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(19) **United States**(12) **Patent Application Publication****Daly et al.**(10) **Pub. No.: US 2006/0058234 A1**(43) **Pub. Date: Mar. 16, 2006**(54) **VEGF TRAPS AND THERAPEUTIC USES
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8, 1999.**Publication Classification**(51) **Int. Cl.****C07K 14/71** (2006.01)**A61K 38/17** (2006.01)**C07H 21/04** (2006.01)**C12P 21/06** (2006.01)**C12N 5/06** (2006.01)(52) **U.S. Cl.** **514/12**; 530/350; 435/69.1;
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(57)

ABSTRACTNucleic acid molecules and multimeric proteins capable of
binding vascular endothelial growth factor (VEGF). VEGF
traps are disclosed which are therapeutically useful for
treating VEGF-associated conditions and diseases, and are
specifically designed for local administration to specific
organs, tissues, and/or cells.

Observed Masses		Expected Masses	Monosaccharide Compositions	Proposed Sugar Chain Structures
VGT C04003 M500	VGT C04008 M500			
1356.4	1356.0	1356.1	(Man) ₂ (Man) ₃ (Glc) ₂	
1380.9	1381.6	1381.2	(Glc)(Man) ₃ (Glc) ₂ (Fuc)	
1397.2	1397.2	1397.3	(Gal)(Glc)(Man) ₃ (Glc) ₂	
1438.6	1438.2	1438.2	(Glc) ₂ (Man) ₃ (Glc) ₂	
1526.7	1525.9	1527.2	(Glc)(Man) ₃ (Glc) ₂ (Fuc) ₂	
1543.4	1542.8	1543.4	(Gal)(Glc)(Man) ₃ (Glc) ₂ (Fuc)	
1559.7	1559.4	1559.4	(Gal)(Glc)(Man)(Man) ₃ (Glc) ₂	
1584.6	1584.0	1584.4	(Glc) ₂ (Man) ₃ (Glc) ₂ (Fuc)	
1600.5	1600.0	1600.4	(Gal)(Glc) ₂ (Man) ₃ (Glc) ₂	
1646.5	1646.6		Adduct of 1584.4	
1688.5	1688.0	1688.4	(SA)(Gal)(Glc)(Man) ₃ (Glc) ₂	
1721.5	1720.8	1721.5	(Gal)(Glc)(Man) ₂ (Man) ₃ (Glc) ₂	

Figure 1A

Observed Masses		Expected Masses	Monosaccharide Compositions	Proposed Sugar Chain Structures
VGTC04003 M500	VGTC04008 M500			
1746.7	1746.2	1746.5	(Gal)(Glc)2(Man)3(Glc)2(Fuc)	
1762.8	1762.6	1762.1	(Gal)2(Glc)2(Man)3(Glc)2	
1809.5	1809.1		Adduct of 1746.5	
1834.8	1834.7	1834.5	(SA)(Gal)(Glc)(Man)3(Glc)2(Fuc)	
1849.9	1851.0	1850.5	(SA)(Gal)2(Glc)(Man)3(Glc)2	
1891.9	1891.1	1891.6	(SA)(Gal)(Glc)2(Man)3(Glc)2	
1908.6	1908.2	1908.6	(Gal)(Glc)2(Man)3(Glc)2(Fuc)	
1996.9	1996.5	1996.6	(SA)(Gal)2(Glc)(Man)3(Glc)2(Fuc)	
2012.8	2012.3	2012.8	(SA)(Gal)(Glc)2(Man)2(Man)3(Glc)2	
2037.7	2037.3	2037.7	(SA)(Gal)(Glc)2(Man)3(Glc)2(Fuc)	
2053.8	2053.2	2053.8	(SA)(Gal)2(Glc)2(Man)3(Glc)2	
2075.8	2074.9		Adduct of 2053.8	
2116.0	2115.7		Adduct of 2053.8	

Figure 1B

Observed Masses		Expected Masses	Monosaccharide Compositions	Proposed Sugar Chain Structures
VGT C04003 M500	VGT C04008 M500			
2200.0	2199.3	2199.9	(SA)(Gal)2(Glc)2(Man)3(Glc)2(Fuc)	
2221.5	2221.5			Na ⁺ Adduct of 2199.9
2262.5	2261.3			Adduct of 2199.9
2345.6	2345.6	2345.0	(SA)2(Gal)2(Glc)2(Man)3(Glc)2	
2407.0	2407.2			Adduct of 2345.0
2492.5	2492.0	2491.2	(SA)2(Gal)2(Glc)2(Man)3(Glc)2(Fuc)	
2554.3	2553.1			Adduct of 2491.2
2564.6	2564.0	2565.2	(SA)(Gal)3(Glc)3(Man)3(Glc)2(Fuc)	
2857.2	2857.3	2856.5	(SA)2(Gal)3(Glc)3(Man)3(Glc)2(Fuc)	
2918.1	2918.9			Adduct of 2856.5
3148.5	3148.5	3147.8	(SA)3(Gal)3(Glc)3(Man)3(Glc)2(Fuc)	
3211.0	3211.0			Adduct of 3147.8

Figure 1C

VEGF TRAPS AND THERAPEUTIC USES THEREOF

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application is a continuation-in-part of application Ser. No. 11/016,097 filed 17 Dec. 2004 and Ser. No. 11/016,503 filed 17 Dec. 2004, which are divisionals of Ser. No. 10/009,852 filed 6 Dec. 2001, which is the National Stage of International Application No. PCT/US00/14142 filed 23 May 2000, which claims the benefit under 35 USC § 119(e) of U.S. provisional Application No. 60/138,133 filed 8 Jun. 1999; and application Ser. No. 10/880,021 filed 29 Jun. 2004, which is a continuation-in-part of Ser. No. 10/609,775 filed 30 Jun. 2003, which is a continuation-in-part of Ser. No. 10/009,852 filed 6 Dec. 2001, which is the National Stage of International Application No. PCT/US00/14142 filed 23 May 2000, which claims the benefit under 35 USC § 119(e) of U.S. provisional Application No. 60/138,133 filed 8 Jun. 1999, which applications are herein specifically incorporated by reference in their entireties.

BACKGROUND OF THE INVENTION

[0002] 1. Field of the Invention

[0003] The invention encompasses fusion polypeptides capable of binding vascular endothelial cell growth factor (VEGF), VEGF family members, and splice variants with specifically desirable characteristics, as well as therapeutic methods of use.

[0004] 2. Brief Summary of the Invention

[0005] In a first aspect, the invention features an isolated nucleic acid molecule encoding a fusion polypeptide comprising receptor components R1-R2-F, wherein R1 is vascular endothelial cell growth factor (VEGF) receptor component Ig domain 2 of Flt-1 (Flt1D2), R2 is VEGF receptor component Ig domain 3 of Flk-1 (Flk1D3) (also known as KDR), and F is a fusion component.

[0006] In a related second aspect, the invention features a VEGF-binding fusion polypeptide comprising VEGF receptor components R1-R2-F, wherein R1, R2, and F are as defined above. The components may be connected directly to each other or connected via one or more spacer sequences. In a preferred embodiment, R1 and R2 are the only receptor components present. In a specific embodiment, the VEGF-binding fusion polypeptide is amino acids 27-129 (R1) and 130-231 (R2) of SEQ ID NO:8, or a variant thereof.

[0007] The fusion component F is selected from the group consisting of a multimerizing component, a serum protein, or a molecule capable of binding a serum protein. In a preferred embodiment, F is a multimerizing component capable of interacting with a multimerizing component on another fusion polypeptide to form a multimeric structure, e.g., a dimer or trimer. Most preferably, the F is selected from the group consisting of (i) a multimerizing component comprising a cleavable region (C-region), (ii) a truncated multimerizing component, (iii) an amino acid sequence between 1 to about 200 amino acids in length having at least one cysteine residue, (iv) a leucine zipper, (v) a helix loop motif and (vi) a coil-coil motif. Preferably, the multimerizing component is an immunoglobulin domain. In one

embodiment, F is a full-length or truncated immunoglobulin domain consisting of amino acids 232-458, 232-457, or 352-458 of SEQ ID NO:8.

[0008] The receptor components may be arranged in different orders, for example, R1R2F; R2R1F; R1FR2; R2FR1; FR1R2; FR2R1, etc. The components of the fusion polypeptide may be connected directly to each other, or connected via a spacer sequence.

[0009] In a third aspect, the invention features a multimeric VEGF-binding protein, comprising two or more fusion polypeptides of the invention (also called a VEGF "trap"). A VEGF trap composed of two fusion polypeptides having at least one truncated multimerizing component is termed a "truncated mini-trap." The multimeric VEGF-binding protein of the invention is capable of binding VEGF with an affinity (Kd) of at least 1×10^{-10} M, preferably at least 1×10^{-11} M, even more preferably at least 1×10^{-12} M, as measured by Biacore-based assays.

[0010] The C-region may be created in the multimerizing component by insertion, deletion, or mutation, such that an enzymatically or chemically cleavable site is created. The C-region may be created in any multimerizing component and at any position within; preferably, the C-region is created in a full-length Fc domain, or a fragment thereof, or a C_H3 domain. The C-region may be a site cleavable by an enzyme, such as, thrombin, ficin, pepsin, matrilysin, or prolidase or cleavable chemically by, for example, formic acid or CuCl₂.

[0011] In all embodiments of the VEGF-binding fusion polypeptides of the invention (including full length VEGF-binding fusion polypeptides, truncated VEGF-binding fusion polypeptides, etc.), a signal sequence (S) may be included at the beginning (or N-terminus) of the fusion polypeptide of the invention. The signal sequence may be native to the cell, recombinant, or synthetic.

[0012] The components of the fusion polypeptide may be connected directly to each other or be connected via spacers. In specific embodiments, one or more receptor and/or fusion partner components of the fusion polypeptide are connected directly to each other without spacers. In other embodiments, one or more receptor and/or fusion partner components are connected with spacers.

[0013] In a fourth aspect, the invention encompasses vectors comprising the nucleic acid molecules of the invention, including expression vectors comprising the nucleic acid molecule operatively linked to an expression control sequence. In a fifth aspect, the invention encompasses host-vector systems for the production of a fusion polypeptide which comprise the expression vector, in a suitable host cell; host-vector systems wherein the suitable host cell is a bacterial, yeast, insect, mammalian cell; an *E. Coli* cell, or a COS or CHO cell. Additional encompassed in a sixth aspect are VEGF-binding fusion polypeptides of the invention modified by acetylation or pegylation, and other post-translational modifications resulting from expression in a mammalian cell line. Methods for acetylating or pegylating a protein are well known in the art. In specific embodiments, the fusion polypeptide of the invention expressed in a mammalian cell line such as a CHO cell comprises amino acids 27-457 of SEQ ID NO:8 and is glycosylated at Asn residues 62, 94, 149, 222 and 308.

[0014] In a related seventh aspect, the invention features a method of producing a VEGF-binding fusion polypeptides of the invention, comprising culturing a host cell transfected with a vector comprising a nucleic acid sequence of the invention, under conditions suitable for expression of the protein from the host cell, and recovering the fusion polypeptides so produced.

[0015] The VEGF-binding fusion polypeptides of the invention are therapeutically useful for treating any disease or condition which is improved, ameliorated, or inhibited by removal, inhibition, or reduction of VEGF. A non-exhaustive list of specific conditions improved by inhibition or reduction of VEGF include, for example, undesirable plasma leakage or vascular permeability, undesirable blood vessel growth, e.g., such as in a tumor, edema associated with inflammatory disorders such as psoriasis or arthritis, including rheumatoid arthritis; asthma; generalized edema associated with bums; ascites and pleural effusion associated with tumors, inflammation or trauma; chronic airway inflammation; asthma; capillary leak syndrome; sepsis; kidney disease associated with increased leakage of protein; pancreatic ductal adenocarcinoma (PDAC) and eye disorders such as age related macular degeneration and diabetic retinopathy. The VEGF mini-trap is particularly useful in treatment of eye disorders, and as an adjuvant to eye surgeries, including glaucoma surgery; and the treatment of intra-ocular tumors, such as for example, uveal melanoma, retinoblastoma, via intravitreal delivery.

[0016] Accordingly, in an eighth aspect, the invention features a therapeutic method for the treatment of a VEGF-related disease or condition, comprising administering a VEGF-binding fusion polypeptide of the invention to a subject suffering from a VEGF-related disease or condition. Although any mammal can be treated by the therapeutic methods of the invention, the subject is preferably a human patient suffering from or at risk of suffering from a condition or disease which can be improved, ameliorated, inhibited or treated with a VEGF-binding fusion polypeptide of the invention.

[0017] In a ninth aspect, the invention features pharmaceutical compositions comprising a VEGF-binding fusion polypeptide of the invention with a pharmaceutically acceptable carrier. Such pharmaceutical compositions may comprise a dimeric fusion polypeptide trap, or nucleic acids encoding the fusion polypeptide. The mini-traps of the invention find specific uses in conditions in which a VEGF inhibitor with reduced serum half life (e.g., faster clearance), and/or increased tissue penetration due to smaller size is desirable. Specific applications for the VEGF mini-trap include, for example, diseases where local administration to a specific tissue or cell is desirable. Examples of such a condition or disease are ocular diseases of the eye.

[0018] Other objects and advantages will become apparent from a review of the ensuing detailed description.

BRIEF DESCRIPTION OF THE FIGURES

[0019] FIGS. 1A-C provides sugar chain mass assignment for the oligosaccharides of two batches of VEGF trap protein (SEQ ID NO:8) (P3=VGT C04003M500; P3.5=C04008M500).

DETAILED DESCRIPTION OF THE INVENTION

[0020] Before the present methods are described, it is to be understood that this invention is not limited to particular methods, and experimental conditions described, as such methods and conditions may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting, since the scope of the present invention will be limited only the appended claims.

[0021] As used in this specification and the appended claims, the singular forms “a”, “an”, and “the” include plural references unless the context clearly dictates otherwise. Thus for example, a reference to “a method” includes one or more methods, and/or steps of the type described herein and/or which will become apparent to those persons skilled in the art upon reading this disclosure and so forth.

[0022] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, the preferred methods and materials are now described. All publications mentioned herein are incorporated herein by reference to describe the methods and/or materials in connection with which the publications are cited.

General Description

[0023] The invention encompasses multimeric VEGF-binding proteins capable of binding and inhibiting VEGF activity with a K_d of at least $x \times 10^{-10}$ M. The molecules of the invention bind and inhibit the biological action of VEGF and/or the physiological reaction or response. For a description of VEGF-receptor-based antagonist VEGF traps Flt1D2.Flk1D3.FcΔC1(a) (SEQ ID NOs:5-6) and VEGFR1R2-FcΔC1(a) (SEQ ID NOs:7-8), see PCT WO/0075319, the contents of which is incorporated in its entirety herein by reference.

Nucleic Acid Constructs and Expression

[0024] The present invention provides for the construction of nucleic acid molecules encoding fusion polypeptides capable of multimerizing to form VEGF traps capable of binding VEGF with high affinity. The nucleic acid molecules of the invention may encode wild-type R1 and R2 receptor components, or may encode functionally equivalent variants thereof. Amino acid sequence variants of the R1 and R2 receptor components of the traps of the invention may also be prepared by creating mutations in the encoding nucleic acid molecules. Such variants include, for example, deletions from, or insertions or substitutions of, amino acid residues within the amino acid sequence of R1 and R2. Any combination of deletion, insertion, and substitution may be made to arrive at a final construct, provided that the final construct possesses the ability to bind and inhibit VEGF.

[0025] These nucleic acid molecules are inserted into a vector that is able to express the fusion polypeptides when introduced into an appropriate host cell. Appropriate host cells include, but are not limited to, bacterial, yeast, insect, and mammalian cells. Any of the methods known to one skilled in the art for the insertion of DNA fragments into a

vector may be used to construct expression vectors encoding the fusion polypeptides of the invention under control of transcriptional/translational control signals.

[0026] Expression of the nucleic acid molecules of the invention may be regulated by a second nucleic acid sequence so that the molecule is expressed in a host transformed with the recombinant DNA molecule. For example, expression may be controlled by any promoter/enhancer element known in the art. Promoters which may be used to control expression of the chimeric polypeptide molecules include, but are not limited to, a long terminal repeat (Squinto et al. (1991) *Cell* 65:1-20); SV40 early promoter region, CMV, M-MuLV, thymidine kinase promoter, the regulatory sequences of the metallothionein gene; prokaryotic expression vectors such as the β -lactamase promoter, or the tac promoter (see also *Scientific American* (1980) 242:74-94); promoter elements from yeast or other fungi such as Gal 4 promoter, ADH, PGK, alkaline phosphatase, and tissue-specific transcriptional control regions derived from genes such as elastase I.

[0027] Expression vectors capable of being replicated in a bacterial or eukaryotic host comprising the nucleic acid molecules of the invention are used to transfect the host and thereby direct expression of such nucleic acids to produce the fusion polypeptides of the invention, which form traps capable of binding to VEGF. Transfected cells may transiently or, preferably, constitutively and permanently express the VEGF traps of the invention.

[0028] The fusion polypeptides of the invention may be purified by any technique which allows for the subsequent formation of a stable, biologically active trap. For example, and not by way of limitation, the factors may be recovered from cells either as soluble proteins or as inclusion bodies, from which they may be extracted quantitatively by 8M guanidinium hydrochloride and dialysis (see, for example, U.S. Pat. No. 5,663,304). In order to further purify the factors, conventional ion exchange chromatography, hydrophobic interaction chromatography, reverse phase chromatography or gel filtration may be used.

VEGF Receptor Components

[0029] The VEGF receptor components of the VEGF mini trap consist of the Ig domain 2 of Flt-1 (Flt1D2) (R1), the Ig domain 3 of Flk-1 (Flk1D3) (R2) (together, R1R2). The term "Ig domain" of Flt-1 or Flk-1 is intended to encompass not only the complete wild-type domain, but also insertional, deletional, and/or substitutional variants thereof which substantially retain the functional characteristics of the intact domain. It will be readily apparent to one of skill in the art that numerous variants of the above Ig domains can be obtained which will retain substantially the same functional characteristics as the wild-type domain.

[0030] The term "functional equivalents" when used in reference to R1 and R2, is intended to encompass an R1 and R2 domain with at least one alteration, e.g., a deletion, addition, and/or substitution, which retains substantially the same functional characteristics as does the wild type R1 and R2, that is, a substantially equivalent binding to VEGF. It will be appreciated that various amino acid substitutions can be made in R1 and R2 without departing from the spirit of the invention with respect to the ability of these receptor components to bind and inactivate VEGF. The functional

characteristics of the traps of the invention may be determined by any suitable screening assay known to the art for measuring the desired characteristic. Examples of such assays are described in the experimental section below which allow determination of binding affinity of the traps for VEGF (Kd), as well as their half-life of dissociation of the trap-ligand complex ($T_{1/2}$). Other assays, for example, a change in the ability to specifically bind to VEGF can be measured by a competition-type VEGF binding assay. Modifications of protein properties such as thermal stability, hydrophobicity, susceptibility to proteolytic degradation, or tendency to aggregate may be measured by methods known to those of skill in the art.

[0031] The components of the fusion polypeptide may be connected directly to each other or be connected via spacers. Generally, the term "spacer" (or linker) means one or more molecules, e.g., nucleic acids or amino acids, or non-peptide moieties, such as polyethylene glycol, which may be inserted between one or more component domains. For example, spacer sequences may be used to provide a desirable site of interest between components for ease of manipulation. A spacer may also be provided to enhance expression of the fusion polypeptide from a host cell, to decrease steric hindrance such that the component may assume its optimal tertiary structure and/or interact appropriately with its target molecule. For spacers and methods of identifying desirable spacers, see, for example, George et al. (2003) *Protein Engineering* 15:871-879, herein specifically incorporated by reference. A spacer sequence may include one or more amino acids naturally connected to a receptor component, or may be an added sequence used to enhance expression of the fusion polypeptides, provide specifically desired sites of interest, allow component domains to form optimal tertiary structures and/or to enhance the interaction of a component with its target molecule. In one embodiment, the spacer comprises one or more peptide sequences between one or more components which is (are) between 1-100 amino acids, preferably 1-25.

[0032] In the most specific embodiments, R1 is amino acids 27-126 of SEQ ID NO:6, or 1-126 of SEQ ID NO:6 (including the signal sequence 1-26); or amino acids 27-129 of SEQ ID NO:8, or 1-129 of SEQ ID NO:8 (including the signal sequence at 1-26). In the most specific embodiments, R2 is amino acids 127-228 of SEQ ID NO:6, or amino acids 130-231 of SEQ ID NO:8. When, for example, R2 is placed at the N-terminus of the fusion polypeptide, a signal sequence may desirably precede the receptor component. The receptor component(s) attached to the multimerizing component may further comprise a spacer component, for example, the GPG sequence of amino acids 229-231 of SEQ ID NO:5.

Fusion and Multimerizing Components

[0033] The fusion partner is any component that enhances the functionality of the fusion polypeptide. Thus, for example, an fusion partner may enhance the biological activity of the fusion polypeptide, aid in its production and/or recovery, or enhance a pharmacological property or the pharmacokinetic profile of the fusion polypeptide by, for example, enhancing its serum half-life, tissue penetrability, lack of immunogenicity, or stability. In preferred embodiments, the fusion partner is selected from the group consisting of a multimerizing component, a serum protein, or a molecule capable of binding a serum protein.

[0034] When the fusion partner is a serum protein or fragment thereof, it is selected from the group consisting of α -1-microglobulin, AGP-1, orosomucoid, α -1-acid glycoprotein, vitamin D binding protein (DBP), hemoexin, human serum albumin (hSA), transferrin, ferritin, afamin, haptoglobin, α -fetoprotein thyroglobulin, α -2-HS-glycoprotein, β -2-glycoprotein, hyaluronan-binding protein, syntaxin, C1R, C1q a chain, galectin3-Mac2 binding protein, fibrinogen, polymeric Ig receptor (PIGR), α -2-macroglobulin, urea transport protein, haptoglobin, IGFBPs, macrophage scavenger receptors, fibronectin, giantin, Fc, α -1-antichymotrypsin, α -1-antitrypsin, antithrombin III, apolipoprotein A-I, apolipoprotein B, β -2-microglobulin, ceruloplasmin, complement component C3 or C4, CI esterase inhibitor, C-reactive protein, cystatin C, and protein C. In a more specific embodiment, fusion partner is selected from the group consisting of α -1-microglobulin, AGP-1, orosomucoid, α -1-acid glycoprotein, vitamin D binding protein (DBP), hemoexin, human serum albumin (hSA), afamin, and haptoglobin. The inclusion of a fusion partner component may extend the serum half-life of the fusion polypeptide of the invention when desired. See, for example, U.S. Pat. Nos. 6,423,512, 5,876,969, 6,593,295, and 6,548,653, herein specifically incorporated by reference in their entirety, for examples of serum albumin fusion polypeptides. hSA is widely distributed throughout the body, particularly in the intestinal and blood components, and has an important role in the maintenance of osmolarity and plasma volume. It is slowly cleared in the liver, and typically has an in vivo half-life of 14-20 days in humans (Waldmann et al. (1977) *Albumin, Structure Function and Uses*; Pergamon Press; pp. 255-275).

[0035] When a fusion partner is a molecule capable of binding a serum protein, the molecule may be a synthetic small molecule, a lipid or liposome, a nucleic acid, including a synthetic nucleic acid such as an aptamer, a peptide, or an oligosaccharide. The molecule may further be a protein, such as, for example, Fc γ R1, Fc γ R2, Fc γ R3, polymeric Ig receptor (PIGR), ScFv, and other antibody fragments specific for a serum protein.

[0036] When the fusion partner is a multimerizing component (MC), it is any natural or synthetic sequence capable of interacting with another MC to form a higher order structure, e.g., a dimer, a trimer, etc. Suitable MCs may include a leucine zipper, including leucine zipper domains derived from c-jun or c-fos; sequences derived from the constant regions of kappa or lambda light chains; synthetic sequences such as helix-loop-helix motifs (Müller et al. (1998) *FEBS Lett.* 432:45-49), coil-coil motifs, etc., or other generally accepted multimerizing domains known to the art. In some embodiments, the fusion component comprises an immunoglobulin-derived domain from, for example, human IgG, IgM or IgA. In specific embodiments, the immunoglobulin-derived domain may be selected from the group consisting of the Fc domain of IgG, the heavy chain of IgG, and the light chain of IgG. The Fc domain of IgG may be selected from the isotypes IgG1, IgG2, IgG3, and IgG4, as well as any allotype within each isotype group. In one example of the VEGF trap of the invention, the multimerizing component is an IgG4 Fc domain (SEQ ID NO:24).

[0037] The fusion polypeptides of the invention may comprise a truncated multimerizing component. For example, when the multimerizing component is a human Fc, in a

particular embodiment the C_H2 component of Fc may be deleted (239-351 of SEQ ID NO:8) (Larson et al. 2005 *J Mol Biol* 348:1177-90, which publication is herein specifically incorporated by reference in its entirety).

[0038] In specific embodiments, the Fc from IgG1 may be modified to reduce effector functions. For example, the Fc may replace Asn297 (using cabot numbering) with a different amino acid, for example, Ala or Gln, Asp, Met, or Tyr, to eliminate glycosylation (Tao et al. 1989 *J. Immunol* 143: 2595-2601, which publication is herein specifically incorporated by reference in its entirety). Glycosylation may also be modified using mutant CHO cell lines, which either eliminate glycosylation or modify the extent of glycosylation (Wright et al. 1998 *J. Immunol.* 160:3393-3402, which publication is herein specifically incorporated by reference in its entirety). Mutations known by the art to eliminate effector functions are Leu234Ala, Leu235Ala/Glu (U.S. patent publication 2005/0100965; Reddy et al. 2000 *J. Immunol.* 164:1925-1933, which publications are herein specifically incorporated by reference in their entirety), and the class 1 mutations described in Shields et al 2001 *JBC* 276:6591-6604, which publication is herein specifically incorporated by reference in its entirety), such as Arg265Ala and Phe329Ala. An IgG4 or IgG2 Fc can also be used to reduce effector functions. In the case of IgG4, mutations that stabilize the molecule may be desirable, for example, Ser228Pro to stabilize covalent dimer formation (1993 *Mol. Immunol.* 30:105-108, which publication is herein specifically incorporated by reference in its entirety). Alternatively, the molecule may be enhanced for effector function activity by including mutations such as Ser298Ala, Glu33Ala, Lys334Ala (Shields et al supra; U.S. 2005/0054832, which publication is herein specifically incorporated by reference in its entirety, or by decreasing the fucosylation of the sugar side chain (Niwa et al. 2005 *Clin Cancer Res* 11:2327-2336, which publication is herein specifically incorporated by reference in its entirety).

[0039] The in vivo half-life of the antibodies can also be improved by modifying the salvage receptor epitope of the Ig constant domain or an Ig-like constant domain such that the molecule does not comprise an intact CH2 domain (239-351) or an intact Ig Fc region (U.S. Pat. No. 6,121,022; U.S. Pat. No. 6,194,551, which publications are herein specifically incorporated by reference in their entirety). The in vivo half-life can furthermore be increased by making mutations in the Fc region, e.g. by substituting Thr at Leu252, Thr at Ser254, or Thr at Phe256 (U.S. Pat. No. 6,277,375, which publication is herein specifically incorporated by reference in its entirety).

Therapeutic Uses

[0040] The VEGF-binding traps of the invention are therapeutically useful for treating any disease or condition which is improved, ameliorated, inhibited or prevented by removal, inhibition, or reduction of VEGF. A non-exhaustive list of specific conditions improved by inhibition or reduction of VEGF include, clinical conditions that are characterized by excessive vascular endothelial cell proliferation, vascular permeability, edema or inflammation such as brain edema associated with injury, stroke or tumor; edema associated with inflammatory disorders such as psoriasis or arthritis, including rheumatoid arthritis; asthma; generalized edema associated with burns; ascites and pleural effusion associated

with tumors, inflammation or trauma; chronic airway inflammation; capillary leak syndrome; sepsis; kidney disease associated with increased leakage of protein; and eye disorders such as age related macular degeneration and diabetic retinopathy.

[0041] The compositions of the invention are therapeutically useful for treating a wide variety of diseases associated with increased VEGF levels. For example, exaggerated Th2 inflammation and airway remodeling are characteristic in the pathogenesis of asthma (see, for example, Elias et al. (1999) J. Clin. Invest. 104:1001-6). Elevated VEGF levels have been detected in tissues and biologic samples from patients with asthma, which correlate directly with disease activity (Lee et al. (2001) J. Allergy Clin. Immunol. 107:1106-1108) and inversely with airway caliber and airway responsiveness. Further, VEGF has been postulated to contribute to asthmatic tissue edema.

[0042] Another disease associated with increased VEGF is pancreatic ductal adenocarcinoma (PDAC). This malignancy often exhibits enhanced foci of endothelial cell proliferation and frequently overexpresses VEGF (Ferrara (1999) J. Mol. Med. 77:527-543). PDAC is responsible for over 20% of deaths due to gastrointestinal malignancies, making it the fourth most common cause of cancer-related mortality in the U.S. and other industrialized countries. Experimental evidence supports an important role for VEGF in pancreatic cancer, thus a VEGF inhibitor has promise as a therapeutic to attenuate intrapancreatic tumor growth and regional and distal metastasis.

[0043] A smaller, non-glycosylated mini-trap expressed in *E. coli* (Example 4), a glycosylated mini-trap expressed in CHO cells (Example 5), or a receptor-based monomeric trap (Example 6) has optimized characteristics for local/intravitreal delivery, i.e. a shorter serum half life for faster clearance and minimizing unwanted systemic exposure. In addition due to its smaller size, the mini-trap has the ability to penetrate through the inner-limiting membrane (ILM) in the eye, and diffuse through the vitreous to the retina/retinal pigment epithelial (RPE) layer which will help to treat retinal disease. Additionally, the mini-trap can be used for local administration for the treatment of ocular disease such as choroidal neovascularization, diabetic macular edema, proliferative diabetic retinopathy, corneal neovascularization/transplant rejection. Still further, the mini-trap can be used in any situation where transient (short-term) blocking of VEGF is required, e.g., to avoid chronic exposure to VEGF blockade, such as, for example, in the treatment of psoriasis.

[0044] A serious problem leading to failure following glaucoma surgery is early inflammation and angiogenesis, as well as too aggressive wound healing. Accordingly, the VEGF traps of the invention may be usefully employed as an adjuvant to glaucoma surgery to prevent early hem- and lymphangiogenesis and macrophage recruitment to the filterig bleb after glaucoma surgery, and improve surgical outcome.

Combination Therapies

[0045] In numerous embodiments, a VEGF trap may be administered in combination with one or more additional compounds or therapies, including a second VEGF trap molecule, a chemotherapeutic agent, surgery, catheter

devices, and radiation. Combination therapy includes administration of a single pharmaceutical dosage formulation which contains a VEGF trap and one or more additional agents; as well as administration of a VEGF trap and one or more additional agent(s) in its own separate pharmaceutical dosage formulation. For example, a VEGF trap and a cytotoxic agent, a chemotherapeutic agent or a growth inhibitory agent can be administered to the patient together in a single dosage composition such as a combined formulation, or each agent can be administered in a separate dosage formulation. Where separate dosage formulations are used, the VEGF-specific fusion polypeptide of the invention and one or more additional agents can be administered concurrently, or at separately staggered times, i.e., sequentially.

[0046] The term "cytotoxic agent" as used herein refers to a substance that inhibits or prevents the function of cells and/or causes destruction of cells. The term is intended to include radioactive isotopes (e.g. I^{131} , I^{125} , Y^{90} and Re^{186}), chemotherapeutic agents, and toxins such as enzymatically active toxins of bacterial, fungal, plant or animal origin, or fragments thereof.

[0047] A "chemotherapeutic agent" is a chemical compound useful in the treatment of cancer. Examples of chemotherapeutic agents include alkylating agents such as thiotepa and cyclophosphamide (Cytoxan®); alkyl sulfonates such as busulfan, improsulfan and piposulfan; aziridines such as benzodopa, carboquone, meturedopa, and uredopa; ethylenimines and methylamelamines including altretamine, triethylenemelamine, trietylenephosphoramide, triethylenethiophosphoramide and trimethylolomelamine; nitrogen mustards such as chlorambucil, chlornaphazine, cholophosphamide, estramustine, ifosfamide, mechlorethamine, mechlorethamine oxide hydrochloride, melphalan, novembichin, phenesterine, prednimustine, trofosfamide, uracil mustard; nitrosureas such as carmustine, chlorozotocin, fotemustine, lomustine, nimustine, ranimustine; antibiotics such as aclacinomysins, actinomycin, authramycin, azaserine, bleomycins, cactinomycin, calicheamicin, carabacin, carminomycin, carzinophilin, chromomycins, dactinomycin, daunorubicin, detorubicin, 6-diazo-5-oxo-L-norleucine, doxorubicin, epirubicin, esorubicin, idarubicin, marcellomycin, mitomycins, mycophenolic acid, nogalamycin, olivomycins, peplomycin, potfiromycin, puromycin, quelamycin, rodorubicin, streptonigrin, streptozocin, tubercidin, ubenimex, zinostatin, zorubicin; anti-metabolites such as methotrexate and 5-fluorouracil (5-FU); folic acid analogues such as denopterin, methotrexate, pteropterin, trimetrexate; purine analogs such as fludarabine, 6-mercaptopurine, thiamiprine, thioguanine; pyrimidine analogs such as ancitabine, azacitidine, 6-azauridine, carmofur, cytarabine, dideoxyuridine, doxifluridine, enocitabine, floxuridine; androgens such as calusterone, dromostanolone propionate, epitostanol, mepitostane, testolactone; anti-adrenals such as aminoglutethimide, mitotane, trilostane; folic acid replenisher such as frolinic acid; aceglatone; aldophosphamide glycoside; aminolevulinic acid; amsacrine; bestabucil; bisantrene; edatraxate; defofamine; demecolcine; diaziquone; elformithine; elliptinium acetate; etoglucid; gallium nitrate; hydroxyurea; lentinan; lonidamine; mitoguanzone; mitoxantrone; mopidamol; nitracrine; pentostatin; phenamet; pirarubicin; podophyllinic acid; 2-ethylhydrazide; procarbazine; PSK®; razoxane; sizofiran; spirogermanium; tenuazonic acid; triaziquone; 2,2',2"-trichlorotriethylamine;

urethan; vindesine; dacarbazine; mannomustine; mitobronitol; mitolactol; pipobroman; gacytosine; arabinoside ("Ara-C"); cyclophosphamide; thiotepa; taxanes, e.g. paclitaxel (Taxol®, Bristol-Myers Squibb Oncology, Princeton, N.J.) and docetaxel (Taxotere®, Aventis Antony, France); chlorambucil; gemcitabine; 6-thioguanine; mercaptopurine; methotrexate; platinum analogs such as cisplatin and carboplatin; vinblastine; platinum; etoposide (VP-16); ifosfamide; mitomycin C; mitoxantrone; vincristine; vinorelbine; navelbine; novantrone; teniposide; daunomycin; aminopterin; xeloda; ibandronate; CPT-11; topoisomerase inhibitor RFS 2000; difluoromethylornithine (DMFO); retinoic acid; espermicins; capecitabine; and pharmaceutically acceptable salts, acids or derivatives of any of the above. Also included in this definition are anti-hormonal agents that act to regulate or inhibit hormone action on tumors such as anti-estrogens including for example tamoxifen, raloxifene, aromatase inhibiting 4(5)-imidazoles, 4-hydroxytamoxifen, trioxifene, keoxifene, LY 117018, onapristone, and toremifene (Fareston); and anti-androgens such as flutamide, nilutamide, bicalutamide, leuprolide, and goserelin; and pharmaceutically acceptable salts, acids or derivatives of any of the above.

[0048] A "growth inhibitory agent" when used herein refers to a compound or composition which inhibits growth of a cell, especially a cancer cell either in vitro or in vivo. Examples of growth inhibitory agents include agents that block cell cycle progression (at a place other than S phase), such as agents that induce G1 arrest and M-phase arrest. Classical M-phase blockers include the vincas (vincristine and vinblastine), Taxol®, and topo II inhibitors such as doxorubicin, epirubicin, daunorubicin, etoposide, and bleomycin. Those agents that arrest G1 also spill over into S-phase arrest, for example, DNA alkylating agents such as tamoxifen, prednisone, dacarbazine, mechlorethamine, cisplatin, methotrexate, 5-fluorouracil, and ara-C.

Methods of Administration

[0049] The invention provides methods of treatment comprising administering to a subject an effective amount of a VEGF trap of the invention. In a preferred aspect, the trap is substantially purified (e.g., substantially free from substances that limit its effect or produce undesired side-effects). The subject is preferably a mammal, and most preferably a human.

[0050] Various delivery systems are known and can be used to administer an agent of the invention, e.g., encapsulation in liposomes, microparticles, microcapsules, recombinant cells capable of expressing the compound, receptor-mediated endocytosis (see, e.g., Wu and Wu, 1987, J. Biol. Chem. 262:4429-4432), construction of a nucleic acid as part of a retroviral or other vector, etc. Methods of introduction can be enteral or parenteral and include but are not limited to intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal, intraocular, and oral routes. The compounds may be administered by any convenient route, for example by infusion or bolus injection, by absorption through epithelial or mucocutaneous linings (e.g., oral mucosa, rectal and intestinal mucosa, etc.) and may be administered together with other biologically active agents. Administration can be systemic or local. Administration can be acute or chronic (e.g. daily, weekly, monthly, etc.) or in combination with other agents. Pulmonary admin-

istration can also be employed, e.g., by use of an inhaler or nebulizer, and formulation with an aerosolizing agent.

[0051] In another embodiment, the active agent can be delivered in a vesicle, in particular a liposome, in a controlled release system, or in a pump. In another embodiment where the active agent of the invention is a nucleic acid encoding a protein, the nucleic acid can be administered in vivo to promote expression of its encoded protein, by constructing it as part of an appropriate nucleic acid expression vector and administering it so that it becomes intracellular, e.g., by use of a retroviral vector (see, for example, U.S. Pat. No. 4,980,286), by direct injection, or by use of microparticle bombardment, or coating with lipids or cell-surface receptors or transfecting agents, or by administering it in linkage to a homeobox-like peptide which is known to enter the nucleus (see e.g., Joliet et al., 1991, Proc. Natl. Acad. Sci. USA 88:1864-1868), etc. Alternatively, a nucleic acid can be introduced intracellularly and incorporated within host cell DNA for expression, by homologous recombination.

[0052] In a specific embodiment, it may be desirable to administer the pharmaceutical compositions of the invention locally to the area in need of treatment; this may be achieved, for example, and not by way of limitation, by local infusion during surgery, topical application, e.g., by injection, by means of a catheter, or by means of an implant, the implant being of a porous, non-porous, or gelatinous material, including membranes, such as sialastic membranes, fibers, or commercial skin substitutes.

[0053] A composition useful in practicing the methods of the invention may be a liquid comprising an agent of the invention in solution, in suspension, or both. The term "solution/suspension" refers to a liquid composition where a first portion of the active agent is present in solution and a second portion of the active agent is present in particulate form, in suspension in a liquid matrix. A liquid composition also includes a gel. The liquid composition may be aqueous or in the form of an ointment. Further, the composition can take the form of a solid article that can be inserted in the eye, such as for example between the eye and eyelid or in the conjunctival sac, where the VEGF trap is released. Release from such an article is usually to the cornea, either via the lacrimal fluid, or directly to the cornea itself, with which the solid article is generally in direct contact. Solid articles suitable for implantation in the eye are generally composed primarily of bioerodible or nonbioerodible polymers. An aqueous solution and/or suspension can be in the form of eye drops. A desired dosage of the active agent can be measured by administration of a known number of drops into the eye. For example, for a drop volume of 25 μ l, administration of 1-6 drops will deliver 25-150 μ l of the composition.

[0054] An aqueous suspension or solution/suspension useful for practicing the methods of the invention may contain one or more polymers as suspending agents. Useful polymers include water-soluble polymers such as cellulosic polymers and water-insoluble polymers such as cross-linked carboxyl-containing polymers. An aqueous suspension or solution/suspension of the present invention is preferably viscous or muco-adhesive, or even more preferably, both viscous or mucoadhesive.

[0055] In another embodiment, the composition useful in practicing the methods of the invention is an in situ gellable

aqueous composition. Such a composition comprises a gelling agent in a concentration effective to promote gelling upon contact with the eye or with lacrimal fluid. Suitable gelling agents include but are not limited to thermosetting polymers. The term "in situ gellable" as used herein includes not only liquids of low viscosity that form gels upon contact with the eye or with lacrimal fluid, but also includes more viscous liquids such as semi-fluid and thixotropic gels that exhibit substantially increased viscosity or gel stiffness upon administration to the eye.

Pharmaceutical Compositions

[0056] The present invention also provides pharmaceutical compositions comprising a VEGF mini-trap of the invention. Such compositions comprise a therapeutically effective amount of one or more mini-traps, and a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable" 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 term "carrier" refers to a diluent, adjuvant, excipient, or vehicle with which the therapeutic is administered. Such pharmaceutical carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. Suitable pharmaceutical excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc, sodium chloride, dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. These compositions can take the form of solutions, suspensions, emulsion, tablets, pills, capsules, powders, sustained-release formulations and the like. Examples of suitable pharmaceutical carriers are described in "Remington's Pharmaceutical Sciences" by E. W. Martin.

[0057] The VEGF mini-trap of the invention can be formulated as neutral or salt forms. Pharmaceutically acceptable salts include those formed with free amino groups such as those derived from hydrochloric, phosphoric, acetic, oxalic, tartaric acids, etc., and those formed with free carboxyl groups such as those derived from sodium, potassium, ammonium, calcium, ferric hydroxides, isopropylamine, triethylamine, 2-ethylamino ethanol, histidine, procaine, etc.

[0058] Further more, aqueous compositions useful for practicing the methods of the invention have ophthalmically compatible pH and osmolality. One or more ophthalmically acceptable pH adjusting agents and/or buffering agents can be included in a composition of the invention, including acids such as acetic, boric, citric, lactic, phosphoric and hydrochloric acids; bases such as sodium hydroxide, sodium phosphate, sodium borate, sodium citrate, sodium acetate, and sodium lactate; and buffers such as citrate/dextrose, sodium bicarbonate and ammonium chloride. Such acids, bases, and buffers are included in an amount required to maintain pH of the composition in an ophthalmically acceptable range. One or more ophthalmically acceptable salts can be included in the composition in an amount sufficient to bring osmolality of the composition into an ophthalmically acceptable range. Such salts include those having sodium,

potassium or ammonium cations and chloride, citrate, ascorbate, borate, phosphate, bicarbonate, sulfate, thiosulfate or bisulfite anions.

[0059] The amount of the trap that will be effective for its intended therapeutic use can be determined by standard clinical techniques based on the present description. In addition, in vitro assays may optionally be employed to help identify optimal dosage ranges. Generally, suitable dosage ranges for intravenous administration are generally about 50-5000 micrograms of active compound per kilogram body weight. Suitable dosage ranges for intranasal administration are generally about 0.01 pg/kg body weight to 1 mg/kg body weight. Effective doses may be extrapolated from dose-response curves derived from in vitro or animal model test systems.

[0060] For systemic administration, a therapeutically effective dose can be estimated initially from in vitro assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC_{50} as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Initial dosages can also be estimated from in vivo data, e.g., animal models, using techniques that are well known in the art. One having ordinary skill in the art could readily optimize administration to humans based on animal data.

[0061] Dosage amount and interval may be adjusted individually to provide plasma levels of the compounds that are sufficient to maintain therapeutic effect. In cases of local administration or selective uptake, the effective local concentration of the compounds may not be related to plasma concentration. One having skill in the art will be able to optimize therapeutically effective local dosages without undue experimentation.

[0062] The amount of compound administered will, of course, be dependent on the subject being treated, on the subject's weight, the severity of the affliction, the manner of administration, and the judgment of the prescribing physician. The therapy may be repeated intermittently while symptoms are detectable or even when they are not detectable. The therapy may be provided alone or in combination with other drugs.

Specific Embodiments

[0063] In the experiments described below, smaller VEGF traps were generated and their ability to bind VEGF was investigated. Such mini-traps are preferably used in specific applications. For example, certain conditions or diseases may be preferably treated with local administration of a VEGF trap to a specific organ, tissue, or cell, rather than by systemic administration. In one exemplification of the mini-traps of the invention, a smaller VEGF trap was generated by directed cleavage of a dimerized VEGF trap having a cleavage region (C-region) generated in a Fc domain (Example 2). The truncated trap exhibited comparable affinity for VEGF and half-life as the full-sized parent trap. Examples 3-5 describe construction of fusion polypeptides having a VEGF receptor component and a multimerizing component consisting of one or two cysteine residues. Affinity measurements showed that the non-glycosylated fusion polypeptides expressed in *E. coli* or the glycosylated polypeptides expressed in CHO cells had comparable binding affinity for VEGF as the full-sized parent trap. Example

6 further illustrates a monomeric VEGF trap consisting of (R1R2), which is capable of binding and inhibiting VEGF. Example 7 describes the construction of a VEGF mini-trap (SEQ ID NO:21) exhibiting high affinity binding for VEGF comparable to the full length trap (SEQ ID NO:8).

[0064] Proteins expressed in mammalian cell lines may contain multiple chemical modifications. Generally, these modifications of immunoglobulin proteins include removal of the signal peptide, truncation of the C-terminal lysine of the heavy chain (Lazar et al. (2004) Rapid Comm Mass Spec 18:239-244, which publication is herein specifically incorporated by reference in its entirety), and glycosylation. As described in Example 8, fusion polypeptides expressed in CHO cells were analyzed further to determine glycosylation patterns and oligosaccharide content. The fusion proteins were determined to comprise amino acids 28-457 of SEQ ID NO:8 and to be glycosylated at the Asn residues of positions 62, 94, 149, 222, and 308.

[0065] Other features of the invention will become apparent in the course of the following descriptions of exemplary embodiments which are given for illustration of the invention and are not intended to be limiting thereof.

EXAMPLES

[0066] The following example is put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how to make and use the methods and compositions of the invention, and are not intended to limit the scope of what the inventors regard as their invention. Efforts have been made to ensure accuracy with respect to numbers used (e.g., amounts, temperature, etc.) but some experimental errors and deviations should be accounted for. Unless indicated otherwise, parts are parts by weight, molecular weight is average molecular weight, temperature is in degrees Centigrade, and pressure is at or near atmospheric.

Example 1

Construction of Flt1D2.Flk1D3.FcΔC1(a)

[0067] The construction of a parent VEGF trap, Flt1D2.Flk1D3.FcΔC1(a) (SEQ ID NOs:5-6), VEGFR1R2.FcΔC1(a) (SEQ ID NOs:7-8), and Flt1D2.VEGFR3D3.FcΔC1(a) (SEQ ID NOs:9-10) is described in detail in PCT publication WO/0075319, herein specifically incorporated by reference in its entirety. Also described in WO/0075319 are methods of constructing and expressing nucleic acid constructs encoding VEGF traps, methods of detecting and measuring VEGF trap binding to VEGF, methods of determining the stoichiometry of VEGF binding by BIAcore analysis, and pharmacokinetic analyses.

Example 2

Thrombin-Cleaved Dimeric VEGF Mini-Trap

[0068] The VEGFR1R2.FcΔC1(a) (SEQ ID NOs:7-8) construct was modified by insertion of a thrombin cleavage following the CPPC (SEQ ID NO:1) of the Fc domain. Purified VEGF trap (5 μg) was incubated with thrombin (Novagen) in 20 mM Tris-HCl, pH 8.4, 50 mM NaCl, 2.5 mM CaCl₂ for 16 hrs at 37° C. Controls included cleavage control protein (CCP) and parent VEGF trap protein incubated without thrombin.

SDS-PAGE analysis (Tris-Glycine 4-20% gel; 5 μg protein per lane) verified correct cleavage (results not shown).

[0069] Affinity determination. The K_d of binding of each VEGF trap to hVEGF₁₆₅ was determined as described in WO/0075319, for the parent VEGF trap, uncleaved VEGF trap containing a thrombin cleavage site ("uncleaved VEGF trap"), cleaved VEGF mini-trap and recombinant monomeric R1R2-myc myc his. More specifically, the ability of the traps to block VEGF₁₆₅-dependent receptor phosphorylation was determined using primary human endothelial cells (HUVECs). VEGF₁₆₅ was incubated in the presence of varying concentrations of the test traps, and the mixture was added to HUVECs to stimulate tyrosine phosphorylation of VEGFR2. At sub-stoichiometric concentrations of VEGF trap, unbound VEGF induced receptor phosphorylation. However, at a 1:1 molar ratio of greater of a VEGF trap to ligand, complete blocking of receptor signaling was observed, establishing that a single molecule of a trap dimer is capable of blocking a single molecule of human VEGF₁₆₅. Thus, the high binding affinity of the VEGF trap for VEGF results in formation of a complex that prevents VEGF from interaction with cell surface receptors. Equivalent results were obtained for identical phosphorylation inhibition experiments for the parent VEGF trap, uncleaved VEGF trap, and cleaved VEGF mini-trap. The results are shown in Table 1.

TABLE 1

Trap	Kinetic Dissociation Rate (1/s)	T _{1/2} (hr)
parent VEGF trap	$5.51 \times 10^{-5} \pm 0.94\%$	3.5
uncleaved VEGF trap	$4.93 \times 10^{-5} \pm 0.70\%$	3.9
cleaved VEGF mini-trap	$5.46 \times 10^{-5} \pm 0.62\%$	3.53
R1R2-myc myc his monomer	$6.74 \times 10^{-3} \pm 0.38\%$	0.028

Example 3

Construction of Plasmids Encoding VEGF Mini-Traps

[0070] VEGF mini-traps were constructed from a precursor of the parent VEGF trap, VEGFR1R2.FcΔC1(a) (SEQ ID NOs:7-8), in which the three amino acids glycine-alanine-proline served as a linker between the Flk1D3 and FcΔC1(a). This plasmid, pTE115 was used in the construction of the VEGF mini-traps because the linker DNA sequence included a Srf I restriction endonuclease recognition sequence that facilitated engineering the VEGF trap. In all other respects, the VEGF trap encoded by pTE115 is identical to that of the VEGF trap, VEGFR1R2.FcΔC1(a) (SEQ ID NOs:7-8) described in detail in PCT publication WO/0075319.

[0071] Two VEGF mini-traps were constructed with multimerization domains consisting of either a single cysteine residue (R1R2_C) (SEQ ID NO:2) or the amino acids ACGC (SEQ ID NO:3) (R1R2_{ACGC}) (SEQ ID NO:4) added to the C-terminus of receptor components Flt1D2.Flk1D3. Both of these constructs are capable of forming homo-dimeric molecules stabilized by one (R1R2_C) or two (R1R2_{ACGC}) inter-molecular disulfides.

[0072] The plasmid pTE517 was made by removing the 690 bp fragment generated by digestion of pTE115 DNA

with Srf I and Not I and inserting the synthetic DNA fragment formed by annealing the oligos R1R2NC (SEQ ID NO:11) and R1R2CC (SEQ ID NO:12). The resulting plasmid encodes R1R2_C, which consists of the Flt1D2.Flk1D3 domains followed by a cysteine residue (SEQ ID NO:18). Similarly, the plasmid pTE518 was made by removing the 690 bp fragment generated by digestion of pTE115 DNA with Srf I and Not I, followed by ligation with the synthetic DNA fragment formed by annealing the oligos R1R2NACGC (SEQ ID NO:13) and R1R2CACGC (SEQ ID NO:14). The resulting plasmid encodes R1R2_{ACGC}, which consists of the Flt1D2.Flk1D3 domains followed by the amino acids ACGC (SEQ ID NO:20).

[0073] Plasmids were also constructed to direct the expression of these mini-traps in *E. coli*. The primers R1R2N-Nco1 (SEQ ID NO:15) and R1R2CNot1 (SEQ ID NO:16) were used to amplify a DNA fragment from pTE115 that encodes amino acids G30 to K231, relative to the parental VEGF trap (SEQ ID NO:8). Amplification of this sequence resulted in fusion of an initiating methionine codon at the 5' end and fusion of the codon for cysteine, followed by a stop codon, at the 3' end (SEQ ID NO:2). This DNA fragment was then cloned into the Nco I and Not I sites of the *E. coli* expression plasmid pRG663 to yield pRG1102 such that expression of R1R2_C was dependent on transcription from the phage T7 Φ 1.1 promoter. Induction of gene expression from pRG1102 results in accumulation of R1R2Cys in the cytoplasm of the *E. coli* host strain RFJ238. Similarly, the primers R1R2N-Nco1 (SEQ ID NO:15) and R1R2ACGC-Not1 (SEQ ID NO:17) were used to amplify a DNA fragment from pTE115 that encodes amino acids G30 to K231 (SEQ ID NO:8) resulting in fusion of an initiating methionine codon at the 5' end and fusion of codons for ACGC (SEQ ID NO:3), followed by a stop codon, at the 3' end (SEQ ID NO:4). This fragment was then cloned into the Nco I and Not I sites of the *E. coli* expression plasmid pRG663 to yield pRG1103 such that expression of R1R2_{ACGC} was dependent on transcription from the phage T7 Φ 1.1 promoter. Induction of gene expression from both pRG1102 and pRG1103 resulted in accumulation of R1R2_C or R1R2_{ACGC}, respectively, in the cytoplasm of the *E. coli* host strain RFJ238.

Example 4

Purification and Characterization of VEGF Mini-Traps from *E. coli*

[0074] Both R1R2_C and R1R2_{ACGC} were expressed as cytoplasmic proteins in *E. coli* and were purified by the same method. Induction of the phage T7 Φ 1.1 promoter on either pRG1102 or pRG1103 in the *E. coli* K12 strain RFJ238 resulted in accumulation of the protein in the cytoplasm. After induction, cells were collected by centrifugation, resuspended in 50 mM Tris-HCl, pH 7.5, 20 mM EDTA, and lysed by passage through a Niro-Soavi cell homogenizer. Inclusion bodies were collected from lysed cells by centrifugation, washed once in distilled H₂O, then solubilized in 8 M guanidinium-HCl, 50 mM Tris-HCl, pH 8.5, 100 mM sodium sulfite, 10 mM sodium tetrathionate and incubated at room temperature for 16 hours. Clarified supernatant was fractionated on an S300 column equilibrated with 6 M guanidinium-HCl, 50 mM Tris-HCl, pH 7.5. Fractions containing R1R2_C were pooled and dialyzed against 6M Urea, 50 mM Tris-HCl, pH 7.5. Dialyzed protein was diluted to 2M Urea, 50 mM Tris-HCl, pH 8.5, 2 mM cysteine then stirred slowly for 7 days at 4° C. Refolded protein was

dialyzed against 50 mM Tris-HCl, pH 7.5 then loaded onto an SP-sepharose column equilibrated with 50 mM Tris-HCl, pH 7.5 and eluted with a NaCl gradient from 0 to 1 M in 50 mM Tris-HCl, pH 7.5. Fractions containing R1R2_C were pooled, concentrated, and loaded onto a Superdex 200 column equilibrated with 50 mM Tris-HCl, pH 7.5, 150 mM NaCl. Fractions containing mini-trap dimer were collected and pooled. The molecular weight of purified mini-trap was estimated to be about 46 kD by SDS-PAGE.

[0075] BIAcore assays were conducted (as described in WO/0075319) to determine trap affinity for VEGF, and the results showed that the R1R2_C and R1R2_{ACGC} mini-traps had VEGF affinity comparable to the full length VEGF trap (Table 2).

TABLE 2

Trap	Kinetic Dissociation Rate (1/s)	T _{1/2} (hr)
VEGF trap	4.23×10^{-5}	4.53
R1R2 _C	3.39×10^{-5}	5.68
R1R2 _{ACGC}	3.41×10^{-5}	5.65

Example 5

Expression of VEGF Mini-Traps in CHO K1 Cells

[0076] Expression of the VEGF mini-traps encoded by pTE517 and pTE518 is dependent on transcription from the human CMV-MIE promoter and results in secretion of the mini-traps into the culture medium when expressed in CHO cells. When expressed as secreted proteins in CHO K1, both mini-traps were found in the conditioned media and estimation of their molecular weight by SDS-PAGE suggested, as expected, that the proteins were glycosylated. Analysis by SDS-PAGE also indicated that the mini-traps were capable of forming homo-dimeric molecules stabilized by intermolecular disulfide(s) between the C-terminal cysteine(s). Specifically, the R1R2_C mini-trap efficiently formed covalent dimers when expressed as a secreted protein in CHO cells.

Example 6

Construction and Expression of a Single Chain VEGF Mini-Trap

[0077] A VEGF mini-trap was also constructed that did not require a multimerization domain (SEQ ID NO:19). This mini-trap was constructed by direct fusion of one Flt1D2.Flk1D3 domain (R1R2) (amino acids 30-231 of SEQ ID NO:19) to a second Flt1D2.Flk1D3 domain (R1R2) (amino acids 234-435 of SEQ ID NO:19) with a Gly-Pro linker between the tandem receptor domains (amino acids 232-233 of SEQ ID NO:19).

[0078] To construct a gene encoding tandem Flt1D2.Flk1D3 domains, a DNA fragment was synthesized (Blue Heron Biotechnology) that encoded one Flt1D2.Flk1D3 domain that minimized DNA homology with the Flt1D2.Flk1D3 domain-encoding DNA found in pTE115. This synthetic DNA fragment was cloned as a Srf I-Not I fragment into the Srf I-Not I sites of pTE115 to yield pTE570, which expresses the R1R2-R1R2 VEGF mini-trap from the CMV-MIE promoter. When this plasmid is transfected into CHO K1 cells the R1R2-R1R2 VEGF mini-trap accumulates in the culture medium.

Example 7

Construction and Expression of a VEGF Mini-Trap

[0079] A VEGF mini-trap was constructed as described above, by direct fusion of one Flt1D2.Flk1D3 domain (R1R2) (amino acids 30-231 of SEQ ID NO:21) with a C-terminal nine amino acid sequence terminating in CPPC. When this plasmid is transfected into CHO K1 cells the VEGF mini-trap of SEQ ID NO:21 is secreted into the culture medium. Subsequent purification by non-reducing SDS-PAGE electrophoresis as well as native light-scattering analysis identified a trap molecule with molecular weight approximately 64 kDa. This molecular weight indicates that a covalent dimer was formed between two fusion polypeptides of SEQ ID NO:21. Similar experiments were conducted with plasmids encoding the fusion polypeptides of SEQ ID NOs:22 and 23, and similarly showed these molecules formed homodimeric traps. Affinity determinations for human VEGF-165 binding to EGF traps composed of dimers of SEQ ID NO:8 and SEQ ID NO:21 are shown in Table 3.

TABLE 3

VEGF Trap	ka (1/Ms)	kd (1/s)	KD (M)
SEQ ID NO: 8	$2.73 \times 10^{+7}$	1.79×10^{-5}	6.55×10^{-13}
SEQ ID NO: 21	$2.00 \times 10^{+7}$	6.56×10^{-6}	3.28×10^{-13}
SEQ ID NO: 21	$2.61 \times 10^{+7}$	5.77×10^{-6}	2.21×10^{-13}

Example 8

Glycosylation of VEGF-Binding Fusion Polypeptides

[0080] Sialic Acid Content. Sialic acid capping of carbohydrate chains has been identified as an important factor that lowers the clearance of glycoproteins from circulation. The total number of sialic acid residues in two batches, P3 and P3.5 (VGTC04003M500 and VGTC04008M500, respectively) of VEGF trap protein (amino acids 28-457 of SEQ ID NO:8) was determined using a quantitative HPLC assay. In this assay, sialic acid is released from the protein using mild acid hydrolysis, then derivatized with o-phenylenediamine, separated by HPLC, and measured by either UV or fluorescence detectors. Quantitation of sialic acid was assessed relative to a standard curve using sialyllactose. Fetuin is used as a positive control for the reaction. The total number of sialic acids released from the fusion polypeptide was 8-10 M and 9-10 M sialic acid/M of protein for P3 and P3.5, respectively.

[0081] Oligosaccharide Profiling by Normal-Phase Anion Exchange (NPAEC) HPLC. Oligosaccharide profiling was used to examine sugar chain quality of two batches of VEGF trap protein in both a qualitative and quantitative manner. PNGase F was used to remove N-linked sugar chains from the peptide backbone. These sugar chains were modified on the reducing end with anthranilic acid and separated by charge through ion exchange chromatography. Chains containing no sialic acid moieties were eluted separately from chains with a single sialic acid, chains with 2 sialic acids, and chains with 3 sialic acids, etc. Peak areas were determined for each sugar chain species and quantified relative to the total peak area of all chain species. The Z number was calculated from the sum of the areas of the single sialic acid containing chains plus 2 times the area of the two sialic acid

containing species plus 3 times the area of the three sialic acid containing species (etc) divided by the sum of the total peak area. The higher the Z number, the greater the extent of average sialic acid on the oligosaccharide chains. The calculated Z numbers were 1.1 (P3) and 1.0 (P3.5).

[0082] Capillary Electrophoresis Fingerprinting. A quantitative oligosaccharide fingerprint assay was developed using capillary electrophoresis (CE) to examine differences in sugar chain structure between protein lots. Unlike the ion exchange (IE) method used to evaluate the sialic acid oligosaccharide profile, the CE method can more readily separate oligosaccharide chains with equivalent charge. The fusion polypeptide were denatured, and then deglycosylated by addition of PNGase to release N-linked sugar chains. The samples were incubated overnight at 37° C., then spiked with maltose (Fluka) as an internal standard. Released sugar chains were chemically modified in a solution containing the fluorophore labeling reagent, 8-aminopyrene 1,2,6-trisulfonate (APTS). Following modification, the released and labeled oligosaccharides were separated by capillary electrophoresis. Structural assignments for the biantennary structures were based on comigration with synthetic oligosaccharide standards. Other carbohydrate species corresponding to triantennary forms have not yet been assigned, but they constitute a very small fraction of the total carbohydrate. Analysis of electropherograms did not reveal any unique sugar chain peaks.

[0083] Oligosaccharide Analysis by MALDI-TOF MS. A global measurement of all the N-linked sugar chains by mass spectrometry was performed on two batches of the VEGF trap. Oligosaccharides were released by PNGase F, derivatized with anthranilic acid, precleaned by SPE HLB cartridge. The oligosaccharides were further cleaned with Dowex AG-50wx12 resin prior to MALDI analysis. Spectra were collected in negative linear mode. The mass spectrum of each oligosaccharide pool was determined and the structural assignments made (FIGS. 1A-C). The expected masses are the average mass calculated based on the proposed N-linked sugar chains with addition of anthranilic acid derivatization. The monosaccharide compositions are listed based on the proposed N-linked sugar chain structures as well.

[0084] Oligosaccharide Chain Structures on Individual Glycosylation Sites by Electrospray Ionization-Mass Spectrometry (ESI-MS). The carbohydrate structures on each individual glycosylation site of two batches of VEGF trap (P3 and P3.5) were determined by a peptide mapping approach. The protein samples were reduced and blocked with iodoacetamide. The samples were then digested with trypsin and the peptides mixture were analyzed by LC/MS. Glycopeptides typically elutes as a group of poorly resolved peaks on HPLC chromatogram and recognized by its characteristic mass patterns. Sugar chain masses were calculated from observed glycopeptide masses. The following sugar chain structures were observed based on mass match: Asn62 and Asn94 were mainly fucosylated bi-antennary, with 0-2 sialic acid and smaller amount of non-fucosylated; Asn94 was partially glycosylated to a similar extent; Asn149 and Asn222 were mainly non-fucosylated bi-antennary, with 0-2 sialic acid, and smaller amount of fucosylated bi-antennary, Man-5, and hybrid type sugar chains; Asn308 was mainly fucosylated bi-antennary, with no sialic acid and smaller amount of non-fucosylated form.

[0085] Other features of the invention will become apparent in the course of the following descriptions of exemplary embodiments which are given for illustration of the invention and are not intended to be limiting thereof.

SEQUENCE LISTING

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<211> LENGTH: 4

<212> TYPE: PRT

<213> ORGANISM: homo sapiens

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<210> SEQ ID NO 2

<211> LENGTH: 200

<212> TYPE: PRT

<213> ORGANISM: homo sapiens

<400> SEQUENCE: 2

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20 25 30

Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile
35 40 45

Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile
50 55 60

Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr
65 70 75 80

Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr Gln Thr Asn Thr
85 90 95

Ile Ile Asp Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val
100 105 110

Gly Glu Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val
115 120 125

Gly Ile Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys
130 135 140

Lys Leu Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys
145 150 155 160

Lys Phe Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln
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Gly Thr Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr
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Phe Val Arg Val His Glu Lys Cys
195 200

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<212> TYPE: PRT

<213> ORGANISM: homo sapiens

<400> SEQUENCE: 3

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<210> SEQ ID NO 4

<211> LENGTH: 203

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      20             25             30

Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile
      35             40             45

Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile
      50             55             60

Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr
      65             70             75             80

Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr Gln Thr Asn Thr
      85             90             95

Ile Ile Asp Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val
      100            105            110

Gly Glu Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val
      115            120            125

Gly Ile Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys
      130            135            140

Lys Leu Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys
      145            150            155            160

Lys Phe Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln
      165            170            175

Gly Thr Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr
      180            185            190

Phe Val Arg Val His Glu Lys Ala Cys Gly Cys
      195            200

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<213> ORGANISM: homo sapiens

<400> SEQUENCE: 5

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tgcttctcac aggatctagt tccggaggta gacctttcgt agagatgtac agtgaaatcc      180
ccgaaattat acacatgact gaaggaaggg agctcgatcat tccctgccgg gttacgtcac      240
ctaacatcac tgttacttta aaaaagtttc cacttgacac tttgatccct gatggaaaac      300
gcataatctg ggacagtaga aagggttca tcatatcaaa tgcaacgtac aaagaaatag      360
ggcttctgac ctgtgaagca acagtcaatg ggcatttcta taagacaaac tatctcacac      420
atcgacaaac caatacaatc atagatgtgg ttctgagtcg gtctcatgga attgaactat      480
ctgttgagaa aaagcttgct ttaaattgta cagcaagaac tgaactaaat gtggggattg      540
acttcaactg ggaataccct tcttcgaagc atcagcataa gaaacttgta aaccgagacc      600
taaaaaccca gtctgggagt gagatgaaga aatttttgag caccttaact atagatgggtg      660
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ccaaggacac cctcatgac tcccggaccc ctgagggtcac atgcgtgggtg gtggacgtga 900
gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg 960
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtgggtc agcgtcctca 1020
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaagggtc tccaacaaag 1080
ccctcccagc ccccatcgag aaaaccatct ccaaagccaa agggcagccc cgagaaccac 1140
aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccagggtc agcctgacct 1200
gcctggtcaa aggtctctat ccacgcgaca tcgccgtgga gtgggagagc aatgggcagc 1260
cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc ttcttcctct 1320
atagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg 1380
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aatgagcggc cgc 1453

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<210> SEQ ID NO 6
<211> LENGTH: 458
<212> TYPE: PRT
<213> ORGANISM: homo sapiens

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<400> SEQUENCE: 6

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

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Val	His	Glu	Lys	Gly	Pro	Gly	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys
225					230					235					240
Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro
				245					250					255	
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys
			260					265					270		
Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp
		275					280					285			
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu
	290					295					300				
Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu
305					310					315					320
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn
				325					330					335	
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly
			340					345					350		
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu
		355					360					365			
Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr
	370					375					380				
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn
385					390					395					400
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe
				405					410					415	
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn
		420						425				430			
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr
	435						440					445			
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys						
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<210> SEQ ID NO 7

<211> LENGTH: 1377

<212> TYPE: DNA

<213> ORGANISM: homo sapiens

<400> SEQUENCE: 7

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acaggatcta gttccggaag tgataccggt agaccttcg tagagatgta cagtgaatc	120
cccgaatta tacacatgac tgaaggaagg gagctcgtca ttccctgccg ggttacgtca	180
cctaacatca ctgttacttt aaaaaagttt ccacttgaca ctttgatccc tgatggaaaa	240
cgcataatct gggacagtag aaagggttc atcatatcaa atgcaacgta caaagaaata	300
gggtcttcta cctgtgaagc aacagtcaat gggcatttgt ataagacaaa ctatctcaca	360
catcgacaaa ccaatacaat catagatgtg gttctgagtc cgtctcatgg aattgaacta	420
tctgttgagg aaaagcttgt cttaaattgt acagcaagaa ctgaactaaa tgtggggatt	480
gacttcaact gggaataccc ttcttcgaag catcagcata agaaacttgt aaaccgagac	540
ctaaaaaccc agtctgggag tgagatgaag aaatttttga gcaccttaac tatagatggg	600
gtaaccggga gtgaccaagg attgtacacc tgtgcagcat ccagtgggct gatgaccaag	660
aagaacagca catttgtcag ggtccatgaa aaggacaaaa ctcacacatg cccaccgtgc	720

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gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 900
aagccgcggg aggagcagta caacagcacg tacctgtgtg tcacgcctct caccgtcctg 960
caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca 1020
gcccccatcg agaaaacat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac 1080
acctgcccc catcccgga tgagctgacc aagaaccagg tcacgcctgac ctgcctggtc 1140
aaaggtctct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagAAC 1200
aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttctt ctacagcaag 1260
ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgtc cgtgatgcat 1320
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<210> SEQ ID NO 8
<211> LENGTH: 458
<212> TYPE: PRT
<213> ORGANISM: homo sapiens

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<400> SEQUENCE: 8

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

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<212> TYPE: DNA
<213> ORGANISM: homo sapiens

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accctgaggt caagttcaac tggtagctgg acggcgtgga ggtgcataat gccaagacaa   960
agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc accgtcctgc  1020
accaggactg gctgaatggc aaggagtaca agtgcaaggt ctccaacaaa gccctcccag  1080
cccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca caggtgtaca  1140
ccctgcccc atcccgggat gagctgacca agaaccaggt cagcctgacc tgcctgggtca  1200
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tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcagtctcc gtgatgcatg  1380
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<211> LENGTH: 455

<212> TYPE: PRT

<213> ORGANISM: homo sapiens

<400> SEQUENCE: 10

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

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 275 280 285
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
 290 295 300
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 305 310 315 320
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
 325 330 335
 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 340 345 350
 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
 355 360 365
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 370 375 380
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 385 390 395 400
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 405 410 415
 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
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 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
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 Leu Ser Leu Ser Pro Gly Lys
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 <212> TYPE: DNA
 <213> ORGANISM: homo sapiens

<400> SEQUENCE: 11

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<210> SEQ ID NO 12
 <211> LENGTH: 28
 <212> TYPE: DNA
 <213> ORGANISM: homo sapiens

<400> SEQUENCE: 12

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28

<210> SEQ ID NO 13
 <211> LENGTH: 23
 <212> TYPE: DNA
 <213> ORGANISM: homo sapiens

<400> SEQUENCE: 13

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23

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 <211> LENGTH: 27

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<212> TYPE: DNA
<213> ORGANISM: homo sapiens

<400> SEQUENCE: 14
ggccgctctc aacaaccgca tgcgccc                27

<210> SEQ ID NO 15
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: homo sapiens

<400> SEQUENCE: 15
gagagagacc atgggtagac ctttcgtaga gatgta        36

<210> SEQ ID NO 16
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: homo sapiens

<400> SEQUENCE: 16
agagaggcgg ccgctttatc aacacttttc atggaccctg acaaatgt  48

<210> SEQ ID NO 17
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: homo sapiens

<400> SEQUENCE: 17
agagaggcgg ccgctttatc aacaaccgca tgccttttca tggaccctga caaatgt  57

<210> SEQ ID NO 18
<211> LENGTH: 235
<212> TYPE: PRT
<213> ORGANISM: homo sapiens

<400> SEQUENCE: 18
Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
 1           5           10           15
Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Asp Thr Gly Arg Pro
          20           25           30
Phe Val Glu Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu
          35           40           45
Gly Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr
          50           55           60
Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys
          65           70           75           80
Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr
          85           90           95
Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His
          100          105          110
Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile
          115          120          125
Asp Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu
          130          135          140
Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile
          145          150          155          160
Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu

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<210> SEQ ID NO 19
<211> LENGTH: 435
<212> TYPE: PRT
<213> ORGANISM: homo sapiens

<400> SEQUENCE: 19
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Met 1	Val	Ser	Tyr	Trp 5	Asp	Thr	Gly	Val 10	Leu	Cys	Ala	Leu 15	Ser		
Cys	Leu	Leu	Leu 20	Thr	Gly	Ser	Ser	Ser 25	Gly	Ser	Asp	Thr 30	Pro		
Phe	Val	Glu	Met	Tyr	Ser	Glu	Ile 40	Pro	Glu	Ile	Ile 45	Met	Thr	Glu	
Gly	Arg	Glu	Leu	Val	Ile 55	Pro	Cys	Arg	Val	Thr	Ser 60	Pro	Asn	Ile	Thr
Val 65	Thr	Leu	Lys	Lys	Phe 70	Pro	Leu	Asp	Thr	Leu 75	Ile	Pro	Asp	Gly	Lys 80
Arg	Ile	Ile	Trp 85	Asp	Ser	Arg	Lys	Gly	Phe 90	Ile	Ile	Ser	Asn	Ala 95	Thr
Tyr	Lys	Glu	Ile 100	Gly	Leu	Leu	Thr	Cys 105	Glu	Ala	Thr	Val	Asn 110	Gly	His
Leu	Tyr	Lys 115	Thr	Asn	Tyr	Leu	Thr 120	His	Arg	Gln	Thr	Asn 125	Thr	Ile	Ile
Asp	Val 130	Val	Leu	Ser	Pro	Ser 135	His	Gly	Ile	Glu	Leu 140	Ser	Val	Gly	Glu
Lys 145	Leu	Val	Leu	Asn	Cys 150	Thr	Ala	Arg	Thr	Glu 155	Leu	Asn	Val	Gly	Ile 160
Asp	Phe	Asn	Trp 165	Glu	Tyr	Pro	Ser	Ser	Lys 170	His	Gln	His	Lys	Lys 175	Leu
Val	Asn	Arg	Asp 180	Leu	Lys	Thr	Gln	Ser 185	Gly	Ser	Glu	Met	Lys 190	Lys	Phe
Leu	Ser	Thr 195	Leu	Thr	Ile	Asp	Gly 200	Val	Thr	Arg	Ser	Asp 205	Gln	Gly	Leu
Tyr	Thr 210	Cys	Ala	Ala	Ser	Ser 215	Gly	Leu	Met	Thr	Lys 220	Lys	Asn	Ser	Thr
Phe 225	Val	Arg	Val	His	Glu 230	Lys	Gly	Pro	Gly	Arg 235	Pro	Phe	Val	Glu	Met 240
Tyr	Ser	Glu	Ile 245	Pro	Glu	Ile	Ile	His	Met 250	Thr	Glu	Gly	Arg	Glu 255	Leu
Val	Ile	Pro	Cys 260	Arg	Val	Thr	Ser	Pro 265	Asn	Ile	Thr	Val	Thr 270	Leu	Lys
Lys	Phe 275	Pro	Leu	Asp	Thr	Leu	Ile 280	Pro	Asp	Gly	Lys	Arg 285	Ile	Ile	Trp

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Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile
 290 295 300
 Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr
 305 310 315 320
 Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Val Leu
 325 330 335
 Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu Lys Leu Val Leu
 340 345 350
 Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile Asp Phe Asn Trp
 355 360 365
 Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu Val Asn Arg Asp
 370 375 380
 Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe Leu Ser Thr Leu
 385 390 395 400
 Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu Tyr Thr Cys Ala
 405 410 415
 Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr Phe Val Arg Val
 420 425 430
 His Glu Lys
 435

<210> SEQ ID NO 20

<211> LENGTH: 238

<212> TYPE: PRT

<213> ORGANISM: homo sapiens

<400> SEQUENCE: 20

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

-continued

Tyr Thr Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr
210 215 220

Phe Val Arg Val His Glu Lys Gly Pro Gly Ala Cys Gly Cys
225 230 235

<210> SEQ ID NO 21
<211> LENGTH: 240
<212> TYPE: PRT
<213> ORGANISM: homo sapiens

<400> SEQUENCE: 21

Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
1 5 10 15

Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Asp Thr Gly Arg Pro
20 25 30

Phe Val Glu Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu
35 40 45

Gly Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr
50 55 60

Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys
65 70 75 80

Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr
85 90 95

Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His
100 105 110

Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile
115 120 125

Asp Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu
130 135 140

Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile
145 150 155 160

Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu
165 170 175

Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe
180 185 190

Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu
195 200 205

Tyr Thr Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr
210 215 220

Phe Val Arg Val His Glu Lys Asp Lys Thr His Thr Cys Pro Pro Cys
225 230 235 240

<210> SEQ ID NO 22
<211> LENGTH: 240
<212> TYPE: PRT
<213> ORGANISM: homo sapiens

<400> SEQUENCE: 22

Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
1 5 10 15

Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Asp Thr Gly Arg Pro
20 25 30

Phe Val Glu Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu
35 40 45

-continued

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

<210> SEQ ID NO 23

<211> LENGTH: 237

<212> TYPE: PRT

<213> ORGANISM: homo sapiens

<400> SEQUENCE: 23

Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
 1 5 10 15
 Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Asp Thr Gly Arg Pro
 20 25 30
 Phe Val Glu Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu
 35 40 45
 Gly Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr
 50 55 60
 Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys
 65 70 75 80
 Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr
 85 90 95
 Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His
 100 105 110
 Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile
 115 120 125
 Asp Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu
 130 135 140
 Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile
 145 150 155 160
 Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu

-continued

	165		170		175
Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe					
	180		185		190
Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu					
	195		200		205
Tyr Thr Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr					
	210		215		220
Phe Val Arg Val His Glu Lys Asp Lys Thr His Thr Cys					
	225		230		235

<210> SEQ ID NO 24
 <211> LENGTH: 434
 <212> TYPE: PRT
 <213> ORGANISM: homo sapiens
 <400> SEQUENCE: 24

Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu					
1	5		10		15
Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val					
	20		25		30
Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr					
	35		40		45
Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe					
	50		55		60
Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu					
	65		70		75
Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg					
	85		90		95
Gln Thr Asn Thr Ile Ile Asp Val Val Leu Ser Pro Ser His Gly Ile					
	100		105		110
Glu Leu Ser Val Gly Glu Lys Leu Val Leu Asn Cys Thr Ala Arg Thr					
	115		120		125
Glu Leu Asn Val Gly Ile Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys					
	130		135		140
His Gln His Lys Lys Leu Val Asn Arg Asp Leu Lys Thr Gln Ser Gly					
	145		150		155
Ser Glu Met Lys Lys Phe Leu Ser Thr Leu Thr Ile Asp Gly Val Thr					
	165		170		175
Arg Ser Asp Gln Gly Leu Tyr Thr Cys Ala Ala Ser Ser Gly Leu Met					
	180		185		190
Thr Lys Lys Asn Ser Thr Phe Val Arg Val His Glu Lys Glu Ser Lys					
	195		200		205
Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly					
	210		215		220
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile					
	225		230		235
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu					
	245		250		255
Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His					
	260		265		270
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg					
	275		280		285

-continued

Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys
	290						295				300				
Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu
305					310					315					320
Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr
				325					330					335	
Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu
				340				345					350		
Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp
	355						360					365			
Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val
	370					375					380				
Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp
385					390					395					400
Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His
				405				410						415	
Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu
			420					425					430		
Gly	Lys														

We claim:

1. A recombinant nucleic acid molecule encoding a fusion polypeptide R1-R2-F, wherein R1 is vascular endothelial cell growth factor (VEGF) receptor component Ig domain 2 of Flt-1, R2 is Ig domain 3 of Flk-1, and F is a fusion partner.

2. The nucleic acid molecule of claim 1, wherein F is selected from the group consisting of a multimerizing component capable of interacting with another multimerizing component to form a multimeric structure, a serum protein, or a molecule capable of binding a serum protein.

3. The nucleic acid of claim 2, wherein the F is a multimerizing component selected from the group consisting of (i) a truncated multimerizing component, (ii) an amino acid sequence between 1 to about 200 amino acids in length having at least one cysteine residue.

4. The nucleic acid of claim 3, wherein F is a truncated multimerizing component selected from the group consisting of amino acids 232-458, 232-457, 352-458 and 352-457 of SEQ ID NO:8.

5. The nucleic acid of claim 4, wherein R1 is amino acids 27-129 and R2 is amino acids 130-231 of SEQ ID NO:8.

6. The nucleic acid of claim 1, wherein the fusion polypeptide is arranged as R1-R2-F, R2-R1-F, R1-F-R2, R2-F-R1, F-R1-R2, or F-R2-R1.

7. A vector comprising the nucleic acid molecule of claim 1.

8. A method of producing a VEGF fusion polypeptide, comprising the steps of introducing into a suitable host cell the vector of claim 7, and effecting expression of the VEGF fusion polypeptide.

9. The method of claim 8, wherein the host cell is a bacterial, yeast, insect, or mammalian cell.

10. The method of claim 9, wherein the host cell is a CHO cell.

11. A fusion polypeptide produced by the method of claim 10 comprising amino acids 28-457 of SEQ ID NO:8 which is glycosylated at Asn residues at positions 62, 94, 149, 222 and 308.

12. A multimer comprising two or more of the fusion polypeptides of claim 11.

13. The multimer of claim 12 which is a dimer capable of binding VEGF with an affinity (Kd) of at least 1×10^{-10} M, as measured by Biacore assay.

14. The multimer of claim 13 wherein the Kd is at least at least 1×10^{-11} M.

15. The multimer of claim 14, wherein the Kd is at least 1×10^{-12} M.

16. A fusion polypeptide encoded by the nucleic acid molecule of claim 1.

17. The fusion polypeptide of claim 16, wherein R1 comprises amino acids 28-129 and R2 comprises amino acids 130-231 of SEQ ID NO:8, or a variant thereof.

18. The fusion polypeptide of claim 17, wherein F is selected from the group consisting of amino acids 232-458, 232-457, 352-458 and 352-457 of SEQ ID NO:8.

19. A vascular endothelial cell growth factor (VEGF) trap, comprising a multimer of two or more fusion polypeptides of claim 18 and capable of binding VEGF with an affinity (Kd) of at least 1×10^{-10} M, as measured by Biacore-based assay.

20. A pharmaceutical composition comprising the VEGF trap of claim 19, and a pharmaceutically acceptable carrier.

21. A method of treating a disease or condition which is improved, ameliorated, or inhibited by removal or inhibition of vascular endothelial growth factor (VEGF), comprising administering the pharmaceutical composition of claim 20 to a subject in need thereof.

22. The method of claim 21, wherein the disease or condition is an ocular disease or condition.

23. The method of claim 22, wherein the ocular disease or condition is age related macular degeneration, intra-ocular tumors, or diabetic retinopathy.

24. The method of claim 23, wherein the condition is eye surgery.

25. The method of claim 24, wherein the eye surgery is glaucoma surgery.

* * * * *