGALVWCTKVEE	SEQ ID NO: 104	11 nM
WEADCAWHLGEAVWCTKVEE	SEQ ID NO: 105	1890 nM
WEADCAWHLGELAWCTKVEE	SEQ ID NO: 106	4670 nM
WEADCAWHLGELVACTKVEE	SEQ ID NO: 107	3380 nM
WEADCAWHLGELVWCAKVEE	SEQ ID NO: 108	101 nM
WEADCAWHLGELVWCTAVEE	SEQ ID NO: 109	10 nM
WEADCAWHLGELVWCTKAEE	SEQ ID NO: 110	8 nM
WEADCAWHLGELVWCTKVAE	SEQ ID NO: 111	4 nM

EXAMPLE 2

Construction of Anti-VEGF Fabs Tagged with IgG-Fc Peptide Ligands

IgG-Fc peptide ligands may be combined with a bioactive compound to form a hybrid molecule that comprises a peptide ligand domain and an active domain. In this Example, IgG-Fc peptide ligands are combined with a Fab fragment that recognizes human VEGF. A neutralizing antibody to human VEGF has been previously identified from murine hybridoma, humanized, and optimized by phage display. *See* Muller *et al.* (1998), *Structure* 6:1153-1167; Chen *et al.* (1999), *J. Mol. Biol.* 293:865-881; and International Patent Publication No. WO 98/45331. Two humanized Fab forms of this antibody were chosen to test whether binding affinity to an irrelevant

IgG could be added to the Fabs without disrupting their antigen-binding affinity. An IgG-Fc peptide ligand, DCAWHLGELVWCT (SEQ ID NO: 9), identified and optimized by the peptide-phage display method described in Example 1 was used, along with a short peptide linker (Gly-Gly-Gly) to provide flexibility between the peptide and the Fab. The light chain of the Fab was

5   chosen for fusions because in the case of this antibody, the light chain is known to have little contribution to antigen binding (Muller et al., 1998, supra). In principle the peptide ligand domain could function to introduce IgG-binding whether introduced at the N-terminus, C-terminus, or inserted within the original Fab sequence. Described here are N-terminal fusions DCAWHLGELVWCTGGG-(light chain) (SEQ ID NO: 112) as well as C-terminal fusions (light

10   chain)-GGGWEADCAWHLGELVWCT (SEQ ID NO: 113).

An oligodeoxynucleotide, HL-569, was designed and synthesized for mutation of anti-VEGF plasmids to create fusions of the IgG-Fc peptide ligand at the N-terminus of the antibody light chain. The sequence of HL-569 (with added peptide sequence underlined) is: 5'-ACA AAC GCG TAC GCT GAC TGC GCT TGG CAC CTG GGC GAG CTG GTC TGG TGC ACC GGA

15   GGA GGA GAT ATC CAG TTG ACC-3' (SEQ ID NO: 114). The GAC codon follows the STII secretion-signal sequence at the N-terminus of the light chain, and the GAT codon corresponds to the first residue of the mature (wild-type) light chain.

Another oligodeoxynucleotide, HL-570, was designed and synthesized for construction of peptide ligand fusions to the C-terminus of the antibody light chain. The sequence of HL-570

20   (with added peptide sequence underlined) is: 5'-AAC AGG GGA GAG TGT GGA GGA GGA TGG GAA GCA GAC TGC GCT TGG CAC CTG GGC GAG CTG GTC TGG TGC ACC TAA GCT GAT CCT CTA C-3' (SEQ ID NO: 115). The TGT codon preceding the underscored GGA codon corresponds to residue Cys-214 of the light chain, and the TAA "stop codon" marks the end of the translated peptide sequence. Phagemids pY0192 and pY0317 (described Muller et al., 1998,

25   supra; Chen et al., 1999; and International Patent Publication No. WO 98/45331, encoding low-affinity and high-affinity forms of a humanized anti-VEGF antibody, respectively, were mutated with each of the two IgG-peptide oligos to yield constructs pY0192-569, pY0192-570, pY0317-569, and pY0317-570.

EXAMPLE 3

30   ### Phage-ELISA Analysis of Hybrid Molecules Comprising

Peptide-Ligand Tagged Anti-VEGF Fabs

A phage-ELISA competitive binding assay (Lowman (1998), Methods Mol. Biol. 87:249-264) was used to compare the apparent binding affinities of anti-VEGF antibody variants tagged with an IgG-Fc peptide ligand at their N-terminus or C-terminus and displayed monovalently on

35   bacteriophage M13 particles as fusions to the C-terminal domain of the gene III protein.

An irrelevant humanized IgG, 4D5-IgG, also known as Herceptin®, was coated onto Nunc Maxisorp immunosorbant plates at 2 microg/mL in phosphate buffered saline solution (PBS). Phagemid particles from overnight cultures of XL-1 Blue *E. coli* (Stratagene) were diluted in PBS containing 0.5% bovine serum albumin and 0.05% Tween-20. The phagemid particles were mixed

5   with serial dilutions of Herceptin® in solution, equilibrated for 20 min in a non-adsorbent plate (Nunc F96), then transferred to the Herceptin®-coated Maxisorp plate for detection of unbound phage. After 20 min, the plate was washed with PBS/Tween, and developed with an anti-phage monoclonal antibody-HRP conjugate (Pharmacia) and OPD substrate (Sigma). Displacement curves (Fig. 1) showed IC_{50} values of about 100-300 nM for each of the constructs, pY0192-569,

10   pY0192-570, pY0317-569, and pY0317-570.

EXAMPLE 4

BIAcore™ Analysis of IgG Binding to Anti-VEGF Fab

Tagged with an IgG-Fc Peptide Ligand

A surface plasmon resonance instrument (BIAcore, Inc., Piscataway, N.J.) was used to

15   measure binding of an irrelevant IgG, 4D5-IgG, also known as Herceptin®, to Fab that previously had been bound to an immobilized VEGF biosensor chip.

Fab variants encoded by pY0317 and pY0317-570 (control anti-VEGF high affinity, humanized Fab, and anti-VEGF high affinity, humanized Fab tagged with an IgG-Fc peptide ligand domain, respectively; *see* Example 2, *supra,* and WO 98/45331) were expressed in *E. coli*

20   and purified by protein-G (Pharmacia) affinity chromatography. Recombinant human VEGF was immobilized onto BIAcore™ CM-5 biosensor chips (BIAcore, Inc.) as described (Muller *et al.*, 1998, *supra*). After VEGF immobilization, the chip was blocked with ethanolamine, and the peptide-ligand tagged Y0317-570 Fab, or Y0317 control, was injected in PBS buffer containing 0.05% Tween-20 and 0.01% sodium azide. Following Fab injection, Herceptin® was injected, and

25   the dissociation off-rate (k_{off}) following injection was observed.

The results (Fig. 2) show that Herceptin® bound to the tagged but not to the control Y0317 Fab. Using a 1:1 Langmuir binding model (Karlsson *et al.* (1991), *J. Immunol. Methods* **145**:229-240 (1991)), a k_{off} of 2.8 x 10^{-3}, sec^{-1}, and a corresponding dissociation half-life ($t_{1/2}$) of 8.5 min were calculated for Y0317-570. Limitations of material prevented reliable on-rate

30   determinations. However, the observed k_{off} suggests an equilibrium binding affinity, K_d, of 30 nM to 300 nM (assuming k_{on} of 10^4-10^5 M^{-1} sec^{-1}), consistent with peptide binding and phage-ELISA results (above). Importantly, the BIAcore™ results (Fig. 2) also show that the tagged Fab can simultaneously binding both antigen (immobilized VEGF) and an irrelevant IgG.

EXAMPLE 5

IgG-Fc Peptide Ligand Tagged Anti-VEGF Fabs

Have Prolonged Elimination Half Times

The blood clearance rates and tissue distribution of the IgG-Fc peptide ligand-tagged anti-VEGF Fab (Fab-Y0317-570) are compared to those of the untagged control anti-VEGF Fab Y0317. Determinations of the elimination half time and volume of distribution are made in New Zealand White Rabbits of 2.8 to 3 kg weight. The amount of test article present in the plasma samples is determined using any method known in the art, such as, e.g., ELISA, or RIA.

Pharmacokinetic analysis is performed using the test article plasma concentrations. Group mean plasma data for each test article conforms to a multi-exponential profile when plotted against the time post-dosing. The data are fit by a standard two-compartment model with bolus input and first-order rate constants for distribution and elimination phases. The general equation for the best fit of the data for i.v. administration is: $c(t) = Ae^{-\alpha t} + Be^{-\beta t}$, where $c(t)$ is the plasma concentration at time t, A and B are intercepts on the Y-axis, and α and β are the apparent first-order rate constants for the distribution and elimination phases, respectively. The α-phase is the initial phase of the clearance and reflects distribution of the protein into all extracellular fluid of the animal, whereas the second or β-phase portion of the decay curve represents true plasma clearance. Methods for fitting such equations are well known in the art. For example, $A = D/V(\alpha\text{-k21})/(\alpha\text{-}\beta)$, $B = D/V \ (\beta\text{-k21})/(\alpha\text{-}\beta)$, and α and β (for $\alpha > \beta$) are roots of the quadratic equation: $r^2 + (\text{k12} + \text{k21} + \text{k10})r + \text{k21k10} = 0$ using estimated parameters of V = volume of distribution, k10 = elimination rate, k12 = transfer rate from compartment 1 to compartment 2 and k21 = transfer rate from compartment 2 to compartment 1, and D = the administered dose.

On the morning of the study six New Zealand White rabbits (body weight 2.8-3.0 kg) were placed in restrainers. Catheters were installed in an ear artery for blood sample collection and in a contralateral ear vein for dosing.

Rabbits were divided into two groups (n=3/group). Group 1 animals received and IV bolus of control anti-VEGF Fab-Y0317. Rabbits in Group 2 received Fab-Y0317-570. A summary of group assignment and dosing information is presented in the table below.

Group	Weight (kg)	Dose Group	Nominal Dose (mg/kg)	Dose Conc. (mg/mL)	Dose Vol. (mL)
1	2.9	Control-Fab-Y0317	1	3	0.97
1	3.0	Control-Fab-Y0317	1	3	1.00

1	2.9	Control-Fab-Y0317	1	3	0.97
2	2.8	Fab-Y0317-570	1	3	0.93
2	3.0	Fab-Y0317-570	1	3	1.00
2	2.9	Fab-Y0317-570	1	3	0.97

Serial blood samples (0.5 mL) were collected just prior to dosing and at 10, 20 40 min, 1, 2, 3, 4, 6, 8, 24 and 48 hr after dose administration. Blood was collected in serum separator tubes, allowed to clot (~30 min) at room temperature, and centrifuged. Serum was harvested and immediately stored at –70C until analyzed.

ELISA plates were coated with 0.5 microg/ml VEGF in 50 mM carbonate buffer, pH 9.6, at 4°C overnight and blocked with 0.5% bovine serum albumin, 10 ppm Proclin 300 (Supelco, Bellefonte, PA) in PBS (8 mM Na_2HPO_4, 1.5 mM KH_2PO_4, 2.7 mM KCl and 137 mM NaCl, pH 7.2) at room temperature for 1 hour. Standards (0.41-100 ng/ml) and twofold serial dilutions of samples (minimum dilution 1: 100) in PBS containing 0.5% bovine serum albumin, 0.05% polysorbate 20, 0.25% CHAPS, 0.2% bovine gamma globulins (Sigma, St. Louis, MO) and 5 mM EDTA were incubated on the plates for 2 hours. Bound antibody was detected using peroxidase labeled goat F(ab')2 anti-human IgG F(ab')2 (Jackson ImmunoResearch, West Grove, PA), followed by 3,3',5,5'-tetramethyl benzidine (Kirkegaard & Perry Laboratories) as the substrate. Plates were washed between steps. Absorbance was read at 450 nm on a Titerek stacker reader (ICN, Costa Mesa, CA). The standard curve was fitted using a four-parameter regression curve-fitting program (Kaleidagraph, Synergy Software, Reading, PA). Data points which fell in the range of the standard curve were used for calculating the Fab concentrations in samples.

Data analysis: Graphs of concentration versus time profiles were made using KaleidaGraph (KaleidaGraph™ V. 3.09 Copyright 1986-1997. Synergy Software. Reading, PA.). Values reported as less than reportable (LTR) were not included in the PK analysis and are not represented graphically. Pharmacokinetic parameters were determined by compartmental analysis using WinNonlin software (WinNonlin® Professional V. 3.1 WinNonlin™ Copyright 1998-1999. Pharsight Corporation. Mountain View, CA.). Pharmacokinetic parameters were computed as described elsewhere (Ritschel WA and Kearns GL. Handbook of basic pharmacokinetics including clinical applications, 5th edition. American Pharmaceutical Assoc., Washington, DC. Copyright 1999).

The results are reported in Figure 3. A two-compartment model with bolus input and first-order output (WinNonlin) was used to fit observed serum concentration vs. time data. Calculated pharmacokinetic parameters ware presented in the table below.

Pharmacokinetic Parameter Summary

(IV bolus; 1mg/kg)

	Parameter	Group 1	Group 2
		Control Fab-Y0317	Fab-Y0317-570
5			
	AUC (h*µg/mL)	13.6 ± 1.2	215 ± 56
	Cmax (µg/mL)	15.6 ± 0.6	13 ± 0.7
	CL (mL/h/kg)	74.2 ± 6.7	4.8 ± 1.1
	K10 half-life (hr)	0.6 ± 0.02	11.3 ± 3.6
10	alpha half-life (hr)	0.39 ± 0.03	1.15 ± 0.31
	beta half-life (hr)	1.93 ± 0.27	37.6 ± 19
	V1 (mL/kg)	64.1 ± 2.37	75.2 ± 4.23
	Vss (mL/kg)	112 ± 7.7	225 ± 54

15   The initial volume of distribution (V1) for both agents was approximately equal to serum volume. The estimated steady state volume of distribution (Vss) for Fab-Y0317-570 (225 mL/kg) was approximately 2 fold higher than estimated for the control Fab (112 mL/kg) suggesting a significant amount of binding to endogenous IgG. Control Fab-Y0317 was eliminated approximately 15-fold faster from the serum (clearance = 74 mL/h/kg) compared to Fab-Y0317-

20   570 (4.8 mL/h/d). The overall exposure (AUC) of Fab-Y0317-570 was ~16 times higher than for Fab-Y0317. Fab-Y0317 was undetectable in the serum 24 h after dosing but serum concentrations of Fab-Y0317-570 were still above 1 µg/mL 48 h after dosing. Both the distribution (alpha) half-life (1.15 h) and the elimination (beta) half-life (37.6 h) were significantly longer than the control Fab.

25   These results suggest that addition of a 13 amino acid that binds to endogenous IgG to Fab-Y0317 can significantly slow Fab clearance, increase half-life and enhance overall exposure.

EXAMPLE 6

Serum Albumin Peptide Ligands

Phage Libraries and Selection Conditions—Phage-displayed peptide libraries were

30   selected against rabbit, rat and human albumin. Phage libraries expressing random peptide sequences fused to gene 8 (Lowman et al., Biochem. 37, 8870 (1998)) were pooled into 5 groups: Pool A contained CX_2GPX_4C, $X_4CX_2GPX_4CX_4$ and $X_iCX_jCX_k$ where $j = 8\text{-}10$; Pool B contained X_{20} and $X_iCX_jCX_k$ where $j = 4\text{-}7$; Pool C contained X_8 and $X_2CX_jCX_2$ where $j = 4\text{-}6$; Pool D contained $X_2CX_jCX_2$ where $j = 7\text{-}10$; Pool E contained $CX_6CX_6CCX_3CX_6C$,

40

CCX_3CX_6C, $CCX_5CX_4CX_4CC$, $CXCX_7CX_3CX_6$ where X represents any of the 20 naturally occurring L-amino acids. In each case i + j + k = 18 and | i - k | < 2. Each of the 10 libraries has in excess of 108 clones.

5   The phage library pools were suspended in binding buffer (PBS, 1% ovalbumin, 0.005% Tween 20) and sorted against rabbit, rat or human albumin immobilized directly on maxisorp plates (10 μg/ml in PBS, overnight at 4°C; plates were blocked with Blocker Casein (Pierce Chemical, Rockford, IL)). After 2 hours, unbound phage were removed by repetitive washing (PBS, 0.05% Tween 20) and bound phage were eluted with 500 mM KCl, 10 mM HCl, pH 2. Eluted phage were propagated in XL1-Blue cells with VCSM13 helper phage (Stratagene, La
10   Jolla, CA). Enrichment was monitored by titering the number of phage that bound to an albumin coated well compared to a well coated with ovalbumin or casein.

       Phage ELISA—Phage clones (~10^{11} phage) were added to plates coated with rat, rabbit or human albumin. The microtiter plate was washed with wash buffer and bound phage were detected with HRP/Anti-M13 Conjugate. The amount of HRP bound was measured using
15    $ABTS/H_2O_2$ substrate and monitoring the change at 405 nm.

       The peptide sequences displayed by phage clones selected for binding to rabbit, human or rat albumin are shown in Figure 4. Also indicated is the ability of individual phage clones to bind the 3 species of immobilized albumin. This was tested using a phage ELISA. Note that clone RB, selected for binding to rat albumin is also capable of binding human and rabbit albumin.
20   Sequence Maturation on Monovalent Phage—Partially randomized libraries were designed using oligonucleotides coding for each of the selected clones in Figure 4, but synthesized with a 70-10-10-10 mixture of bases as described (Dennis et al., Nature 404, 465 (2000)). Although the potential diversity of these libraries is the same as the initial naïve libraries, each 'soft randomized' library maintains a bias towards the selected sequence in Figure 4. Each library was again selected
25   for binding to rat, rabbit or human albumin regardless of its origin. For example, the library resulting from soft randomization of clone RB was selected against rat, rabbit or human albumin even though it was originally identified for binding to rat albumin. Sequences identified following soft randomization are shown in Figure 5 along with their species specificity as determined by phage ELISA. Most clones appear to be specific for the species of albumin for which they were
30   selected, however, clones from the RB soft randomization library bind to all three species.

       Phage clones were also tested for binding to rhesus, mouse and bovine albumin. Clones originating from the RB soft randomization library were found to bind each of these species of albumin as well and were specific for albumin based upon their lack of binding to ovalbumin and

41

casein (Figure 6). Clones that bind to multiple species of albumin (multi-species binders) are listed in Figure 7.

Hard randomization—Sequences from soft randomization of the RB sequence were further matured using a hard randomization strategy. A new library was designed that kept highly selected residues (underlined) constant $X_5DXCLPXWGCLWX_4$, while fully randomizing the remaining positions. A second library, one residue shorter at both the N and C terminus was also constructed. Sequences from these libraries selected against rat, rabbit and human albumin are shown in Figures 8A, 8B, and 8C respectively.

Peptide Synthesis—Peptides were synthesized by either manual or automated (Milligen 9050) Fmoc-based solid (phase synthesis on a 0.25 mmol scale using a PEG-polystyrene resin (Bodanszky M., (1984) Principles of Peptide Synthesis, Springer, Berlin). Side chain protecting groups were removed and the peptides were cleaved from the resin with 95% trifluoroacetic acid (TFA) and 5% triisopropylsilane. A saturated iodine solution in acetic acid was added for oxidation of disulfide bonds. Peptides were purified by reversed phase HPLC using a water/acetonitrile gradient containing 0.1% TFA. Peptides were >95% pure by analytical HPLC and its identity verified by mass spectrometry.

The carboxy terminal lysine of peptide SA08 was derivatized with NHS-LC-biotin (Pierce Chemical, Rockford, IL) and purified by HPLC as above yielding SA08b (Ac-QGLIGDICLPRWGCLWGDSVK$_b$-n where K$_b$ refers to lysine-biotin).

SA08b Binding Assay—Rabbit, rat or mouse albumin was immobilized directly on maxisorp plates at 10 µg/ml in PBS, overnight at 4°C. Plates were blocked using Blocker Casein (Pierce Chemical, Rockford, IL) for1 hr, at 25°C. Serially diluted samples were suspended in binding buffer (above) and added to the plate followed by the addition of 10 nM SA08b for 1 hr, at 25°C. The microtiter plate was washed with PBS, 0.05 % Tween 20 and the SA08b bound to albumin was detected with Streptavidin/HRP. The amount of HRP bound was measured using ABTS/H_2O_2 substrate and monitoring the change at 405 nm.

Peptides corresponding to identified phage sequences were synthesized and their affinity for rat, rabbit or mouse albumin measured using the SA08b binding assay (Figure 9 and 10).

Construction, Expression and Purification of Albumin Binding Fab Fusions—In order to test whether association with albumin could increase the half-life of proteins and peptides in vivo, the sequence of SA06 was fused to a Fab fragment (D3H44) directed for binding tissue factor (TF). The SA06 sequence was added to the carboxy terminus of either the light chain (D3H44-L) or heavy chain (D3H44-Ls) of the Fab. In addition, as a precaution against folding problems,

42

identical constructions were made but with the intra-chain disulfide replaced by alanines (D3H44-Ls and D3H44-Hs, respectively) as depicted in Figure 11.

The fusions were expressed under control of the alkaline phosphatase promoter and secreted from E. coli using the stII secretion signal. Fab fusions were recovered from the periplasm
5   by suspending cells in 1 mM EDTA, 10 mM Tris-HCl, pH8, for 1 hr at 4°C. Cell debris was removed by centrifugation and the anti-TF Fab was selectively purified using a Hi-Trap (Amersham Pharmacia Biotech, Piscataway, NJ) TF affinity column. Properly folded D3H44-L or D3H44-Ls was further purified using a rabbit albumin affinity column (rabbit albumin coupled to CNBr-activated Sepharose 4B, Amersham Pharmacia Biotech, Piscataway, NJ). Both columns
10   were washed with PBS and eluted with 50 mM HCl. Eluted fractions were neutralized with 1 M Tris pH 8. Endotoxin was further removed following extraction with triton X114 (Aida and Pabst, J. Immunol. Methods 132, 191 (1990)).

Purified D3H44 fusions retained their ability to bind TF as measured using a FX activation assay (Figure 12), and a prothrombin time assay that measures prolongation of tissue factor
15   dependent clotting (Figure 13)(for methods see Dennis et al., Nature 404, 465 (2000)). Unlike D3H44 lacking the albumin binding sequence (WT), both D3H44-L and D3H44-Ls are able to bind to albumin as measured in the SA08b binding assay (Figure 14). Further, both D3H44 albumin-binding fusions are capable of binding TF and albumin simultaneously as judged by a biotin-TF binding assay (Figure 15). In this assay, the binding of the D3H44 fusions to
20   immobilized albumin is detected with biotinylated TF. Wild-type D3H44 (WT) is unable to bind albumin and thus does not generate a signal upon addition of biotinylated TF.

Pharmacokinetics of D3H44 albumin-binding fusions—D3H44 variants were given as a 0.5 mg/kg bolus in rabbit. Each group consisted of 3 rabbits (5 in the F(ab')2 group). Serum samples taken at the indicated time points were serially diluted and the concentration of D3H44
25   determined using a TF binding ELISA.

Pharmacokinetic analysis is performed using the test article plasma concentrations. Group mean plasma data for each test article conforms to a multi-exponential profile when plotted against the time post-dosing. The data are fit by a standard two-compartment model with bolus input and first-order rate constants for distribution and elimination phases. The general equation for the best
30   fit of the data for i.v. administration is: $c(t) = Ae^{-\alpha t} + Be^{-\beta t}$, where $c(t)$ is the plasma concentration at time t, A and B are intercepts on the Y-axis, and α and β are the apparent first-order rate constants for the distribution and elimination phases, respectively. The α-phase is the initial phase of the clearance and reflects distribution of the protein into all extracellular fluid of the animal, whereas the second or β-phase portion of the decay curve represents true plasma clearance.

Methods for fitting such equations are well known in the art. For example, $A = D/V(\alpha\text{-}k21)/(\alpha\text{-}\beta)$,

$B = D/V$ $(\beta\text{-}k21)/(\alpha\text{-}\beta)$, and α and β (for $\alpha > \beta$) are roots of the quadratic equation:

$r^2 + (k12 + k21 + k10)r + k21k10 = 0$ using estimated parameters of V = volume of distribution,

k10 = elimination rate, k12 = transfer rate from compartment 1 to compartment 2 and k21 =

5   transfer rate from compartment 2 to compartment 1, and D = the administered dose.

Data analysis: Graphs of concentration versus time profiles were made using
KaleidaGraph (KaleidaGraph™ V. 3.09 Copyright 1986-1997. Synergy Software. Reading, PA.).
Values reported as less than reportable (LTR) were not included in the PK analysis and are not
represented graphically. Pharmacokinetic parameters were determined by compartmental analysis

10   using WinNonlin software (WinNonlin® Professional V. 3.1 WinNonlin™ Copyright 1998-1999.
Pharsight Corporation. Mountain View, CA.). Pharmacokinetic parameters were computed as
described elsewhere (Ritschel WA and Kearns GL. Handbook of basic pharmacokinetics
including clinical applications, 5th edition. American Pharmaceutical Assoc., Washington, DC.
Copyright 1999).

15   Fusion of the albumin binding peptide to D3H44 results in a protein having improved
pharmacokinetic parameters (Figure 16 and 17). D3H44-L has a 70-fold increase in half-life (K10-
HL) relative to wild-type Fab and a comparable half-life to D3H44 Fabs derivatized with 20K or
40K polyethylene glycol (PEG).

All publications cited herein are expressly incorporated by reference in their entirety.

20

CLAIMS

What is claimed is:

1.   A conjugate for prolonging the elimination half time of a therapeutic or diagnostic substance, comprising a peptide having an engineered amino acid sequence capable of binding a plasma protein, said peptide conjugated to the therapeutic or diagnostic substance, wherein the elimination half time of the conjugate exceeds that of the unconjugated therapeutic or diagnostic substance.

2.   The conjugate of claim 1, wherein the sequence is selected by screening a peptide library.

3.   The conjugate of claim 2, wherein the library screening comprises phage display of the peptides.

4.   The conjugate of claim 1, wherein the peptide is shorter than about 40 residues.

5.   The conjugate of claim 4, wherein the peptide is shorter than about 30 residues.

6.   The conjugate of claim 5, wherein the peptide is shorter than about 20 residues.

7.   The conjugate of claim 1, wherein the sequence is Xaa_i-Cys-Xaa_j-Cys-Xaa_k, wherein the sum of i, j, and k is less than or equal to about 25.

8.   The conjugate of claim 1, wherein the plasma protein is an immunoglobulin.

9.   The conjugate of claim 8, wherein the immunoglobulin is IgG.

10.   The conjugate of claim 9, wherein the sequence is Xaa_i-Cys-Xaa_j-Cys-Xaa_k, wherein the sum of i, j, and k is less than or equal to about 25.

11.   The conjugate of claim 10, wherein the sum of i, j, and k is less than or equal to about 18.

12.   The conjugate of claim 11, wherein the sum of i, j, and k is less than or equal to about 11.

13.   The conjugate of claim 8, wherein the immunoglobulin is IgM.

14.   The conjugate of claim 1, wherein the plasma protein is serum albumin.

15.   The conjugate of claim 1, wherein the therapeutic or diagnostic substance comprises a protein.

16.   The conjugate of claim 1, wherein the affinity of the peptide for the plasma protein is characterized by an equilibrium dissociation constant, K_d, less than or equal to about 500 nM.

17.   The conjugate of claim 15, wherein K_d is less than or equal to about 100 nM.

18.   The conjugate of claim 17, wherein K_d is less than or equal to about 50 nM.

19.   The conjugate of claim 15, wherein the peptide is conjugated to the amino terminus of the protein.

20.   The conjugate of claim 19, further comprising a linker between the peptide and the protein.

21.   The conjugate of claim 15, wherein the peptide is conjugated to the carboxy terminus of the protein.

22.   The conjugate of claim 21, further comprising a linker between the peptide and the protein.

23.   The conjugate of claim 15, wherein the peptide is conjugated to a region of the protein other than the amino or carboxy terminus.

24.   A polynucleotide encoding the conjugate of claim 19.

25.   A polynucleotide encoding the conjugate of claim 20.

26.   A polynucleotide encoding the conjugate of claim 21.

27.   A polynucleotide encoding the conjugate of claim 22.

28.   A polynucleotide encoding the conjugate of claim 23.

29.   The conjugate of claim 1, wherein the peptide sequence is selected from the group consisting of SEQ ID NOS.: 3, 4, 9, and 17 through 111.

30.   The conjugate of claim 29, wherein the peptide sequence is SEQ ID NO: 9.

31.   A method of prolonging the elimination half time of a therapeutic substance, comprising conjugating the substance to a peptide having an engineered amino acid sequence capable of binding a plasma protein, wherein the elimination half time of the conjugated substance exceeds that of the unconjugated therapeutic substance.

32.   A peptide which:

i)   comprises the sequence Trp_1-Glu_1-Ala_1-Asp_1-Cys_1-Ala_2-Trp_2-His-Leu_1-Gly-Glu_2-Leu_2-Val-Trp_3-Cys_2-Thr-Pro-Met-Glu_3-Phe (SEQ ID NO: 18); or

ii) competes with SEQ ID NO: 18 for binding IgG-Fc in an *in vitro* assay, and has between 1 and 6 amino acids of SEQ ID NO: 18 substituted according to the following:

Xaa_1-Xaa_2-Xaa_3-Xaa_4-Cys-Xaa_5-Xaa_6-Xaa_7-Xaa_8-Gly-Glu-Leu-Val-Trp-Cys-Xaa_9-Xaa_{10}-Xaa_{11}-Xaa_{12}-Xaa_{13} (SEQ ID NO: 16), wherein Xaa_4 is Ser, Arg, or Asp; Xaa_5 is Ala, Ser, or Thr; Xaa_6 is Trp, Tyr; Xaa_7 is His, Trp; Xaa_8 is Leu or Met; and Xaa_9 is Glu, Ser, Thr or Val; and

iii) comprises the peptide of ii).

33.   The peptide of claim 32 having the following formula: Xaa_i-Cys_1-Xaa_j-Cys_2-Xaa_k, wherein Xaa_i is absent or is between 1 and 4 amino acids; Xaa_j is 9 amino acids, and Xaa_k is absent or between 1 and 5 amino acids.

34.   The peptide of claim 32 having an IC_{50} for IgG-Fc of less than about 1 TM.

35.   The peptide of claim 34 having an IC_{50} for IgG-Fc of less than about 100 nM.

36.   The peptide of claim 35 having an IC_{50} for IgG-Fc of less than about 10 nM.

37.   An isolated polynucleotide encoding the peptide of claim 32.

38.   The complement of an isolated polynucleotide encoding the peptide of claim 32.

39.   A peptide having between 11 and 20 amino acids which competes for binding to IgG-Fc in an *in vitro* assay with Trp_1-Glu_1-Ala_1-Asp-Cys_1-Ala_2-Trp_2-His-Leu_1-Gly-Glu_2-Leu_2-Val-Trp_3-Cys_2-Thr-Pro-Met-$Glu3$-Phe (SEQ ID NO: 18) and having the formula Xaa_1-Xaa_2-Xaa_3-Xaa_4-Cys-Xaa_5-Xaa_6-Xaa_7-Xaa_8-Gly-Glu-Leu-Val-Trp-Cys-Xaa_9-Xaa_{10}-Xaa_{11}-Xaa_{12}-

Xaa$_{13}$ (SEQ ID NO: 14), wherein Xaa$_{(1-4)}$ is absent or between one and four amino acids; Xaa$_5$ is selected from the group consisting of Ala, Ser, or Thr; Xaa$_6$ is selected from the group consisting of Trp or Tyr; Xaa$_7$ is selected from the group consisting of His or Trp; and Xaa$_8$ is selected from the group consisting of Leu or Met; and Xaa$_{(9-13)}$ is between one and five amino acids.

5   40.   An isolated polynucleotide encoding the peptide of claim 39.

41.   The complement of an isolated polynucleotide encoding the peptide of claim 39.

42.   A peptide conjugated to a therapeutic or diagnostic substance, wherein said peptide has an engineered amino acid sequence capable of binding a plasma protein, and

10   wherein the elimination half time of the conjugate exceeds that of the unconjugated therapeutic or diagnostic substance.

43.   A peptide which:

i)   comprises the sequence (Xaa)$_5$-Asp-Xaa-Cys-Leu-Pro-Xaa-Trp-Gly-Cys-Leu-Trp-(Xaa)$_4$ wherein Xaa is an amino acid or

15   ii)   competes for binding human serum albumin in an in vitro assay with a peptide having the sequence (Xaa)$_5$-Asp-Xaa-Cys-Leu-Pro-Xaa-Trp-Gly-Cys-Leu-Trp-(Xaa)$_4$ wherein Xaa is an amino acid or

iii)   comprises the sequence of ii).

44.   The conjugate of claim 1 wherein the peptide sequence is the peptide of

20   claim 43.

45.   A peptide having the sequence Asp-Leu-Cys-Leu-Arg-Asp-Trp-Gly-Cys-Leu-Trp   (SEQ ID NO: z1)

46.   A peptide having the sequence Asp-Ile-Cys-Leu-Pro-Arg-Trp-Gly-Cys-Leu-Trp   (SEQ ID NO: z2)

25   47.   A peptide having the sequence Met-Glu-Asp-Ile-Cys-Leu-Pro-Arg-Trp-Gly-Cys-Leu-Trp-Glu-Asp   (SEQ ID NO: z3)

48.   A peptide having the sequence Gln-Arg-Leu-Met-Glu-Asp-Ile-Cys-Leu-Pro-Arg-Trp-Gly-Cys-Leu-Trp-Glu-Asp-Asp-Phe   (SEQ ID NO: z4)

49.   A peptide having the sequence Gln-Gly-Leu-Ile-Gly-Asp-Ile-Cys-Leu-Pro-Arg-Trp-Gly-Cys-Leu-Trp-Gly-Asp-Ser-Val   (SEQ ID NO: z5)

50.   A peptide having the sequence Gln-Gly-Leu-Ile-Gly-Asp-Ile-Cys-Leu-Pro-Arg-Trp-Gly-Cys-Leu-Trp-Gly-Asp-Ser-Val-Lys   (SEQ ID NO: z6)

51.   A peptide having the sequence Glu-Asp-Ile-Cys-Leu-Pro-Arg-Trp-Gly-Cys-Leu-Trp-Glu-Asp-Asp   (SEQ ID NO: z7)

52.   A peptide having the sequence Arg-Leu-Met-Glu-Asp-Ile-Cys-Leu-Pro-Arg-Trp-Gly-Cys-Leu-Trp-Glu-Asp-Asp   (SEQ ID NO: z8)

53.   A peptide having the sequence Met-Glu-Asp-Ile-Cys-Leu-Pro-Arg-Trp-Gly-Cys-Leu-Trp-Glu-Asp-Asp   (SEQ ID NO: z9)

54.   A peptide having the sequence Met-Glu-Asp-Ile-Cys-Leu-Pro-Arg-Trp-Gly-Cys-Leu-Trp-Glu-Asp   (SEQ ID NO: z10)

55.   A peptide having the sequence Arg-Leu-Met-Glu-Asp-Ile-Cys-Leu-Ala-Arg-Trp-Gly-Cys-Leu-Trp-Glu-Asp-Asp   (SEQ ID NO: z11)

56.   The conjugate of claim 1 wherein the peptide sequence is the peptide of any of claims 44-55.

57.   A peptide which:
i)   comprises the sequence $(Xaa)_x$-Phe-Cys-Xaa-Asp-Trp-Pro-Xaa-Xaa-Xaa-Ser-Cys $(Xaa)_z$ wherein Xaa is an amino acid or
ii)   competes for binding human serum albumin in an in vitro assay with a peptide having the sequence $(Xaa)_x$-Phe-Cys-Xaa-Asp-Trp-Pro-Xaa-Xaa-Xaa-Ser-Cys-$(Xaa)_z$ wherein Xaa is an amino acid or
iii)   comprises the sequence of ii).

58.   A peptide which:
i)   comprises the sequence $(Xaa)_x$-Val-Cys-Tyr-Xaa-Xaa-Xaa-Ile-Cys-Phe-$(Xaa)_z$ wherein Xaa is an amino acid or

ii)   competes for binding human serum albumin in an in vitro assay with a peptide having the sequence $(Xaa)_X$-Val-Cys-Tyr-Xaa-Xaa-Xaa-Ile-Cys-Phe-$(Xaa)_Z$ wherein Xaa is an amino acid or

iii)   comprises the sequence of ii).

59.   A peptide which:

i)   comprises the sequence $(Xaa)_X$-Cys-Tyr-Xaa_1-Pro-Gly-Xaa-Cys-$(Xaa)_Z$ wherein Xaa is an amino acid and Xaa_1 is selected from the group consisting of Ile, Phe, Tyr and Val or

ii)   competes for binding human serum albumin in an in vitro assay with a peptide having the sequence $(Xaa)_X$-Cys-Tyr-Xaa_1-Pro-Gly-Xaa-Cys-$(Xaa)_Z$ wherein Xaa is an amino acid and Xaa_1 is selected from the group consisting of Ile, Phe, Tyr and Val or

iii)   comprises the sequence of ii).

60.   The conjugate of claim 1 wherein the peptide sequence is the peptide of any of claims 57, 58 or 59.
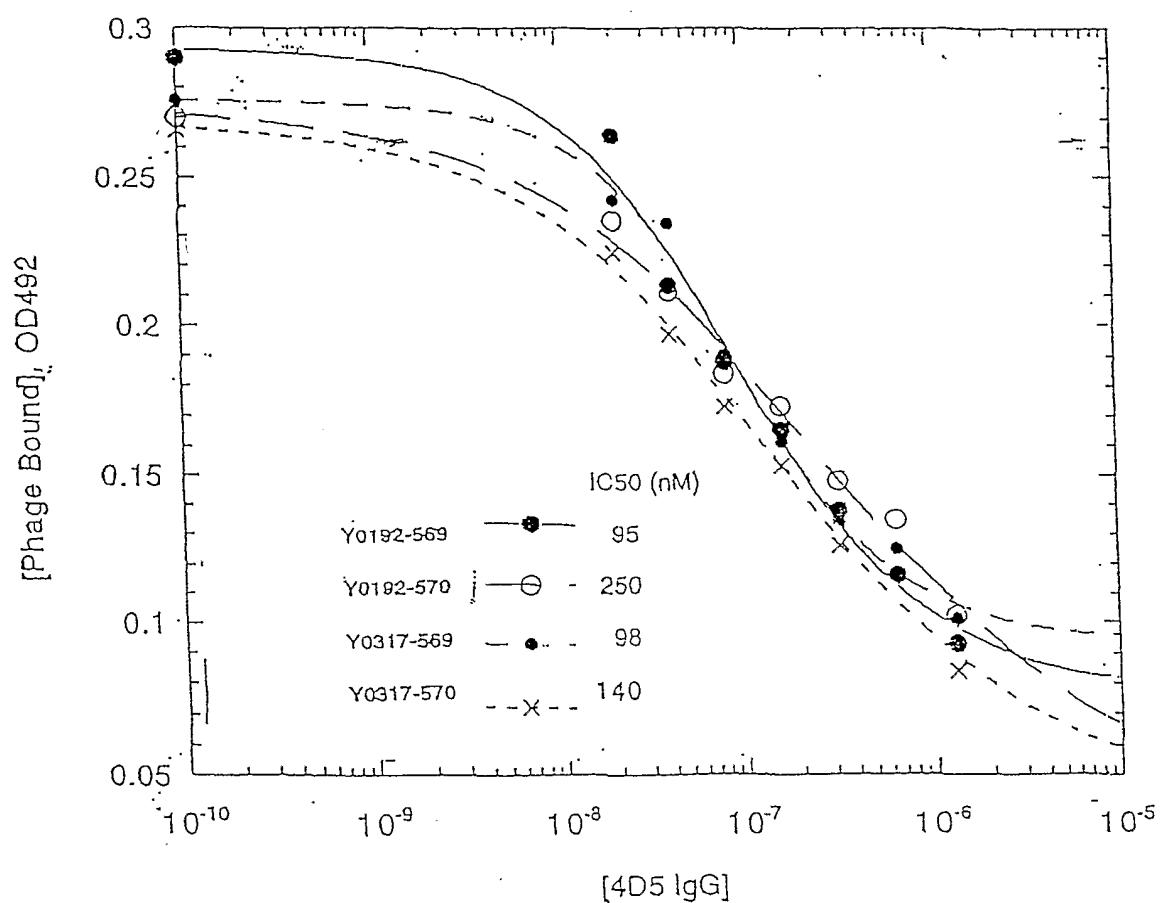
FIG. 1

BIAcore Shows peptide-tagged

Y0317 Can Bind Both VEGF, IgG
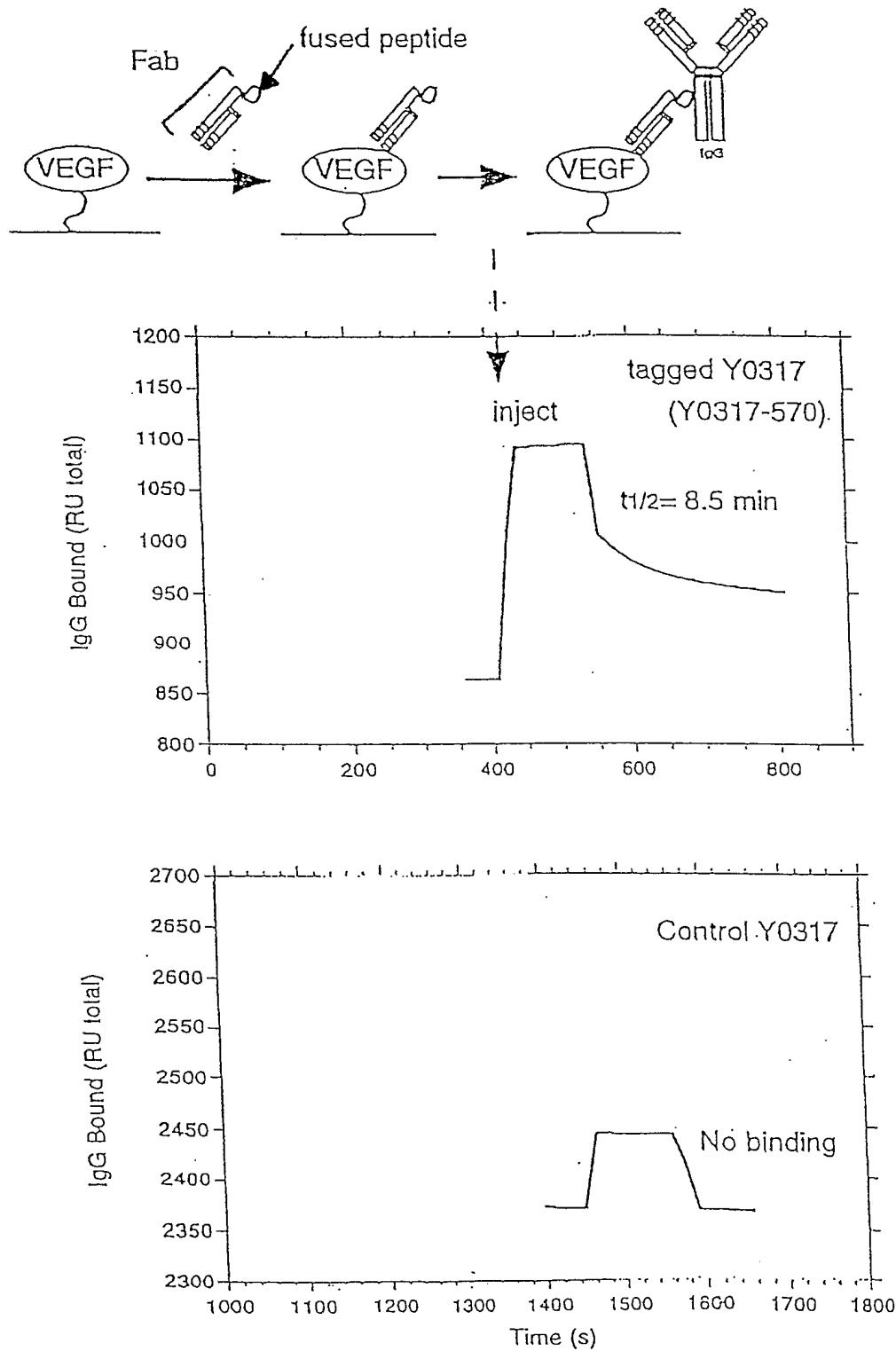
FIG. 2
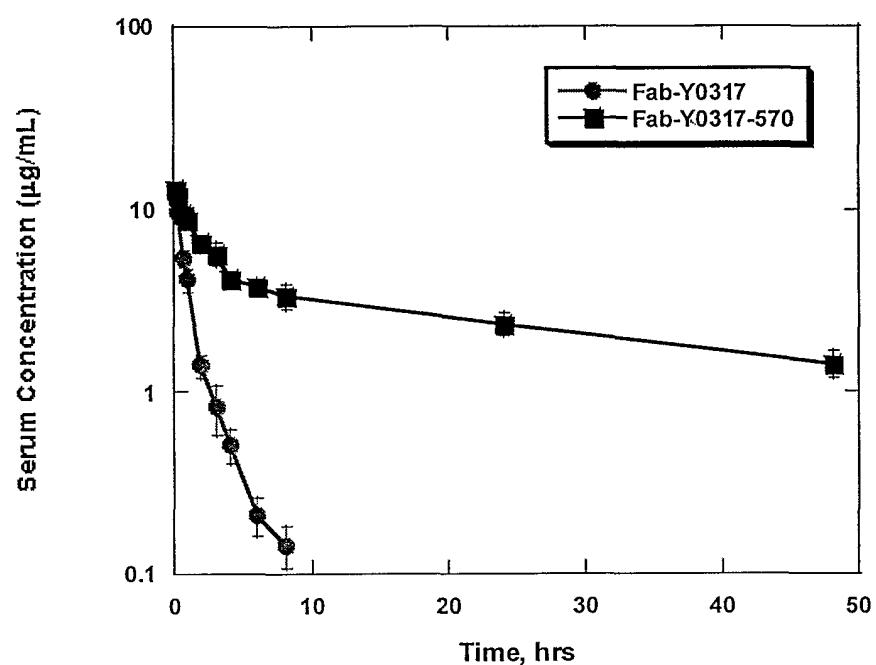
FIG. 3

Species Specificity of Albumin-Binding Phage Peptides

Library		Phage Binding		
	Selected on Rabbit SA	Rabbit	Human	Rat
BA	G E N W C D S T L M A Y D L C G Q V N M	+++	-	-
BB	M D E L A F Y C G I W E C L M H Q E Q K	+++	-	-
BC	D L C D V D F C W F	+++	-	-
BD	K S C S E L H W L L V E E C L F	+++	-	-
	Selected on Human SA			
HA	E V R S F C T D W P A E K S C K P L R G	-	+++	-
HB	R A P E S F V C Y W E T I C F E R S E Q	-	++	(+)
HC	E M C Y F P G I C W M	-	+++	++
HE	C E V A L D A C R G G E S G C C R H I C E L I R Q L C	-	(+)	-
	Selected on Rat SA			
RA	R N E D P C V V L L E M G L E C W E G V	-	-	+++
RD	D T C V D L V R L G L E C W G	-	-	+++
RB	Q R Q M V D F C L P Q W G C L W G D G F	++	+	+++
RC	D L C L R D W G C L W	-	-	+++
RE	C G C V D V S D W D C W S E C L W S H G A	-	-	+++

FIG. 4

Sequences Selected on Rabbit Albumin	Human	Binds Rabbit	Rat
Library BA G E N W C D S T L M A Y D L C G Q V N M			
BA-B44 G E D W C D S T L L A F D L C G E G A R	-	+++	-
BA-B37 G E N W C D W V L L A Y D L C G E D N T	-	+++	-
BA-B39 M E L W C D S T L M A Y D L C G D F N M	-	+++	-

Sequences Selected on Human Albumin	Human	Binds Rabbit	Rat
Library HA E V R S F C T D W P A E K S C K P L R G			
HA-H74 E V R S F C T D W P A H Y S C T S L Q G	+++	-	-
HA-H83 G - R S F C M D W P A H K S C T P L M L	+++	-	-
HA-H73 G V R T F C Q D W P A H N S C K L L R G	+++	-	-
HA-H76 Q T R S F C A D W P R H E S C K P L R G	+++	-	-
HA-H84 R - R T - C - D W P - H N S C K '- L R G	+++	-	-
Library HB R A P E S F V C Y W E T I C F E R S E Q			
HB-H2 R A A E S S V C Y W P G I C F D R T E Q	+++	-	-
HB-H8 M E P S R S V C Y A E G I C F D R G E Q	+++	-	-
HB-H3 R E P A S L V C Y F E D I C F V R A E A	+	-	-
HB-H6 R G P D - V - C Y W P S I C F E R S M P	+	-	-
HB-H4 L V P E R I V C Y F E S I C Y E R S E L	+	-	-
HB-H16 R M P A S L P C Y W E T I C Y E S S E Q	+	-	-
HB-H18 R T A E S L V C Y W P G I C F A Q S E R	+	-	-
HB-H1 R A P E R W V C Y W E G I C F D R Y E Q	(+)	-	-
Library HC E M C Y F P G I C W M			
HB-H12 E I C Y F P G I C W I	++	-	-
HB-H13 E L C Y F P G I C W T	++	-	-
HC-H6 D I C Y I P G I C W M	++	-	-
HC-H2 K L C Y F P G I C W S	++	-	-
HC-H3 D L C Y F P G I C W M	++	-	-
HC-H4 G M C Y F P G I C W A	++	-	-
HC-H7 E M C Y F P G I C W S	++	-	-
HC-H9 E M C Y F P G I C W T	++	-	-
HC-H10 K T C Y F P G I C W M	++	-	-
HC-H5 K V C Y F P G I C W M	++	-	-
HC-H8 D V C Y F P G I C W M	++	-	-
HC-H17 E I C Y F P G I C W M	++	-	-
HC-H14 A L C Y F P G I C W M	++	-	-
HC-H15 E L C Y F P G I C W P	++	-	-
HC-H20 E L C Y F P G I C W M	++	-	-
HC-H13 D M C Y F P G I C W L	++	-	-
HC-H18 D M C Y F P G I C F N	++	-	-
HC-H12 E T C Y F P G I C W L	++	-	-
HC-H11 E V C Y F P G I C W F	++	-	-
HC-H16 E V C Y F P G I C W E	++	-	-
HC-H19 E V C Y F P G I C W M	++	-	-
Library HBC X X E M C Y F P G I C W M X X			
HBC-H7 L A E M C Y F P G I C W M S A	+++	-	-
HBC-H4 G G E I C Y F P G I C R V L P	+++	-	-
HBC-H6 E H D M C Y F P G I C W I A D	+++	-	-
HBC-H10 V Q E V C Y F P G I C W M Q E	+++	-	-
HBC-H2 S R E V C Y Y P G I C W N G A	+++	-	-
HBC-H1 D S E V C Y F P G I C W S G T	+++	-	-
HBC-H3 G T E V C Y F P G I C W G G G	+++	-	-
HBC-H8 S Y A P C Y F P G I C W M G N	+++	-	-
HBC-H17 H A E I C Y F P G I C W T E R	+++	-	-
HBC-H11 N D E I C Y F P G V C W K S G	+++	-	-
HBC-H18 R D T V C Y F P G I C W M A S	+++	-	-
HBC-H19 V R D M C Y F P G I C W K S E	+++	-	-
HBC-H12 A S E I C Y F P G I C W M V E	+++	-	-
HBC-H13 Q T E L C Y F P G I C W N E S	+++	-	-
HBC-H14 T T E M C Y F P G I C W K T E	+++	-	-
HBC-H15 K T E I C Y F P G I C W M S G	+++	-	-
HBC-H16 Q - - - C - F P G - - W V - K	+++	-	-
HB-H10 I V E M C Y Y P G I C W I S P	+++	-	-
HB-H7 S G A I C Y V P G I C W T H A	+++	-	-

Sequences Selected on Rat Albumin	Human	Binds Rabbit	Rat
Library RB Q R Q M V D F C L P Q W G C L W G D G F			
RB-H1 Q R H P E D I C L P R W G C L W G D D D	++	+++	+++
RB-H6 N R Q M E D I C L P Q W G C L W G D D F	++	+++	+++

FIG. 5A

	Sequence			
RB-B2	Q R L M E D I C L P R W G C L W G D R F	++	+++	+++
RB-B5	Q W H M E D I C L P Q W G C L W G D V L	++	+++	+++
RB-B6	Q W Q M E N V C L P K W G C L W E E L D	++	+++	+++
RB-B4	L W A M E D I C L P K W G C L W E D D F	++	+++	+++
RB-B7	L R L M D N I C L P R W G C L W D D G F	++	+++	+++
RB-B8	H S Q M E D I C L P R W G C L W G D E L	++	+++	+++
RB-B11	Q W Q V M D I C L P R W G C L W A D E Y	++	+++	+++
RB-B12	Q G L I G D I C L P R W G C L W G D S V	++	+++	+++
RB-B16	H R L V E D I C L P R W G C L W G N D F	++	+++	+++
RB-B9	Q M H M M D I C L P K W G C L W G D T S	(+)	+++	+++
RB-B14	L R I F E D I C L P K W G C L W G E G F	(+)	+++	+++
RB-B3	Q S Y M E D I C L P R W G C L S D D A S	(+)	+++	+++
RB-B10	Q G D F W D I C L P R W G C L S G E G Y	-	+++	+++
RB-B1	R W Q T E D V C L P K W G C L F G D G V	-	+++	+++
RB-R8	Q G L I G D I C L P R W G C L W G D S V	++	+++	+++
RB-R16	L I F M E D V C L P Q W G C L W E D G V	++	+++	+++
HC-R10	Q R D M G D I C L P R W G C L W E D G V	++	+++	+++
RB-R4	Q R H M M D F C L P K W G C L W G D G Y	-	(+)	+++
RB-R7	Q R P I M D F C L P K W G C L W E D G F	-	(+)	+++
RB-R11	E R Q M V D F C L P K W G C L W G D G F	-	(+)	+++
RB-R12	Q G Y M V D F C L P R W G C L W G D A N	-	(+)	+++
RB-R13	K M G R V D F C L P K W G C L W G D E L	-	(+)	+++
RB-R15	Q S Q L E D F C L P K W G C L W G D G F	-	(+)	+++
RB-R17	Q G G M G D F C L P Q W G C L W G E D L	-	(+)	+++
RB-R5	Q R L M W E I C L P L W G C L W G D G L	-	-	+++
RB-R10	Q R Q I M D F C L P H W G C L W G D G F	-	-	+++
RB-R2	G R Q V V D F C L P K W G C L W E E G L	-	-	+++
RB-R3	Q M Q M S D F C L P Q W G C L W G D G Y	-	-	+++
RB-R9	K S R M G D F C L P E W G C L W G D E L	-	-	+++
RB-R1	E R Q M E D F C L P Q W G C L W G D G V	-	-	+++
RB-R14	Q R Q V V D F C L P Q W G C L W G D G S	-	-	+++

Library RC   *D L C L R D W G C L W*

	Sequence			
RC-R6	D I C L P E W G C L W	-	-	++
RC-R8	D I C L P E W G C L W	-	-	++
RC-R15	D I C L P E W G C L W	-	-	++
RC-R1	D I C L P V W G C L W	-	-	++
RC-R2	D I C L P V W G C L W	-	-	++
RC-R3	D I C L P V W G C L W	-	-	++
RC-R10	D I C L P V W G C L W	-	-	++
RC-R12	D I C L P V W G C L W	-	-	++
RC-R18	D I C L P V W G C L W	-	-	++
RC-R9	D L C L P E W G C L W	-	-	(+)
RC-R4	D L C L P K W G C L W	-	-	++
RC-R5	D L C L P V W G C L W	-	-	(+)
RC-R20	D I C L P A W G C L W	-	-	++
RC-R17	D I C L P D W G C L W	-	-	++
RC-R13	D I C L P R W G C L W	-	-	++
RC-R16	D I C L E R W G C L W	-	-	++

Library RBC   *X X D L C L R D W G C L W X X*

	Sequence			
RBC-R16	E W D V C L P H W G C L W D G	-	(+)	+++
RBC-R7	W D D I C F R D W G C L W G S	-	-	+++
RBC-R1	M D D I C L H H W G C L W D E	-	-	+++
RBC-R2	M D D L C L P N W G C L W G D	-	-	+++
RBC-R4	F E D F C L P N W G C L W G S	-	-	+++
RBC-R6	F E D L C V V R W G C L W G D	-	-	+++
RBC-R5	W E D L C L P D W G C L W E D	-	-	+++
RBC-R9	S E D F C L P V W G C L W E D	-	-	+++
RBC-R10	D F D L C L P D W G C L W D D	-	-	+++
RBC-R8	N W D L C F P D W G C L W D D	-	-	+++
RBC-R14	E E D L C L P V W G C L W G A	-	-	+++
RBC-R20	E E D V C L P V W G C L W E G	-	-	+++
RBC-R12	M F D L C L P K W G C L W G N	-	-	+++
RBC-R13	E F D L C L P T W G C L W E D	-	-	+++
RBC-R15	M W D V C F P D W G C L W D V	-	-	+++
RBC-R18	E W D V C F P A W G C L W D Q	-	-	+++
RBC-R11	V W D L C L P Q W G C L W D E	-	-	+++

Library RD   *D T C V D L V R L G L E C W G*

	Sequence			
RD-R2	D T C A D L V R L G L E C W A	-	-	+++
RD-R7	N T C A D L V R L G L E C W A	-	-	+++
RD-R11	D T C D D L V Q L G L E C W A	-	-	+++
RD-R5	D T C E D L V R L G L E C W A	-	-	+++
RD-R6	D S C G D L L R L G L E C W A	-	-	+++
RD-R1	D T C S D L V G L G L E C W A	-	-	+++

FIG. 5B
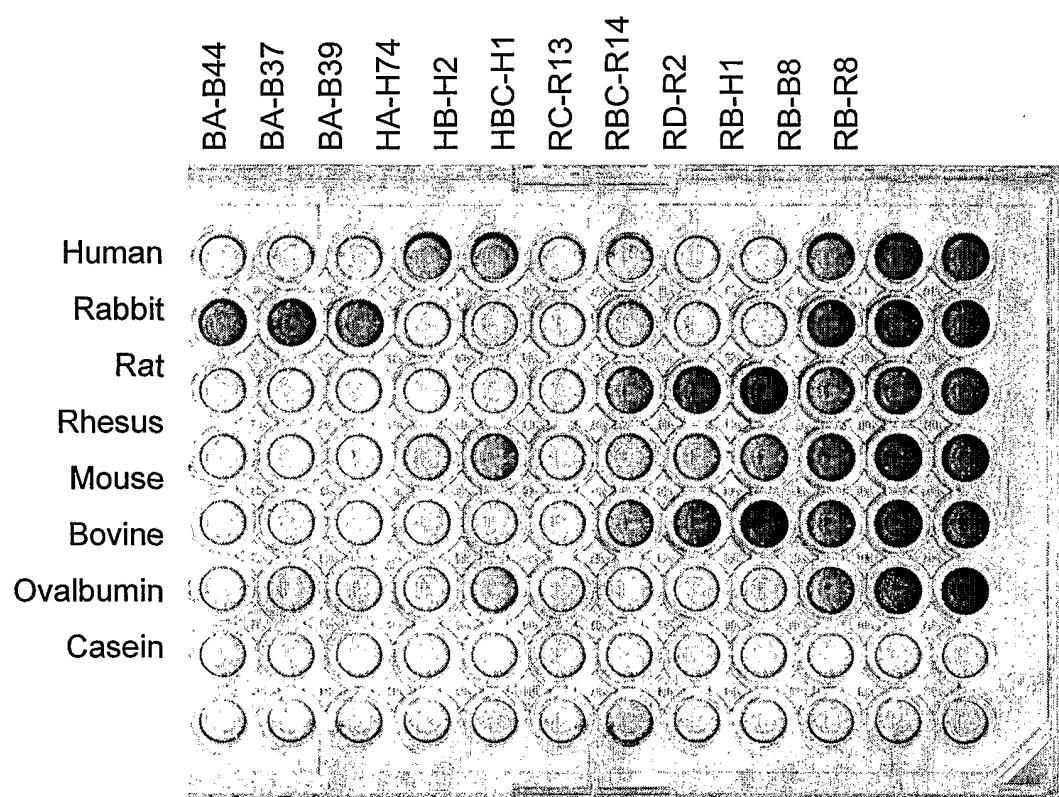
FIG. 6

PHAGE																					Binds		
																					Human	Rabbit	Rat
RB	Q	R	Q	M	V	D	F	C	L	P	Q	W	G	C	L	W	G	D	G	F	+	++	+++
RB-H1	Q	R	H	P	E	D	I	C	L	P	R	W	G	C	L	W	G	D	D	D	++	+++	+++
RB-H6	N	R	Q	M	E	D	I	C	L	P	Q	W	G	C	L	W	G	D	D	F	++	+++	+++
RB-B12	Q	G	L	I	G	D	I	C	L	P	R	W	G	C	L	W	G	D	S	V	++	+++	+++
RB-B8	H	S	Q	M	E	D	I	C	L	P	R	W	G	C	L	W	G	D	E	L	++	+++	+++
RB-B7	L	R	L	M	D	N	I	C	L	P	R	W	G	C	L	W	D	D	G	F	++	+++	+++
RB-B5	Q	W	H	M	E	D	I	C	L	P	Q	W	G	C	L	W	G	D	V	L	++	+++	+++
RB-B6	Q	W	Q	M	E	N	V	C	L	P	K	W	G	C	L	W	E	E	L	D	++	+++	+++
RB-B4	L	W	A	M	E	D	I	C	L	P	K	W	G	C	L	W	E	D	D	F	++	+++	+++
RB-B11	Q	W	Q	V	M	D	I	C	L	P	R	W	G	C	L	W	A	D	E	Y	++	+++	+++
RB-B16	H	R	L	V	E	D	I	C	L	P	R	W	G	C	L	W	G	N	D	F	++	+++	+++
RB-B2	Q	R	L	M	E	D	I	C	L	P	R	W	G	C	L	W	G	D	R	F	++	+++	+++
RB-R8	Q	G	L	I	G	D	I	C	L	P	R	W	G	C	L	W	G	D	S	V	++	+++	+++
RB-R16	L	I	F	M	E	D	V	C	L	P	Q	W	G	C	L	W	E	D	G	V	++	+++	+++
HC-R10	Q	R	D	M	G	D	I	C	L	P	R	W	G	C	L	W	E	D	G	V	++	+++	+++

FIG. 7

Sequences selected on rat albumin

Hard Randomization Library
```
       X X X X X D X C L P X W G C L W X X X X

35   A  A  Q  V  G  D  I  C  L  P  R  W  G  C  L  W  S  E  Y  A
33   A  G  W  A  A  D  V  C  L  P  R  W  G  C  L  W  E  E  D  V
60   A  S  V  V  D  D  I  C  L  P  V  W  G  C  L  W  G  E  D  I
84   A  T  M  E  D  D  I  C  L  P  R  W  G  C  L  W  G  A  E  E
10   D  E  D  F  E  D  Y  C  L  P  P  W  G  C  L  W  G  S  S  M
34   E  G  T  W  D  D  F  C  L  P  R  W  G  C  L  W  L  G  E  R
93   E  R  W  E  G  D  V  C  L  P  R  W  G  C  L  W  G  E  S  G
23   G  D  W  M  H  D  I  C  L  P  K  W  G  C  L  W  D  E  K  A
71   G  I  E  W  G  D  T  C  L  P  K  W  G  C  L  W  R  V  E  G
36   G  Q  Q  G  E  D  V  C  L  P  V  W  G  C  L  W  D  T  S  S
48   G  R  Y  P  M  D  L  C  L  P  R  W  G  C  L  W  E  D  S  A
24   G  S  A  G  D  D  L  C  L  P  R  W  G  C  L  W  E  R  G  A
9    H  A  S  D  W  D  V  C  L  P  G  W  G  C  L  W  E  E  D  D
47   L  G  V  T  H  D  T  C  L  P  R  W  G  C  L  W  D  E  V  G
72   L  V  W  E  E  D  F  C  L  P  K  W  G  C  L  W  G  A  E  D
11   N  V  G  W  N  D  I  C  L  P  R  W  G  C  L  W  A  Q  E  S
83   Q  G  V  E  W  D  V  C  L  P  Q  W  G  C  L  W  T  R  E  V
58   R  L  D  A  W  D  I  C  L  P  Q  W  G  C  L  W  E  E  P  S
96   S  E  A  P  G  D  Y  C  L  P  R  W  G  C  L  W  A  Q  E  K
94   T  A  M  D  E  D  V  C  L  P  R  W  G  C  L  W  G  S  G  S
81   T  E  I  G  Q  D  F  C  L  P  R  W  G  C  L  W  V  P  G  T
57   T  L  G  W  P  D  F  C  L  P  K  W  G  C  L  W  R  E  S  D
12   T  L  S  N  Q  D  I  C  L  P  G  W  G  C  L  W  G  G  I  N
46   T  S  T  G  G  D  L  C  L  P  R  W  G  C  L  W  D  S  S  E
22   V  S  E  M  D  D  I  C  L  P  L  W  G  C  L  W  A  D  A  P
59   V  S  E  W  E  D  I  C  L  P  S  W  G  C  L  W  E  T  Q  D
45   V  V  G  D  G  D  F  C  L  P  K  W  G  C  L  W  D  Q  A  R
21   V  V  W  D  D  D  V  C  L  P  R  W  G  C  L  W  E  E  Y  G
69   W  S  D  S  D  D  V  C  L  P  R  W  G  C  L  W  G  N  V  A
95   W  V  E  E  G  D  I  C  L  P  R  W  G  C  L  W  E  S  V  E
33   A  Q  A  M  G  D  I  C  L  P  R  W  G  C  L  W  E  A  E  I
10   A  S  D  R  G  D  L  C  L  P  Y  W  G  C  L  W  G  P  D  G
93   A  S  D  P  G  D  V  C  L  P  R  W  G  C  L  W  G  E  S  F
71   A  S  N  W  E  D  V  C  L  P  R  W  G  C  L  W  G  E  R  N
22   A  S  T  P  R  D  I  C  L  P  R  W  G  C  L  W  S  E  D  A
23   D  G  E  E  G  D  L  C  L  P  R  W  G  C  L  W  A  L  E  H
24   E  G  E  E  V  D  I  C  L  P  Q  W  G  C  L  W  G  Y  P  V
82   E  V  G  D  L  D  L  C  L  P  R  W  G  C  L  W  G  N  D  K
81   F  R  D  G  E  D  F  C  L  P  Q  W  G  C  L  W  A  D  T  S
46   G  D  M  V  N  D  F  C  L  P  R  W  G  C  L  W  G  S  E  N
83   G  R  M  G  T  D  L  C  L  P  R  W  G  C  L  W  G  E  V  E
94   H  E  W  E  R  D  I  C  L  P  R  W  G  C  L  W  R  D  G  D
35   K  K  V  S  G  D  I  C  L  P  I  W  G  C  L  W  D  N  D  Y
96   L  L  E  S  D  D  I  C  L  P  R  W  G  C  L  W  H  E  D  G
21   M  Q  A  E  S  D  F  C  L  P  H  W  G  C  L  W  D  E  G  T
36   M  Q  G  P  L  D  I  C  L  P  R  W  G  C  L  W  G  G  V  D
48   Q  M  P  L  E  D  I  C  L  P  R  W  G  C  L  W  E  G  R  E
95   R  E  E  W  G  D  L  C  L  P  T  W  G  C  L  W  E  T  K  K
47   R  V  W  T  E  D  V  C  L  P  R  W  G  C  L  W  S  E  G  N
11   S  I  R  E  Y  D  V  C  L  P  K  W  G  C  L  W  E  P  S  A
34   S  P  T  E  W  D  M  C  L  P  K  W  G  C  L  W  G  D  A  L
69   S  S  G  L  E  D  I  C  L  P  N  W  G  C  L  W  A  D  G  S
9    S  V  G  W  G  D  I  C  L  P  V  W  G  C  L  W  G  E  G  G
57   T  E  E  N  W  D  L  C  L  P  R  W  G  C  L  W  G  D  D  W
84   T  S  G  S  D  D  I  C  L  P  V  W  G  C  L  W  G  E  D  S
58   T  W  P     G  D  L  C  L  P  R  W  G  C  L  W  E  A  E  S
72   W  D  H  E  L  D  F  C  L  P  V  W  G  C  L  W  A  E  D  V
60   W  T  E  S  E  D  I  C  L  P  G  W  G  C  L  W  G  P  E  V
59   W  V  P  F  E  D  V  C  L  P  R  W  G  C  L  W  S  S  Y  Q
```

Hard Randomization Library
```
       X X X X D X C L P X W G C L W X X X

93   E  E  D  S  D  I  C  L  P  R  W  G  C  L  W  N  T  S
81   E  G  Y  W  D  L  C  L  P  R  W  G  C  L  W  E  L  E
10   E  L  G  E  D  L  C  L  P  R  W  G  C  L  W  G  S  E
24   E  T  W  S  D  V  C  L  P  R  W  G  C  L  W  G  A  S
83   G  D  Y  V  D  L  C  L  P  G  W  G  C  L  W  E  D  G
23   G  V  L  D  D  I  C  L  P  R  W  G  C  L  W  G  P  K
94   H  M  M  D  D  V  C  L  P  G  W  G  C  L  W  A  S  E
59   I  D  Y  T  D  L  C  L  P  A  W  G  C  L  W  E  L  E
36   I  E  H  E  D  L  C  L  P  R  W  G  C  L  W  A  V  D
11   I  S  E  W  D  L  C  L  P  R  W  G  C  L  W  D  R  S
12   I  S  W  A  D  V  C  L  P  K  W  G  C  L  W  G  K  D
47   I  S  W  G  D  L  C  L  P  R  W  G  C  L  W  E  G  S
22   K  L  W  D  D  I  C  L  P  R  W  G  C  L  W  S  P  L
84   L  A  W  P  D  V  C  L  P  R  W  G  C  L  W  G  G  M
71   L  N  E  S  D  I  C  L  P  T  W  G  C  L  W  G  V  D
46   L  P  E  Q  D  V  C  L  P  V  W  G  C  L  W  D  A  N
35   M  A  W  G  D  V  C  L  P  R  W  G  C  L  W  A  G  G
48   N  E  E  W  D  V  C  L  P  R  W  G  C  L  W  G  G  V
60   Q  E  L  Q  D  F  C  L  P  R  W  G  C  L  W  G  V  G
21   Q  R  E  W  D  V  C  L  P  R  W  G  C  L  W  S  D  V
9    Q  R  F  W  D  T  C  L  P  R  W  G  C  L  W  G  G  D
57   R  V  F  T  D  V  C  L  P  R  W  G  C  L  W  D  L  G
58   S  G  W  D  D  V  C  L  P  V  W  G  C  L  W  G  P  S
96   S  S  A  S  D  Y  C  L  P  R  W  G  C  L  W  G  D  L
72   S  W  Q  G  D  I  C  L  P  R  W  G  C  L  W  G  V  D
69   S  Y  E  T  D  V  C  L  P  Y  W  G  C  L  W  E  D  A
34   S  Y  W  G  D  V  C  L  P  R  W  G  C  L  W  S  E  A
45   T  L  E  W  D  M  C  L  P  R  W  G  C  L  W  T  E  Q
95   V  G  E  F  D  I  C  L  P  R  W  G  C  L  W  D  A  E
33   V  T  S  W  D  V  C  L  P  R  W  G  C  L  W  E  E  D
82   W  L  W  E  D  L  C  L  P  K  W  G  C  L  W  E  E  D
82   A  L  F  E  D  V  C  L  P  V  W  G  C  L  W  G  G  E
45   A  S  E  W  D  V  C  L  P  T  W  G  C  L  W  M  E  G
34   A  Y  S  A  D  I  C  L  P  R  W  G  C  L  W  M  S  E
35   E  D  W  E  D  I  C  L  P  Q  W  G  C  L  W  E  G  M
83   E  D  W  T  D  L  C  L  P  A  W  G  C  L  W  D  T  E
```

FIG. 8A

Sequences selected on rabbit albumin

Hard Randomization Library

```
          X  X  X  X  X  D  X  C  L  P  X  W  G  C  L  W  X  X  X  X
75        A  G  L  D  E  D  I  C  L  P  R  W  G  C  L  W  G  K  E  A
39        A  G  M  M  G  D  I  C  L  P  R  W  G  C  L  W  Q  G  E  P
76        A  P  G  D  W  D  F  C  L  P  K  W  G  C  L  W  D  D  D  A
74        A  Q  L  E  D  D  I  C  L  P  R  W  G  C  L  W  S  D  G  Y
86        A  R  T  M  G  D  T  C  L  P  R  W  G  C  L  W  G  A  S  D
63        A  W  Q  D  F  D  V  C  L  P  R  W  G  C  L  W  E  P  E  S
26        D  T  T  W  G  D  I  C  L  P  R  W  G  C  L  W  S  E  E  A
4         E  G  F  L  G  D  I  C  L  P  R  W  G  C  L  W  G  H  Q  A
2         E  Q  W  L  H  D  I  C  L  P  K  W  G  C  L  W  D  D  T  D
61        E  T  G  W  P  D  I  C  L  P  R  W  G  C  L  W  E  E  G  E
52        F  E  L  G  E  D  I  C  L  P  R  W  G  C  L  W  E  E  H  N
38        G  A  S  L  G  D  I  C  L  P  R  W  G  C  L  W  G  P  E  D
88        G  E  W  W  E  D  I  C  L  P  R  W  G  C  L  W  G  S  S  S
1         G  S  L  E  S  D  I  C  L  P  R  W  G  C  L  W  G  I  D  E
13        G  W  L  E  E  D  I  C  L  P  K  W  G  C  L  W  G  A  D  N
64        H  E  Q  W  D  D  I  C  L  P  R  W  G  C  L  W  G  G  S  Y
49        Q  R  V  D  D  D  I  C  L  P  R  W  G  C  L  W  G  E  N  S
50        S  V  G  W  G  D  I  C  L  P  K  W  G  C  L  W  A  E  S  D
40        T  L  M  S  N  D  I  C  L  P  R  W  G  C  L  W  D  E  P  K
28        T  L  V  L  D  D  I  C  L  P  R  W  G  C  L  W  D  M  T  D
14        T  W  Q  G  E  D  I  C  L  P  R  W  G  C  L  W  D  T  E  V
73        V  G  V  F  D  D  I  C  L  P  R  W  G  C  L  W  E  O  P  V
25        V  P  A  M  G  D  I  C  L  P  R  W  G  C  L  W  E  A  R  N
16        V  S  L  G  D  D  I  C  L  P  K  W  G  C  L  W  E  P  E  A
15        V  W  I  D  R  D  I  C  L  P  R  W  G  C  L  W  D  T  E  N
51        W  R  W  N  E  D  I  C  L  P  R  W  G  C  L  W  E  E  E  A
73        A  V  S  W  A  D  I  C  L  P  R  W  G  C  L  W  E  R  A  D
37        A  W  L  D  E  D  I  C  L  P  K  W  G  C  L  W  N  T  G  V
16        F  S  L  D  E  D  I  C  L  P  K  W  G  C  L  W  G  A  E  K
3         G  D  L  G  D  D  I  C  L  P  R  W  G  C  L  W  D  E  Y  P
87        G  E  G  W  S  D  I  C  L  P  R  W  G  C  L  W  A  E  D  E
38        G  L  M  G  E  D  I  C  L  P  R  W  G  C  L  W  K  G  D  I
75        G  W  H  D  R  D  I  C  L  P  R  W  G  C  L  W  E  Q  N  D
63        L  L  G  G  H  D  I  C  L  P  R  W  G  C  L  W  G  G  D  V
64        M  R  W  S  S  D  I  C  L  P  K  W  G  C  L  W  G  D  E  E
13        Q  F  E  W  D  D  I  C  L  P  R  W  G  C  L  W  E  V  E  V
49        Q  G  W  W  H  D  I  C  L  P  R  W  G  C  L  W  E  E  G  E
51        R  E  G  W  P  D  I  C  L  P  R  W  G  C  L  W  S  E  T  G
40        R  E  L  W  G  D  I  C  L  P  R  W  G  C  L  W  E  H  A  T
76        R  L  E  L  M  D  I  C  L  P  R  W  G  C  L  W  D  P  Q  D
2         S  G  V  L  G  D  I  C  L  P  R  W  G  C  L  W  E  E  A  G
14        S  L  G  L  T  D  L  C  L  P  R  W  G  C  L  W  E  E  E  Q
27        S  S  L  E  Q  D  I  C  L  P  R  W  G  C  L  W  G  Q  D  A
74        S  V  L  S  D  D  I  C  L  P  R  W  G  C  L  W  W  D  F  S
15        T  S  L  L  D  D  I  C  L  P  R  W  G  C  L  W  Y  E  E  G
50        T  S  L  A  D  D  I  C  L  P  R  W  G  C  L  W  S  E  D  G
25        V  E  M  W  H  D  I  C  L  P  R  W  G  C  L  W  D  S  N  A
4         W  D  L  A  S  D  I  C  L  P  R  W  G  C  L  W  E  E  E  A
```

Hard Randomization Library

```
          X  X  X  X  D  X  C  L  P  X  W  G  C  L  W  X  X  X
40        F  I  T  Q  D  I  C  L  P  R  W  G  C  L  W  G  E  N
13        F  L  W  R  D  I  C  L  P  R  W  G  C  L  W  S  E  G
50        F  V  H  E  D  I  C  L  P  R  W  G  C  L  W  G  E  G
26        G  L  G  D  D  I  C  L  P  R  W  G  C  L  W  G  R  D
63        G  M  F  D  D  I  C  L  P  K  W  G  C  L  W  G  L  G
37        G  P  G  W  D  I  C  L  P  R  W  G  C  L  W  G  E  E
87        G  P  W  Y  D  I  C  L  P  R  W  G  C  L  W  D  G  V
4         G  W  D  D  D  I  C  L  P  R  W  G  C  L  W  G  D  G
39        L  E  Y  E  D  I  C  L  P  K  W  G  C  L  W  G  G  E
14        L  L  D  E  D  I  C  L  P  R  W  G  C  L  W  G  V  R
28        L  M  S  P  D  I  C  L  P  K  W  G  C  L  W  E  G  D
52        L  V  L  G  D  I  C  L  P  R  W  G  C  L  W  E  S  D
75        M  L  S  R  D  I  C  L  P  R  W  G  C  L  W  E  E  E
61        M  P  W  T  D  I  C  L  P  R  W  G  C  L  W  S  E  S
25        R  L  G  S  D  I  C  L  P  R  W  G  C  L  W  G  A  G
51        R  L  G  S  D  I  C  L  P  R  W  G  C  L  W  D  Y  Q
49        S  P  W  M  D  I  C  L  P  R  W  G  C  L  W  E  S  G
38        S  T  F  T  D  I  C  L  P  R  W  G  C  L  W  E  L  E
74        S  V  L  S  D  I  C  L  P  R  W  G  C  L  W  E  E  S
86        T  W  F  S  D  I  C  L  P  R  W  G  C  L  W  E  P  G
88        V  H  Q  A  D  I  C  L  P  R  W  G  C  L  W  G  D  T
1         V  L  L  G  D  I  C  L  P  L  W  G  C  L  W  G  E  D
15        V  N  W  G  D  I  C  L  P  R  W  G  C  L  W  G  E  S
76        V  V  W  S  D  I  C  L  P  R  W  G  C  L  W  D  K  E
73        V  W  Y  K  D  I  C  L  P  R  W  G  C  L  W  E  A  E
85        W  D  Y  G  D  I  C  L  P  R  W  G  C  L  W  E  E  G
2         W  E  V  Q  D  I  C  L  P  R  W  G  C  L  W  G  D  D
27        Y  I  W  R  D  I  C  L  P  R  W  G  C  L  W  E  G  E
3         Y  R  D  Y  D  I  C  L  P  R  W  G  C  L  W  D  E  R
64        A  F  W  S  D  I  C  L  P  R  W  G  C  L  W  E  E  D
49        D  W  G  R  D  I  C  L  P  R  W  G  C  L  W  D  E  E
28        E  A  W  G  D  I  C  L  P  R  W  G  C  L  W  E  L  E
61        L  I  L  S  D  I  C  L  P  R  W  G  C  L  W  D  D  T
25        L  K  L  E  D  I  C  L  P  R  W  G  C  L  W  G  E  S
52        L  L  T  R  D  I  C  L  P  K  W  G  C  L  W  G  S  D
4         L  R  W  S  D  I  C  L  P  R  W  G  C  L  W  E  E  T
87        L  Y  L  R  D  I  C  L  P  K  W  G  C  L  W  E  A  D
76        N  W  Y  D  D  I  C  L  P  R  W  G  C  L  W  D  V  E
1         Q  D  W  E  D  I  C  L  P  R  W  G  C  L  W  G  D  -
38        Q  S  W  P  D  I  C  L  P  K  W  G  C  L  W  G  E  G
88        T  L  L  Q  D  I  C  L  P  R  W  G  C  L  W  E  S  D
74        V  R  L  M  D  I  C  L  P  R  W  G  C  L  W  G  E  E
26        V  R  W  E  D  I  C  L  P  R  W  G  C  L  W  G  E  E
40        W  D  V  A  D  I  C  L  P  R  W  G  C  L  W  A  E  D
15        W  H  M  G  D  I  C  L  P  R  W  G  C  L  W  S  E  V
14        W  K  D  F  D  I  C  L  P  R  W  G  C  L  W  D  D  H
3         W  L  S  E  D  I  C  L  P  Q  W  G  C  L  W  E  E  S
27        W  L  S  E  D  I  C  L  P  R  W  G  C  L  W  A  A  D
37        W  L  S  D  D  I  C  L  P  R  W  G  C  L  W  D  D  L
```

FIG. 8B

Sequences selected on human albumin

Hard Randomization Library

	X	X	X	X	X	D	X	C	L	P	X	W	G	C	L	W	X	X	X	X
68	E	V	R	E	W	D	I	C	L	P	R	W	G	C	L	W	E	N	W	R
6	F	G	Q	E	W	D	I	C	L	P	R	W	G	C	L	W	G	N	E	Q
17	I	W	Q	L	E	D	I	C	L	P	R	W	G	C	L	W	E	D	G	L
53	N	T	P	T	Y	D	I	C	L	P	R	W	G	C	L	W	G	D	V	P
5	Q	P	V	W	S	D	I	C	L	P	R	W	G	C	L	W	G	E	D	H
18	S	W	Y	G	G	D	I	C	L	P	J	W	G	C	L	W	S	E	E	S
80	W	G	M	A	R	D	W	C	L	P	M	W	G	C	L	W	R	G	G	G
7	W	H	L	T	D	D	I	C	L	P	R	W	G	C	L	W	G	D	E	Q
54																				
67	N	W	A	E	N	D	I	C	L	P	R	W	G	C	L	W	G	D	E	N
68	S	A	R	E	W	D	I	C	L	P	T	W	G	C	L	W	E	K	D	I

Hard Randomization Library

	X	X	X	X	D	X	C	L	P	X	W	G	C	L	W	X	X	X
42	A	G	E	W	D	I	C	L	P	R	W	G	C	L	W	D	V	E
56	E	I	R	W	D	F	C	L	P	R	W	G	C	L	W	D	E	D
8	E	S	L	G	D	I	C	L	P	R	W	G	C	L	W	G	S	G
30	E	Y	W	G	D	I	C	L	P	R	W	G	C	L	W	D	W	Q
80	K	M	W	S	D	I	C	L	P	R	W	G	C	L	W	E	E	E
90	M	G	T	K	D	I	C	L	P	R	W	G	C	L	W	A	E	A
7	M	H	E	W	D	I	C	L	P	R	W	G	C	L	W	E	S	S
78	R	G	L	H	D	A	C	L	P	W	W	G	C	L	W	A	G	S
19	R	L	F	G	D	I	C	L	P	R	W	G	C	L	W	Q	G	E
5	S	G	E	W	D	I	C	L	P	R	W	G	C	L	W	G	E	G
6	S	M	F	F	D	H	C	L	P	M	W	G	C	L	W	A	E	Q
44	V	G	E	W	D	I	C	L	P	N	W	G	C	L	W	E	R	E
32	W	W	M	A	D	R	C	L	P	L	W	G	C	L	W	R	G	D
29	W	W	V	R	D	L	C	L	P	T	W	G	C	L	W	S	G	K
54	Y	F	D	G	D	I	C	L	P	R	W	G	C	L	W	G	S	D
32	T	L	F	Q	D	I	C	L	P	R	W	G	C	L	W	E	E	S
68	W	F	P	K	D	R	C	L	P	V	W	G	C	L	W	E	R	H

FIG. 8C

PEPTIDE	Sequence	Rabbit SA IC$_{50}$ (nM)	Rat SA IC$_{50}$ (nM)	Mouse SA IC$_{50}$ (nM)
SA02	D L C L R D W G C L W -n			
SA04	D I C L P R W G C L W -n	8543	787	40
SA05	M E D I C L P R W G C L W E D -n	804	161	6
SA06	Q R L M E D I C L P R W G C L W E D D F -n	128	68	8
SA07	Q G L I G D I C L P R W G C L W G D S V -n	30	35	6
SA08	Ac- Q G L I G D I C L P R W G C L W G D S V K -n	63	68	10
SA09	Ac- E D I C L P R W G C L W E D D -n	1687	258	6
SA10	Ac- R L M E D I C L P R W G C L W E D D -n	86	77	4
SA11	Ac- M E D I C L P R W G C L W E D D -n	1213	232	17
SA12	Ac- M E D I C L P R W G C L W E D -n	1765	205	13
SA13	Ac- R L M E D I C L A R W G C L W E D D -n	3200	2480	188
D3H44-L	Q R L M E D I C L P R W G C L W E D D F -n	241		
D3H44-Ls	Q R L M E D I C L P R W G C L W E D D F -n	75		

FIG. 9

Peptide SA06 in the
SA08b Competition Binding Assay
## with a Mouse, Rat, or Rabbit Albumin Coat
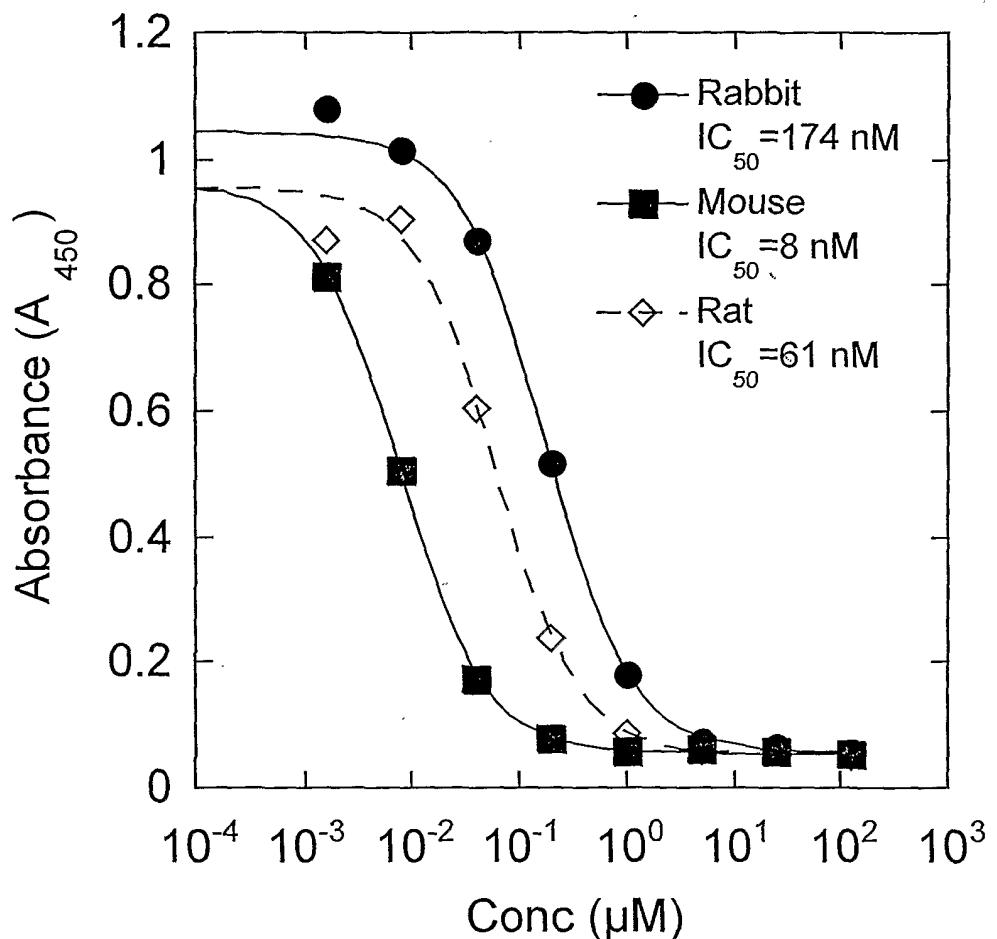

FIG. 10
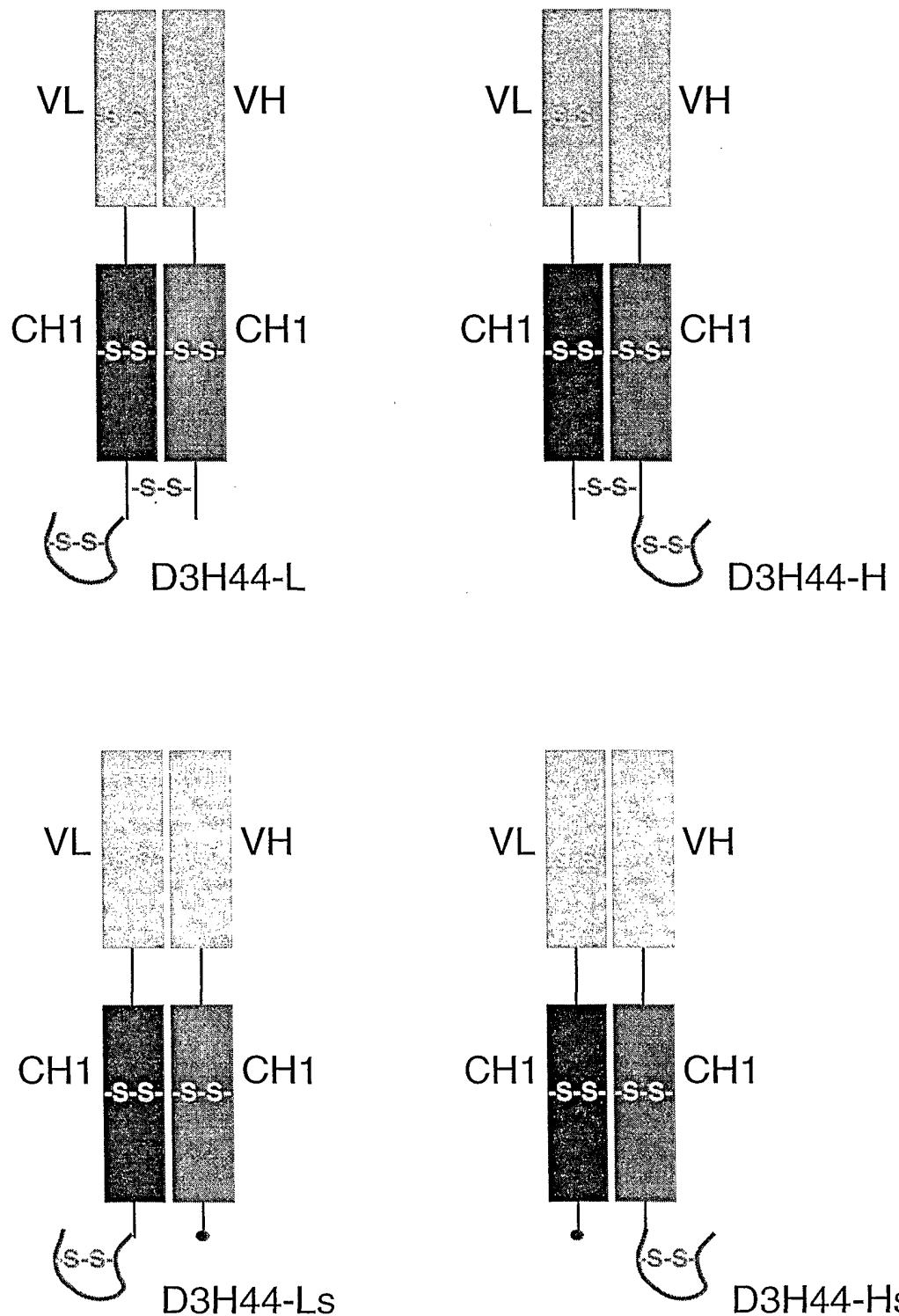
FIG. 11

Inhibition of FX Activation
by D3H44-L

FIG. 12

Human Prothrombin Time (PT) of
D3H44 Fab or D3H44-L


FIG. 13

SA08b Competition Binding Assay
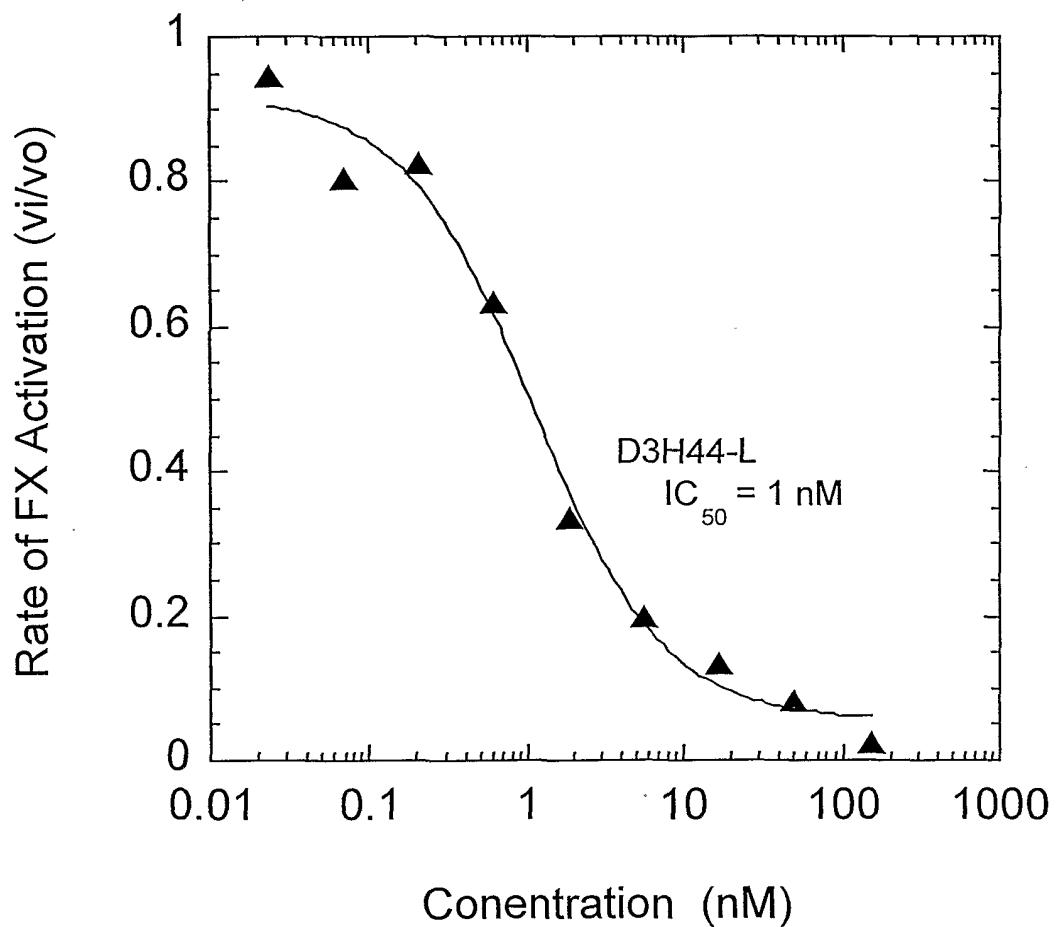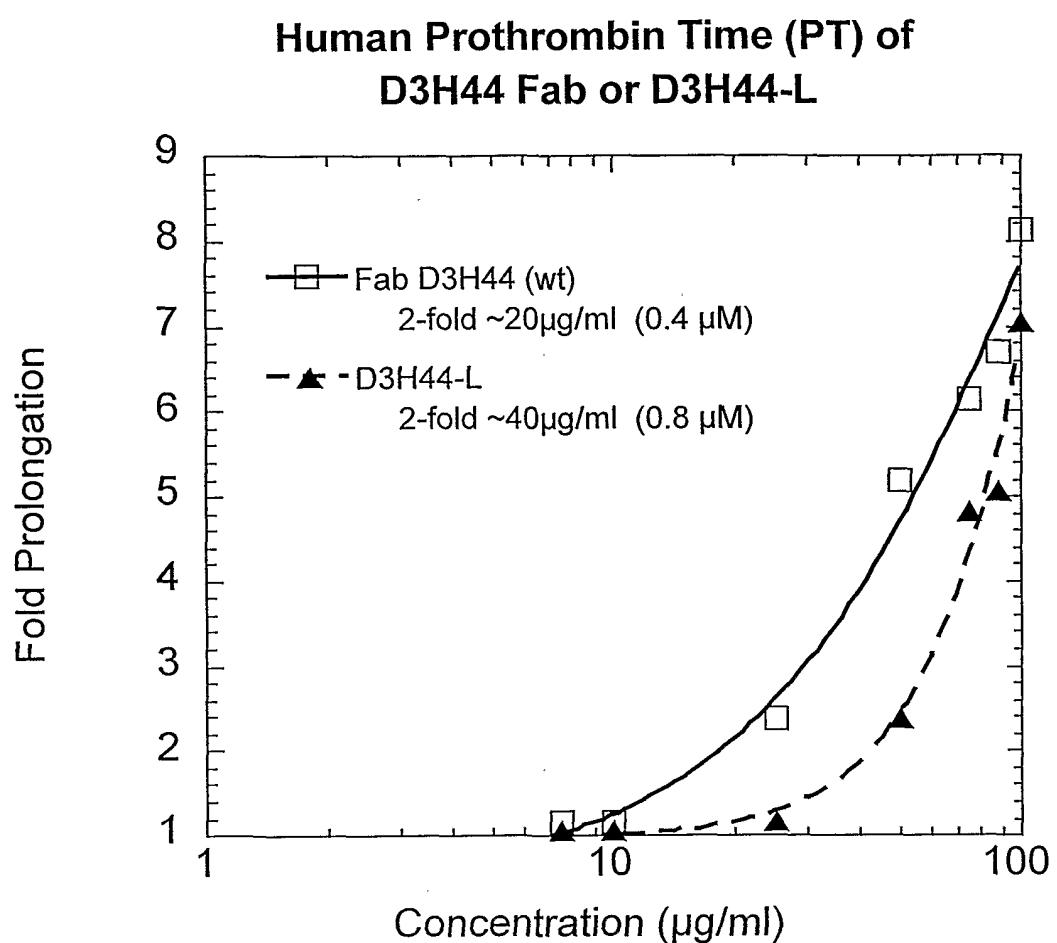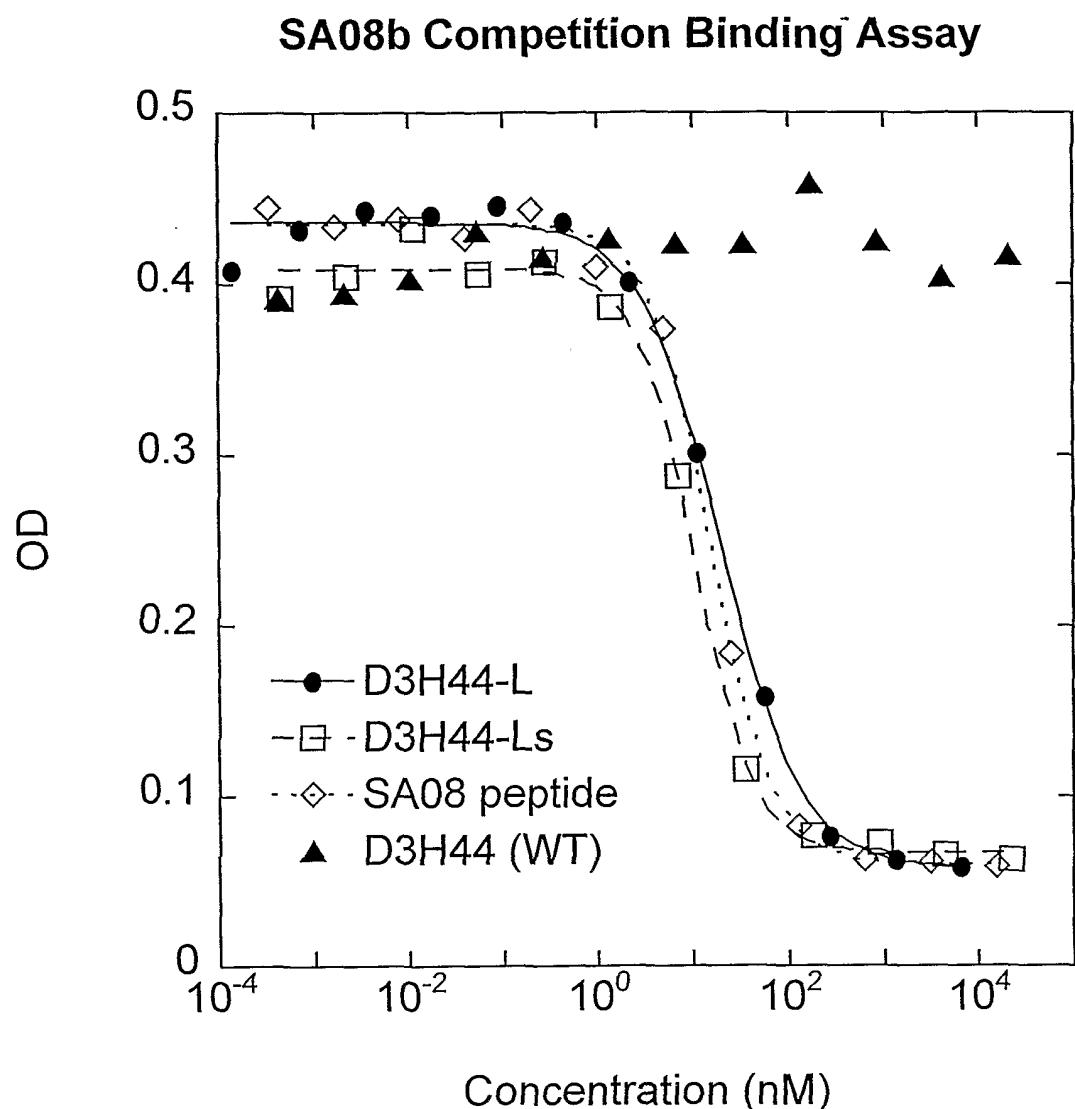

FIG. 14
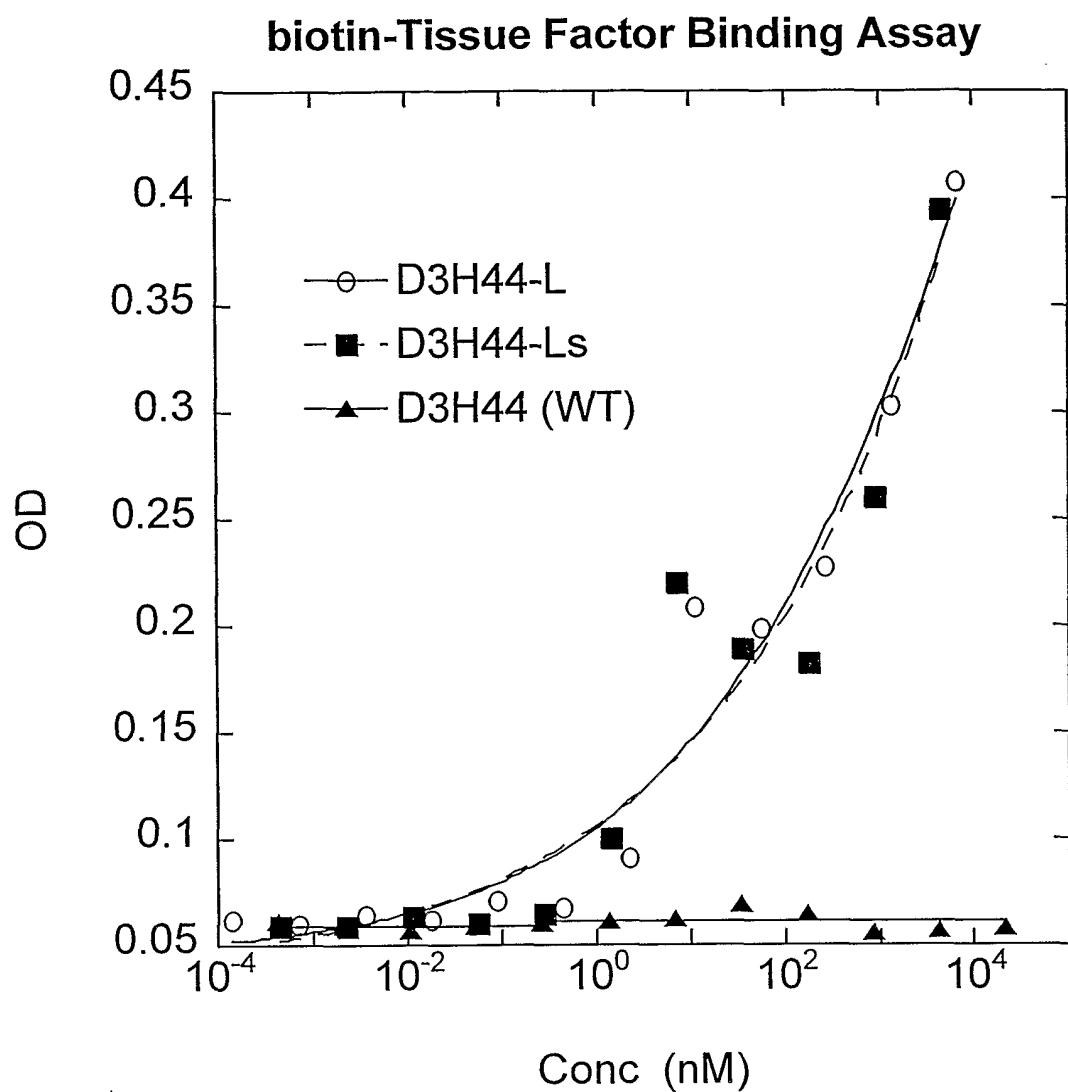
FIG. 15

Pharmacokinetics of D3H44 variants in Rabbit
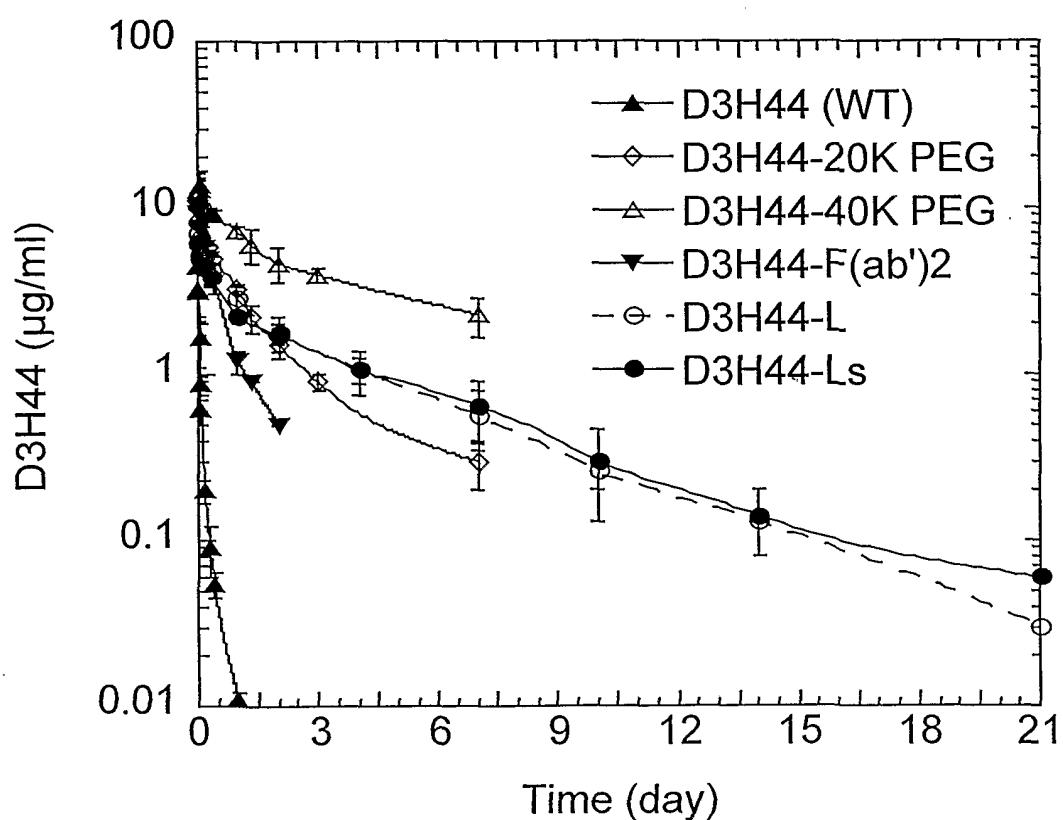
FIG. 16

00-331 Summarized PK Data

ParameterUnits		D3H44-Fab		D3H44-L		D3H44-Ls		
		Average	Stdev	Average	Stdev	Average	Stdev	
Dose	ug/kg	396		416		524		
AUC	hr*ug/mL	5.86	1.23	349	33	332	82	
AUC/Dose	(hr*ug/mL)/(mg/kg)	14.8	3.1	840	78	633	157	
CL	mL/hr/kg	69.9	16.2	1.20	0.11	1.64	0.37	
Cmax	ug/mL	5.00	2.30	7.55	1.23	5.98	0.11	
K10-HL	hr	0.876	0.213	32.4	3.2	38.3	8.8	
MRT	hr	3.07	0.62	95.0	13.1	110	20	
V1	mL/kg	90.6	38.4	56.2	10.1	87.6	1.7	$p < 0.05$ RC20L vs RC20Ls
Vss	mL/kg	221	95	113	7	176	11	$p < 0.05$ RC20L vs RC20Ls

99-133 Summarized PK data (historical)

ParameterUnits		D3H44-20K PEG		D3H44-40K PEG		D3H44-Fab		D3H44-Fab'2	
		Average	Stdev	Average	Stdev	Average	Stdev	Average	Stdev
AUC	hr*ug/mL	271	33	1255	383	9.8	1.6	120	13
CL	mL/hr/kg	1.87	0.23	0.422	0.119	51.8	9.2	4.21	0.51
K10-HL	hr	18.0	4.2	68.9	28.5	0.760	0.123	8.84	0.73
V1	ug/mL	47.4	5.4	39.2	7.4	55.9	4.7	53.5	5.3
Vss	mL/kg	109	14	78.8	13.7	127	13	84.5	11.4
Dose	ug/kg	509		493		500		500	
AUC/Dose	(hr*ug/mL)/(mg/kg)	532	65	2546	777	19.7	3.2	240	26

AUC = area under the curve   MRT = mean residence time
CL = clearance   V1 = initial distribution volume
K10-HL = half-life from compartment   Vss = distribution volume at steady state

FIG. 17