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CA 2376379 A1 2000/12/14

(21) **2 376 379**

(12) **DEMANDE DE BREVET CANADIEN
CANADIAN PATENT APPLICATION**

(13) **A1**

(86) Date de dépôt PCT/PCT Filing Date: 2000/05/23

(87) Date publication PCT/PCT Publication Date: 2000/12/14

(85) Entrée phase nationale/National Entry: 2001/12/06

(86) N° demande PCT/PCT Application No.: US 2000/014142

(87) N° publication PCT/PCT Publication No.: 2000/075319

(30) Priorité/Priority: 1999/06/08 (60/138,133) US

(51) Cl.Int.⁷/Int.Cl.⁷ C12N 15/12, A61P 43/00, A61K 38/17,
C12N 5/10, C07K 14/71, C12N 15/62

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(54) Titre : POLYPEPTIDES CHIMERIQUES MODIFIES A PHARMACOCINETIQUE AMELIOREE

(54) Title: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED PHARMACOKINETIC PROPERTIES

(57) **Abrégé/Abstract:**

Modified chimeric polypeptides with improved pharmacokinetics are disclosed. Specifically, modified chimeric Flt1 receptor polypeptides that have been modified in such a way as to improve their pharmacokinetic profile are disclosed. Also disclosed are methods of making and using the modified polypeptides including but not limited to using the modified polypeptides to decrease or inhibit plasma leakage and/or vascular permeability in a mammal.



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

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
14 December 2000 (14.12.2000)

PCT

(10) International Publication Number
WO 00/75319 A1

(51) International Patent Classification⁷: C12N 15/12, 15/62, 5/10, C07K 14/71, A61K 38/17, A61P 43/00

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(21) International Application Number: PCT/US00/14142

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

(22) International Filing Date: 23 May 2000 (23.05.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/138,133 8 June 1999 (08.06.1999) US

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

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Published:

- With international search report.
- Before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments.

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

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**MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
PHARMACOKINETIC PROPERTIES**

5 The application claims priority of U.S. Provisional Application No. 60/138,133, filed on June 8, 1999. Throughout this application various publications are referenced. The disclosures of these publications in their entireties are hereby incorporated by reference into this application.

10

INTRODUCTION

The field of this invention is modified polypeptides with improved pharmacokinetics. Specifically, the field of this invention relates to
15 Flt1 receptor polypeptides that have been modified in such a way as to improve their pharmacokinetic profile. The field of this invention also relates to methods of making and using the modified polypeptides including but not limited to using the modified polypeptides to decrease or inhibit plasma leakage and/or vascular permeability in a mammal.

20

BACKGROUND

The ability of polypeptide ligands to bind to cells and thereby elicit a phenotypic response such as cell growth, survival, cell product
25 secretion, or differentiation is often mediated through transmembrane receptors on the cells. The extracellular domain of such receptors (i.e. that portion of the receptor that is displayed on the surface of the cell) is generally the most distinctive portion of the molecule, as it provides the protein with its ligand binding characteristic. Binding of a ligand

to the extracellular domain generally results in signal transduction which transmits a biological signal to intracellular targets. Often, this signal transduction acts via a catalytic intracellular domain. The particular array of sequence motifs of this catalytic intracellular domain determines its access to potential kinase substrates (Mohammadi, et al., 1990, Mol. Cell. Biol. 11:5068-5078; Fantl, et al., 1992, Cell 69:413-413). Examples of receptors that transduce signals via catalytic intracellular domains include the receptor tyrosine kinases (RTKs) such as the Trk family of receptors which are generally limited to cells of the nervous system, the cytokine family of receptors including the tripartate CNTF receptor complex (Stahl & Yancopoulos, 1994, J. Neurobio. 25:1454-1466) which is also generally limited to the cells of the nervous system, G-protein coupled receptors such as the β_2 -adrenergic receptor found on, for instance, cardiac muscle cells, and the multimeric IgE high affinity receptor Fc ϵ RI which is localized, for the most part, on mast cells and basophils (Sutton & Gould, 1993, Nature 366:421-428).

All receptors identified so far appear to undergo dimerization, multimerization, or some related conformational change following ligand binding (Schlessinger, J., 1988, Trend Biochem. Sci. 13:443-447; Ullrich & Schlessinger, 1990, Cell 61:203-212; Schlessinger & Ullrich, 1992, Neuron 9:383-391) and molecular interactions between dimerizing intracellular domains lead to activation of catalytic function. In some instances, such as platelet-derived growth factor (PDGF), the ligand is a dimer that binds two receptor molecules (Hart, et al., 1988, Science, 240:1529-1531; Heldin, 1989, J. Biol. Chem. 264:8905-8912) while, for example, in the case of epidermal growth

factor (EGF), the ligand is a monomer (Weber, et al., 1984, J. Biol. Chem. 259:14631-14636). In the case of the Fc ϵ RI receptor, the ligand, IgE, exists bound to Fc ϵ RI in a monomeric fashion and only becomes activated when antigen binds to the IgE/Fc ϵ RI complex and cross-links adjacent IgE molecules (Sutton & Gould, 1993, Nature 366:421-428).

Often, the tissue distribution of a particular receptor within higher organisms provides insight into the biological function of the receptor.

The RTKs for some growth and differentiation factors, such as

fibroblast growth factor (FGF), are widely expressed and therefore appear to play some general role in tissue growth and maintenance.

Members of the Trk RTK family (Glass & Yancopoulos, 1993, Trends in Cell Biol. 3:262-268) of receptors are more generally limited to cells

of the nervous system, and the Nerve Growth Factor family consisting

of nerve growth factor (NGF), brain-derived neurotrophic factor (BDNF), neurotrophin-3 (NT-3) and neurotrophin-4/5 (NT-4/5), which bind the Trk RTK family receptors, promote the differentiation of diverse groups of neurons in the brain and periphery (Lindsay, R. M, 1993, in

Neurotrophic Factors, S.E. Loughlin & J.H. Fallon, eds., pp. 257-284, San

Diego, CA, Academic Press). Fc ϵ RI is localized to a very limited number

of types of cells such as mast cells and basophils. Mast cells derive

from bone marrow pluripotent hematopoietic stem cell lineage, but complete their maturation in the tissue following migration from the blood stream (See Janeway & Travers, 1996, in Immunobiology, 2d.

Edition, M. Robertson & E. Lawrence, eds., pp. 1:3-1:4, Current Biology Ltd., London, UK, Publisher) and are involved in the allergic response.

Many studies have demonstrated that the extracellular domain of a receptor provides the specific ligand binding characteristic.

Furthermore, the cellular environment in which a receptor is expressed may influence the biological response exhibited upon binding of a ligand to the receptor. For example, when a neuronal cell expressing a Trk receptor is exposed to a neurotrophin which binds to that receptor, neuronal survival and differentiation results. When the same receptor is expressed by a fibroblast, exposure to the neurotrophin results in proliferation of the fibroblast (Glass, et al., 1991, Cell 66:405-413).

A class of cell-derived dimeric mitogens with selectivity for vascular endothelial cells has been identified and designated vascular endothelial cell growth factor (VEGF). VEGF has been purified from conditioned growth media of rat glioma cells [Conn et al., (1990), Proc. Natl. Acad. Sci. U.S.A., 87, pp 2628-2632]; and conditioned growth media of bovine pituitary follicle stellate cells [Ferrara and Henzel, (1989), Biochem. Biophys. Res. Comm., 161, pp. 851-858; Gozpadarowicz et al., (1989), Proc. Natl. Acad. Sci. U.S.A., 86, pp. 7311-7315] and conditioned growth medium from human U937 cells [Connolly, D. T. et al. (1989), Science, 246, pp. 1309-1312]. VEGF is a dimer with an apparent molecular mass of about 46 kDa with each subunit having an apparent molecular mass of about 23 kDa. VEGF has some structural similarities to platelet derived growth factor (PDGF), which is a mitogen for connective tissue cells but not mitogenic for vascular endothelial cells from large vessels.

The membrane-bound tyrosine kinase receptor, known as Flt, was shown to be a VEGF receptor [DeVries, C. et al., (1992), Science, 255, pp.989-

991]. The Flt receptor specifically binds VEGF which induces mitogenesis. Another form of the VEGF receptor, designated KDR, is also known to bind VEGF and induce mitogenesis. The partial cDNA sequence and nearly full length protein sequence of KDR is known as well [Terman, B. I. et al., (1991) Oncogene 6, pp. 1677-1683; Terman, B. I. et al., (1992) Biochem. Biophys. Res. Comm. 187, pp. 1579-1586].

Persistent angiogenesis may cause or exacerbate certain diseases such as psoriasis, rheumatoid arthritis, hemangiomas, angiofibromas, diabetic retinopathy and neovascular glaucoma. An inhibitor of VEGF activity would be useful as a treatment for such diseases and other VEGF-induced pathological angiogenesis and vascular permeability conditions, such as tumor vascularization. The present invention relates to a VEGF inhibitor that is based on the VEGF receptor Flt1.

Plasma leakage, a key component of inflammation, occurs in a distinct subset of microvessels. In particular, in most organs plasma leakage occurs specifically in the venules. Unlike arterioles and capillaries, venules become leaky in response to numerous inflammatory mediators including histamine, bradykinin, and serotonin. One characteristic of inflammation is the plasma leakage that results from intercellular gaps that form in the endothelium of venules. Most experimental models of inflammation indicate that these intercellular gaps occur between the endothelial cells of postcapillary and collecting venules (Baluk, P., et al., Am. J. Pathol. 1998 152:1463-76). It has been shown that certain lectins may be used to reveal features of focal sites of plasma leakage, endothelial gaps, and finger-like processes at endothelial cell borders in inflamed venules (Thurston, G., et al., Am. J.

Physiol, 1996, 271: H2547-62). In particular, plant lectins have been used to visualize morphological changes at endothelial cell borders in inflamed venules of, for example, the rat trachea. Lectins, such as conconavalin A and ricin, that bind focally to inflamed venules reveal
5 regions of the subendothelial vessel wall exposed by gaps that correspond to sites of plasma leakage (Thurston, G., et al., Am J Physiol, 1996, 271: H2547-62).

The properties of the microvessels are dynamic. Chronic inflammatory
10 diseases, for example, are associated with microvascular remodeling, including angiogenesis and microvessel enlargement. Microvessels can also remodel by acquiring abnormal phenotypic properties. In a murine model of chronic airway inflammation, airway capillaries acquire properties of venules, including widened vessel diameter, increased
15 immunoreactivity for von Willebrand factor, and increased immunoreactivity for P-selectin. In addition, these remodeled vessels leak in response to inflammatory mediators, whereas vessels in the same position in the airways of normal mice do not.

20 Certain substances have been shown to decrease or inhibit vascular permeability and/or plasma leakage. For example, mystixins are synthetic polypeptides that have been reported to inhibit plasma leakage without blocking endothelial gap formation (Baluk, P., et al., J. Pharmacol. Exp. Ther., 1998, 284: 693-9). Also, the beta 2-adrenergic
25 receptor agonist formoterol reduces microvascular leakage by inhibiting endothelial gap formation (Baluk, P. and McDonald, D.M., Am. J. Physiol., 1994, 266:L461-8).

The angiopoietins and members of the vascular endothelial growth factor (VEGF) family are the only growth factors thought to be largely specific for vascular endothelial cells. Targeted gene inactivation studies in mice have shown that VEGF is necessary for the early stages
5 of vascular development and that Ang-1 is required for later stages of vascular remodeling.

US Patent No. 6,011,003, issued January 4, 2000, in the name of Metris Therapeutics Limited, discloses an altered, soluble form of FLT
10 polypeptide being capable of binding to VEGF and thereby exerting an inhibitory effect thereon, the polypeptide comprising five or fewer complete immunoglobulin domains.

US Patent No. 5,712,380, issued January 27, 1998 and assigned to Merck
15 & Co., discloses vascular endothelial cell growth factor (VEGF) inhibitors that are naturally occurring or recombinantly engineered soluble forms with or without a C-terminal transmembrane region of the receptor for VEGF.

20 Also assigned to Merck & Co. is PCT Publication No. WO 98/13071, published April 2, 1998, which discloses gene therapy methodology for inhibition of primary tumor growth and metastasis by gene transfer of a nucleotide sequence encoding a soluble receptor protein which binds to VEGF.

25

PCT Publication No. WO 97/44453, published November 27, 1997, in the name of Genentech, Inc., discloses novel chimeric VEGF receptor proteins comprising amino acid sequences derived from the vascular

endothelial growth factor (VEGF) receptors Flt1 and KDR, including the murine homologue to the human KDR receptor FLK1, wherein said chimeric VEGF receptor proteins bind to VEGF and antagonize the endothelial cell proliferative and angiogenic activity thereof.

5

PCT Publication No. WO 97/13787, published April 17, 1997, in the name of Toa Gosei Co., LTD., discloses a low molecular weight VEGF inhibitor usable in the treatment of diseases accompanied by neovascularization such as solid tumors. A polypeptide containing the first immunoglobulin-like domain and the second immunoglobulin-like domain in the extracellular region of a VEGF receptor FLT but not containing the sixth immunoglobulin-like domain and the seventh immunoglobulin-like domain thereof shows a VEGF inhibitory activity.

10

Sharifi, J. et al., 1998, The Quarterly Jour. of Nucl. Med. 42:242-249, disclose that because monoclonal antibodies (MAbs) are basic, positively charged proteins, and mammalian cells are negatively charged, the electrostatic interactions between the two can create higher levels of background binding resulting in low tumor to normal organ ratios. To overcome this effect, the investigators attempted to improve MAb clearance by using various methods such as secondary agents as well as chemical and charge modifications of the MAb itself.

20

Jensen-Pippo, et al., 1996, Pharmaceutical Research 13:102-107, disclose that pegylation of a therapeutic protein, recombinant human granulocyte colony stimulating factor (PEG-G-CSF), results in an increase in stability and in retention of *in vivo* bioactivity when administered by the intraduodenal route.

25

Tsutsumi, *et al.*, 1997, Thromb Haemost. 77:168-73, disclose experiments wherein the *in vivo* thrombopoietic activity of polyethylene glycol-modified interleukin-6 (MPEG-IL-6), in which 54%
5 of the 14 lysine amino groups of IL-6 were coupled with PEG, was compared to that of native IL-6.

Yang, *et al.*, 1995, Cancer 76:687-94, disclose that conjugation of polyethylene glycol to recombinant human interleukin-2 (IL-2) results
10 in a compound, polyethylene glycol-modified IL-2 (PEG-IL-2) that retains the *in vitro* and *in vivo* activity of IL-2, but exhibits a markedly prolonged circulating half-life.

R. Duncan and F. Spreafico, Clin. Pharmacokinet. 27: 290-306, 296
15 (1994) review efforts to improve the plasma half-life of asparaginase by conjugating polyethylene glycol.

PCT International Publication No. WO 99/03996 published January 28, 1999 in the name of Regeneron Pharmaceuticals, Inc. and The Regents of
20 The University of California describes modified human noggin polypeptides having deletions of regions of basic amino acids. The modified human noggin polypeptides are described as retaining biological activity while having reduced affinity for heparin and superior pharmacokinetics in animal sera as compared to the
25 unmodified human noggin.

SUMMARY OF THE INVENTION

The present invention is directed to VEGF antagonists with improved pharmacokinetic properties. A preferred embodiment is an isolated
5 nucleic acid molecule encoding a fusion polypeptide capable of binding a VEGF polypeptide comprising (a) a nucleotide sequence encoding a VEGF receptor component operatively linked to (b) a nucleotide sequence encoding a multimerizing component, wherein the VEGF receptor component is the only VEGF receptor component of the fusion
10 polypeptide and wherein the nucleotide sequence of (a) consists essentially of a nucleotide sequence encoding the amino acid sequence of Ig domain 2 of the extracellular domain of a first VEGF receptor and a nucleotide sequence encoding the amino acid sequence of Ig domain 3 of the extracellular domain of a second VEGF receptor.

15 In a further embodiment, the isolated nucleic acid of the first VEGF receptor is Flt1.

In a further embodiment, the isolated nucleic acid of the second VEGF
20 receptor is Flk1.

In yet another embodiment, the isolated nucleic acid of the second VEGF receptor is Flt4.

25 In another preferred embodiment, the nucleotide sequence encoding Ig domain 2 of the extracellular domain of the first VEGF receptor is upstream of the nucleotide sequence encoding Ig domain 3 of the extracellular domain of the second VEGF receptor.

In still another preferred embodiment, the nucleotide sequence encoding Ig domain 2 of the extracellular domain of the first VEGF receptor is downstream of the nucleotide sequence encoding Ig domain
5 3 of the extracellular domain of the second VEGF receptor.

In a preferred embodiment of the invention, the multimerizing component comprises an immunoglobulin domain.

10 In another embodiment, the immunoglobulin domain is selected from the group consisting of the Fc domain of IgG, the heavy chain of IgG, and the light chain of IgG.

Preferred embodiments include an isolated nucleic acid molecule
15 comprising a nucleotide sequence encoding a modified Flt1 receptor fusion polypeptide, wherein the coding region of the nucleic acid molecule consists of a nucleotide sequence selected from the group consisting of

- (a) the nucleotide sequence set forth in Figure 13A-13D;
- 20 (b) the nucleotide sequence set forth in Figure 14A-14C;
- (c) the nucleotide sequence set forth in Figure 15A-15C;
- (d) the nucleotide sequence set forth in Figure 16A-16D;
- (e) the nucleotide sequence set forth in Figure 21A-21C;
- (f) the nucleotide sequence set forth in Figure 22A-22C;
- 25 (g) the nucleotide sequence set forth in Figure 24A-24C; and
- (h) a nucleotide sequence which, as a result of the degeneracy of the genetic code, differs from the nucleotide sequence of (a), (b), (c), (d), (e), (f), or (g) and which encodes a fusion polypeptide molecule having

the biological activity of the modified Flt1 receptor fusion polypeptide.

In a further embodiment of the invention, a fusion polypeptide is encoded by the isolated nucleic acid molecules described above.

5

A preferred embodiment is a composition capable of binding a VEGF molecule to form a nonfunctional complex comprising a multimer of the fusion polypeptide.

10 Also preferred is a composition wherein the multimer is a dimer.

In yet another embodiment, the composition is in a carrier.

Another embodiment is a vector which comprises the nucleic acid
15 molecules described above, including an expression vector comprising a the nucleic acid molecules described wherein the nucleic acid molecule is operatively linked to an expression control sequence.

Other included embodiments are a host-vector system for the
20 production of a fusion polypeptide which comprises the expression vector, in a suitable host cell; the host-vector system wherein the suitable host cell is a bacterial cell, yeast cell, insect cell, or mammalian cell; the host-vector system wherein the suitable host cell is E. Coli; the host-vector system wherein the suitable host cell is a
25 COS cell; the host-vector system wherein the suitable host cell is a CHO cell.

Another embodiment of the invention is a method of producing a fusion polypeptide which comprises growing cells of the host-vector system under conditions permitting production of the fusion polypeptide and recovering the fusion polypeptide so produced.

5

Additional embodiments include a fusion polypeptide encoded by the nucleic acid sequence set forth in Figure 10A-10D or Figure 24A-24C, which has been modified by acetylation or pegylation wherein the acetylation is accomplished with at least about a 100 fold molar
10 excess of acetylation reagent or wherein acetylation is accomplished with a molar excess of acetylation reagent ranging from at least about a 10 fold molar excess to about a 100 fold molar excess or wherein the pegylation is 10K or 20K PEG.

15 A preferred embodiment includes a method of decreasing or inhibiting plasma leakage in a mammal comprising administering to the mammal the fusion polypeptide described above, including embodiments wherein the mammal is a human, the fusion polypeptide is acetylated or the fusion polypeptide is pegylated.

20

A further embodiments is a fusion polypeptide which specifically binds the VEGF receptor ligand VEGF.

A preferred embodiment of the invention is a method of blocking blood
25 vessel growth in a human comprising administering an effective amount of the fusion polypeptide described above.

Also preferred is a method of inhibiting VEGF receptor ligand activity in a mammal comprising administering to the mammal an effective amount of the fusion polypeptide described above.

- 5 Preferred embodiments of these methods are wherein the mammal is a human.

Further embodiments of the methods of the invention include attenuation or prevention of tumor growth in a human; attenuation or
10 prevention of edema in a human, especially wherein the edema is brain edema; attenuation or prevention of ascites formation in a human, especially wherein the ascites is ovarian cancer-associated ascites.

Preferred embodiments of the invention include a fusion polypeptide
15 capable of binding a VEGF polypeptide comprising (a) a VEGF receptor component operatively linked to (b) a multimerizing component, wherein the VEGF receptor component is the only VEGF receptor component in the fusion polypeptide and consists essentially of the amino acid sequence of Ig domain 2 of the extracellular domain of a
20 first VEGF receptor and the amino acid sequence of Ig domain 3 of the extracellular domain of a second VEGF receptor.

In a further embodiment of the fusion polypeptide, the first VEGF receptor is Flt1.

25

In yet a further embodiment of the fusion polypeptide, the second VEGF receptor is Flk1.

Still another embodiment of the fusion polypeptide is one in which the second VEGF receptor is Flt4.

Preferred embodiments include a fusion polypeptide wherein amino acid
5 sequence of Ig domain 2 of the extracellular domain of the first VEGF
receptor is upstream of the amino acid sequence of Ig domain 3 of the
extracellular domain of the second VEGF receptor and a fusion
polypeptide wherein the amino acid sequence of Ig domain 2 of the
extracellular domain of the first VEGF receptor is downstream of the
10 amino acid sequence of Ig domain 3 of the extracellular domain of the
second VEGF receptor.

In yet another embodiment, the fusion polypeptide multimerizing
component comprises an immunoglobulin domain including an
15 embodiment wherein the immunoglobulin domain is selected from the
group consisting of the Fc domain of IgG, the heavy chain of IgG, and the
light chain of IgG.

Preferred embodiments include a fusion polypeptide comprising an
20 amino acid sequence of a modified Flt1 receptor, wherein the amino
acid sequence selected from the group consisting of (a) the amino acid
sequence set forth in Figure 13A-13D; (b) the amino acid sequence set
forth in Figure 14A-14C; (c) the amino acid sequence set forth in Figure
15A-15C; (d) the amino acid sequence set forth in Figure 16A-16D; (e)
25 the amino acid sequence set forth in Figure 21A-21C; (f) the amino acid
sequence set forth in Figure 22A-22C; and (g) the amino acid sequence
set forth in Figure 24A-24C.

Another preferred embodiment is a method of decreasing or inhibiting plasma leakage in a mammal comprising administering to the mammal the fusion polypeptide described above.

- 5 An alternative preferred embodiment is a method of inhibiting VEGF receptor ligand activity in a mammal comprising administering to the mammal an effective amount of the fusion polypeptide described above.

BRIEF DESCRIPTION OF THE FIGURES

10

Figure 1. IEF gel analysis of unmodified and acetylated Flt1(1-3)-Fc proteins. Unmodified Flt1(1-3)-Fc protein is unable to enter the gel due to its >9.3 pI, whereas acetylated Flt1(1-3)-Fc is able to enter the gel and equilibrate at pI 5.2.

15

Figure 2. Binding of unmodified Flt1(1-3)-Fc and acetylated Flt1(1-3)-Fc proteins to Matrigel® coated plates. Unmodified Flt1(1-3)-Fc proteins binds extensive to extracellular matrix components in Matrigel®, whereas acetylated Flt1(1-3)-Fc does not bind.

20

Figure 3. Binding of unmodified Flt1(1-3)-Fc, acetylated Flt1(1-3)-Fc, and pegylated Flt1(1-3)-Fc in a Biacore-based assay. Acetylated (columns 13-16), pegylated (columns 17-20), and heparin-treated Flt1(1-3)-Fc (columns 21-24) are each able to completely compete with the Biacore chip-bound Flt1(1-3)-Fc for VEGF binding as compared to control (columns 1-4) and irrelevant protein (columns 5-8).

25

Unmodified Flt1(1-3)-Fc (columns 5-6) appears to only partially compete with Biacore chip-bound Flt1(1-3)-Fc for VEGF binding.

However, washing the bound samples with 0.5M NaCl (columns 7-8) results in a binding profile similar to the modified forms of Flt1(1-3)-Fc, indicating that the unmodified protein is exhibiting non-specific binding to the chip that can be eliminated by the salt wash.

5

Figure 4. Binding of unmodified Flt1(1-3)-Fc, acetylated Flt1(1-3)-Fc, and pegylated Flt1(1-3)-Fc to VEGF in an ELISA-based assay. Both pegylated and acetylated Flt1(1-3)-Fc proteins bind to VEGF with affinities approaching that of unmodified Flt1(1-3)-Fc.

10

Figure 5. Pharmacokinetic profiles of unmodified Flt1(1-3)-Fc, acetylated Flt1(1-3)-Fc, and pegylated Flt1(1-3)-Fc. Balb/c mice (23-28g) were injected subcutaneously with 4mg/kg of unmodified, acetylated, or pegylated Flt1(1-3)-Fc. The mice were tail bled at 1, 2, 4, 6, 24 hours, 2 days, and 3 days after injection of protein and the sera were assayed in a standard ELISA-based assay designed to detect Flt1(1-3)-Fc protein. The T_{max} for all of the Flt1(1-3)-Fc proteins was between the 6 hour and 24 hour time points. The C_{max} for the different proteins was as follows: Unmodified: 0.06 μ g/ml - 0.15 μ g/ml; acetylated: 1.5 μ g/ml - 4.0 μ g/ml; and pegylated: approximately 5 μ g/ml.

20

Figure 6A-6B. IEF gel analysis of unmodified and step-acetylated Flt1(1-3)-Fc proteins. Unmodified Flt1(1-3)-Fc protein is unable to enter the gel due to its >9.3 pI, whereas most of the step-acetylated Flt1(1-3)-Fc samples (30-100 fold excess samples) were able to migrate into the gel and equilibrate at pIs ranging between 4.55 - 8.43, depending on the degree of acetylation.

25

Figure 7. Binding of unmodified Flt1(1-3)-Fc and step-acetylated Flt1(1-3)-Fc proteins to Matrigel® coated plates. As with the irrelevant control protein, rTie2-Fc, step-acetylated Flt1(1-3)-Fc (20 and 30 fold excess samples) does not exhibit any binding to the Matrigel coated plate, whereas the non-acetylated Flt1(1-3)-Fc protein exhibits significant binding. The 10 fold excess sample shows reduced binding, but the degree of acetylation is not enough to completely block binding to extracellular matrix components.

10

Figure 8. Binding of unmodified Flt1(1-3)-Fc and step-acetylated Flt1(1-3)-Fc in a Biacore-based assay. At a sub-stoichiometric ratio (0.5 µg/ml of either unmodified Flt1(1-3) or step-acetylated Flt1(1-3)-Fc vs. 0.2 µg/ml VEGF), there is not enough Flt1(1-3)-Fc (either unmodified or step-acetylated) in the solution to completely bind the VEGF. At 1.0 µg/ml, which approximates a 1:1 stoichiometric ratio, the both unmodified and step-acetylated Flt1(1-3)-Fc are better able to compete for VEGF binding, but there is still insufficient Flt1(1-3)-Fc protein (either unmodified or step-acetylated) to completely saturate the available VEGF. However, at 5.0 µg/ml, which is several times greater than a 1:1 stoichiometric ratio, both the Flt1(1-3)-Fc and the step-acetylated Flt1(1-3)-Fc proteins are able to saturate the VEGF, regardless of the degree of acetylation.

20

Figure 9. Pharmacokinetic profiles of unmodified Flt1(1-3)-Fc and step-acetylated Flt1(1-3)-Fc. Balb/c mice (23-28g) were injected subcutaneously with 4mg/kg of unmodified or 10, 20, 40, 60 and 100 fold excess samples of step-acetylated Flt1(1-3)-Fc (3 mice for

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unmodified, 10, 20 and 40 fold excess samples and 2 mice for 60 and 100 fold excess samples). The mice were tail bled at 1, 2, 4, 6, 24 hours, 2 days and 3 days after injection. The sera were assayed in an ELISA-based assay designed to detect Flt1(1-3)-Fc. The T_{max} for all of the Flt1(1-3)-Fc proteins tested was at the 6 hour time point but the C_{max} was as follows: Unmodified Flt1(1-3)-Fc: 0.06 μ g/ml; 10 fold excess sample: - 0.7 μ g/ml, 20 fold excess sample - 2 μ g/ml, 40 fold excess sample - 4 μ g/ml, 60 fold excess sample - 2 μ g/ml, 100 fold excess sample - 1 μ g/ml.

Figure 10A-10D. Nucleic acid and deduced amino acid sequence of Flt1(1-3)-Fc.

Figure 11. Schematic diagram of the structure of Flt1.

Figure 12A and 12B. Hydrophilicity analysis of the amino acid sequences of Ig domain 2 and Ig domain 3 of Flt1.

Figure 13A-13D. Nucleic acid and deduced amino acid sequence of Mut1: Flt1(1-3 $_{\Delta B}$)-Fc.

Figure 14A-14 C. Nucleic acid and deduced amino acid sequence of Mut2: Flt1(2-3 $_{\Delta B}$)-Fc.

Figure 15A-15C. Nucleic acid and deduced amino acid sequence of Mut3: Flt1(2-3)-Fc.

Figure 16A-16D. Nucleic acid and deduced amino acid sequence of Mut4: Flt1(1-3_{R->N})-Fc.

Figure 17. Binding of unmodified Flt1(1-3)-Fc, basic region deletion mutant Flt1(1-3)-Fc, and Flt1(1-3)_{R->N} mutant proteins in a Biacore-based assay. At the sub-stoichiometric ratio (0.25 µg/ml Flt1(1-3)-Fc of unmodified, acetylated or genetically modified samples vs. 01. µg/ml VEGF), there is insufficient Flt1(1-3)-Fc protein to block binding of VEGF to the Flt1(1-3)-Fc immobilized on the Biacore chip. At 0.5 µg/ml of unmodified, acetylated or genetically modified Flt1(1-3)-Fc proteins, the stoichiometric ratio approximates 1:1 and there is an increased ability to block VEGF binding to the Biacore chip. At 1.0 µg/ml of unmodified, acetylated or genetically modified Flt1(1-3)-Fc proteins, which is approximately a 10:1 stoichiometric ratio, the Flt1(1-3)-Fc proteins are able to block binding of VEGF to the Biacore chip, but they are not equivalent. Unmodified, acetylated, and Mut1: Flt1(1-3_{ΔB})-Fc are essentially equal in their ability to block VEGF binding, whereas Mut4: Flt1(1-3_{R->N})-Fc is somewhat less efficient at blocking binding

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Figure 18. Binding of unmodified Flt1(1-3)-Fc, Mut1: Flt1(1-3_{ΔB})-Fc, Mut2: Flt1(2-3_{ΔB})-Fc, and Flt1(2-3) mutant proteins to Matrigel® coated plates. Unmodified Flt1(1-3)-Fc protein binds avidly to these wells, the Mut3: Flt1(2-3)-Fc protein binds somewhat more weakly, the Mut1: Flt1(1-3_{ΔB})-Fc protein binds more weakly still, and the Mut2: Flt1(2-3_{ΔB})-Fc protein shows the best profile, binding more weakly than any of the other mutant proteins. The Mut4: Flt1(1-3_{R->N})-Fc

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glycosylation mutant protein shows only marginal benefit on the Matrigel assay.

Figure 19. Binding of unmodified Flt1(1-3)-Fc, Mut1: Flt1(1-3_{ΔB})-Fc, Mut2: Flt1(2-3_{ΔB})-Fc, and Flt1(2-3) mutant proteins in an ELISA-based assay. At the concentrations tested, unmodified Flt1(1-3)-Fc, Mut1: Flt1(1-3_{ΔB})-Fc, Mut2: Flt1(2-3_{ΔB})-Fc, and Flt1(2-3) mutant proteins bind VEGF similarly.

Figure 20. Pharmacokinetic profiles of unmodified Flt1(1-3)-Fc, Mut1: Flt1(1-3_{ΔB})-Fc, Mut2: Flt1(2-3_{ΔB})-Fc, and Flt1(2-3) mutant proteins. the C_{max} for these reagents was as follows: Unmodified Flt1(1-3)-Fc - 0.15μg/ml; 40 fold molar excess acetylated Flt1(1-3)-Fc - 1.5μg/ml; and Mut1: Flt1(1-3_{ΔB})-Fc - 0.7μg/ml.

Figure 21A-21C. Nucleotide and deduced amino acid sequence of the modified Flt1 receptor termed Flt1D2.Flk1D3.FcΔC1(a).

Figure 22A-22C. Nucleotide and deduced amino acid sequence of the modified Flt1 receptor termed Flt1D2.VEGFR3D3.FcΔC1(a).

Figure 23. Extracellular Matrix (ECM) Assay. The results of this assay demonstrate that the Flt1D2.Flk1D3.FcΔC1(a) and Flt1D2.VEGFR3D3.FcΔC1(a) proteins are considerably less sticky to the ECM as compared to the Flt1(1-3)-Fc protein.

Figure 24A-24C. Nucleotide and deduced amino acid sequence of the modified Flt1 receptor termed VEGFR1R2-Fc Δ C1(a).

Figure 25A-25C. Phosphorylation assay. At a 1.5 molar excess of either Flt1(1-3)-Fc , Flt1(1-3)-Fc (A40) or transient Flt1D2Flk1D3.Fc Δ C1(a) there is complete blockage of receptor stimulation by these three modified Flt1 receptors as compared to control media challenge. In contrast, transient Flt1D2VEGFR3D3.Fc Δ C1(a) does not show significant blockage at this molar excess, as compared with VEGF positive control challenge. Similar results are seen in Figure 25B, where the modified Flt receptors are in a 3-fold molar excess to VEGF165 ligand. In Figure 25C, where the modified Flt1 receptors are in a 6-fold molar excess to VEGF165 ligand, transient Flt1D2VEGFR3D3.Fc Δ C1(a) can now be shown to be partially blocking VEGF165-induced stimulation of cell-surface receptors.

Figure 26A-26B. Phosphorylation assay. Detection by Western blot of tyrosine phosphorylated VEGFR2(Flk1) by VEGF165 ligand stimulation shows that cell-surface receptors are not phosphorylated by challenge samples which have VEGF165 preincubated with 1 and 2 fold molar excess (Figure 26A) or 3 and 4 fold molar excess (Figure 26B) of either transient Flt1D2Flk1D3.Fc Δ C1(a), stable Flt1D2Flk1D3.Fc Δ C1(a), or transient VEGFR1R2-Fc Δ C1(a). At all modified Flt1 receptor concentrations tested there is complete binding of VEGF165 ligand

during the preincubation, resulting in no detectable stimulation of cell-surface receptors by unbound VEGF165 as compared to control media challenge.

5 **Figure 27.** MG/R2 Cell proliferation assay. The following modified Flt receptors Flt1(1-3)-Fc, Flt1D2.FlklD3.Fc Δ C1(a) and Flt1D2.VEGFR3D3.Fc Δ C1(a), plus an irrelevant receptor termed Tie2-Fc as a negative control, were titrated from 40nM to 20pM and incubated on the cells for 1hr at 37°C. Human recombinant VEGF165 in defined
10 media was then added to all the wells at a concentration of 1.56nM. The negative control receptor Tie2-Fc does not block VEGF165-induced cell proliferation at any concentration whereas Flt1D2.FlklD3.Fc Δ C1(a) blocks 1.56nM VEGF165 with a half maximal dose of 0.8nM. Flt1(1-3)-Fc and Flt1D2.VEGFR3D3.Fc Δ C1(a) are less effective in blocking
15 VEGF165 in this assay with a half maximal dose of ~ 2nM. VEGF165 alone gives a reading of 1.2 absorbance units and the background is 0.38 absorbance units.

Figure 28. Biacore analysis of Binding Stoichiometry. Binding
20 stoichiometry was calculated as a molar ratio of bound VEGF165 to the immobilized Flt1D2FlklD3.Fc Δ C1(a) or VEGFR1R2-Fc Δ C1(a), using the conversion factor of 1000 RU equivalent to 1 ng/ml. The results indicated binding stoichiometry of one VEGF165 dimeric molecule per one Flt1D2FlklD3.Fc Δ C1(a) or VEGFR1R2-Fc Δ C1(a) molecule.

Figure 29 and Figure 30. Size Exclusion Chromatography

Stoichiometry. Flt1D2Flk1D3.FcΔC1(a) or VEGFR1R2-FcΔC1(a) at a concentration of 1nM (estimated to be 1000 times higher than the KD of the Flt1D2Flk1D3.FcΔC1(a) or VEGFR1R2-FcΔC1(a)/VEGF165

5 interaction) were mixed with varied concentrations of VEGF165. After incubation, concentrations of the free Flt1D2Flk1D3.FcΔC1(a) in solution were measured. The data shows that the addition of 1 nM VEGF165 into the Flt1D2Flk1D3.FcΔC1(a) solution completely blocks Flt1D2Flk1D3.FcΔC1(a) binding to the VEGF165 surface. This result
10 suggested the binding stoichiometry of one VEGF165 molecule per one Flt1D2Flk1D3.FcΔC1(a) molecule.

Figure 31. Size Exclusion Chromatography (SEC) under native conditions. Peak #1 represents the Flt1D2Flk1D3.FcΔC1(a)/ VEGF165
15 complex and peak #2 represents unbound VEGF165. Fractions eluted between 1.1 and 1.2 ml were combined and guanidinium hydrochloride (GuHCl) was added to a final concentration 4.5M to dissociate the complex.

20 **Figure 32.** Size Exclusion Chromatography (SEC) under dissociative conditions. To separate the components of the receptor-ligand complex and to determine their molar ratio, 50μl of dissociated complex was loaded onto a Superose 12 PC 3.2/30 equilibrated in 6M GuHCl and eluted. Peak #1 represents Flt1D2Flk1D3.FcΔC1(a) and peak #2
25 represents VEGF165.

Figure 33, Figure 34 and Figure 35. Size Exclusion

Chromatography (SEC) with On-Line Light Scattering. Size exclusion chromatography column with a MiniDawn on-line light scattering

5 detector (Wyatt Technology, Santa Barbara, California) and refractive index (RI) detectors (Shimadzu, Kyoto, Japan) was used to determine the molecular weight (MW) of the receptor-ligand complex. As shown in Figure 33, the elution profile shows two peaks. Peak #1 represents the receptor-ligand complex and peak #2 represents the unbound VEGF165.

10 MW was calculated from LS and RI signals. The same procedure was used to determine MW of the individual components of the receptor-ligand complex. The results of these determinations are as follows: MW of the Flt1D2Flk1D3.FcΔC1(a)/VEGF165 complex at the peak position is 157 300 (Figure 33), the MW of VEGF165 at the peak
15 position is 44 390 (Figure 34) and the MW of R1R2 at the peak is 113 300 (Figure 35).

Figure 36. Peptide mapping and glycosylation analysis. The disulfide structures and glycosylation sites in Flt1D2.Flk1D3.FcΔC1(a) were

20 determined by a peptide mapping method. There are a total of ten cysteines in Flt1D2.Flk1D3.FcΔC1(a); six of them belong to the Fc region. Cys27 is disulfide bonded to Cys76. Cys121 is disulfide bonded to Cys 182. The first two cysteines in the Fc region (Cys211 and Cys214) form an intermolecular disulfide bond with the same two
25 cysteines in another Fc chain. However, it can not be determined

whether disulfide bonding is occurring between same cysteines (Cys211 to Cys211, for example) or between Cys211 and Cys214. Cys216 is disulfide bonded to Cys306. Cys 352 is disulfide bonded to Cys410.

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There are five possible N-linked glycosylation sites in Flt1D2.Flk1D3.FcΔC1(a) and are found to be glycosylated to varying degrees. Complete glycosylation is observed at Asn33, Asn193, and Asn282. Partial glycosylation is observed on Asn65 and Asn120. Sites
10 of glycosylation are highlighted by underline in the Figure.

Figure 37. Pharmacokinetics of Flt1(1-3)-Fc (A40), Flt1D2.Flk1D3.FcΔC1(a) and VEGFR1R2-FcΔC1(a). Balb/c mice were injected subcutaneously with 4mg/kg of Flt1(1-3)-Fc (A40), CHO
15 transiently expressed Flt1D2.Flk1D3.FcΔC1(a), CHO stably expressed Flt1D2.Flk1D3.FcΔC1(a), and CHO transiently expressed VEGFR1R2-FcΔC1(a). The mice were tail bled at 1, 2, 4, 6, 24 hrs, 2 days, 3 days and 6 days after injection. The sera were assayed in an ELISA designed to detect Flt1(1-3)-Fc (A40), Flt1D2.Flk1D3.FcΔC1(a) or VEGFR1R2-FcΔC1(a).
20 The Tmax for Flt1(1-3)-Fc (A40) was at 6 hrs while the Tmax for the transient and stable Flt1D2.Flk1D3.FcΔC1(a) and the transient VEGFR1R2-FcΔC1(a) was 24hrs. The Cmax for Flt1(1-3)-Fc (A40) was 8μg/ml, For both transients (Flt1D2.Flk1D3.FcΔC1(a) and VEGFR1R2-FcΔC1(a)) the Cmax was 18μg/ml and the Cmax for the
25 stable VEGFR1R2-FcΔC1(a) was 30μg/ml.

Figure 38. Pharmacokinetics of Flt1(1-3)-Fc (A40), Flt1D2.Flk1D3.FcΔC1(a) and Flt1D2.VEGFR3D3.FcΔC1(a). Balb/c mice were injected subcutaneously with 4mg/kg of Flt1(1-3)-Fc (A40), CHO transiently expressed Flt1D2.Flk1D3.FcΔC1(a) and CHO transiently expressed Flt1D2.VEGFR3D3.FcΔC1(a). The mice were tail bled at 1, 2, 5, 6, 7, 8, 12, 15 and 20 days after injection. The sera were assayed in an ELISA designed to detect Flt1(1-3)-Fc, Flt1D2.Flk1D3.FcΔC1(a) and Flt1D2.VEGFR3D3.FcΔC1(a). Flt1(1-3)-Fc (A40) could no longer be detected in the serum after day 5 whereas Flt1D2.Flk1D3.FcΔC1(a) and Flt1D2.VEGFR3D3.FcΔC1(a) were detectable for 15 days or more.

Figure 39. The Ability of Flt1D2.Flk1D3.FcΔC1(a) to Inhibit HT-1080 Fibrosarcoma Tumor Growth In Vivo. Every other day or 2 times per week treatment of SCID mice with Flt1D2.Flk1D3.FcΔC1(a) at 25mg/Kg significantly decreases the growth of subcutaneous HT-1080 fibrosarcoma tumors.

Figure 40. The Ability of Flt1D2.Flk1D3.FcΔC1(a) to Inhibit C6 Glioma Tumor Growth In Vivo. Every other day or 2 times a week treatment of SCID mice with Flt1D2.Flk1D3.FcΔC1(a) significantly decreases the growth of subcutaneous C6 glioma tumors at doses as low as 2.5mg/Kg.

Figure 41. VEGF-Induced Uterine Hyperpermeability. PMSG injected subcutaneously (5 IU) to induce ovulation in prepubertal female rats

results in a surge of estradiol after 2 days which in turn causes an induction of VEGF in the uterus. This induction results in hyperpermeability of the uterus and an increase in uterine wet.

Subcutaneous injection of Flt1(1-3)-Fc (A40), Flt1D2.Flk1D3.FcΔC1(a)

5 and Flt1D2.VEGFR3D3.FcΔC1(a) at 25mg/kg at 1hr after PMSG injection results in about a 50% inhibition of the increase in uterine wet weight.

Figure 42A-42B. Assessment of Corpus Luteum Angiogenesis Using Progesterone as a Readout. PMSG was injected subcutaneously (5 IU) to induce ovulation in prepubertal female rats, resulting in a fully functioning corpus luteum containing a dense network of blood vessels that secretes progesterone into the blood stream to prepare the uterus for implantation. The induction of angiogenesis in the corpus luteum requires VEGF. Resting levels of progesterone are about 5ng/ml and can be induced to 25-40ng/ml after PMSG. Subcutaneous injection of Flt1(1-3)-Fc (A40) or Flt1D2.Flk1D3.FcΔC1(a) at 25mg/kg or 5mg/kg at 1hr. after PMSG injection resulted in a complete inhibition of the progesterone induction on day 4.

20 DETAILED DESCRIPTION OF THE INVENTION

It has been a long standing problem in the art to produce a receptor based VEGF antagonist that has a pharmacokinetic profile that is appropriate for consideration of the antagonist as a therapeutic

25 candidate. Applicants describe herein, for the first time, a chimeric

polypeptide molecule, capable of antagonizing VEGF activity, that exhibits improved pharmacokinetic properties as compared to other known receptor-based VEGF antagonists. The chimeric polypeptide molecules described herein thus provide for the first time appropriate
5 molecules for use in therapies in which antagonism of VEGF is a desired result.

The present invention provides for novel chimeric polypeptide molecules formed by fusing a modified extracellular ligand binding
10 domain of the Flt1 receptor to the Fc region of IgG.

The extracellular ligand binding domain is defined as the portion of a receptor that, in its native conformation in the cell membrane, is oriented extracellularly where it can contact with its cognate ligand.
15 The extracellular ligand binding domain does not include the hydrophobic amino acids associated with the receptor's transmembrane domain or any amino acids associated with the receptor's intracellular domain. Generally, the intracellular or cytoplasmic domain of a receptor is usually composed of positively charged or polar amino acids
20 (i.e. lysine, arginine, histidine, glutamic acid, aspartic acid). The preceding 15-30, predominantly hydrophobic or apolar amino acids (i.e. leucine, valine, isoleucine, and phenylalanine) comprise the transmembrane domain. The extracellular domain comprises the amino acids that precede the hydrophobic transmembrane stretch of amino
25 acids. Usually the transmembrane domain is flanked by positively

charged or polar amino acids such as lysine or arginine. von Heijne has published detailed rules that are commonly referred to by skilled artisans when determining which amino acids of a given receptor belong to the extracellular, transmembrane, or intracellular domains (See von Heijne, 1995, BioEssays 17:25-30). Alternatively, websites on the Internet, such as http://ulrec3.unil.ch/software/TMPRED_form.html. have become available to provide protein chemists with information about making predictions about protein domains.

The present invention provides for the construction of nucleic acid molecules encoding chimeric polypeptide molecules that are inserted into a vector that is able to express the chimeric polypeptide molecules when introduced into an appropriate host cell. Appropriate host cells include, but are not limited to, bacterial cells, yeast cells, insect cells, 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 chimeric polypeptide molecules under control of transcriptional/translational control signals. These methods may include in vitro recombinant DNA and synthetic techniques and in vivo recombinations (genetic recombination) (See Sambrook, et al., Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory; Current Protocols in Molecular Biology, Eds. Ausubel, et al., Greene Publ. Assoc., Wiley-Interscience, NY).

Expression of nucleic acid molecules encoding the chimeric polypeptide molecules may be regulated by a second nucleic acid sequence so that the chimeric polypeptide molecule is expressed in a host transformed with the recombinant DNA molecule. For example, expression of the chimeric polypeptide molecules described herein 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, the long terminal repeat as described in Squinto et al., (1991, Cell 65:1-20); the SV40 early promoter region (Bernoist and Chambon, 1981, Nature 290:304-310), the CMV promoter, the M-MuLV 5' terminal repeat the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto, et al., 1980, Cell 22:787-797), the herpes thymidine kinase promoter (Wagner et al., 1981, Proc. Natl. Acad. Sci. U.S.A. 78:144-1445), the regulatory sequences of the metallothionine gene (Brinster et al., 1982, Nature 296:39-42); prokaryotic expression vectors such as the β -lactamase promoter (Villa-Kamaroff, et al., 1978, Proc. Natl. Acad. Sci. U.S.A. 75:3727-3731), or the *tac* promoter (DeBoer, et al., 1983, Proc. Natl. Acad. Sci. U.S.A. 80:21-25, see also "Useful proteins from recombinant bacteria" in Scientific American, 1980, 242:74-94); promoter elements from yeast or other fungi such as the Gal 4 promoter, the ADH (alcohol dehydrogenase) promoter, PGK (phosphoglycerol kinase) promoter, alkaline phosphatase promoter, and the following animal transcriptional control regions, which exhibit tissue specificity and

have been utilized in transgenic animals: elastase I gene control region which is active in pancreatic acinar cells (Swift et al., 1984, Cell 38:639-646; Ornitz et al., 1986, Cold Spring Harbor Symp. Quant. Biol. 50:399-409; MacDonald, 1987, Hepatology 7:425-515); insulin gene
5 control region which is active in pancreatic beta cells (Hanahan, 1985, Nature 315:115-122), immunoglobulin gene control region which is active in lymphoid cells (Grosschedl et al., 1984, Cell 38:647-658; Adames et al., 1985, Nature 318:533-538; Alexander et al., 1987, Mol. Cell. Biol. 7:1436-1444), mouse mammary tumor virus control region
10 which is active in testicular, breast, lymphoid and mast cells (Leder et al., 1986, Cell 45:485-495), albumin gene control region which is active in liver (Pinkert et al., 1987, Genes and Devel. 1:268-276), alpha-fetoprotein gene control region which is active in liver (Krumlauf et al., 1985, Mol. Cell. Biol. 5:1639-1648; Hammer et al., 1987, Science
15 235:53-58); alpha 1-antitrypsin gene control region which is active in the liver (Kelsey et al, 1987, Genes and Devel. 1:161-171), beta-globin gene control region which is active in myeloid cells (Mogam et al., 1985, Nature 315:338-340; Kollias et al., 1986, Cell 46:89-94); myelin basic protein gene control region which is active in oligodendrocyte
20 cells in the brain (Readhead et al., 1987, Cell 48:703-712); myosin light chain-2 gene control region which is active in skeletal muscle (Shani, 1985, Nature 314:283-286), and gonadotropic releasing hormone gene control region which is active in the hypothalamus (Mason et al., 1986, Science 234:1372-1378).

Thus, according to the invention, expression vectors capable of being replicated in a bacterial or eukaryotic host comprising chimeric polypeptide molecule-encoding nucleic acid as described herein, are used to transfect the host and thereby direct expression of such nucleic acids to produce the chimeric polypeptide molecules, which may then be recovered in a biologically active form. As used herein, a biologically active form includes a form capable of binding to VEGF.

Expression vectors containing the chimeric nucleic acid molecules described herein can be identified by three general approaches: (a) DNA-DNA hybridization, (b) presence or absence of "marker" gene functions, and (c) expression of inserted sequences. In the first approach, the presence of a foreign gene inserted in an expression vector can be detected by DNA-DNA hybridization using probes comprising sequences that are homologous to the inserted chimeric polypeptide molecule sequences. In the second approach, the recombinant vector/host system can be identified and selected based upon the presence or absence of certain "marker" gene functions (e.g., thymidine kinase activity, resistance to antibiotics, transformation phenotype, occlusion body formation in baculovirus, etc.) caused by the insertion of foreign genes in the vector. For example, if the chimeric polypeptide molecule DNA sequence is inserted within the marker gene sequence of the vector, recombinants containing the insert can be identified by the absence of the marker gene function. In the third approach, recombinant expression vectors can be identified by assaying

the foreign gene product expressed by the recombinant. Such assays can be based, for example, on the physical or functional properties of the chimeric polypeptide molecules.

- 5 Cells of the present invention may transiently or, preferably, constitutively and permanently express the chimeric polypeptide molecules.

The chimeric polypeptide molecules may be purified by any technique
10 which allows for the subsequent formation of a stable, biologically active chimeric polypeptide molecule. 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
15 example, Builder, et al., US Patent 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.

- 20 In one embodiment of the invention, the nucleotide sequence encoding the first component is upstream of the nucleotide sequence encoding the second component. In another embodiment of the invention, the nucleotide sequence encoding the first component is downstream of the nucleotide sequence encoding the second component. Further
25 embodiments of the invention may be prepared in which the order of the

first, second and third fusion polypeptide components are rearranged.

For example, if the nucleotide sequence encoding the first component is designated 1, the nucleotide sequence encoding the second component is designated 2, and the nucleotide sequence of the third component is designated 3, then the order of the components in the isolated nucleic acid of the invention as read from 5' to 3' may be any of the following six combinations: 1,2,3; 1,3,2; 2,1,3; 2,3,1; 3,1,2; or 3,2,1.

The present invention also has diagnostic and therapeutic utilities. In particular embodiments of the invention, methods of detecting aberrancies in the function or expression of the chimeric polypeptide molecules described herein may be used in the diagnosis of disorders. In other embodiments, manipulation of the chimeric polypeptide molecules or agonists or antagonists which bind the chimeric polypeptide molecules may be used in the treatment of diseases. In further embodiments, the chimeric polypeptide molecule is utilized as an agent to block the binding of a binding agent to its target.

By way of example, but not limitation, the method of the invention may be useful in treating clinical conditions that are characterized by 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.

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An amino acid sequence analysis of Flt1(1-3)-Fc revealed the presence of an unusually high number (46) of the basic amino acid residue lysine. An IEF analysis of Flt1(1-3)-Fc showed that this protein has pI greater than 9.3, confirming the prediction that the protein is very basic. It was hypothesized that the basic nature of Flt1(1-3)-Fc protein was causing it to bind to extracellular matrix components and that this interaction might be the cause of the extremely short detectable circulating serum half-life exhibited by Flt1(1-3)-Fc when injected into mice. In order to test this hypothesis, Flt1(1-3)-Fc protein was acetylated at the lysine residues to reduce the basic charge. Acetylated Flt1(1-3)-Fc was then tested in the assays described *infra*.

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The following examples are offered by way of illustration and not by way of limitation.

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EXAMPLES

Example 1: Expression of Flt1(1-3)-Fc protein in CHO K1 cells.

Using standard molecular biology techniques (see e.g., Molecular Cloning, A Laboratory Manual (Sambrook, et al., Cold Spring Harbor

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Laboratory), Current Protocols in Molecular Biology (Eds. Ausubel, et al., Greene Publ. Assoc., Wiley-Interscience, NY), the gene encoding Flt1(1-3)-Fc was inserted into the expression vector pEE14.1 (Lonza Biologics, plc) at a multiple cloning site downstream of the CMV promoter. CHO

5 K1 cells were transfected with the pEE14.1/Flt1(1-3)-Fc DNA construct using lipofectamine (Gaithersburg, MD). The transfected CHO K1 cells were grown in glutamine-free DMEM (JRH, Kansas City, MO) containing 25 μ M methionine sulfoximine (MSX) from Sigma Inc., St. Louis, MO, and high recombinant protein expressors were obtained by

10 screening the CHO K1 cell supernatants from over 100 hand-picked colony isolates using a standard immunoassay which captures and detects human Fc. The selected hand-picked clone was amplified in the presence of 100 μ M MSX followed by a second round of screening of the amplified clones. The highest producing clone had a specific

15 productivity of recombinant Flt1(1-3)-Fc protein of 55 pg/cell/day.

The selected clone was expanded in 225cm² T-flasks (Corning, Acton, MA) and then into 8.5L roller bottles (Corning, Acton, MA) using the cell culture media described *supra*. Cells were removed from the roller

20 bottles by standard trypsinization and put into 3.5L of suspension medium. The suspension medium is comprised of glutamine-free ISCHO medium (Irvine Scientific, Santa Ana, CA) containing 5% fetal bovine serum (FBS from Hyclone Labs, Logan, UT), 100 μ M MSX and GS supplement (JRH Scientific, Kansas City, MO) in a 5L Celligen

25 bioreactor (New Brunswick Scientific, New Brunswick, NJ) at a density

of 0.3×10^6 cells/mL. After the cells reached a density of 3.6×10^6 /mL and were adapted to suspension they were transferred to a 60L bioreactor (ABEC, Allentown, PA) at a density of 0.5×10^6 cells/mL in 20L of ISCHO medium with 5% fetal bovine serum. After two days an additional 20L of ISCHO + 5% fetal bovine serum was added to the bioreactor. The cells were allowed to grow for an additional two days reaching a final density of 3.1×10^6 cells/mL, and a final Flt1(1-3)-Fc concentration at harvest was 95 mg/L. At harvest the cells were removed by tangential flow filtration using 0.45 μ m ProstaK Filters (Millipore, Inc., Bedford, MA).

Example 2: Purification of Flt1(1-3)-Fc protein obtained from CHO K1 cells

Flt1(1-3)-Fc protein was initially purified by affinity chromatography. A Protein A column was used to bind, with high specificity, the Fc portion of the molecule. This affinity-purified protein was then concentrated and passed over a SEC column. The protein was then eluted into the formulation buffer. The following describes these procedures in detail.

Materials and Methods

All chemicals were obtained from J.T. Baker, Phillipsburg, NJ with the exception of PBS; which was obtained as a 10X concentrate from Life

Technologies, Gaithersburg, MD. Protein A Fast Flow and Superdex 200 preparation grade resins were obtained from Pharmacia, Piscataway, NJ. Equipment and membranes for protein concentration were obtained from Millipore, Bedford, MA.

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Approximately 40L of 0.45 μ m-filtered CHO conditioned media containing Flt1(1-3)-Fc protein was applied to a 290mL Protein A Fast Flow column (10cm diameter) that had been equilibrated with PBS. The column was washed with PBS containing 350mM NaCl and 0.02% CHAPS
10 and the bound protein was eluted with 20mM Citric Acid containing 10mM Na₂HPO₄. The single peak in the elution was collected and its pH was raised to neutrality with 1M NaOH. The eluate fractions was concentrated to approximately 9 mg/mL using 10K regenerated
cellulose membranes by both tangential flow filtration and by stirred
15 cell concentration. To remove aggregates and other contaminants, the concentrated protein was applied to a column packed with Superdex 200 preparation grade resin (10cm x 55cm) and run in PBS containing 5 % glycerol. The main peak fractions were pooled, sterile filtered, aliquoted and stored at -80°C.

20

Example 3: Acetylation of Flt1(1-3)-Fc protein.

Two milligrams of Flt1(1-3)-Fc protein were acetylated as described in the instruction manual provided with the sulfo-NHS-acetate
25 modification kit (Pierce Chemical Co., Rockford, IL, Cat.#26777).

Example 4: Characterization of acetylated Flt1(1-3)-Fc protein.

5 **(a.) IEF analysis:** Flt1(1-3)-Fc and acetylated Flt1(1-3)-Fc were analyzed by standard IEF analysis. As shown in Figure 1, Flt1(1-3)-Fc protein is not able to migrate into the gel and therefore must have a pI greater than 9.3, the highest pI in the standard. However, acetylated Flt1(1-3)-Fc is able to migrate into the gel and equilibrate at a pI of
10 approximately 5.2. This result demonstrates that acetylation reduces the net positive charge of the protein and therefore its pI considerably.

(b.) Binding to extracellular matrix components

15 To test for binding to extracellular matrix components, Flt1(1-3)-Fc and acetylated Flt1(1-3)-Fc were tested in an assay designed to mimic the interaction with extracellular matrix components. In this assay, 96-well tissue culture plates are coated with Matrigel (Biocoat MATRIGEL® matrix thin layer 96 well plate, Catalog #40607, Becton
20 Dickinson Labware, Bedford, MA). The plates are incubated with varying concentrations of either Flt1(1-3)-Fc, acetylated Flt1(1-3)-Fc, or rTie2-Fc (an irrelevant control) protein are added to the wells. The plates are incubated for 1-2 hours at either room temperature or 37°C degrees and then detection of bound proteins is accomplished by adding
25 a secondary alkaline phosphatase-conjugated anti-human Fc antibody to

the wells. Finally, alkaline phosphatase substrate is added to the wells and optical density is measured. Figure 2 shows the results of this assay. Like the irrelevant control protein rTie2-Fc, acetylated Flt1(1-3)-Fc does not exhibit any binding to the Matrigel coated plate, whereas the non-acetylated Flt1(1-3)-Fc protein exhibits significant binding. This result indicates that acetylation of basic amino acid residues is an effective way to interfere with the charge interactions that exist between positively charged proteins and the negatively charged extracellular matrix components they are exposed to *in vivo*.

Example 5: Pegylation of Flt1(1-3)-Fc protein.

Although pegylation (polyethylene glycol - PEG) of proteins has been shown to increase their *in vivo* potency by enhancing stability and bioavailability while minimizing immunogenicity (see references cited *supra*), it is counter-intuitive that pegylating molecules that are too large to be filtered by the kidney glomeruli would improve their pharmacokinetic properties. Without being bound by theory, Applicants postulated that pegylation of the Flt1(1-3)-Fc molecules could improve the pharmacokinetic properties, possibly not by altering the positive charge or by decreasing the pI of Flt1(1-3)-Fc, but rather by physically shielding the positive charges from interacting with the extracellular matrix. Applicants decided to attempt to improve the pharmacokinetic properties of Flt1(1-3)-Fc molecules by attaching strands of 20K PEGs as described *infra*.

Materials and Methods

Purified Flt1(1-3)-Fc derived from CHO cells (see *supra*) was used in
5 the following pegylation experiments. Functionalized PEGs were
obtained from Shearwater Polymers, Huntsville, AL; Bicine from Sigma,
St Louis, MO; Superose 6 column from Pharmacia, Piscataway, NJ; PBS
as a 10X concentrate from Life Technologies, Gaithersburg, MD; Glycerol
from J.T. Baker, Phillipsburg, NJ; and Bis-Tris precast gels from Novex,
10 CA.

20K PEG strands functionalized with amine-specific terminal moieties
were used in small-scale reaction studies that were set-up to evaluate
different reaction conditions in which the PEG:protein stoichiometry
15 was varied. Based on these reactions and the analyses of samples on
standard SDS-PAGE, Flt1(1-3)-Fc at a concentration of 1.5 mg/mL was
reacted at pH 8.1 with 20K SPA-PEG (PEG succinimidyl propionate)
molecules at a PEG-to-Flt1(1-3)-Fc monomer molar ratio of 1:6. The
reaction was allowed to proceed at 8°C overnight. For initial
20 purification, the reaction products were applied to a 10mm x 30cm
Superose 6 column equilibrated with PBS containing 5% Glycerol. The
column appeared to separate pegylated Flt1(1-3)-Fc molecules based on
the extent of pegylation. Fractions corresponding to what appeared to
be primarily mono-pegylated and di-pegylated dimeric Flt1(1-3)-Fc, as
25 judged by banding patterns on reducing and non-reducing SDS-PAGE gels

were pooled. The protein concentration was determined by measuring absorbance at 280 nm. The pegylated Flt1(1-3)-Fc protein was sterile filtered, aliquoted and stored at -40°C.

5 **Example 6: Binding of unmodified, acetylated, and pegylated Flt1(1-3)-Fc in a Biacore-based assay.**

Unmodified, acetylated, and pegylated Flt1(1-3)-Fc proteins were tested in a Biacore-based assay to evaluate their ability to bind to the
10 Flt1 ligand, VEGF. In this assay, unmodified Flt1(1-3)-Fc protein was immobilized on the surface of a Biacore chip (see Biacore Instruction Manual, Pharmacia, Inc., Piscataway, NJ, for standard procedures) and a sample containing 0.2 µg/ml VEGF and either unmodified Flt1(1-3)-Fc, acetylated Flt1(1-3)-Fc or pegylated Flt1(1-3)-Fc (each at 25 µg/ml)
15 was passed over the Flt1(1-3)-Fc-coated chip. To minimize the effects of non-specific binding, the bound samples were washed with a 0.5M NaCl wash. In one sample, unmodified Flt1(1-3)-Fc was mixed with heparin. Heparin is a negatively charged molecule and the Flt1(1-3)-Fc protein is a positively charged molecule, so when the two molecules
20 are mixed together, they should interact through their respective charges. This essentially neutralizes Flt1(1-3)-Fc's inherent positive charge making the molecule behave as if it has been chemically or genetically modified so as to reduce its charge and its tendency to bind via charge interactions. As shown in Figure 3, acetylated (columns 13-
25 16), pegylated (columns 17-20), and heparin-treated Flt1(1-3)-Fc

(columns 21-24) are each able to completely compete with the Biacore chip-bound Flt1(1-3)-Fc for VEGF binding as compared to control (columns 1-4) and irrelevant protein (columns 5-8). Unmodified Flt1(1-3)-Fc (columns 5-6) appeared to only partially compete with Biacore chip-bound Flt1(1-3)-Fc for VEGF binding. However, washing the bound samples with 0.5M NaCl (columns 7-8) resulted in a binding profile similar to the modified forms of Flt1(1-3)-Fc, indicating that the unmodified protein was exhibiting non-specific binding to the chip that could be eliminated by the salt wash.

10

Example 7: Binding of unmodified, acetylated, and pegylated Flt1(1-3)-Fc in an ELISA-based assay.

Unmodified, acetylated, and pegylated Flt1(1-3)-Fc proteins were tested in a standard ELISA-based assay to evaluate their ability to bind the Flt1 receptor ligand VEGF. As shown in Figure 4, both pegylated and acetylated Flt1(1-3)-Fc proteins are capable of binding to VEGF, demonstrating that modifying the protein either by pegylation or acetylation does not destroy its ability to bind its ligand.

20

Example 8: Pharmacokinetic analysis of unmodified Flt1(1-3)-Fc, acetylated Flt1(1-3)-Fc, and pegylated Flt1(1-3)-Fc.

In vivo experiments were designed to assess the pharmacokinetic profiles of unmodified Flt1(1-3)-Fc, acetylated Flt1(1-3)-Fc, and

25

pegylated Flt1(1-3)-Fc protein. Balb/c mice (23-28g; 3 mice/group) were injected subcutaneously with 4mg/kg of unmodified, acetylated, or pegylated Flt1(1-3)-Fc. The mice were tail bled at 1, 2, 4, 6, 24 hours, 2 days, and 3 days after injection of protein. The sera were
5 assayed in a standard ELISA-based assay designed to detect Flt1(1-3)-Fc protein. Briefly, the assay involves coating an ELISA plate with VEGF, binding the unmodified, acetylated, or pegylated Flt1(1-3)-Fc-containing sera, and reporting with an anti-Fc antibody linked to alkaline phosphatase. As shown in Figure 5, the T_{max} for all of the
10 Flt1(1-3)-Fc proteins was between the 6 hour and 24 hour time points. The C_{max} for the different proteins was as follows: Unmodified: 0.06 µg/ml - 0.15 µg/ml; acetylated: 1.5 µg/ml - 4.0 µg/ml; and pegylated: approximately 5 µg/ml.

15 **Example 9: Step-acetylation of Flt1(1-3)-Fc**

To determine what minimal amount of acetylation is necessary to eliminate binding to extracellular matrix components, an experiment was designed that acetylated the Flt1(1-3)-Fc protein in a step-wise
20 fashion by using increasing amounts of molar excess of acetylation reagent in the acetylation reaction mixture. The range of molar excess was as follows: 0, 10, 20, 30, 40, 50, 60, 70, 80, 90, and 100 moles of acetylation reagent per 1 mole of Flt1(1-3)-Fc monomer. The reactions were performed as detailed in the instruction manual provided with the

sulfo-NHS-Acetate modification kit (Pierce Chemical Co., Rockford, IL, Cat.# 26777).

Example 10: Characterization of step-acetylated Flt1(1-3)-

5 **Fc.**

(a.) IEF analysis Unmodified Flt1(1-3)-Fc and step-acetylated Flt1(1-3)-Fc proteins were analyzed by standard IEF analysis. As shown in Figure 6A-6B, unmodified Flt1(1-3)-Fc protein was not able
10 to migrate into the gel due to its extremely high pI (greater than 9.3). However, most of the step-acetylated Flt1(1-3)-Fc samples (30-100 fold molar excess samples) were able to migrate into the gel and equilibrate at pIs ranging between 4.55 - 8.43, depending on the degree of acetylation of the protein. This result demonstrates that
15 acetylation can change the positive charge of the protein in a dose-dependent manner and that reduction of the pI can be controlled by controlling the degree of acetylation.

20 **(b.) Binding of step-acetylated Flt1(1-3)-Fc to extracellular matrix components**

To test for binding to extracellular matrix components, Flt1(1-3)-Fc and step-acetylated Flt1(1-3)-Fc were tested in the above-described assay designed to mimic the interaction with extracellular matrix
25 components. Varying concentrations of either unmodified Flt1(1-3)-Fc,

step-acetylated Flt1(1-3)-Fc (10, 20, and 30 fold molar excess samples), or rTie2-Fc (an irrelevant control) protein were added to the wells. The plates were incubated for 1-2 hours at room temperature or 37°C and then detection of bound proteins was accomplished by adding a secondary alkaline phosphatase-conjugated anti-human Fc antibody to the wells. Alkaline phosphatase substrate was subsequently added to the wells and optical density measured. Figure 7 shows the results of this assay. Like the irrelevant control protein rTie2-Fc, step-acetylated Flt1(1-3)-Fc (20 and 30 fold molar excess samples) did not exhibit any significant binding to the Matrigel coated plate, whereas the non-acetylated Flt1(1-3)-Fc protein exhibited significant binding. The binding is saturable, indicating that the Flt1(1-3)-Fc protein may be binding to specific sites, rather than a more general charge-mediated interaction that might not be saturable. The 10 fold molar excess sample showed reduced binding, but the degree of acetylation was not enough to completely block binding to extracellular matrix components. The 20 fold molar excess and higher samples displayed no detectable binding, despite the fact that by IEF analysis (Figure 6A and 6B) the lower molar excess samples still had a large net positive charge. This result demonstrates that it is not necessary to completely acetylate all available basic amino acids in order to eliminate binding to extracellular matrix components.

(c.) Binding of step-acetylated Flt1(1-3)-Fc in a Biacore-based assay.

Unmodified and step-acetylated Flt1(1-3)-Fc proteins were tested in a Biacore-based assay to evaluate their ability to bind to the Flt1 ligand, VEGF. In this assay, unmodified Flt1(1-3)-Fc protein (0.5, 1.0, or 5.0 $\mu\text{g/ml}$) was immobilized on the surface of a Biacore chip (see Biacore Instruction Manual, Pharmacia, Inc., Piscataway, NJ, for standard procedures) and a solution containing 0.2 $\mu\text{g/ml}$ VEGF and either unmodified Flt1(1-3)-Fc (at either 0.5, 1.0, or 5.0 $\mu\text{g/ml}$) or different step-acetylated Flt1(1-3)-Fc samples (at 0.5, 1.0, or 5.0 $\mu\text{g/ml}$ each) were passed over the Flt1(1-3)-Fc-coated chip. As shown in Figure 8, at a sub-stoichiometric ratio (0.5 $\mu\text{g/ml}$ of either unmodified Flt1(1-3) or step-acetylated Flt1(1-3)-Fc vs. 0.2 $\mu\text{g/ml}$ VEGF), there is not enough Flt1(1-3)-Fc (either unmodified or step-acetylated) in the solution to completely bind the VEGF. At 1.0 $\mu\text{g/ml}$, which approximates a 1:1 stoichiometric ratio, both unmodified and step-acetylated Flt1(1-3)-Fc are better able to compete for VEGF binding, but there is still insufficient Flt1(1-3)-Fc protein (either unmodified or step-acetylated) to completely bind the available VEGF. However, at 5.0 $\mu\text{g/ml}$, which is several times greater than a 1:1 stoichiometric ratio, both the Flt1(1-3)-Fc and the step-acetylated Flt1(1-3)-Fc proteins are able to bind the VEGF, regardless of the degree of acetylation. This clearly demonstrates that acetylation does not alter Flt1(1-3)-Fc's ability to bind VEGF.

(d.) Pharmacokinetic analysis of step-acetylated Flt1(1-3)-Fc

In vivo experiments were designed to assess the pharmacokinetic profiles of unmodified Flt1(1-3)-Fc and step-acetylated Flt1(1-3)-Fc protein. Balb/c mice (23-28g) were injected subcutaneously with 4mg/kg of unmodified or 10, 20, 40, 60 and 100 fold molar excess samples of step-acetylated Flt1(1-3)-Fc (3 mice for unmodified, 10, 20 and 40 fold molar excess samples and 2 mice for 60 and 100 fold molar excess samples). The mice were tail bled at 1, 2, 4, 6, 24 hours, 2 days and 3 days after injection. The sera were assayed in an ELISA-based assay designed to detect Flt1(1-3)-Fc (described *supra*). Figure 9 details the results of this study. The T_{max} for all of the Flt1(1-3)-Fc proteins tested was at the 6 hour time point but the C_{max} was as follows: Unmodified Flt1(1-3)-Fc: 0.06µg/ml; 10 fold molar excess sample: - 0.7µg/ml, 20 fold molar excess sample - 2µg/ml, 40 fold molar excess sample - 4µg/ml, 60 fold molar excess sample - 2µg/ml, 100 fold molar excess sample - 1µg/ml. This results demonstrates that acetylation or pegylation of Flt1(1-3)-Fc significantly improves its pharmacokinetic profile.

Example 11: Construction of Flt1(1-3)-Fc basic region deletion mutant designated Mut1: Flt1(1-3)_{ΔB})-Fc.

Based on the observation that acetylated Flt1(1-3)-Fc, which has a pI

below 6, has much better pharmacokinetics than the highly positive unmodified Flt1(1-3)-Fc (pI > 9.3), it was asked whether the difference in pharmacokinetics could be attributed to the net charge of the protein, which made it stick to negatively charged extracellular matrix components, or whether there were perhaps specific locations on the surface of the Flt1(1-3)-Fc protein that constituted specific binding sites for extracellular matrix components. For example, many proteins are known to have heparin binding sites, often consisting of a cluster of basic residues. Sometimes these residues are found in a cluster on the primary sequence of the protein; some of the literature has identified "consensus sequences" for such heparin binding sites (see for example Hileman, et al., 1998, Bioessays 20(2):156-67). In other cases, the known crystal structure of a protein reveals a cluster of positively charged residues on the surface of a protein, but the residues come from different regions of the primary sequence and are only brought together when the protein folds into its tertiary structure. Thus it is difficult to deduce whether an isolated amino acid residue forms part of a cluster of basic residues on the surface of the protein. However, if there is a cluster of positively charged amino acid residues in the primary sequence, it is not unreasonable to surmise that the residues are spatially close to one another and might therefore be part of an extracellular matrix component binding site. Flt1 receptor has been studied extensively and various domains have been described (see for example Tanaka et al., 1997, Jpn. J. Cancer Res 88:867-876). Referring to the nucleic acid and amino acid sequence set forth in Figure 10A-10D

of this application, one can identify the signal sequence for secretion which is located at the beginning of the sequence and extends to the glycine coded for by nucleotides 76-78. The mature protein begins with Ser-Lys-Leu-Lys, starting at nucleotide 79 of the nucleic acid
5 sequence. Flt1 Ig domain 1 extends from nucleotide 79 to 393, ending with the amino acids Ser-Asp-Thr. Flt1 Ig domain 2 extends from nucleotide 394 to 687 (encoding Gly-Arg-Pro to Asn-Thr-Ile), and Flt1 Ig domain 3 extends from nucleotides 688 to 996 (encoding Ile-Asp-Val to Asp-Lys-Ala). There is a bridging amino acid sequence, Gly-Pro-Gly,
10 encoded by nucleotides 997-1005, followed by the nucleotide sequence encoding human Fc (nucleotides 1006-1701 or amino acids Glu-Pro-Lys to Pro-Gly-Lys-stop).

A more detailed analysis of the Flt1 amino acid sequence reveals that
15 there is a cluster, namely, amino acid residues 272-281 (KNKRASVRR) of Figure 10A-10D, in which 6 out of 10 amino acid residues are basic. This sequence is located in Flt1 Ig domain 3 of the receptor (see Figure 11), which is not itself essential for binding of VEGF ligand, but which confers a higher affinity binding to ligand. An alignment of the
20 sequence of Ig domain 3 with that of Ig domain 2 reveals that in this region, there is very poor alignment between the two Ig domains, and that there are about 10 additional amino acids in Ig domain 3. An analysis of the hydrophilicity profiles (MacVector computer software) of these two domains clearly indicates the presence of a hydrophilic
25 region in the protein (Figure 12A-12B). These observations raised the

possibility that the actual three dimensional conformation of Flt1 Ig domain 3 allowed for some type of protrusion that is not in Flt1 Ig domain 2. To test this hypothesis, the 10 additional amino acids were deleted and the resulting protein was tested to see whether the deletion would affect the pharmacokinetics favorably without seriously compromising the affinity of the receptor for VEGF. This DNA construct, which was constructed using standard molecular biology techniques (see e.g., Molecular Cloning, A Laboratory Manual (Sambrook, et al., Cold Spring Harbor Laboratory), Current Protocols in Molecular Biology (Eds. Ausubel, et al., Greene Publ. Assoc., Wiley-Interscience, NY) in the mammalian expression vector pMT21 (Genetics Institute, Inc., Cambridge, MA), is referred to as Mut1: Flt1(1-3_{ΔB})-Fc. The Mut1: Flt1(1-3_{ΔB})-Fc construct was derived from Flt1(1-3)-Fc by deletion of nucleotides 814-843 (set forth in Figure 10A-10D), which deletes the highly basic 10-amino acid residue sequence Lys-Asn-Lys-Arg-Ala-Ser-Val-Arg-Arg-Arg from Flt1 Ig domain 3.

The final DNA construct was sequence-verified using an ABI 373A DNA sequencer and Taq Dideoxy Terminator Cycle Sequencing Kit (Applied Biosystems, Inc., Foster City, CA). The sequence of Mut1: Flt1(1-3_{ΔB})-Fc is set forth in Figure 13A-13D.

Example 12: Construction of Flt1(1-3)-Fc basic region deletion mutant designated Mut2: Flt1(2-3_{ΔB})-Fc.

A second deletion mutant construct, designated Mut2: Flt1(2-3_{ΔB})-Fc, was derived from the Mut1: Flt1(1-3_{ΔB})-Fc construct by deletion of Flt1 Ig domain 1 encoded by nucleotides 79-393 (see Figure 10A-10D); for convenience, nucleotides 73-78 (TCA GGT) were changed to TCC GGA. This introduced a restriction site (BspE1) without altering the associated amino acid sequence, Ser-Gly. This DNA construct, which was constructed using standard molecular biology techniques (see e.g., Molecular Cloning, A Laboratory Manual (Sambrook, et al., Cold Spring Harbor Laboratory), Current Protocols in Molecular Biology (Eds. Ausubel, et al., Greene Publ. Assoc., Wiley-Interscience, NY) in the mammalian expression vector pMT21 (Genetics Institute, Inc., Cambridge, MA), was also sequence-verified using an ABI 373A DNA sequencer and Taq Dideoxy Terminator Cycle Sequencing Kit (Applied Biosystems, Inc., Foster City, CA). The sequence of Mut2: Flt1(2-3_{ΔB})-Fc is set forth in Figure 14A-14C.

Example 13: Construction of Flt1(1-3)-Fc deletion mutant designated Mut3: Flt1(2-3)-Fc.

A third deletion mutant construct, designated Mut3: Flt1(2-3)-Fc, was constructed the same way as the Mut2: Flt1(2-3_{ΔB})-Fc construct, except that Flt1 Ig domain 3 was left intact (the basic region amino

acids were not deleted). The construct was constructed using standard molecular biology techniques and the final construct was sequence-verified as described *supra*. The sequence of Mut3: Flt1(2-3)-Fc is set forth in Figure 15A-15C.

5

Example 14: Construction of Flt(1-3)-Fc basic region N-glycosylation mutant designated Mut4: Flt1(1-3_{R->N})-Fc.

A final construct was made in which a N-glycosylation site was introduced into the middle of the basic region of Flt1 Ig domain 3. This construct was designated Mut4: Flt1(1-3_{R->N})-Fc and was made by changing nucleotides 824-825 from GA to AC, consequently changing the coded Arg residue (AGA) into an Asn residue (AAC) (see Figure 10A-10D). The resulting amino acid sequence is therefore changed from Arg-Ala-Ser to Asn-Ala-Ser, which matches the canonical signal (Asn-Xxx-Ser/Thr) for the addition of a N-glycosylation site at the Asn residue. The sequence of Mut4: Flt1(1-3_{R->N})-Fc is set forth in Figure 16A-16D.

Example 15: Characterization of acetylated Flt1(1-3)-Fc, Mut1: Flt1(1-3_{ΔB})-Fc, and Mut4: Flt1(1-3_{R->N})-Fc mutants.

(a.) Binding to extracellular matrix components

To determine whether the three modified proteins were more or less

likely to have improved pharmacokinetic properties, Matrigel coated 96-well dishes (as described *supra*) were incubated with varying concentrations of the mutant proteins and detected with anti-human Fc/alkaline-phosphatase conjugated antibodies. As shown in Figure 18, this experiment showed that while the unmodified Flt1(1-3)-Fc protein could bind avidly to these wells, the Mut3: Flt1(2-3)-Fc protein bound somewhat more weakly, the Mut1: Flt1(1-3_{ΔB})-Fc protein bound more weakly still, and the Mut2: Flt1(2-3_{ΔB})-Fc protein showed the best profile, binding more weakly than any of the other mutant proteins. The Mut4: Flt1(1-3_{R->N})-Fc glycosylation mutant protein showed only marginal benefit on the Matrigel assay. These results confirm the hypothesis that a linear sequence of positive amino acids can be deleted from the primary sequence resulting in a decrease in charge interaction with extracellular matrix components.

15

(b.) Binding of Mut1: Flt1(1-3_{ΔB})-Fc and Mut4: Flt1(1-3_{R->N})-Fc in a Biacore-based assay.

Unmodified and acetylated Flt1(1-3)-Fc and genetically modified Mut1: Flt1(1-3_{ΔB})-Fc and Mut4: Flt1(1-3_{R->N})-Fc proteins were tested in a Biacore-based assay to evaluate their ability to bind to the Flt1 ligand, VEGF. In this assay, unmodified Flt1(1-3)-Fc protein (0.25, 0.5, or 1.0 μg/ml) was immobilized on the surface of a Biacore chip (see Biacore Instruction Manual, Pharmacia, Inc., Piscataway, NJ, for standard procedures) and a solution containing 0.1 μg/ml VEGF and either

25

purified or COS cell supernatant containing unmodified Flt1(1-3)-Fc (at approximately (0.25, 0.5, or 1.0 $\mu\text{g/ml}$), purified acetylated Flt1(1-3)-Fc (at (0.25, 0.5, or 1.0 $\mu\text{g/ml}$), COS cell supernatant containing Mut1: Flt1(1-3 $_{\Delta\text{B}}$)-Fc (at approximately (0.25, 0.5, or 1.0 $\mu\text{g/ml}$), or COS cell
5 supernatant containing Mut4: Flt1(1-3 $_{\text{R} \rightarrow \text{N}}$)-Fc (at approximately (0.25, 0.5, or 1.0 $\mu\text{g/ml}$) were passed over the Flt1(1-3)-Fc-coated chip. As shown in Figure 17, at the sub-stoichiometric ratio (0.25 $\mu\text{g/ml}$ Flt1(1-3)-Fc of unmodified, acetylated or genetically modified samples vs. 01. $\mu\text{g/ml}$ VEGF), there is insufficient Flt1(1-3)-Fc protein to block
10 binding of VEGF to the Flt1(1-3)-Fc immobilized on the Biacore chip. At 0.5 $\mu\text{g/ml}$ of unmodified, acetylated or genetically modified Flt1(1-3)-Fc proteins, the stoichiometric ratio approximates 1:1 and there is an increased ability to block VEGF binding to the Biacore chip. At 1.0 $\mu\text{g/ml}$ of unmodified, acetylated or genetically modified Flt1(1-3)-Fc
15 proteins, which is approximately a 10:1 stoichiometric ratio, the Flt1(1-3)-Fc proteins are able to block binding of VEGF to the Biacore chip, but they are not equivalent. Unmodified, acetylated, and Mut1: Flt1(1-3 $_{\Delta\text{B}}$)-Fc are essentially equal in their ability to block VEGF binding, whereas Mut4: Flt1(1-3 $_{\text{R} \rightarrow \text{N}}$)-Fc is somewhat less efficient at
20 blocking binding. These results confirm the hypothesis that it is possible to reduce the non-specific binding of a positively charged molecule by genetically removing a linear sequence of predominantly negatively charged amino acids.

(c.) Binding of Mut1: Flt1(1-3_{ΔB})-Fc, Mut2: Flt1(2-3_{ΔB})-Fc, Mut3: Flt1(2-3)-Fc, and in an ELISA-based assay.

To determine whether the three mutant proteins could bind the Flt1
5 ligand VEGF, binding experiments were done in which 96-well plates
coated with VEGF were incubated with varying concentrations of the
respective mutant protein, and after washing, the amount bound was
detected by incubating with an alkaline phosphatase conjugated anti-
human Fc antibody and quantitated colorimetrically by the addition of
10 an appropriate alkaline phosphatase substrate. As shown in Figure 19,
this experiment showed that all the mutant proteins could bind VEGF
similarly, at the concentrations tested.

**Example 16: Pharmacokinetic analysis of acetylated Flt1(1-
15 3)-Fc, Mut1: Flt1(1-3_{ΔB})-Fc, and unmodified Flt1(1-3)-Fc.**

In vivo experiments were designed to assess the pharmacokinetic
profiles of unmodified Flt1(1-3)-Fc, Mut1: Flt1(1-3_{ΔB})-Fc, and 40 fold
molar excess acetylated Flt1(1-3)-Fc protein. Balb/c mice (25-30g)
20 were injected subcutaneously with 4mg/kg of unmodified Flt1(1-3)-Fc,
40 fold molar excess acetylated Flt1(1-3)-Fc, and Mut1: Flt1(1-3_{ΔB})-Fc
proteins (4 mice each). These mice were tail bled at 1, 2, 4, 6, 24
hours, 2 days, 3 days, and 5 days after injection. The sera were
assayed in an ELISA designed to detect Flt1(1-3)-Fc protein which
25 involves coating an ELISA plate with VEGF, binding the Flt1(1-3)-Fc and

reporting with an anti-Fc antibody linked to alkaline phosphatase. As shown in Figure 20, the C_{max} for these reagents was as follows:

Unmodified Flt1(1-3)-Fc - 0.15 μ g/ml; 40 fold molar excess acetylated Flt1(1-3)-Fc - 1.5 μ g/ml; and Mut1: Flt1(1-3 _{Δ B})-Fc - 0.7 μ g/ml.

5

Example 17: Modified Flt1 receptor vector construction

The rationale for constructing modified versions of the Flt1 receptor (also known as VEGFR1) was based on the observation that the protein sequence of Flt1 was highly basic, and was therefore likely to stick to extracellular matrix (ECM). The highly basic nature of Flt1 probably explains why unmodified Flt1(1-3)-Fc (described *supra*) has poor pharmacokinetics that make it difficult to use as a therapeutic agent. As described *supra*, the chemically modified form of 40 fold molar excess acetylated Flt1(1-3)-Fc, hereinafter termed A40, exhibited a greatly improved pharmacokinetic (PK) profile over the non-acetylated Flt1(1-3)-Fc. Therefore, attempts were made to engineer DNA molecules that could be used to recombinantly express modified forms of a Flt1 receptor molecule that would possess the improved PK profile exhibited by A40 and still maintain the ability to bind tightly to VEGF.

It is known in the literature that the first Ig domain of Flt1 (which has a net charge of +5 at neutral pH) is not essential for tight binding to VEGF, so this domain was deleted. The third Ig domain (having a net charge of +11) is not essential for binding, but confers higher affinity

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for VEGF than the second Ig domain, so instead of deleting it entirely, it was replaced with the equivalent domains of the Flt1 receptor relatives Flk1 (also known as VEGFR2) and Flt4 (also known as VEGFR3). These chimeric molecules (denoted R1R2 (Flt1.D2.FlklD3.FcΔC1(a) and
5 VEGFR1R2-FcΔC1(a) and R1R3 (Flt1D2.VEGFR3D3-FcΔC1(a) and VEGFR1R3-FcΔC1(a) respectively, wherein R1 and Flt1D2 = Ig domain 2 of Flt1 (VEGFR1); R2 and FlklD3 = Ig domain 3 of Flk1 (VEGFR2); and R3 and VEGFR3D3 = Ig domain 3 of Flt4 (VEGFR3)) were much less sticky to ECM, as judged by an *in vitro* ECM binding assay as described *infra*, had
10 greatly improved PK as described *infra*. In addition, these molecules were able to bind VEGF tightly as described *infra* and block phosphorylation of the native Flk1 receptor expressed in endothelial cells as described *infra*.

15 **(a) Construction of the expression plasmid**

pFlt1D2.FlklD3.FcΔC1(a)

Expression plasmids pMT21.Flt1(1-3).Fc (6519bp) and pMT21.Flkl-1(1-3).Fc (5230bp) are plasmids that encode ampicillin resistance and Fc-
20 tagged versions of Ig domains 1-3 of human Flt1 and human Flkl, respectively. These plasmids were used to construct a DNA fragment consisting of a fusion of Ig domain 2 of Flt1 with Ig domain 3 of Flkl, using PCR amplification of the respective Ig domains followed by further rounds of PCR to achieve fusion of the two domains into a

single fragment. For Ig domain 2 of Flt1, the 5' and 3' amplification primers were as follows:

5': bsp/flt1D2 (5'-GACTAGCAGTCCGGAGGTAGACCTTTCGTAGAGATG-3')

5

3': Flt1D2-Flk1D3.as (5'-CGGACTCAGAACCACATCTATGATTGTATTGGT-3')

The 5' amplification primer encodes a BspE1 restriction enzyme site upstream of Ig domain 2 of Flt1, defined by the amino acid sequence
 10 GRPFVEM (corresponding to amino acids 27-33 of Figure 21A-21C). The
 3' primer encodes the reverse complement of the 3' end of Flt1 Ig
 domain 2 fused directly to the 5' beginning of Flk1 Ig domain 3, with
 the fusion point defined as TIID of Flt1 (corresponding to amino acids
 123-126 of Figure 21A-21C) and continuing into VVLS (corresponding
 15 to amino acids 127-130 of Figure 21A-21C) of Flk1.

For Ig domain 3 of Flk1, the 5' and 3' amplification primers were as follows:

20 5': Flt1D2-Flk1D3.s (5'-ACAATCATAGATGTGGTTCTGAGTCCGTCTCATG
 G-3')

3': Flk1D3/apa/srf.as (5'-GATAATGCCCGGGCCCTTTTCATGGACCCTGAC
 AAATG-3')

25

The 5' amplification primer encodes the end of Flt1 Ig domain 2 fused directly to the beginning of Flk1 Ig domain 3, as described above. The 3' amplification primer encodes the end of Flk1 Ig domain 3, defined by the amino acids VRVHEK (corresponding to amino acids 223-228 of Figure 21A-21C), followed by a bridging sequence that includes a recognition sequence for the restriction enzyme Srf1, and encodes the amino acids GPG. The bridging sequence corresponds to amino acids 229-231 of Figure 21A-21C.

After a round of PCR amplification to produce the individual domains, the products were combined in a tube and subjected to a further round of PCR with the primers bsp/flt1D2 and Flk1D3/apa/srf.as (described *supra*) to produce the fusion product. This PCR product was subsequently digested with the restriction enzymes BspEI and SmaI and the resulting 614bp fragment was subcloned into the BspEI to SrfI restriction sites of the vector pMT21/ Δ B2.Fc, to create the plasmid pMT21/Flt1D2.FlklD3.Fc. The nucleotide sequence of the Flt1D2-FlklD3 gene fusion insert was verified by standard sequence analysis. This plasmid was then digested with the restriction enzymes EcoRI and SrfI and the resulting 702bp fragment was transferred into the EcoRI to SrfI restriction sites of the plasmid pFlt1(1-3)B2-Fc Δ C1(a) to produce the plasmid pFlt1D2.FlklD3.Fc Δ C1(a). The complete DNA and deduced amino acid sequences of the Flt1D2.FlklD3.Fc Δ C1(a) chimeric molecule is set forth in Figure 21A-21C.

(b) Construction of the expression plasmid**pFlt1D2VEGFR3D3Fc Δ C1(a)**

The expression plasmid pMT21.Flt1(1-3).Fc (6519bp) encodes ampicillin
 5 resistance and an Fc-tagged version of Ig domains 1-3 of human Flt1
 receptor. This plasmid was used to produce a DNA fragment containing
 Ig domain 2 of Flt1 by PCR. RNA from the cell line HEL921.7 was used
 to produce Ig domain 3 of Flk1, using standard RT-PCR methodology. A
 further round of PCR amplification was used to achieve fusion of the
 10 two Ig domains into a single fused fragment. For Ig domain 2 of Flt1,
 the 5' and 3' amplification primers were as follows:

5': bsp/flt1D2 (5'-GACTAGCAGTCCGGAGGTAGACCTTTCGTAGAGATG-3')

15 3': Flt1D2.VEGFR3D3.as(TTCCTGGGCAACAGCTGGATATCTATGATTGTA
 TTGGT)

The 5' amplification primer encodes a BspE1 restriction site upstream
 of Ig domain 2 of Flt1, defined by the amino acid sequence GRPFVEM
 20 (corresponding to amino acids 27-33 of Figure 22A-22C). The 3'
 amplification primer encodes the reverse complement of the end of Flt1
 Ig domain 2 fused directly to the beginning of VEGFR3 Ig domain 3, with
 the fusion point defined as TIID of Flt1 (corresponding to amino acids
 123-126 of Figure 22A-22C) and continuing into IQLL of VEGFR3
 25 (corresponding to amino acids 127-130 of Figure 22A-22C).

For Ig domain 3 of VEGFR3, the 5' and 3' primers used for RT-PCR were as follows:

5 5': R3D3.s (ATCCAGCTGTTGCCCAGGAAGTCGCTGGAGCTGCTGGTA)

3': R3D3.as (ATTTTCATGCACAATGACCTCGGTGCTCTCCCGAAATCG)

Both the 5' and 3' amplification primers match the sequence of VEGFR3.

10 The 296bp amplification product of this RT-PCR reaction was isolated by standard techniques and subjected to a second round of PCR to add suitable sequences to allow for fusion of the Flt1D2 with the Flk1D3 domains and fusion of the Flk1D3 and Fc domains via a GPG bridge (see below). The amplification primers were as follows:

15

5':Flt1D2.VEGFR3D3.s

(TCATAGATATCCAGCTGTTGCCCAGGAAGTCGCTGGAG)

3': VEGFR3D3/srf.as

20 (GATAATGCCCGGGCCATTTTCATGCACAATGACCTCGGT)

The 5' amplification primer encodes the 3' end of Flt1 Ig domain 2 fused directly to the beginning (5' end) of VEGFR3 Ig domain 3, as described above. The 3' amplification primer encodes the 3' end of

25 VEGFR3 Ig domain 3, defined by the amino acids VIVHEN (corresponding

to amino acids 221-226 of Figure 22A-22C), followed by a bridging sequence that includes a recognition sequence for Srf1, and encodes the amino acids GPG. The bridging sequence corresponds to amino acids 227-229 of Figure 22A-22C.

5

After one round (for Flt1 Ig domain 2) or two rounds (for Flt4 Ig domain 3) of PCR to produce the individual Ig domains, the PCR products were combined in a tube and subjected to a further round of PCR amplification with the amplification primers bsp/flt1D2 and VEGFR3D3/srf.as described *supra*, to produce the fusion product. This PCR product was subsequently digested with the restriction enzymes BspEI and SmaI and the resulting 625bp fragment was subcloned into the BspEI to SrfI restriction sites of the vector pMT21/Flt1ΔB2.Fc (described *supra*), to create the plasmid pMT21/Flt1D2.VEGFR3D3.Fc.

15 The sequence of the Flt1D2-VEGFR3D3 gene fusion insert was verified by standard sequence analysis. This plasmid was then digested with the restriction enzymes EcoRI and SrfI and the resulting 693bp fragment was subcloned into the EcoRI to SrfI restriction sites of the plasmid pFlt1(1-3)ΔB2-FcΔC1(a) to produce the plasmid designated

20 pFlt1D2.VEGFR3D3.FcΔC1(a). The complete DNA deduced amino acid sequence of the Flt1D2.VEGFR3D3.FcΔC1(a) chimeric molecule is set forth in Figure 22A-22C.

Example 18: Extracellular Matrix Binding (ECM) Binding Assay

ECM-coated plates (Becton Dickinson catalog # 35-4607) were rehydrated with warm DME supplemented with glutamine (2mM), 100U penicillin, 100U streptomycin, and 10% BCS for at least 1 hr. before adding samples. The plates were then incubated for 1 hr. at room temperature with varying concentrations of Flt1D2.FlklD3.FcΔC1(a) and Flt1D2.VEGFR3D3.FcΔC1(a) starting at 10nM with subsequent 2-fold dilutions in PBS plus 10% BCS. The plates were then washed 3 times with PBS plus 0.1% Triton-X and incubated with alkaline phosphatase-conjugated anti-human Fc antibody (Promega, 1:4000 in PBS plus 10% BCS) for 1 hr. at room temperature. The plates were then washed 4 times with PBS 0.1% Triton-X and alkaline phosphatase buffer/pNPP solution (Sigma) was added for color development. Plates were read at $\lambda = 405-570\text{nm}$. The results of this experiment are shown in Figure 23 and demonstrate that the Flt1D2.FlklD3.FcΔC1(a) and Flt1D2.VEGFR3D3.FcΔC1(a) proteins are considerably less sticky to the ECM as compared to the Flt1(1-3)-Fc protein.

Example 19: Transient expression of pFlt1D2.FlklD3.FcΔC1(a) in CHO-K1 (E1A) cells

A large scale (2L) culture of E. coli DH10B cells carrying the pFlt1D2.FlklD3.FcΔC1(a) plasmid described *supra* in Example 17(a) was grown overnight in Terrific Broth (TB) plus 100μg/ml ampicillin. The

next day, the plasmid DNA was extracted using a QIAgen Endofree Megaprep kit following the manufacturer's protocol. The concentration of the purified plasmid DNA was determined by standard techniques using a UV spectrophotometer and fluorometer. The plasmid DNA was
5 verified by standard restriction enzyme digestion of aliquots using the restriction enzymes EcoRI plus NotI and AseI. All restriction enzyme digest fragments corresponded to the predicted sizes when analyzed on a 1% agarose gel.

10 Forty 15 cm petri plates were seeded with CHO-K1/E1A cells at a density of 4×10^6 cells/plate. Plating media was Gibco Ham's F-12 supplemented with 10% Hyclone Fetal Bovine Serum (FBS), 100U penicillin/100U streptomycin and glutamine (2mM). The following day each plate of cells was transfected with 6 μ g of the
15 pFlt1D2.Flk1D3.Fc Δ C1(a) plasmid DNA using Gibco Optimem and Gibco Lipofectamine in 12 ml volume, following the manufacturer's protocol. Four hours after adding the transfection mix to the cells, 12 ml/plate of Optimem supplemented with 10% FBS was added. Plates were incubated at 37°C in a 5% CO₂ incubator overnight. The following day
20 the media was removed from each plate and 25 ml expression media (Gibco CHO-S-SFM II supplemented with glutamine (2mM) and 1mM sodium butyrate) was added. The plates were incubated at 37°C for 3 days. After 3 days of incubation, the media was aspirated from each plate and centrifuged at 400 rpm in a swinging bucket rotor to pellet

cells. The supernatant was decanted into sterile 1L bottles and purification of the expressed protein was performed as described *infra*.

Example 20: Construction pVEGFR1R2-Fc Δ C1(a) expression

5 **vector**

The pVEGFR1R2.Fc Δ C1(a) expression plasmid was constructed by insertion of DNA encoding amino acids SDT (corresponding to amino acids 27-29 of Figure 24A-24C) between Flt1d2-Flk1d3-Fc Δ C1(a) amino acids 26 and 27 of Figure 21A-21C (GG) and removal of DNA encoding amino acids GPG corresponding to amino acids 229-231 of Figure. The SDT amino acid sequence is native to the Flt1 receptor and was added back in to decrease the likelihood of heterogeneous N-terminal processing. The GPG (bridging sequence) was removed so that the Flt1 and Flk1 Ig domains were fused directly to one another. The complete DNA and deduced amino acid sequences of the pVEGFR1R2.Fc Δ C1(a) chimeric molecule is set forth in Figure 24A-24C.

Example 21: Cell Culture Process Used to Produce Modified

20 **Flt1 Receptors**

(a) Cell Culture Process Used to Produce

Flt1D2.Flk1D3.Fc Δ C1(a)

25 The process for production of Flt1D2.Flk1D3.Fc Δ C1(a) protein using the

expression plasmid pFlt1D2.Flk1D3.FcΔC1(a) described *supra* in Example 1 involves suspension culture of recombinant Chinese hamster ovary (CHO K1/E1A) cells which constitutively express the protein product.

The cells are grown in bioreactors and the protein product is isolated

5 and purified by affinity and size exclusion chromatography. The process is provided in greater detail below.

Cell Expansion

10 Two confluent T-225 cm² flasks containing the Flt1D2.Flk1D3.FcΔC1(a) expressing cell line were expanded by passaging cells into eight T-225 cm² flasks in medium (GMEM + 10% serum, GIBCO) and incubated at 37°C and 5% CO₂. When the flasks approached confluence (approximately 3 to 4 days) the cells were detached using trypsin. Fresh medium was added
15 to protect the cells from further exposure to the trypsin. The cells were centrifuged and resuspended in fresh medium then transferred to eight 850 cm² roller bottles and incubated at 37°C and 5% CO₂ until confluent.

20 Suspension Culture in Bioreactors

Cells grown in roller bottles were trypsinized to detach them from the surface and washed with suspension culture medium. The cells are aseptically transferred to a 5L bioreactor (New Brunswick Celligen

25 Plus) where the cells are grown in 3.5L of suspension culture. The

suspension culture medium was a glutamine-free low glucose modification of IS-CHO (Irvine Scientific) to which 5% fetal bovine serum (Hyclone), GS supplement (Life Technologies) and 25 μ M methionine sulfoximine (Sigma) was added. The pH was controlled at 7.2 by addition of carbon dioxide to the inlet gas or by addition of a liquid solution of sodium carbonate to the bioreactor. Dissolved oxygen level was maintained at 30% of saturation by addition of oxygen or nitrogen to the inlet gas and temperature controlled at 37°C. When a density of 4 x10⁶ cells/mL was reached the cells were transferred to a 40L bioreactor containing the same medium and setpoints for controlling the bioreactor. The temperature setpoint was reduced to 34°C to slow cell growth and increase the relative rate of protein expression.

(b) Cell Culture Process Used to Produce Flt1D2.VEGFR3D3.Fc Δ C1(a)

The same methodologies as described *supra* for Flt1D2.FlklD3.Fc Δ C1(a) were used to produce Flt1D2.VEGFR3D3.Fc Δ C1(a).

Example 22: Harvest and Purification of Modified Flt1 Receptors

(a) Harvest and Purification of Flt1D2.Flk1D3.FcΔC1(a)

The product protein was aseptically harvested from the bioreactor while retaining cells using Millipore Prostak tangential-flow filtration modules and a low-shear mechanical pump (Fristam). Fresh medium was added to the bioreactor to replace that removed during the harvest filtration. Approximately 40L of harvest filtrate was then loaded onto a 400 mL column containing Protein A Sepharose resin (Amersham Pharmacia). After loading the resin was washed with buffer containing 10 mM sodium phosphate, 500 mM sodium chloride, pH 7.2 to remove any unbound contaminating proteins. Flt1D2.Flk1D3.FcΔC1(a) protein was eluted with a pH 3.0 citrate buffer. The eluted protein was neutralized by addition of Tris base and frozen at -20°C.

Several frozen lots of Flt1D2.Flk1D3.FcΔC1(a) protein from the Protein A step above were thawed, pooled and concentrated using a Millipore 30kD nominal molecular weight cutoff (NMWCO) tangential flow filtration membrane. The protein was transferred to a stirred cell concentrator (Millipore) and further concentrated to 30 mg/mL using a 30kD NMWCO membrane. The concentrated protein was loaded onto a size exclusion column packed with Superdex 200 resin (Amersham Pharmacia) that was equilibrated with phosphate buffered saline plus 5% glycerol. The same buffer was used to run the column. The fractions corresponding to Flt1D2.Flk1D3.FcΔC1(a) dimer were pooled, sterile filtered through a 0.22 micron filter, aliquoted and frozen.

(b) Harvest and Purification of Flt1D2.VEGFR3D3.FcΔC1(a)

The same methodologies as described *supra* for Flt1D2.FlklD3.FcΔC1(a)
5 were used to harvest and purify Flt1D2.VEGFR3D3.FcΔC1(a).

Example 23: Phosphorylation Assay for Transiently Expressed VEGFR2

10 Primary human umbilical vein endothelial cells (HUVECs), passage 4-6, were starved for 2 hrs in serum-free DME high glucose media. Samples containing 40 ng/ml (1nM) human VEGF165, which is a ligand for the VEGF receptors Flt1, Flk1 and Flt4(VEGFR3) were prepared and were preincubated for 1 hr. at room temperature with varying amounts of the
15 modified Flt1 receptors Flt1(1-3)-Fc, Flt1(1-3)-Fc (A40), Flt1D2FlklD3.FcΔC1(a) and Flt1D2VEGFR3D3.FcΔC1(a) in serum-free DME-high glucose media containing 0.1% BSA. Cells were challenged for 5 minutes with the samples prepared above +/- VEGF165, followed by whole cell lysis using complete lysis buffer. Cell lysates were
20 immunoprecipitated with an antibody directed against the C-terminus of VEGFR2 receptor. The immunoprecipitated lysates were loaded onto 4-12% SDS-PAGE Novex gel and then transferred to PVDF membrane using standard transfer methodologies. Detection of phosphorylated VEGFR2 was done by immunoblotting with the anti-phospho Tyrosine
25 mAb called 4G10 (UBI) and developed using ECL-reagent (Amersham).

Figures 25A-25C and 26A-26B show the results of this experiment.

Figure 25A-25C reveals that detection by Western blot of tyrosine phosphorylated VEGFR2(Flk1) by VEGF165 ligand stimulation shows that cell-surface receptors are phosphorylated to varying levels depending on which modified Flt1 receptor is used during the preincubations with VEGF. As is seen in Figure 25A, at a 1.5 molar excess of either Flt1(1-3)-Fc, Flt1(1-3)-Fc (A40) or transient Flt1D2Flk1D3.Fc Δ C1(a) there is complete blockage of receptor stimulation by these three modified Flt1 receptors as compared to control media challenge. In contrast, transient Flt1D2VEGFR3D3.Fc Δ C1(a) does not show significant blockage at this molar excess, as compared with VEGF positive control challenge. Similar results are seen in Figure 25B, where the modified Flt receptors are in a 3-fold molar excess to VEGF165 ligand. In Figure 25C, where the modified Flt1 receptors are in a 6-fold molar excess to VEGF165 ligand, transient Flt1D2VEGFR3D3.Fc Δ C1(a) can now be shown to be partially blocking VEGF165-induced stimulation of cell-surface receptors.

In Figure 26A-26B, detection by Western blot of tyrosine

phosphorylated VEGFR2(Flk1) by VEGF165 ligand stimulation shows that cell-surface receptors are not phosphorylated by challenge samples which have VEGF165 preincubated with 1 and 2 fold molar excess (Figure 26A) or 3 and 4 fold molar excess (Figure 26B) of either transient Flt1D2Flk1D3.Fc Δ C1(a), stable Flt1D2Flk1D3.Fc Δ C1(a), or transient VEGFR1R2-Fc Δ C1(a). At all modified Flt1 receptor

concentrations tested there is complete binding of VEGF165 ligand during the preincubation, resulting in no detectable stimulation of cell-surface receptors by unbound VEGF165 as compared to control media challenge.

5

Example 24: Cell Proliferation Bioassay

The test cell population is MG87 cells that have been stably transfected with a expression plasmid that contains a DNA insert encoding the VEGFR2(Flk1) extracellular domain fused to the TrkB intracellular kinase domain, thus producing a chimeric molecule. The reason the TrkB intracellular kinase domain was used rather than the native VEGFR2(Flk1) intracellular kinase domain is that the intracellular kinase domain of VEGFR2(Flk1) does not cause a strong proliferative response when stimulated by VEGF165 in these cells. It is known that MG87 cells containing full length TrkB receptor give a robust proliferative response when stimulated with BDNF, so the TrkB intracellular kinase domain was engineered to replace the intracellular kinase domain of VEGFR2(Flk1) to take advantage of this proliferative response capability.

5×10^3 cells/well were plated in a 96 well plate and allowed to settle for 2 hrs at 37°C. The following modified Flt receptors Flt1(1-3)-Fc, Flt1D2.FlklD3.Fc Δ C1(a) and Flt1D2.VEGFR3D3.Fc Δ C1(a), plus an irrelevant receptor termed Tie2-Fc as a negative control, were titrated

25

from 40nM to 20pM and incubated on the cells for 1hr at 37°C. Human recombinant VEGF165 in defined media was then added to all the wells at a concentration of 1.56nM. The plates were incubated for 72 hrs at 37°C and then MTS (Owen's reagent, Promega) added and the plates were incubated for an additional for 4 hrs. Finally, the plates were read on a spectrophotometer at 450/570nm. The results of this experiment are shown in Figure 27. The control receptor Tie2-Fc does not block VEGF165-induced cell proliferation at any concentration whereas Flt1D2.Flk1D3.FcΔC1(a) blocks 1.56nM VEGF165 with a half maximal dose of 0.8nM. Flt1(1-3)-Fc and Flt1D2.VEGFR3D3.FcΔC1(a) are less effective in blocking VEGF165 in this assay with a half maximal dose of ~ 2nM. VEGF165 alone gives a reading of 1.2 absorbance units and the background is 0.38 absorbance units.

Example 25: Binding Stoichiometry of Modified Flt Receptors to VEGF165

(a) BIAcore Analysis

The stoichiometry of Flt1D2Flk1D3.FcΔC1(a) and VEGFR1R2-FcΔC1(a) interaction with human VEGF165 was determined by measuring either the level of VEGF saturation binding to the Flt1D2Flk1D3.FcΔC1(a) or VEGFR1R2-FcΔC1(a) surfaces or measuring concentration of VEGF165 needed to completely prevent binding of Flt1D2Flk1D3.FcΔC1(a) or VEGFR1R2-FcΔC1(a) to VEGF BIAcore chip surface.

Modified Flt receptors Flt1D2Flk1D3.FcΔC1(a) and VEGFR1R2-FcΔC1(a), were captured with an anti-Fc specific antibody that was first immobilized on a Biacore chip (BIAcore) using amine-coupling chemistry. A blank antibody surface was used as a negative control. VEGF165 was injected at a concentration of 1 nM, 10 nM, and 50 nM over the Flt1D2Flk1D3.FcΔC1(a) and VEGFR1R2-FcΔC1(a) surfaces at 10 μl/min for one hour. A real-time binding signal was recorded and saturation binding was achieved at the end of each injection. Binding stoichiometry was calculated as a molar ratio of bound VEGF165 to the immobilized Flt1D2Flk1D3.FcΔC1(a) or VEGFR1R2-FcΔC1(a), using the conversion factor of 1000 RU equivalent to 1 ng/ml. The results indicated binding stoichiometry of one VEGF165 dimeric molecule per one Flt1D2Flk1D3.FcΔC1(a) or VEGFR1R2-FcΔC1(a) molecule (Figure 28).

In solution, Flt1D2Flk1D3.FcΔC1(a) or VEGFR1R2-FcΔC1(a) at a concentration of 1nM (estimated to be 1000 times higher than the KD of the Flt1D2Flk1D3.FcΔC1(a) or VEGFR1R2-FcΔC1(a)/VEGF165 interaction) were mixed with varied concentrations of VEGF165. After one hour incubation, concentrations of the free Flt1D2Flk1D3.FcΔC1(a) in solution were measured as a binding signal to an amine-coupled VEGF165 surface. A calibration curve was used to convert the Flt1D2Flk1D3.FcΔC1(a) BIAcore binding signal to its molar concentration. The data showed that the addition of 1 nM VEGF165 into

the Flt1D2Flk1D3.Fc Δ C1(a) solution completely blocked Flt1D2Flk1D3.Fc Δ C1(a) binding to the VEGF165 surface. This result suggested the binding stoichiometry of one VEGF165 molecule per one Flt1D2Flk1D3.Fc Δ C1(a) molecule (Figure 29 and Figure 30). When the
5 concentration of Flt1D2Flk1D3.Fc Δ C1(a) was plotted as a function of added concentration of VEGF165, the slope of the linear portion was -1.06 for Flt1D2Flk1D3.Fc Δ C1(a) and -1.07 for VEGFR1R2-Fc Δ C1(a). The magnitude of the slope, very close to negative one, was indicative that one molecule of VEGF165 bound to one molecule of either
10 Flt1D2Flk1D3.Fc Δ C1(a) or VEGFR1R2-Fc Δ C1(a).

(b) Size Exclusion Chromatography

Flt1D2Flk1D3.Fc Δ C1(a) was mixed with a 3-fold excess of VEGF165 and
15 the receptor-ligand complex was purified using a Pharmacia Superose 6 size exclusion chromatography column. The receptor-ligand complex was then incubated in a buffer containing 6M guanidine hydrochloride in order to dissociate it into its component proteins.

Flt1D2Flk1D3.Fc Δ C1(a) was separated from VEGF165 using Superose 6
20 size exclusion chromatography column run in 6M guanidium chloride. In order to determine complex stoichiometry, several injections of Flt1D2Flk1D3.Fc Δ C1(a) and VEGF165 were made and peak height or peak integrated intensity was plotted as a function of the concentration of injected protein. The calibration was done under condition identical to
25 one used in separating components of Flt1D2Flk1D3.Fc Δ C1(a)/VEGF

complex. Quantification of the Flt1D2Flk1D3.Fc Δ C1(a)/VEGF complex composition was based on the calibration curves. The results of this experiment are set forth in Figure 28, which shows the ratio of VEGF165 to Flt1D2Flk1D3.Fc Δ C1(a) in a complex to be 1:1.

5

Example 26: Determination of the Binding Stoichiometry of Flt1D2Flk1D3.Fc Δ C1(a)/VEGF165 Complex by Size Exclusion Chromatography

10 **Flt1D2Flk1D3.Fc Δ C1(a)/VEGF165 Complex Preparation**

VEGF165 (concentration = 3.61 mg/ml) was mixed with CHO cell transiently expressed Flt1D2.Flk1D3.Fc Δ C1(a) (concentration = 0.9 mg/ml) in molar ratio of 3:1 (VEGF165:Flt1D2.Flk1D3.Fc Δ C1(a)) and
15 incubated overnight at 4°C.

(a) Size Exclusion Chromatography (SEC) under native conditions

20 To separate the complex from excess of unbound VEGF165, 50 μ l of the complex was loaded on a Pharmacia Superose 12 PC 3.2/30 which was equilibrated in PBS buffer. The sample was eluted with the same buffer at flow rate 40 μ l/min. at room temperature. The results of this SEC are shown in Figure 31. Peak #1 represents the complex and peak
25 #2 represents unbound VEGF165. Fractions eluted between 1.1 and 1.2

ml were combined and guanidinium hydrochloride (GuHCl) was added to a final concentration 4.5M to dissociate the complex.

(b) Size Exclusion Chromatography (SEC) under dissociative

5 conditions

To separate the components of the receptor-ligand complex and to determine their molar ratio, 50 μ l of dissociated complex as described *supra* was loaded onto a Superose 12 PC 3.2/30 equilibrated in 6M GuHCl and eluted with the same solution at a flow rate 40 μ l/min. at room temperature. The results of this SEC are shown in Figure 32. Peak #1 represents Flt1D2Flk1D3.Fc Δ C1(a) and peak #2 represents VEGF165.

15 (c) Calculation of Flt1D2Flk1D3.Fc Δ C1(a):VEGF165 Complex Stoichiometry

The stoichiometry of the receptor-ligand complex was determined from the peak area or the peak height of the components. Concentrations of VEGF165 and Flt1D2Flk1D3.Fc Δ C1(a) corresponding to the peak height or peak area, respectively, were obtained from the standard curves for VEGF165 and Flt1D2Flk1D3.Fc Δ C1(a). To obtain a standard curve, four different concentrations (0.04 mg/ml -0.3mg/ml) of either component were injected onto a Pharmacia Superose 12 PC 3.2/30 column equilibrated in 6M guanidinium chloride and eluted with the same

solution at flow rate 40 μ l/min. at room temperature. The standard curve was obtained by plotting peak area or peak height vs protein concentration. The molar ratio of VEGF165:Flt1D2Flk1D3.Fc Δ C1(a) determined from the peak area of the components was 1.16. The molar ratio of VEGF165:Flt1D2Flk1D3.Fc Δ C1(a) determined from the peak height of the components was 1.10.

Example 27: Determination of the Stoichiometry of the Flt1D2Flk1D3.Fc Δ C1(a)/VEGF165 Complex by Size Exclusion Chromatography with On-Line Light Scattering

Complex preparation

VEGF165 was mixed with CHO transiently expressed Flt1D2.Flk1D3.Fc Δ C1(a) protein in molar ratio of 3:1 (VEGF165:Flt1D2Flk1D3.Fc Δ C1(a)) and incubated overnight at 4°C.

(a) Size Exclusion Chromatography (SEC) with On-Line Light Scattering

Size exclusion chromatography column with a MiniDawn on-line light scattering detector (Wyatt Technology, Santa Barbara, California) and refractive index (RI) detectors (Shimadzu, Kyoto, Japan) was used to determine the molecular weight (MW) of the receptor-ligand complex.

Samples were injected onto a Superose 12 HR 10/30 column

(Pharmacia) equilibrated in PBS buffer and eluted with the same buffer at flow rate 0.5 ml/min. at room temperature. As shown in Figure 33, the elution profile shows two peaks. Peak #1 represents the receptor-ligand complex and peak #2 represents the unbound VEGF165. MW was
5 calculated from LS and RI signals. The same procedure was used to determine MW of the individual components of the receptor-ligand complex. The results of these determinations are as follows: MW of the Flt1D2Flk1D3.FcΔC1(a)/VEGF165 complex at the peak position is 157 300 (Figure 33), the MW of VEGF165 at the peak position is 44 390
10 (Figure 34) and the MW of R1R2 at the peak is 113 300 (Figure 35).

These data indicated that the stoichiometry of the Flt1D2Flk1D3.FcΔC1(a)/VEGF complex is 1:1 as its corresponds to the sum of molecular weights for Flt1D2Flk1D3.FcΔC1(a) and VEGF165.
15 Importantly, this method conclusively proved that the Flt1D2Flk1D3.FcΔC1(a)/VEGF165 complex was indeed composed of only one molecule of VEGF165 ligand and only one molecule of the Flt1D2Flk1D3.FcΔC1(a).

20 **Example 28: Peptide Mapping of Flt1D2.Flk1D3.FcΔC1(a)**

The disulfide structures and glycosylation sites in Flt1D2.Flk1D3.FcΔC1(a) were determined by a peptide mapping method. In this method, the protein was first cleaved with trypsin. Tryptic
25 fragments were analyzed and identified by HPLC coupled with mass

spectrometry, in addition to an N-terminal sequencing technique. Reduction of the tryptic digest was employed to help identify disulfide-bond-containing fragments. Treatment of the tryptic digest with PNGase F (Glyko, Novato, CA) was employed to help identify
5 fragments with N-linked glycosylation sites. The results are summarized in the accompanying Figure 36.

There are a total of ten cysteines in Flt1D2.Flk1D3.FcΔC1(a); six of them belong to the Fc region. Cys27 has been confirmed to be disulfide
10 bonded to Cys76. Cys121 is confirmed to be disulfide bonded to Cys182. The first two cysteines in the Fc region (Cys211 and Cys214) form an intermolecular disulfide bond with the same two cysteines in another Fc chain. However, because these two cysteines can not be separated enzymatically from each other, it can not be determined
15 whether disulfide bonding is occurring between same cysteines (Cys211 to Cys211, for example) or between Cys211 and Cys214. Cys216 is confirmed to be disulfide bonded to Cys306. Cys 352 is confirmed to be disulfide bonded to Cys410.

20 There are five possible N-linked glycosylation sites in Flt1D2.Flk1D3.FcΔC1(a). All five of them are found to be glycosylated to varying degrees. Complete glycosylation was observed at Asn33 (amino acid sequence NIT), Asn193 (amino acid sequence NST), and Asn282 (amino acid sequence NST). In addition, partial glycosylation is

observed on Asn65 and Asn120. Sites of glycosylation are highlighted by underline in the Figure 36.

Example 29: Pharmacokinetic Analysis of Modified Flt

5 Receptors

(a) Pharmacokinetic analysis of Flt1(1-3)-Fc (A40), Flt1D2.Flk1D3.Fc Δ C1(a) and VEGFR1R2-Fc Δ C1(a)

10 Balb/c mice (25-30g) were injected subcutaneously with 4mg/kg of Flt1(1-3)-Fc (A40), CHO transiently expressed Flt1D2.Flk1D3.Fc Δ C1(a), CHO stably expressed Flt1D2.Flk1D3.Fc Δ C1(a), and CHO transiently expressed VEGFR1R2-Fc Δ C1(a). The mice were tail bled at 1, 2, 4, 6, 24hrs, 2 days, 3 days and 6 days after injection. The sera were assayed
15 in an ELISA designed to detect Flt1(1-3)-Fc (A40), Flt1D2.Flk1D3.Fc Δ C1(a) or VEGFR1R2-Fc Δ C1(a). The ELISA involves coating an ELISA plate with VEGF165, binding the detect Flt1(1-3)-Fc (A40), Flt1D2.Flk1D3.Fc Δ C1(a) or VEGFR1R2-Fc Δ C1(a) and reporting with an anti-Fc antibody linked to horse radish peroxidase. The results
20 of this experiments are shown in Figure 37. The T_{max} for Flt1(1-3)-Fc (A40) was at 6 hrs while the T_{max} for the transient and stable Flt1D2.Flk1D3.Fc Δ C1(a) and the transient VEGFR1R2-Fc Δ C1(a) was 24hrs. The C_{max} for Flt1(1-3)-Fc (A40) was 8 μ g/ml. For both transients (Flt1D2.Flk1D3.Fc Δ C1(a) and VEGFR1R2-Fc Δ C1(a)) the C_{max}

was 18 μ g/ml and the C_{max} for the stable VEGFR1R2-Fc Δ C1(a) was 30 μ g/ml.

(b) Pharmacokinetic analysis of Flt1(1-3)-Fc (A40),

5 Flt1D2.Flk1D3.Fc Δ C1(a) and Flt1D2.VEGFR3D3.Fc Δ C1(a)

Balb/c mice (25-30g) were injected subcutaneously with 4mg/kg of Flt1(1-3)-Fc (A40), CHO transiently expressed Flt1D2.Flk1D3.Fc Δ C1(a) and CHO transiently expressed Flt1D2.VEGFR3D3.Fc Δ C1(a). The mice
10 were tail bled at 1, 2, 5, 6, 7, 8, 12, 15 and 20 days after injection. The sera were assayed in an ELISA designed to detect Flt1(1-3)-Fc, Flt1D2.Flk1D3.Fc Δ C1(a) and Flt1D2.VEGFR3D3.Fc Δ C1(a). The ELISA involves coating an ELISA plate with 165, binding the Flt1(1-3)-Fc, Flt1D2.Flk1D3.Fc Δ C1(a) or Flt1D2.VEGFR3D3.Fc Δ C1(a) and reporting
15 with an anti-Fc antibody linked to horse radish peroxidase. Flt1(1-3)-Fc (A40) could no longer be detected in the serum after day 5 whereas , Flt1D2.Flk1D3.Fc Δ C1(a) and Flt1D2.VEGFR3D3.Fc Δ C1(a) were detectable for 15 days or more. The results of this experiment are shown in Figure 38.

20

Example 30: Evaluation of the Ability of
Flt1D2.Flk1D3.Fc Δ C1(a) to Inhibit Tumor Growth In Vivo

To evaluate the ability of Flt1D2.Flk1D3.Fc Δ C1(a) to inhibit tumor
25 growth in vivo a model in which tumor cell suspensions are implanted

subcutaneously on the right flank of male severe combined immunodeficiency (SCID) mice was employed. Two cell lines, the human HT-1080 fibrosarcoma cell line (ATCC accession no. CCL-121) and the rat C6 glioma cell line (ATCC accession no. CCL-107), each of which exhibit distinctly different morphologies and growth characteristics, were used in the assay. The first dose of Flt1D2.Flk1D3.Fc Δ C1(a) (at 25mg/Kg or as indicated in Figures 39 and 40) was given on the day of tumor implantation. Animals subsequently received subcutaneous injections of Flt1(1-3)-Fc (A40), Flt1D2.Flk1D3.Fc Δ C1(a) or vehicle either every other day (EOD) or two times per week (2X/wk) for a period of 2 weeks. After 2 weeks, animals were perfused with fixative, tumors were removed and samples were blinded. Tumor volume was determined by measuring the length and width of visible subcutaneous tumors. Both of Flt1(1-3)-Fc (A40) and Flt1D2.Flk1D3.Fc Δ C1(a) significantly reduced the growth of tumors formed by HT-1080 and C6 cells. The results of these experiments are shown in Figure 39 and Figure 40.

Example 31: The Effect of VEGF165 and Modified Flt
Receptors in Female Reproductive System

The stereotypic pattern of vascular remodeling which occur in the uterus and ovary over the course of the reproductive cycle has been well characterized, making these tissues particularly well suited to the study of mechanisms which regulate angiogenesis, vascular

remodeling and vascular regression. Indeed, *in situ* hybridization studies in the reproductive tissues provided the first clear evidence that VEGF acts as a mediator of physiological angiogenesis in mature rodents, as well as humans and non-human primates (Phillips et al, 5 1990; Ravindranath et al, 1992; Shweiki et al, 1993; Kamat et al, 1995). As cyclic angiogenesis and vascular remodeling are prominent features of the normal ovary and uterus, it is not surprising that abnormal blood vessel growth and/or vascular dysfunction have been found to characterize many pathological conditions which affect these 10 organs. Furthermore, these pathogenic vascular abnormalities are thought to be caused or perpetuated by the dysregulated expression of one or more angiogenic or anti-angiogenic factors, most prominently VEGF.

15 For example, abnormal angiogenesis is characteristic of polycystic ovary disease, endometriosis and endometrial carcinoma, and in each case VEGF is over expressed in the affected tissue (Kamat et al, 1995; Shifren et al, 1996; Guidi et al, 1996; Donnez et al, 1998).

Overexpression of VEGF is also thought to play a pathogenic role in the 20 establishment of systemic vascular hyperpermeability in ovarian hyperstimulation syndrome (McClure et al, 1994; Levin et al, 1998) and preeclampsia (Baker et al, 1995; Sharkey et al, 1996). In addition, VEGF has been implicated as the permeability factor responsible for the production of ascites associated with ovarian carcinoma and other 25 tumors (Senger et al, 1983; Boockock et al, 1995). Agents which effectively neutralize the biological actions of VEGF can reasonably be

anticipated to be of therapeutic benefit in the above and related conditions.

Angiogenesis and vascular remodeling are also hallmarks of blastocyst
5 implantation and placental development (Findlay, 1986). VEGF is
strongly expressed both in the maternal decidua and in embryonic
trophoblasts, where it is thought to first stimulate expansion and
hyperpermeability of the uterine vasculature during the peri-
implantation period and subsequently mediate formation of both the
10 maternal and embryonic components of the placental vasculature
(Shweiki et al, 1993; Cullinan-Bove and Koos, 1993; Chakraborty et al,
1995; Das et al, 1997). VEGF is also required for luteal angiogenesis
and associated progesterone secretion necessary to prepare the uterus
for implantation (Ferrara et al, 1998). Thus, agents which inhibit the
15 biological actions of VEGF may prove to be useful as contraceptive
agents (by preventing implantation), or as abortifacients in the early
stages of gestation. The latter application might find particular use as
a non-surgical intervention for the termination of ectopic pregnancies.

20 While the expression of VEGF receptors is largely confined to the
vascular endothelium in normal reproductive tissues, Flt1 is also
expressed by trophoblasts in the placenta in both humans and animals
(Clark et al, 1996; He et al, 1999) where it has been proposed to play a
role in trophoblast invasion. Interestingly, both Flt1 and KDR (Flk1) are
25 expressed by choriocarcinoma cell line BeWo (Charnock-Jones et al,
1994), and VEGF has been shown to promote DNA synthesis and tyrosine
phosphorylation of MAP kinase in these cells. Furthermore, primary and

metastatic ovarian carcinomas not only to express high levels of VEGF, but - in addition to the vascular endothelium - the tumor cells themselves express KDR and/ or Flt1 (Boock et al, 1995). These findings suggest that VEGF may not only be critically involved in the generation and maintenance of tumor vasculature, but that at least in some tumors of reproductive origin VEGF may subserve an autocrine role, directly supporting the survival and proliferation of the tumor cells. Thus agents which block the actions of VEGF may have particularly beneficial applications to the treatment of tumors of reproductive origin.

Methods and Results

(a) Assessment of VEGF-Induced Uterine Hyperpermeability

Pregnant mare's serum gonadotrophin (PMSG) was injected subcutaneously (5 IU) to induce ovulation in prepubertal female rats. This results in a surge of estradiol after 2 days which in turn causes an induction of VEGF in the uterus. It is reported that this induction results in hyperpermeability of the uterus and an increase in uterine wet weight 6 hrs. later and, therefore, could potentially be blocked by the modified Flt receptors Flt1(1-3)-Fc (A40), Flt1D2.Flk1D3.Fc Δ C1(a) and Flt1D2.VEGFR3D3.Fc Δ C1(a). In this in vivo model, the normal weight of the rat uterus is about 50 mg and this can be induced to 300-350 mg by PMSG. Desiccation of the tissue reveals that this is all water weight. Subcutaneous injection of Flt1(1-3)-Fc (A40),

Flt1D2.Flk1D3.Fc Δ C1(a) and Flt1D2.VEGFR3D3.Fc Δ C1(a) at 25mg/kg at 1hr. after PMSG injection results in about a 50% inhibition of the increase in uterine wet weight. Increasing the dose of modified Flt receptor does not further reduce the increase in wet weight suggesting that there is a VEGF-independent component to this model. The results of this experiment are shown in Figure 41.

(a) Assessment of corpus luteum angiogenesis using progesterone as a readout

Pregnant mare's serum gonadotrophin (PMSG) is injected subcutaneously (5 IU) to induce ovulation in prepubertal female rats. This results in a fully functioning corpus luteum containing a dense network of blood vessels after 4 days that allows for the secretion of progesterone into the blood stream in order to prepare the uterus for implantation. The induction of angiogenesis in the corpus luteum requires VEGF; therefore, blocking VEGF would result in a lack of new blood vessels and thus a lack of progesterone secreted into the blood stream. In this in vivo model, resting levels of progesterone are about 5ng/ml and this can be induced to a level of 25-40ng/ml after PMSG. Subcutaneous injection of Flt1(1-3)-Fc (A40) or Flt1D2.Flk1D3.Fc Δ C1(a) at 25mg/kg or 5mg/kg at 1hr. after PMSG injection results in a complete inhibition of the progesterone induction on day 4. The results of this experiment are shown in Figure 42A-42B.

Example 33: Pharmacokinetic Analysis of Flt1(1-3)-Fc (A40) and Pegylated Flt1(1-3)-Fc

Flt1(1-3)-Fc was PEGylated with either 10kD PEG or 20kD PEG and tested in balb/c mice for their pharmacokinetic profile. Both PEGylated forms of Flt1(1-3)-Fc were found to have much better PK profiles than Flt1(1-3)-Fc (A40), with the T_{max} occurring at 24 hrs. for the PEGylated molecules as opposed to 6 hrs. for Flt1(1-3)-Fc (A40).

Example 34: VEGF165 ELISA to Test Affinity of Modified Flt1 Receptor Variants

10pM of VEGF165 was incubated overnight at room temperature with modified Flt1 receptor variants ranging from 160pM to 0.1pM. The modified Flt1 receptor variants used in this experiment were Flt1(1-3)-Fc, Flt1(1-3)-Fc (A40), transiently expressed Flt1D2Flk1D3.FcΔC1(a), transiently expressed Flt1D2VEFGFR3D3-FcΔC1(a), Flt1-(1-3_{NAS})-Fc, Flt1(1-3_{R->C})-Fc and Tie2-Fc. Flt1(1-3_{NAS})-Fc is a modified version of Flt1(1-3)-Fc in which the highly basic amino acid sequence KNKRASVRRR is replaced by NASVNGSR, resulting in the incorporation of two new glycosylation sites and a net reduction of five positive charges, both with the purpose of reducing the unfavorable effects of this sequence on PK. Flt1(1-3_{R->C})-Fc is a modification in which a single arginine (R) residue within the same basic amino acid sequence is changed to a cysteine (C) (KNKRASVRRR ->

KNKCASVRRR) to allow for pegylation at that residue, which could then shield the basic region from exerting its unfavorable effects on PK. After incubation the solution was transferred to a plate containing a capture antibody for VEGF165 (R&D). The amount of free VEGF165 was

5 then determined using an antibody to report free VEGF165. This showed that the modified Flt1 receptor variant with the highest affinity for VEGF165 (determined as the lowest amount of free VEGF165) was Flt1D2FIk1D3.FcΔC1(a), followed by Flt1(1-3)-Fc and Flt1(1-3)-Fc (A40) and then by Flt1(1-3_{R->C})-Fc, Flt1(1-3_{NAS})-Fc and

10 Flt1D2VEFGFR3D3-FcΔC1(a). Tie2Fc has no affinity for VEGF165.

WE CLAIM:

1. An isolated nucleic acid molecule encoding a fusion polypeptide capable of binding a VEGF polypeptide comprising:

5 (a) a nucleotide sequence encoding a VEGF receptor component operatively linked to

(b) a nucleotide sequence encoding a multimerizing component, wherein the VEGF receptor component is the only VEGF receptor component of the fusion polypeptide and wherein the nucleotide

10 sequence of (a) consists essentially of a nucleotide sequence encoding the amino acid sequence of Ig domain 2 of the extracellular domain of a first VEGF receptor and a nucleotide sequence encoding the amino acid sequence of Ig domain 3 of the extracellular domain of a second VEGF receptor.

15

2. The isolated nucleic acid of claim 1 wherein the first VEGF receptor is Flt1.

3. The isolated nucleic acid of claim 1 wherein the second VEGF
20 receptor is Flk1.

4. The isolated nucleic acid of claim 1 wherein the second VEGF receptor is Flt4.

25

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5. The isolated nucleic acid molecule of claim 1, wherein the nucleotide sequence encoding Ig domain 2 of the extracellular domain of the first VEGF receptor is upstream of the nucleotide sequence encoding Ig domain 3 of the extracellular domain of the second VEGF receptor.

5

6. The isolated nucleic acid molecule of claim 1, wherein the nucleotide sequence encoding Ig domain 2 of the extracellular domain of the first VEGF receptor is downstream of the nucleotide sequence encoding Ig domain 3 of the extracellular domain of the second VEGF receptor.

10

7. The isolated nucleic acid molecule of claim 1, wherein the multimerizing component comprises an immunoglobulin domain.

8. The isolated nucleic acid molecule of claim 1, wherein the immunoglobulin domain is selected from the group consisting of the Fc domain of IgG, the heavy chain of IgG, and the light chain of IgG.

9. An isolated nucleic acid molecule comprising a nucleotide sequence encoding a modified Flt1 receptor fusion polypeptide, wherein the coding region of the nucleic acid molecule consists essentially of a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence set forth in Figure 21A-21C
- (b) the nucleotide sequence set forth in Figure 22A-22C;
- (c) the nucleotide sequence set forth in Figure 24A-24C; and
- (d) a nucleotide sequence which, as a result of the degeneracy of the genetic code, differs from the nucleotide sequence of (a), (b) or (c) and which encodes a fusion polypeptide molecule having the biological activity of the modified Flt1 receptor fusion polypeptide.

10. An isolated nucleic acid molecule comprising a nucleotide sequence encoding a modified Flt1 receptor fusion polypeptide, wherein the coding region of the nucleic

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acid molecule consists essentially of a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence set forth in Figure 13A-13D;
 - (b) the nucleotide sequence set forth in Figure 14A-14C;
 - 5 (c) the nucleotide sequence set forth in Figure 15A-15C;
 - (d) the nucleotide sequence set forth in Figure 16A-16D; and
 - (e) a nucleotide sequence which as a result of the degeneracy of the genetic code, differs from the nucleotide sequence of (a), (b), (c) or (d) and which encodes a fusion polypeptide molecule having the biological activity of the modified
 - 10 Flt1 receptor fusion polypeptide.
11. A fusion polypeptide encoded by the isolated nucleic acid molecule of claim 1, 2, 3, 4, 9 or 10.
 - 15 12. A composition capable of binding a VEGF molecule to form a nonfunctional complex comprising a multimer of the fusion polypeptide of claim 10.
 13. The composition of claim 12, wherein the multimer is a dimer.
 - 20 14. The composition of claim 13 and a carrier.
 15. A vector which comprises the nucleic acid molecule of claim 1, 2, 3, 4, 9 or 10.
 - 25 16. An expression vector comprising a nucleic acid molecule of claim 1, 2, 3, 4, 9 or 10 wherein the nucleic acid molecule is operatively linked to an expression control sequence.
 17. A host-vector system for the production of a fusion polypeptide which
 - 30 comprises the expression vector of claim 16, in a suitable host cell.

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18. The host-vector system of claim 17, wherein the suitable host cell is a bacterial cell, yeast cell, insect cell, or mammalian cell.
19. The host-vector system of claim 17, wherein the suitable host cell is E. coli.
- 5 20. The host-vector system of claim 17, wherein the suitable host cell is a COS cell or a CHO cell.
21. A method of producing a fusion polypeptide which comprises growing cells
- 10 of the host-vector system of claim 17, under conditions permitting production of the fusion polypeptide and recovering the fusion polypeptide so produced.

22. A fusion polypeptide encoded by the nucleic acid sequence set forth in Figure 10A-10D, ^{Figure 21A-21C, Figure 22A-22C} or Figure 24A-24C, which has been modified by acetylation or pegylation.

5 23. The fusion polypeptide of claim 22 wherein the modification is acetylation.

24. The fusion polypeptide of claim 22 wherein the modification is pegylation.

10

25. The fusion polypeptide of claim 23 wherein the acetylation is accomplished with at least about a 100 fold molar excess of acetylation reagent.

15 26. The fusion polypeptide of claim 23 wherein acetylation is accomplished with a molar excess of acetylation reagent ranging from at least about a 10 fold molar excess to about a 100 fold molar excess.

20 27. The fusion polypeptide of claim 24 wherein the pegylation is 10K or 20K PEG.

28. A method of decreasing or inhibiting plasma leakage in a mammal comprising administering to the mammal fusion polypeptide of claim 10.

25

29. The method of claim 28, wherein the mammal is a human.

30. The method of claim 29, wherein the fusion polypeptide is acetylated.

5

31. The method of claim 29, wherein the fusion polypeptide is pegylated.

32. The fusion polypeptide of claims ¹¹~~10~~ which specifically binds the
10 VEGF receptor ligand VEGF.

33. A method of blocking blood vessel growth in a human comprising administering an effective amount of the fusion polypeptide of claim ¹¹~~10~~.

15

34. A method of inhibiting VEGF receptor ligand activity in a mammal comprising administering to the mammal an effective amount of the fusion polypeptide of claim ¹¹~~10~~.

20 35. The method of claim 34, wherein the mammal is a human.

36. The method of claim 34, used to attenuate or prevent tumor growth in a human.

25

37. The method of claim 34, used to attenuate or prevent edema in a human.

38. The method of claim 34, used to attenuate or prevent ascites
5 formation in a human.

39. The method of claim 37, wherein the edema is brain edema.

40. The method of claim 38, wherein the ascites is ovarian cancer
10 associated ascites.

41. A fusion polypeptide capable of binding a VEGF polypeptide comprising:

- (a) a VEGF receptor component operatively linked to
- 15 (b) a multimerizing component,

wherein the VEGF receptor component is the only VEGF receptor component in the fusion polypeptide and consists essentially of the amino acid sequence of Ig domain 2 of the extracellular domain of a first VEGF receptor and the amino acid sequence of Ig domain 3 of the
20 extracellular domain of a second VEGF receptor.

42. The fusion polypeptide of claim 41 wherein the first VEGF receptor is Flt1.

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43. The fusion polypeptide of claim 41 wherein the second VEGF receptor is Flk1.
44. The fusion polypeptide of claim 41 wherein the second VEGF receptor is
5 Flt4.
45. The fusion polypeptide claim 41, wherein amino acid sequence of Ig domain
2 of the extracellular domain of the first VEGF receptor is upstream of the amino
acid sequence of Ig domain 3 of the extracellular domain of the second VEGF
10 receptor.
46. The fusion polypeptide of claim 41, wherein the amino acid sequence of Ig
domain 2 of the extracellular domain of the first VEGF receptor is downstream of the
amino acid sequence of Ig domain 3 of the extracellular domain of the second VEGF
15 receptor.
47. The fusion polypeptide of claim 41, wherein the multimerizing component
comprises an immunoglobulin domain.
- 20 48. The fusion polypeptide of claim 41, wherein the immunoglobulin domain is
selected from the group consisting of the Fc domain of IgG, the heavy chain of IgG,
and the light chain of IgG.
49. A fusion polypeptide consisting essentially of an amino acid sequence of a
25 modified Flt1 receptor, wherein the amino acid sequence is selected from the group
consisting of:
- (a) the amino acid sequence set forth in Figure 21A-21C
 - (b) the amino acid sequence set forth in Figure 22A-22C; and
 - (c) the amino acid sequence set forth in Figure 24A-24C.

30

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50. A fusion polypeptide comprising an amino acid sequence of a modified Flt1 receptor, wherein the amino acid sequence is selected from the group consisting of:

- (a) the amino acid sequence set forth in Figure 13A-13D;
- (b) the amino acid sequence set forth in Figure 14A-14C;
- 5 (c) the amino acid sequence set forth in Figure 15A-15C; and
- (d) the amino acid sequence set forth in Figure 16A-16D;

51. A method of decreasing or inhibiting plasma leakage in a mammal comprising administering to the mammal fusion polypeptide of claim 41, 42, 43, 44,
10 49 or 50.

52. A method of inhibiting VEGF receptor ligand activity in a mammal comprising administering to the mammal an effective amount of the fusion polypeptide of claim 41, 42, 43, 44, 49 or 50.

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Fig.1.

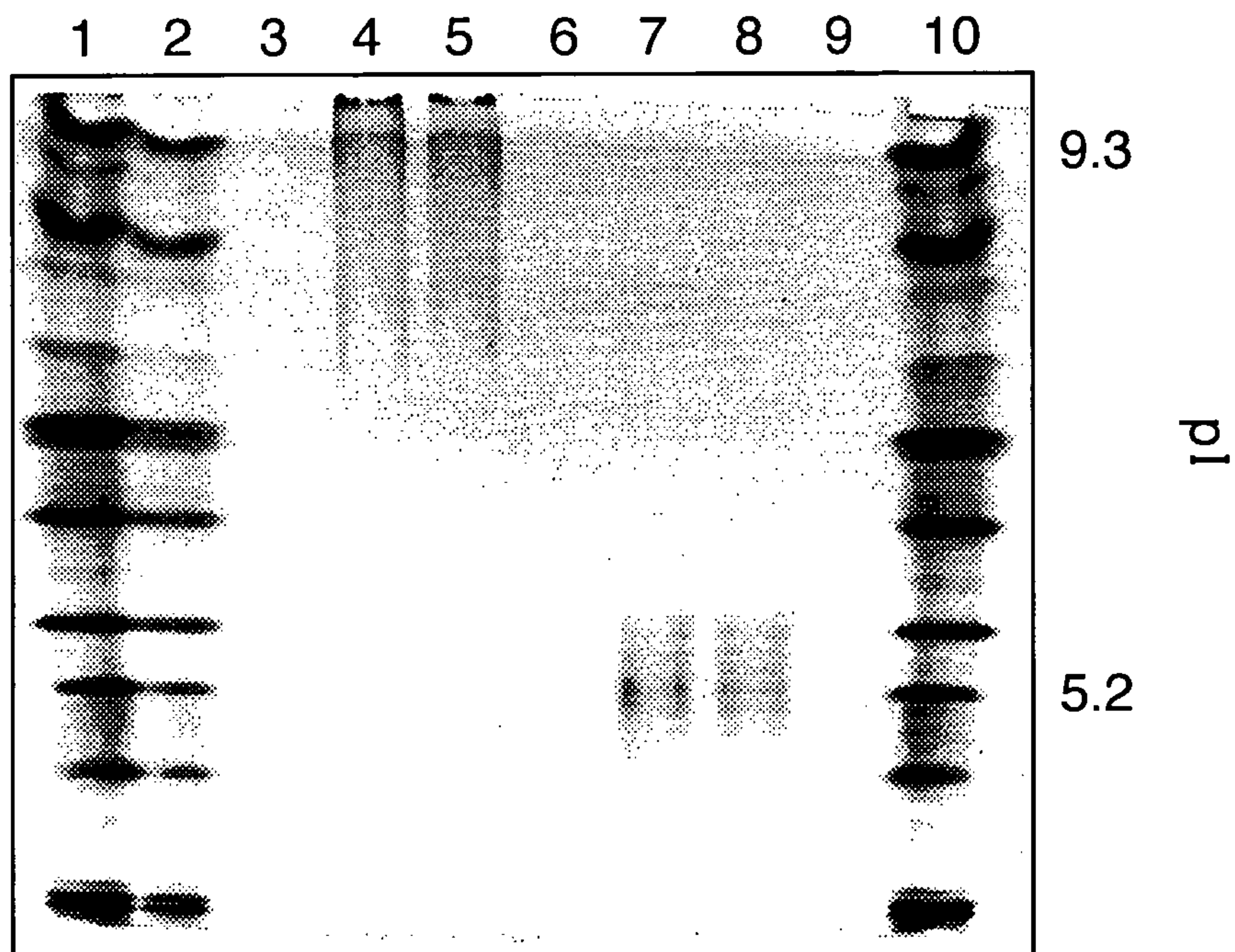


Fig.2.

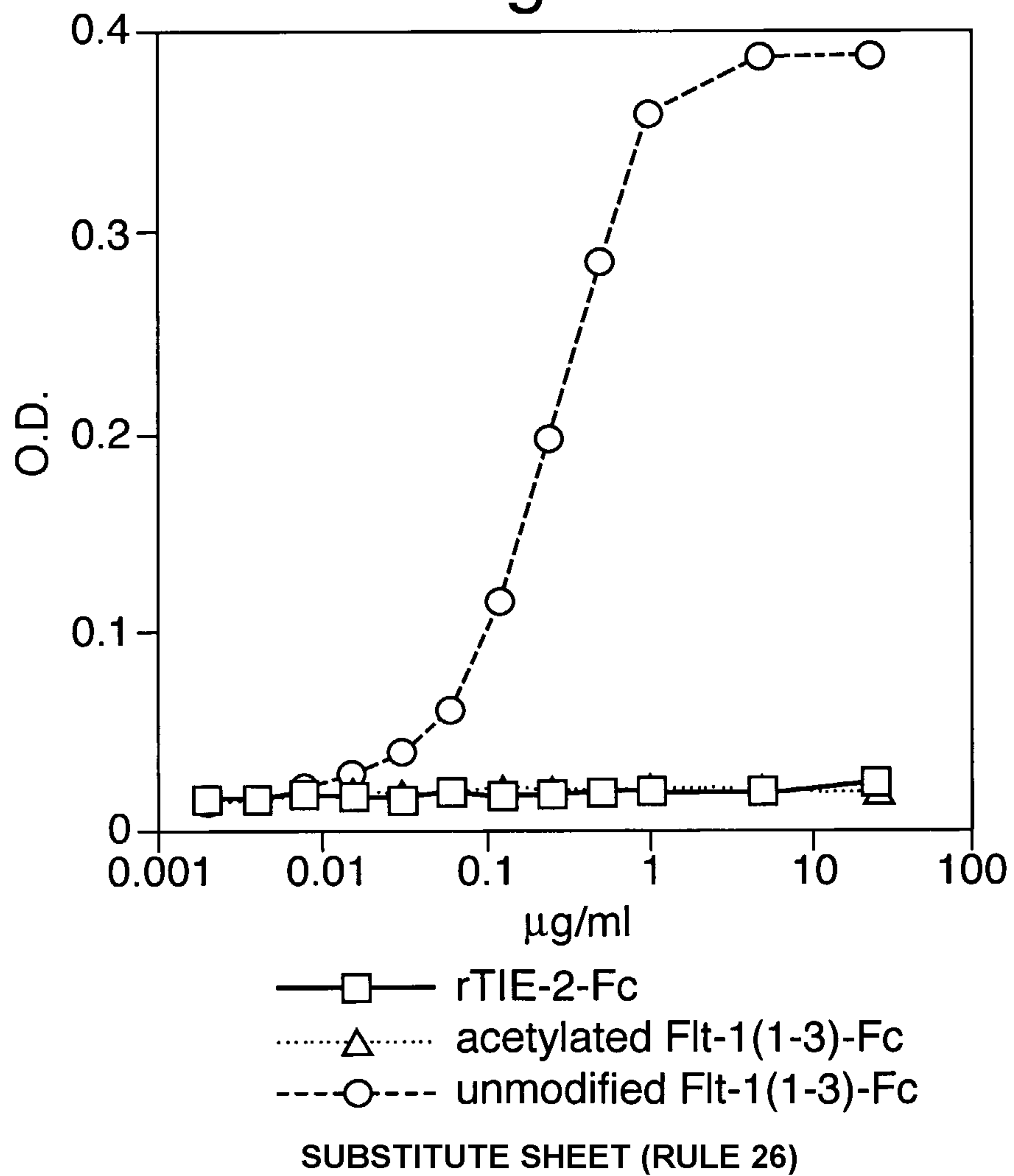
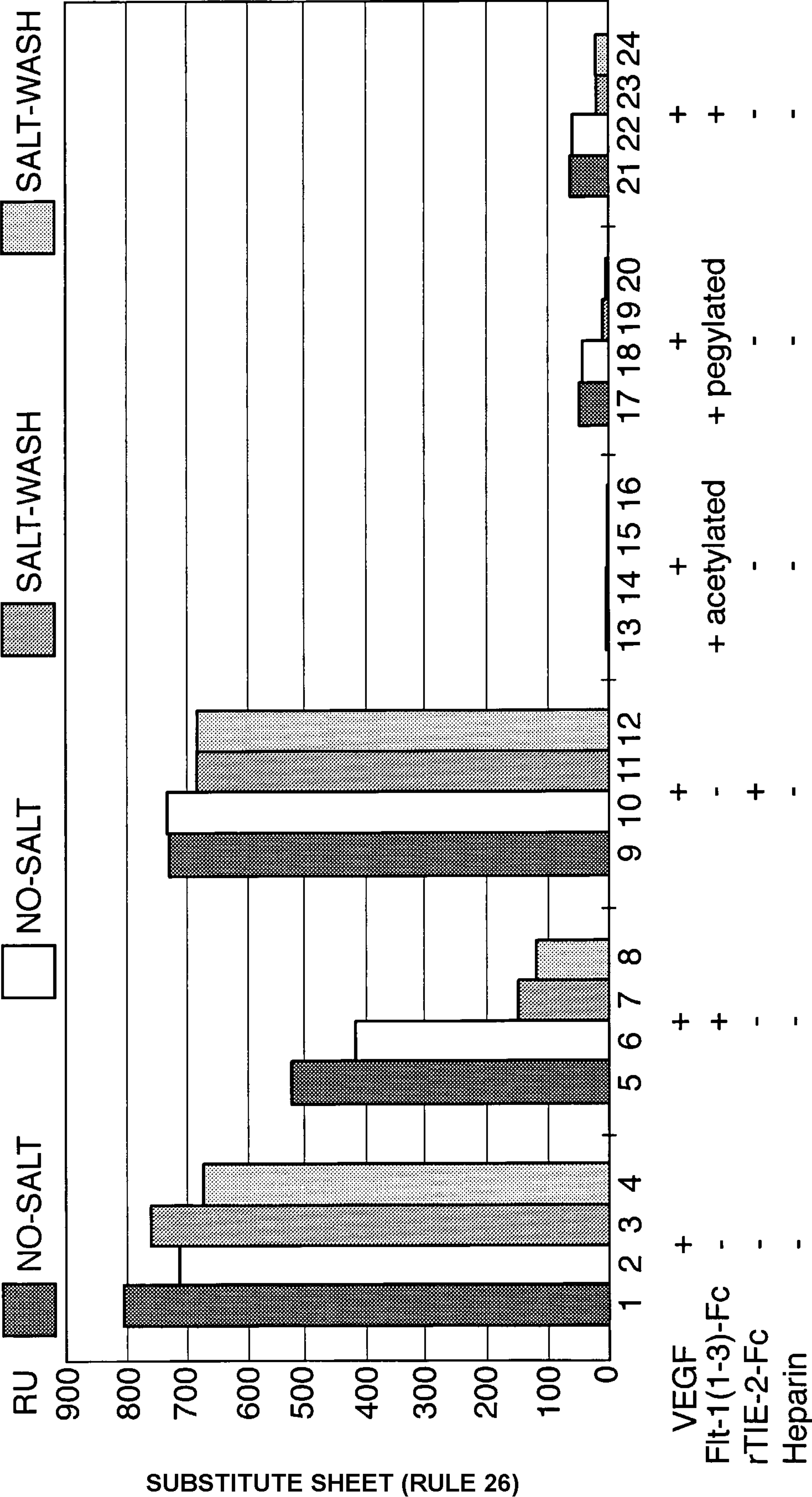
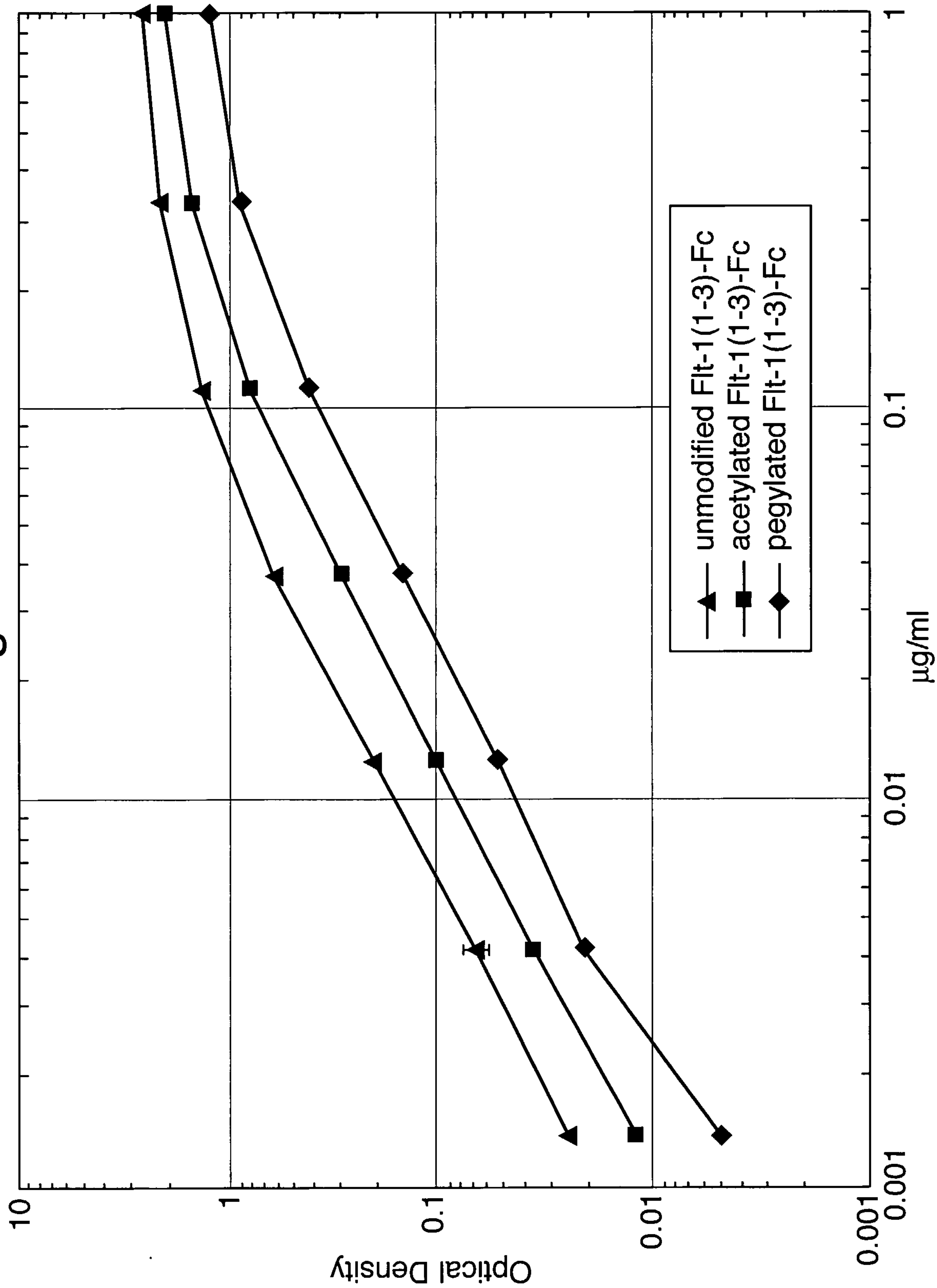


Fig.3.



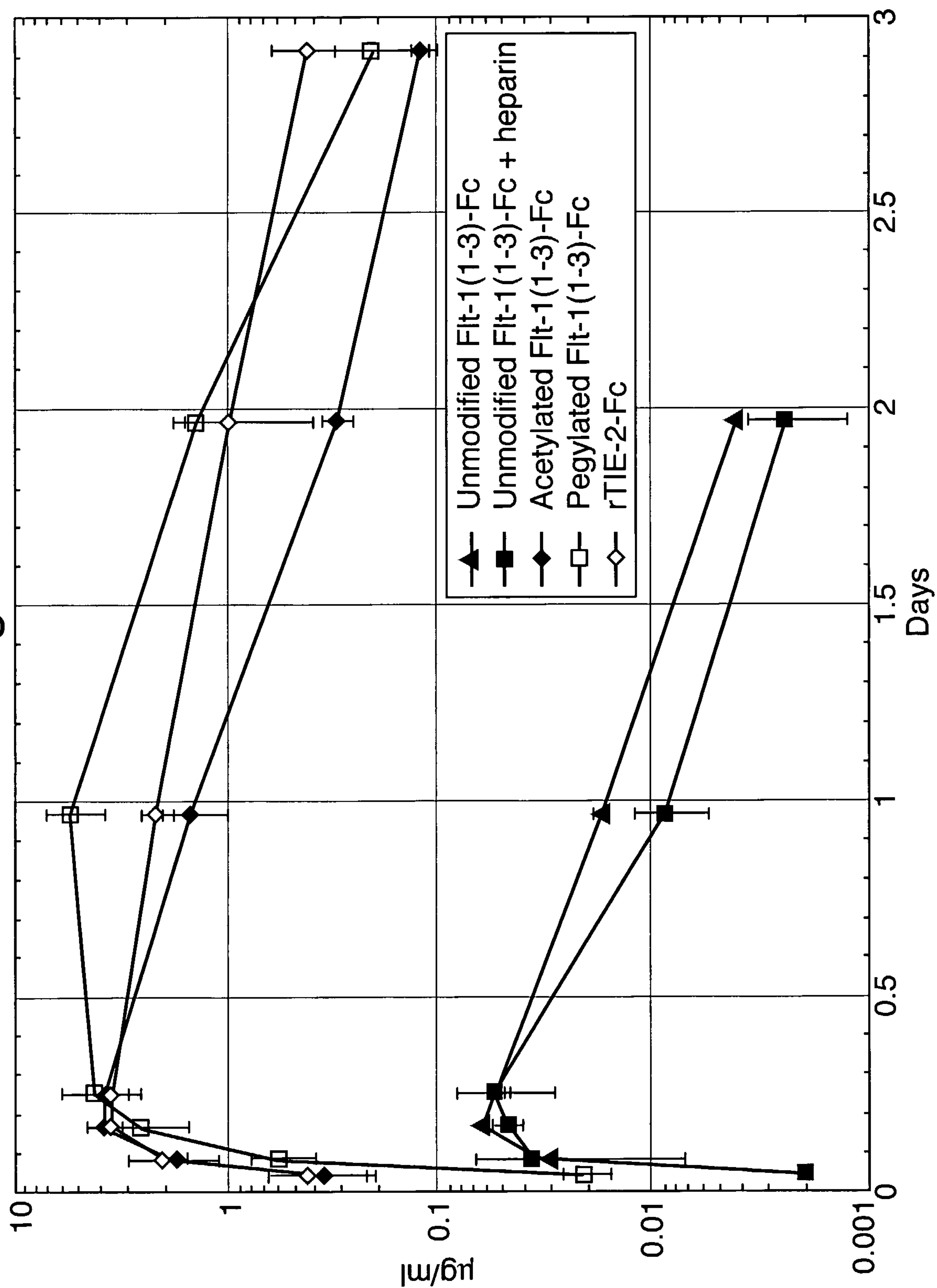
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Fig.4.



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Fig.5.



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Fig.6A.

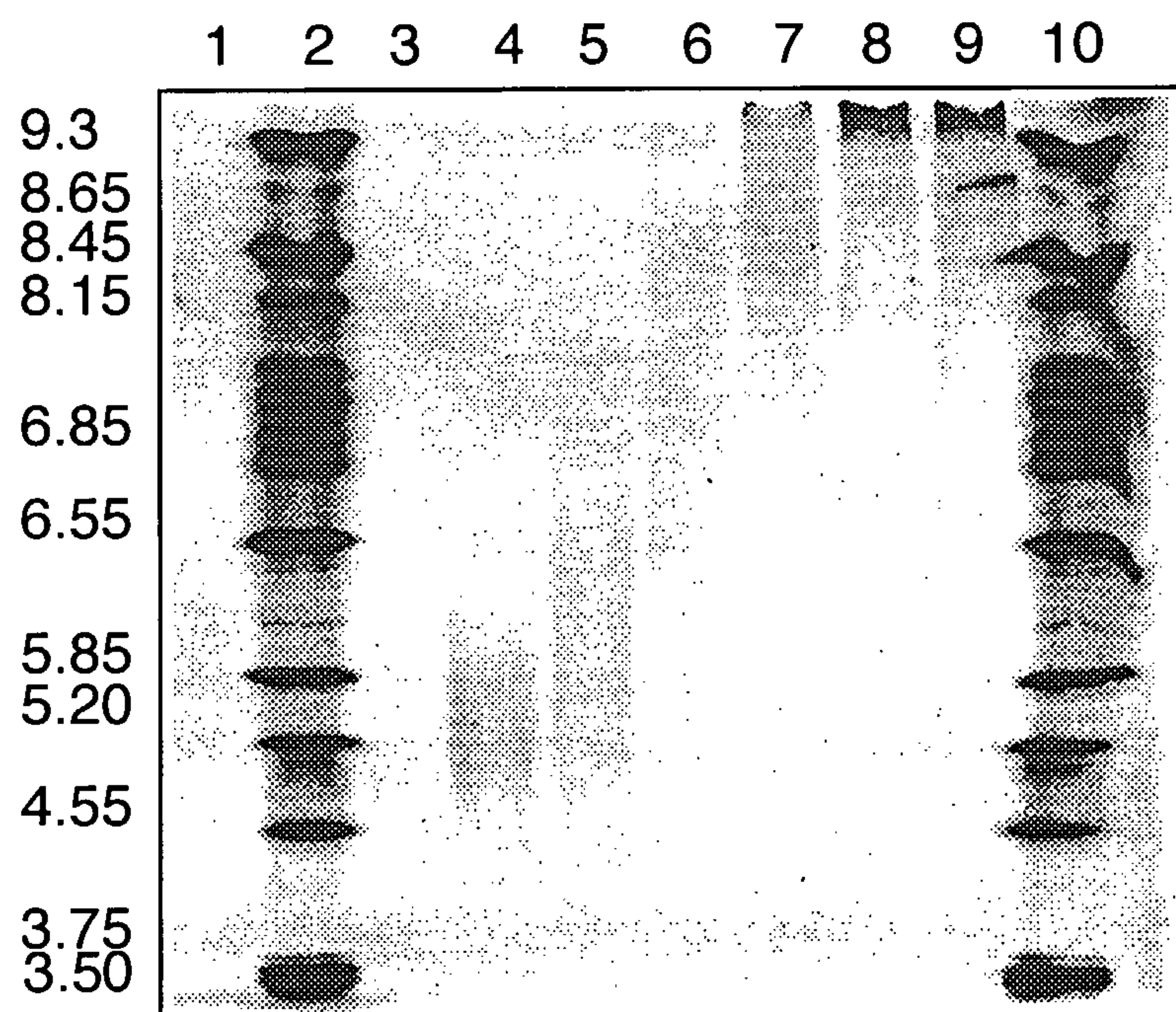
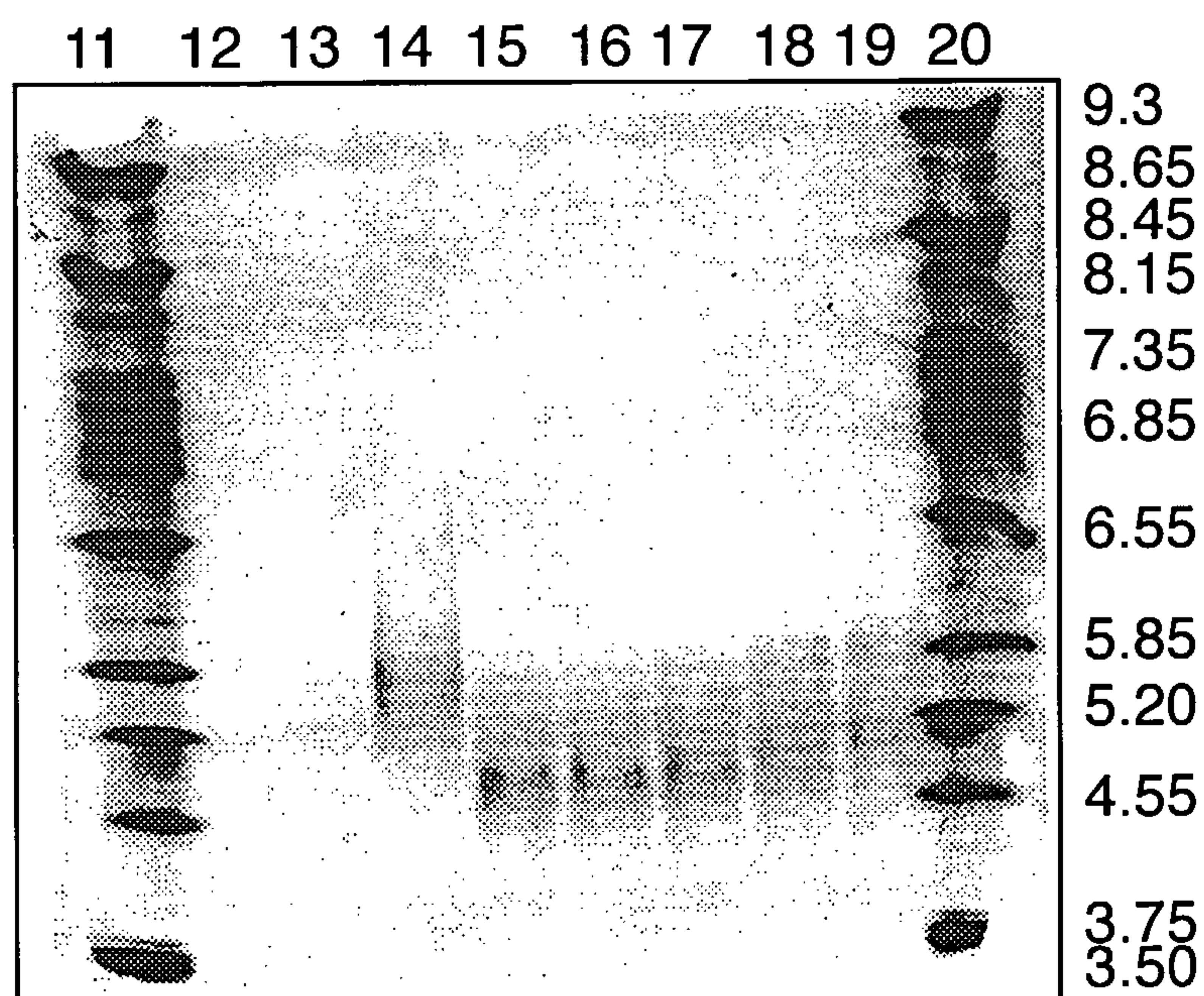
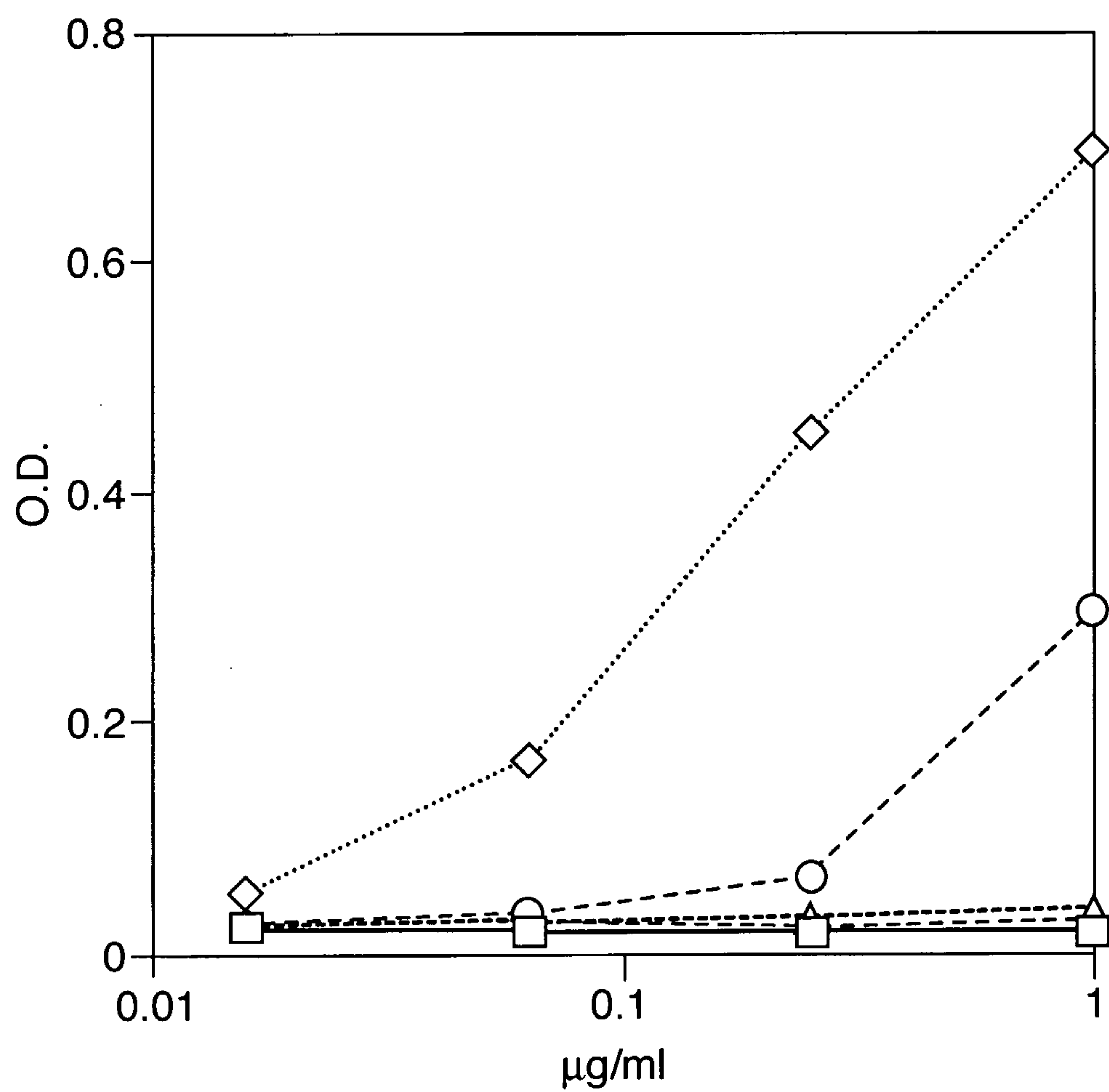


Fig.6B.



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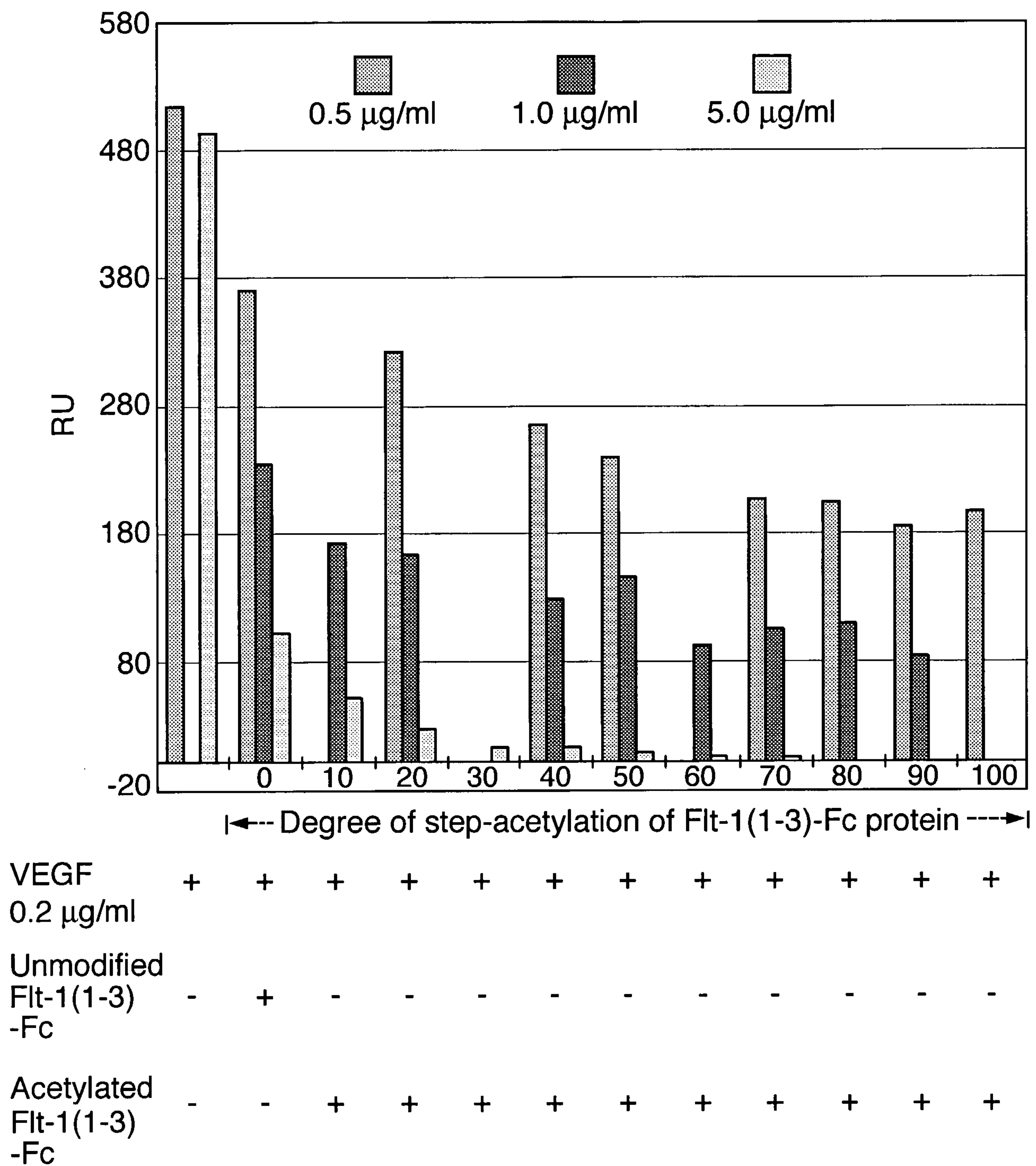
Fig.7.



- rTIE-2-Fc
.....◇..... unmodified Flt-1(1-3)-Fc
---○--- acetylated Flt-1(1-3)-Fc (10X)
-.-△-.- acetylated Flt-1(1-3)-Fc (20X)
---⊞--- acetylated Flt-1(1-3)-Fc (30X)

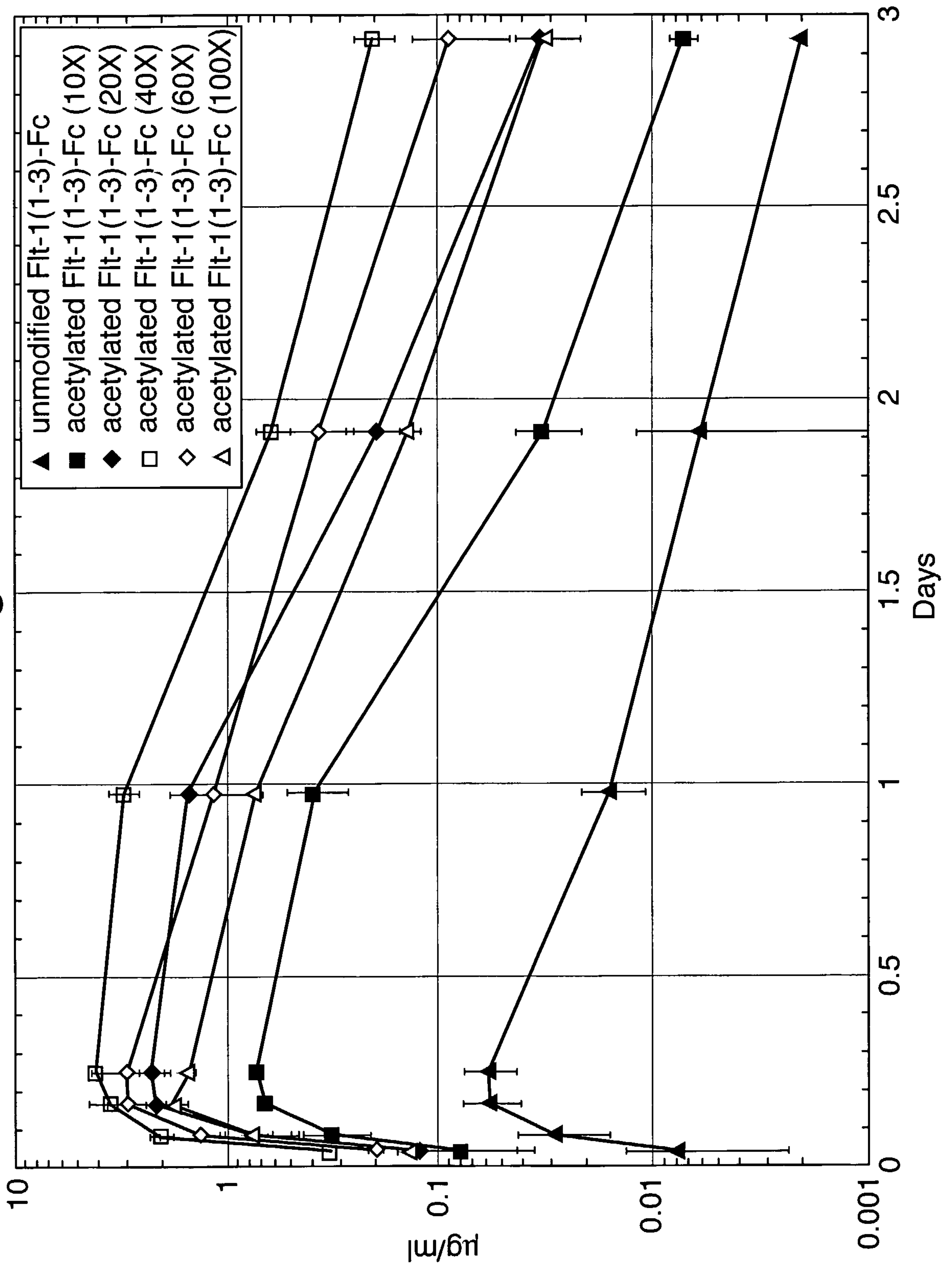
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Fig.8.



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Fig.9.



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Fig.10A.

	10		20		30		40		50		60								
*	*	*	*	*	*	*	*	*	*	*	*								
ATG	GTC	AGC	TAC	TGG	GAC	ACC	GGG	GTC	CTG	CTG	TGC	GCG	CTG	CTC	AGC	TGT	CTG	CTT	CTC
TAC	CAG	TCG	ATG	ACC	CTG	TGG	CCC	CAG	GAC	GAC	ACG	CGC	GAC	GAG	TCG	ACA	GAC	GAA	GAG
Met	Val	Ser	Tyr	Trp	Asp	Thr	Gly	Val	Leu	Leu	Cys	Ala	Leu	Leu	Ser	Cys	Leu	Leu	Leu>

	70		80		90		100		110		120								
*	*	*	*	*	*	*	*	*	*	*	*								
ACA	GGA	TCT	AGT	TCA	GGT	TCA	AAA	TTA	AAA	GAT	CCT	GAA	CTG	AGT	TTA	AAA	GGC	ACC	CAG
TGT	CCT	AGA	TCA	AGT	CCA	AGT	TTT	AAT	TTT	CTA	GGA	CTT	GAC	TCA	AAT	TTT	CCG	TGG	GTC
Thr	Gly	Ser	Ser	Ser	Gly	Ser	Lys	Leu	Lys	Asp	Pro	Glu	Leu	Ser	Leu	Lys	Gly	Thr	Gln>

	130		140		150		160		170		180								
*	*	*	*	*	*	*	*	*	*	*	*								
CAC	ATC	ATG	CAA	GCA	GGC	CAG	ACA	CTG	CAT	CTC	CAA	TGC	AGG	GGG	GAA	GCA	GCC	CAT	AAA
GTG	TAG	TAC	GTT	CGT	CCG	GTC	TGT	GAC	GTA	GAG	GTT	ACG	TCC	CCC	CTT	CGT	CGG	GTA	TTT
His	Ile	Met	Gln	Ala	Gly	Gln	Thr	Leu	His	Leu	Gln	Cys	Arg	Gly	Glu	Ala	Ala	His	Lys>

	190		200		210		220		230		240								
*	*	*	*	*	*	*	*	*	*	*	*								
TGG	TCT	TTG	CCT	GAA	ATG	GTG	AGT	AAG	GAA	AGC	GAA	AGG	CTG	AGC	ATA	ACT	AAA	TCT	GCC
ACC	AGA	AAC	GGA	CTT	TAC	CAC	TCA	TTC	CTT	TCG	CTT	TCC	GAC	TCG	TAT	TGA	TTT	AGA	CGG
Trp	Ser	Leu	Pro	Glu	Met	Val	Ser	Lys	Glu	Ser	Glu	Arg	Leu	Ser	Ile	Thr	Lys	Ser	Ala>

	250		260		270		280		290		300								
*	*	*	*	*	*	*	*	*	*	*	*								
TGT	GGA	AGA	AAT	GGC	AAA	CAA	TTC	TGC	AGT	ACT	TTA	ACC	TTG	AAC	ACA	GCT	CAA	GCA	AAC
ACA	CCT	TCT	TTA	CCG	TTT	GTT	AAG	ACG	TCA	TGA	AAT	TGG	AAC	TTG	TGT	CGA	GTT	CGT	TTG
Cys	Gly	Arg	Asn	Gly	Lys	Gln	Phe	Cys	Ser	Thr	Leu	Thr	Leu	Asn	Thr	Ala	Gln	Ala	Asn>

	310		320		330		340		350		360								
*	*	*	*	*	*	*	*	*	*	*	*								
CAC	ACT	GGC	TTC	TAC	AGC	TGC	AAA	TAT	CTA	GCT	GTA	CCT	ACT	TCA	AAG	AAG	AAG	GAA	ACA
GTG	TGA	CCG	AAG	ATG	TCG	ACG	TTT	ATA	GAT	CGA	CAT	GGA	TGA	AGT	TTC	TTC	TTC	CTT	TGT
His	Thr	Gly	Phe	Tyr	Ser	Cys	Lys	Tyr	Leu	Ala	Val	Pro	Thr	Ser	Lys	Lys	Lys	Glu	Thr>

	370		380		390		400		410		420								
*	*	*	*	*	*	*	*	*	*	*	*								
GAA	TCT	GCA	ATC	TAT	ATA	TTT	ATT	AGT	GAT	ACA	GGT	AGA	CCT	TTC	GTA	GAG	ATG	TAC	AGT
CTT	AGA	CGT	TAG	ATA	TAT	AAA	TAA	TCA	CTA	TGT	CCA	TCT	GGA	AAG	CAT	CTC	TAC	ATG	TCA
Glu	Ser	Ala	Ile	Tyr	Ile	Phe	Ile	Ser	Asp	Thr	Gly	Arg	Pro	Phe	Val	Glu	Met	Tyr	Ser>

	430		440		450		460		470		480								
*	*	*	*	*	*	*	*	*	*	*	*								
GAA	ATC	CCC	GAA	ATT	ATA	CAC	ATG	ACT	GAA	GGA	AGG	GAG	CTC	GTC	ATT	CCC	TGC	CGG	GTT
CTT	TAG	GGG	CTT	TAA	TAT	GTG	TAC	TGA	CTT	CCT	TCC	CTC	GAG	CAG	TAA	GGG	ACG	GCC	CAA
Glu	Ile	Pro	Glu	Ile	Ile	His	Met	Thr	Glu	Gly	Arg	Glu	Leu	Val	Ile	Pro	Cys	Arg	Val>

	490		500		510		520		530		540								
*	*	*	*	*	*	*	*	*	*	*	*								
ACG	TCA	CCT	AAC	ATC	ACT	GTT	ACT	TTA	AAA	AAG	TTT	CCA	CTT	GAC	ACT	TTG	ATC	CCT	GAT
TGC	AGT	GGA	TTG	TAG	TGA	CAA	TGA	AAT	TTT	TTC	AAA	GGT	GAA	CTG	TGA	AAC	TAG	GGA	CTA
Thr	Ser	Pro	Asn	Ile	Thr	Val	Thr	Leu	Lys	Lys	Phe	Pro	Leu	Asp	Thr	Leu	Ile	Pro	Asp>

10/55

Fig.10B.

550	560	570	580	590	600
* * *	* * *	* * *	* * *	* * *	* * *
GGA AAA CGC ATA ATC TGG GAC AGT AGA AAG GGC TTC ATC ATA TCA AAT GCA ACG TAC AAA					
CCT TTT GCG TAT TAG ACC CTG TCA TCT TTC CCG AAG TAG TAT AGT TTA CGT TGC ATG TTT					
Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys>					
610	620	630	640	650	660
* * *	* * *	* * *	* * *	* * *	* * *
GAA ATA GGG CTT CTG ACC TGT GAA GCA ACA GTC AAT GGG CAT TTG TAT AAG ACA AAC TAT					
CTT TAT CCC GAA GAC TGG ACA CTT CGT TGT CAG TTA CCC GTA AAC ATA TTC TGT TTG ATA					
Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr>					
670	680	690	700	710	720
* * *	* * *	* * *	* * *	* * *	* * *
CTC ACA CAT CGA CAA ACC AAT ACA ATC ATA GAT GTC CAA ATA AGC ACA CCA CGC CCA GTC					
GAG TGT GTA GCT GTT TGG TTA TGT TAG TAT CTA CAG GTT TAT TCG TGT GGT GCG GGT CAG					
Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val>					
730	740	750	760	770	780
* * *	* * *	* * *	* * *	* * *	* * *
AAA TTA CTT AGA GGC CAT ACT CTT GTC CTC AAT TGT ACT GCT ACC ACT CCC TTG AAC ACG					
TTT AAT GAA TCT CCG GTA TGA GAA CAG GAG TTA ACA TGA CGA TGG TGA GGG AAC TTG TGC					
Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr>					
790	800	810	820	830	840
* * *	* * *	* * *	* * *	* * *	* * *
AGA GTT CAA ATG ACC TGG AGT TAC CCT GAT GAA AAA AAT AAG AGA GCT TCC GTA AGG CGA					
TCT CAA GTT TAC TGG ACC TCA ATG GGA CTA CTT TTT TTA TTC TCT CGA AGG CAT TCC GCT					
Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys Asn Lys Arg Ala Ser Val Arg Arg>					
850	860	870	880	890	900
* * *	* * *	* * *	* * *	* * *	* * *
CGA ATT GAC CAA AGC AAT TCC CAT GCC AAC ATA TTC TAC AGT GTT CTT ACT ATT GAC AAA					
GCT TAA CTG GTT TCG TTA AGG GTA CGG TTG TAT AAG ATG TCA CAA GAA TGA TAA CTG TTT					
Arg Ile Asp Gln Ser Asn Ser His Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys>					
910	920	930	940	950	960
* * *	* * *	* * *	* * *	* * *	* * *
ATG CAG AAC AAA GAC AAA GGA CTT TAT ACT TGT CGT GTA AGG AGT GGA CCA TCA TTC AAA					
TAC GTC TTG TTT CTG TTT CCT GAA ATA TGA ACA GCA CAT TCC TCA CCT GGT AGT AAG TTT					
Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys>					
970	980	990	1000	1010	1020
* * *	* * *	* * *	* * *	* * *	* * *
TCT GTT AAC ACC TCA GTG CAT ATA TAT GAT AAA GCA GGC CCG GGC GAG CCC AAA TCT TGT					
AGA CAA TTG TGG AGT CAC GTA TAT ATA CTA TTT CGT CCG GGC CCG CTC GGG TTT AGA ACA					
Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Gly Pro Gly Glu Pro Lys Ser Cys>					
1030	1040	1050	1060	1070	1080
* * *	* * *	* * *	* * *	* * *	* * *
GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC					
CTG TTT TGA GTG TGT ACG GGT GGC ACG GGT CGT GGA CTT GAG GAC CCC CCT GGC AGT CAG					
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val>					

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Fig.10C.

1090					1100					1110					1120					1130					1140				
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*					
TTC	CTC	TTC	CCC	CCA	AAA	CCC	AAG	GAC	ACC	CTC	ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACA										
AAG	GAG	AAG	GGG	GGT	TTT	GGG	TTC	CTG	TGG	GAG	TAC	TAG	AGG	GCC	TGG	GGA	CTC	CAG	TGT										
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr>										

1150					1160					1170					1180					1190					1200				
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*					
TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAC	GAA	GAC	CCT	GAG	GTC	AAG	TTC	AAC	TGG	TAC	GTG	GAC										
ACG	CAC	CAC	CAC	CTG	CAC	TCG	GTG	CTT	CTG	GGA	CTC	CAG	TTC	AAG	TTG	ACC	ATG	CAC	CTG										
Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp>										

1210					1220					1230					1240					1250					1260				
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*					
GGC	GTG	GAG	GTG	CAT	AAT	GCC	AAG	ACA	AAG	CCG	CGG	GAG	GAG	CAG	TAC	AAC	AGC	ACG	TAC										
CCG	CAC	CTC	CAC	GTA	TTA	CGG	TTC	TGT	TTC	GGC	GCC	CTC	CTC	GTC	ATG	TTG	TCG	TGC	ATG										
Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr>										

1270					1280					1290					1300					1310					1320				
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*					
CGT	GTG	GTC	AGC	GTC	CTC	ACC	GTC	CTG	CAC	CAG	GAC	TGG	CTG	AAT	GGC	AAG	GAG	TAC	AAG										
GCA	CAC	CAG	TCG	CAG	GAG	TGG	CAG	GAC	GTG	GTC	CTG	ACC	GAC	TTA	CCG	TTC	CTC	ATG	TTC										
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys>										

1330					1340					1350					1360					1370					1380				
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*					
TGC	AAG	GTC	TCC	AAC	AAA	GCC	CTC	CCA	GCC	CCC	ATC	GAG	AAA	ACC	ATC	TCC	AAA	GCC	AAA										
ACG	TTC	CAG	AGG	TTG	TTT	CGG	GAG	GGT	CGG	GGG	TAG	CTC	TTT	TGG	TAG	AGG	TTT	CGG	TTT										
Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys>										

1390					1400					1410					1420					1430					1440				
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*					
GGG	CAG	CCC	CGA	GAA	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CGG	GAT	GAG	CTG	ACC	AAG										
CCC	GTC	GGG	GCT	CTT	GGT	GTC	CAC	ATG	TGG	GAC	GGG	GGT	AGG	GCC	CTA	CTC	GAC	TGG	TTC										
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys>										

1450					1460					1470					1480					1490					1500				
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*					
AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GGC	TTC	TAT	CCC	AGC	GAC	ATC	GCC	GTG	GAG										
TTG	GTC	CAG	TCG	GAC	TGG	ACG	GAC	CAG	TTT	CCG	AAG	ATA	GGG	TCG	CTG	TAG	CGG	CAC	CTC										
Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu>										

1510					1520					1530					1540					1550					1560				
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*					
TGG	GAG	AGC	AAT	GGG	CAG	CCG	GAG	AAC	AAC	TAC	AAG	ACC	ACG	CCT	CCC	GTG	CTG	GAC	TCC										
ACC	CTC	TCG	TTA	CCC	GTC	GGC	CTC	TTG	TTG	ATG	TTC	TGG	TGC	GGA	GGG	CAC	GAC	CTG	AGG										
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser>										

1570					1580					1590					1600					1610					1620				
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*					
GAC	GGC	TCC	TTC	TTC	CTC	TAC	AGC	AAG	CTC	ACC	GTG	GAC	AAG	AGC	AGG	TGG	CAG	CAG	GGG										
CTG	CCG	AGG	AAG	AAG	GAG	ATG	TCG	TTC	GAG	TGG	CAC	CTG	TTC	TCG	TCC	ACC	GTC	GTC	CCC										
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly>										

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Fig.10D.

1630				1640				1650				1660				1670				1680	
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*			
AAC	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG	GCT	CTG	CAC	AAC	CAC	TAC	ACG	CAG	AAG	AGC		
TTG	CAG	AAG	AGT	ACG	AGG	CAC	TAC	GTA	CTC	CGA	GAC	GTG	TTG	GTG	ATG	TGC	GTC	TTC	TCG		
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser>		

1690				1700			
*	*	*	*	*	*	*	*
CTC	TCC	CTG	TCT	CCG	GGT	AAA	TGA
GAG	AGG	GAC	AGA	GGC	CCA	TTT	ACT
Leu	Ser	Leu	Ser	Pro	Gly	Lys	***>

Fig.11.

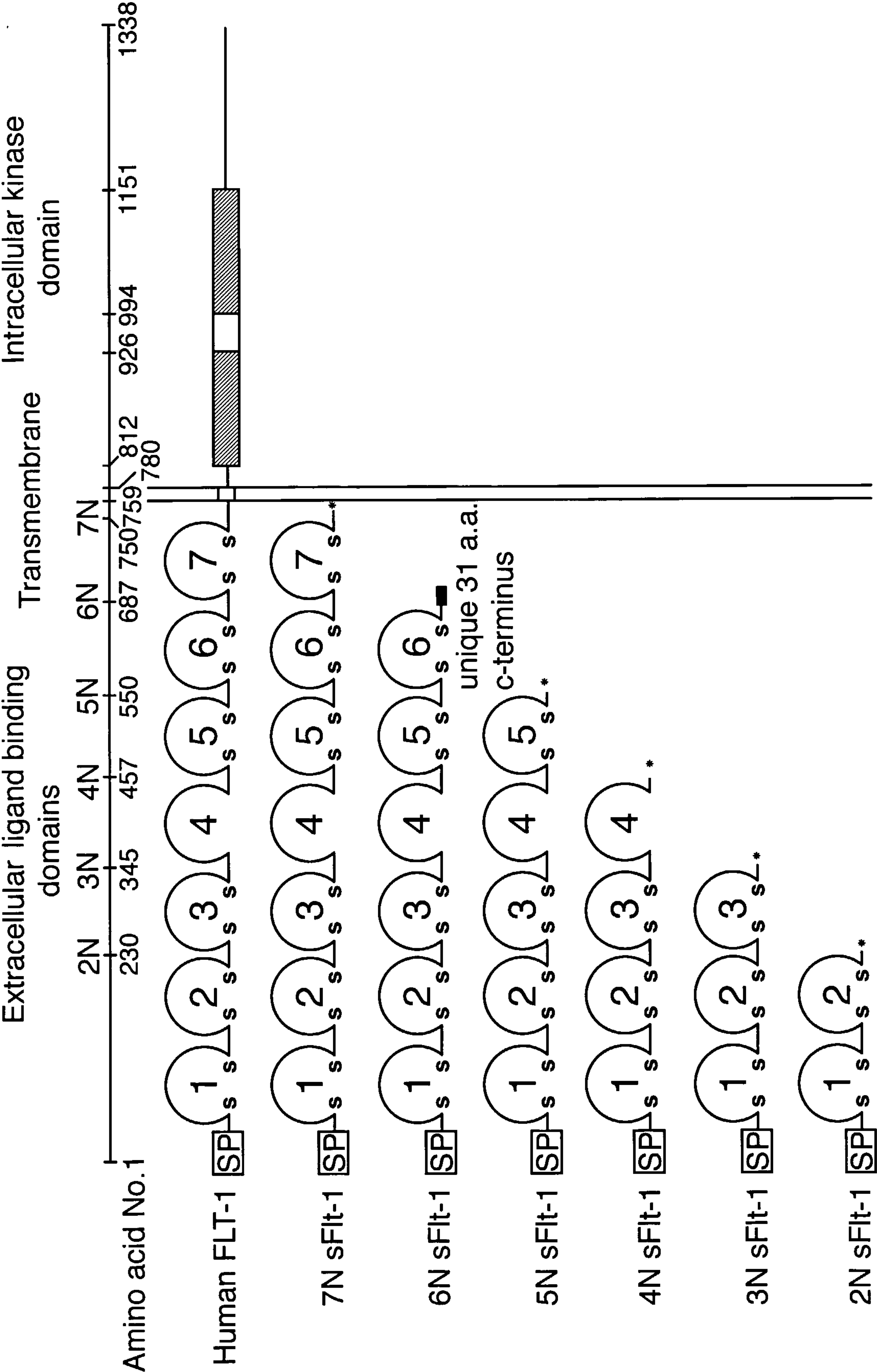


Fig.12A.

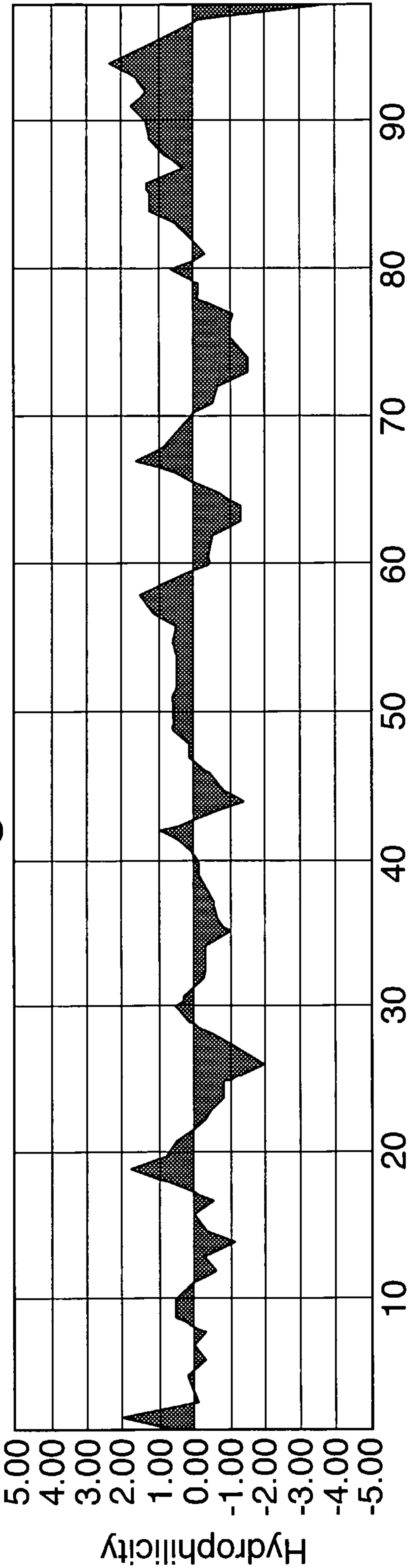


Fig.12B.



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Fig.13A.

	10		20		30		40		50		60								
*	*	*	*	*	*	*	*	*	*	*	*								
ATG	GTC	AGC	TAC	TGG	GAC	ACC	GGG	GTC	CTG	CTG	TGC	GCG	CTG	CTC	AGC	TGT	CTG	CTT	CTC
TAC	CAG	TCG	ATG	ACC	CTG	TGG	CCC	CAG	GAC	GAC	ACG	CGC	GAC	GAG	TCG	ACA	GAC	GAA	GAG
Met	Val	Ser	Tyr	Trp	Asp	Thr	Gly	Val	Leu	Leu	Cys	Ala	Leu	Leu	Ser	Cys	Leu	Leu	Leu>

	70		80		90		100		110		120								
*	*	*	*	*	*	*	*	*	*	*	*								
ACA	GGA	TCT	AGT	TCA	GGT	TCA	AAA	TTA	AAA	GAT	CCT	GAA	CTG	AGT	TTA	AAA	GGC	ACC	CAG
TGT	CCT	AGA	TCA	AGT	CCA	AGT	TTT	AAT	TTT	CTA	GGA	CTT	GAC	TCA	AAT	TTT	CCG	TGG	GTC
Thr	Gly	Ser	Ser	Ser	Gly	Ser	Lys	Leu	Lys	Asp	Pro	Glu	Leu	Ser	Leu	Lys	Gly	Thr	Gln>

	130		140		150		160		170		180								
*	*	*	*	*	*	*	*	*	*	*	*								
CAC	ATC	ATG	CAA	GCA	GGC	CAG	ACA	CTG	CAT	CTC	CAA	TGC	AGG	GGG	GAA	GCA	GCC	CAT	AAA
GTG	TAG	TAC	GTT	CGT	CCG	GTC	TGT	GAC	GTA	GAG	GTT	ACG	TCC	CCC	CTT	CGT	CGG	GTA	TTT
His	Ile	Met	Gln	Ala	Gly	Gln	Thr	Leu	His	Leu	Gln	Cys	Arg	Gly	Glu	Ala	Ala	His	Lys>

	190		200		210		220		230		240								
*	*	*	*	*	*	*	*	*	*	*	*								
TGG	TCT	TTG	CCT	GAA	ATG	GTG	AGT	AAG	GAA	AGC	GAA	AGG	CTG	AGC	ATA	ACT	AAA	TCT	GCC
ACC	AGA	AAC	GGA	CTT	TAC	CAC	TCA	TTC	CTT	TCG	CTT	TCC	GAC	TCG	TAT	TGA	TTT	AGA	CGG
Trp	Ser	Leu	Pro	Glu	Met	Val	Ser	Lys	Glu	Ser	Glu	Arg	Leu	Ser	Ile	Thr	Lys	Ser	Ala>

	250		260		270		280		290		300								
*	*	*	*	*	*	*	*	*	*	*	*								
TGT	GGA	AGA	AAT	GGC	AAA	CAA	TTC	TGC	AGT	ACT	TTA	ACC	TTG	AAC	ACA	GCT	CAA	GCA	AAC
ACA	CCT	TCT	TTA	CCG	TTT	GTT	AAG	ACG	TCA	TGA	AAT	TGG	AAC	TTG	TGT	CGA	GTT	CGT	TTG
Cys	Gly	Arg	Asn	Gly	Lys	Gln	Phe	Cys	Ser	Thr	Leu	Thr	Leu	Asn	Thr	Ala	Gln	Ala	Asn>

	310		320		330		340		350		360								
*	*	*	*	*	*	*	*	*	*	*	*								
CAC	ACT	GGC	TTC	TAC	AGC	TGC	AAA	TAT	CTA	GCT	GTA	CCT	ACT	TCA	AAG	AAG	AAG	GAA	ACA
GTG	TGA	CCG	AAG	ATG	TCG	ACG	TTT	ATA	GAT	CGA	CAT	GGA	TGA	AGT	TTC	TTC	TTC	CTT	TGT
His	Thr	Gly	Phe	Tyr	Ser	Cys	Lys	Tyr	Leu	Ala	Val	Pro	Thr	Ser	Lys	Lys	Lys	Glu	Thr>

	370		380		390		400		410		420								
*	*	*	*	*	*	*	*	*	*	*	*								
GAA	TCT	GCA	ATC	TAT	ATA	TTT	ATT	AGT	GAT	ACA	GGT	AGA	CCT	TTC	GTA	GAG	ATG	TAC	AGT
CTT	AGA	CGT	TAG	ATA	TAT	AAA	TAA	TCA	CTA	TGT	CCA	TCT	GGA	AAG	CAT	CTC	TAC	ATG	TCA
Glu	Ser	Ala	Ile	Tyr	Ile	Phe	Ile	Ser	Asp	Thr	Gly	Arg	Pro	Phe	Val	Glu	Met	Tyr	Ser>

	430		440		450		460		470		480								
*	*	*	*	*	*	*	*	*	*	*	*								
GAA	ATC	CCC	GAA	ATT	ATA	CAC	ATG	ACT	GAA	GGA	AGG	GAG	CTC	GTC	ATT	CCC	TGC	CGG	GTT
CTT	TAG	GGG	CTT	TAA	TAT	GTG	TAC	TGA	CTT	CCT	TCC	CTC	GAG	CAG	TAA	GGG	ACG	GCC	CAA
Glu	Ile	Pro	Glu	Ile	Ile	His	Met	Thr	Glu	Gly	Arg	Glu	Leu	Val	Ile	Pro	Cys	Arg	Val>

	490		500		510		520		530		540								
*	*	*	*	*	*	*	*	*	*	*	*								
ACG	TCA	CCT	AAC	ATC	ACT	GTT	ACT	TTA	AAA	AAG	TTT	CCA	CTT	GAC	ACT	TTG	ATC	CCT	GAT
TGC	AGT	GGA	TTG	TAG	TGA	CAA	TGA	AAT	TTT	TTC	AAA	GGT	GAA	CTG	TGA	AAC	TAG	GGA	CTA
Thr	Ser	Pro	Asn	Ile	Thr	Val	Thr	Leu	Lys	Lys	Phe	Pro	Leu	Asp	Thr	Leu	Ile	Pro	Asp>

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Fig.13B.

550	560	570	580	590	600
* * *	* * *	* * *	* * *	* * *	* * *
GGA AAA CGC ATA ATC TGG GAC AGT AGA AAG GGC TTC ATC ATA TCA AAT GCA ACG TAC AAA	CCT TTT GCG TAT TAG ACC CTG TCA TCT TTC CCG AAG TAG TAT AGT TTA CGT TGC ATG TTT	Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys>			
610	620	630	640	650	660
* * *	* * *	* * *	* * *	* * *	* * *
GAA ATA GGG CTT CTG ACC TGT GAA GCA ACA GTC AAT GGG CAT TTG TAT AAG ACA AAC TAT	CTT TAT CCC GAA GAC TGG ACA CTT CGT TGT CAG TTA CCC GTA AAC ATA TTC TGT TTG ATA	Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr>			
670	680	690	700	710	720
* * *	* * *	* * *	* * *	* * *	* * *
CTC ACA CAT CGA CAA ACC AAT ACA ATC ATA GAT GTC CAA ATA AGC ACA CCA CGC CCA GTC	GAG TGT GTA GCT GTT TGG TTA TGT TAG TAT CTA CAG GTT TAT TCG TGT GGT GCG GGT CAG	Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val>			
730	740	750	760	770	780
* * *	* * *	* * *	* * *	* * *	* * *
AAA TTA CTT AGA GGC CAT ACT CTT GTC CTC AAT TGT ACT GCT ACC ACT CCC TTG AAC ACG	TTT AAT GAA TCT CCG GTA TGA GAA CAG GAG TTA ACA TGA CGA TGG TGA GGG AAC TTG TGC	Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr>			
790	800	810	820	830	840
* * *	* * *	* * *	* * *	* * *	* * *
AGA GTT CAA ATG ACC TGG AGT TAC CCT GAT GAA ATT GAC CAA AGC AAT TCC CAT GCC AAC	TCT CAA GTT TAC TGG ACC TCA ATG GGA CTA CTT TAA CTG GTT TCG TTA AGG GTA CGG TTG	Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Ile Asp Gln Ser Asn Ser His Ala Asn>			
850	860	870	880	890	900
* * *	* * *	* * *	* * *	* * *	* * *
ATA TTC TAC AGT GTT CTT ACT ATT GAC AAA ATG CAG AAC AAA GAC AAA GGA CTT TAT ACT	TAT AAG ATG TCA CAA GAA TGA TAA CTG TTT TAC GTC TTG TTT CTG TTT CCT GAA ATA TGA	Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr>			
910	920	930	940	950	960
* * *	* * *	* * *	* * *	* * *	* * *
TGT CGT GTA AGG AGT GGA CCA TCA TTC AAA TCT GTT AAC ACC TCA GTG CAT ATA TAT GAT	ACA GCA CAT TCC TCA CCT GGT AGT AAG TTT AGA CAA TTG TGG AGT CAC GTA TAT ATA CTA	Cys Arg Val Arg Ser Gly Pro Ser Phe Lys Ser Val Asn Thr Ser Val His Ile Tyr Asp>			
970	980	990	1000	1010	1020
* * *	* * *	* * *	* * *	* * *	* * *
AAA GCA GGC CCG GGC GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA	TTT CGT CCG GGC CCG CTC GGG TTT AGA ACA CTG TTT TGA GTG TGT ACG GGT GGC ACG GGT	Lys Ala Gly Pro Gly Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro>			
1030	1040	1050	1060	1070	1080
* * *	* * *	* * *	* * *	* * *	* * *
GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC	CGT GGA CTT GAG GAC CCC CCT GGC AGT CAG AAG GAG AAG GGG GGT TTT GGG TTC CTG TGG	Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr>			

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Fig.13C.

1090	1100	1110	1120	1130	1140
* * *	* * *	* * *	* * *	* * *	* * *
CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC					
GAG TAC TAG AGG GCC TGG GGA CTC CAG TGT ACG CAC CAC CAC CTG CAC TCG GTG CTT CTG					
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp>					
1150	1160	1170	1180	1190	1200
* * *	* * *	* * *	* * *	* * *	* * *
CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG					
GGA CTC CAG TTC AAG TTG ACC ATG CAC CTG CCG CAC CTC CAC GTA TTA CGG TTC TGT TTC					
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys>					
1210	1220	1230	1240	1250	1260
* * *	* * *	* * *	* * *	* * *	* * *
CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC					
GGC GCC CTC CTC GTC ATG TTG TCG TGC ATG GCA CAC CAG TCG CAG GAG TGG CAG GAC GTG					
Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His>					
1270	1280	1290	1300	1310	1320
* * *	* * *	* * *	* * *	* * *	* * *
CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC					
GTC CTG ACC GAC TTA CCG TTC CTC ATG TTC ACG TTC CAG AGG TTG TTT CGG GAG GGT CGG					
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala>					
1330	1340	1350	1360	1370	1380
* * *	* * *	* * *	* * *	* * *	* * *
CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC					
GGG TAG CTC TTT TGG TAG AGG TTT CGG TTT CCC GTC GGG GCT CTT GGT GTC CAC ATG TGG					
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr>					
1390	1400	1410	1420	1430	1440
* * *	* * *	* * *	* * *	* * *	* * *
CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA					
GAC GGG GGT AGG GCC CTA CTC GAC TGG TTC TTG GTC CAG TCG GAC TGG ACG GAC CAG TTT					
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys>					
1450	1460	1470	1480	1490	1500
* * *	* * *	* * *	* * *	* * *	* * *
GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC					
CCG AAG ATA GGG TCG CTG TAG CGG CAC CTC ACC CTC TCG TTA CCC GTC GGC CTC TTG TTG					
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn>					
1510	1520	1530	1540	1550	1560
* * *	* * *	* * *	* * *	* * *	* * *
TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC					
ATG TTC TGG TGC GGA GGG CAC GAC CTG AGG CTG CCG AGG AAG AAG GAG ATG TCG TTC GAG					
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu>					
1570	1580	1590	1600	1610	1620
* * *	* * *	* * *	* * *	* * *	* * *
ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG					
TGG CAC CTG TTC TCG TCC ACC GTC GTC CCC TTG CAG AAG AGT ACG AGG CAC TAC GTA CTC					
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu>					

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Fig.13D.

1630				1640				1650				1660				1670			
*		*		*		*		*		*		*		*		*			
GCT	CTG	CAC	AAC	CAC	TAC	ACG	CAG	AAG	AGC	CTC	TCC	CTG	TCT	CCG	GGT	AAA	TGA		
CGA	GAC	GTG	TTG	GTG	ATG	TGC	GTC	TTC	TCG	GAG	AGG	GAC	AGA	GGC	CCA	TTT	ACT		
Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	***>		

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Fig.14A.

			10				20				30				40				50			60
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
ATG	GTC	AGC	TAC	TGG	GAC	ACC	GGG	GTC	CTG	CTG	TGC	GCG	CTG	CTC	AGC	TGT	CTG	CTT	CTC			
TAC	CAG	TCG	ATG	ACC	CTG	TGG	CCC	CAG	GAC	GAC	ACG	CGC	GAC	GAG	TCG	ACA	GAC	GAA	GAG			
Met	Val	Ser	Tyr	Trp	Asp	Thr	Gly	Val	Leu	Leu	Cys	Ala	Leu	Leu	Ser	Cys	Leu	Leu	Leu	>		
			70				80				90				100				110			120
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
ACA	GGA	TCT	AGT	TCC	GGA	GGT	AGA	CCT	TTC	GTA	GAG	ATG	TAC	AGT	GAA	ATC	CCC	GAA	ATT			
TGT	CCT	AGA	TCA	AGG	CCT	CCA	TCT	GGA	AAG	CAT	CTC	TAC	ATG	TCA	CTT	TAG	GGG	CTT	TAA			
Thr	Gly	Ser	Ser	Ser	Gly	Gly	Arg	Pro	Phe	Val	Glu	Met	Tyr	Ser	Glu	Ile	Pro	Glu	Ile	>		
			130				140				150				160				170			180
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
ATA	CAC	ATG	ACT	GAA	GGA	AGG	GAG	CTC	GTC	ATT	CCC	TGC	CGG	GTT	ACG	TCA	CCT	AAC	ATC			
TAT	GTG	TAC	TGA	CTT	CCT	TCC	CTC	GAG	CAG	TAA	GGG	ACG	GCC	CAA	TGC	AGT	GGA	TTG	TAG			
Ile	His	Met	Thr	Glu	Gly	Arg	Glu	Leu	Val	Ile	Pro	Cys	Arg	Val	Thr	Ser	Pro	Asn	Ile	>		
			190				200				210				220				230			240
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
ACT	GTT	ACT	TTA	AAA	AAG	TTT	CCA	CTT	GAC	ACT	TTG	ATC	CCT	GAT	GGA	AAA	CGC	ATA	ATC			
TGA	CAA	TGA	AAT	TTT	TTC	AAA	GGT	GAA	CTG	TGA	AAC	TAG	GGA	CTA	CCT	TTT	GCG	TAT	TAG			
Thr	Val	Thr	Leu	Lys	Lys	Phe	Pro	Leu	Asp	Thr	Leu	Ile	Pro	Asp	Gly	Lys	Arg	Ile	Ile	>		
			250				260				270				280				290			300
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
TGG	GAC	AGT	AGA	AAG	GGC	TTC	ATC	ATA	TCA	AAT	GCA	ACG	TAC	AAA	GAA	ATA	GGG	CTT	CTG			
ACC	CTG	TCA	TCT	TTC	CCG	AAG	TAG	TAT	AGT	TTA	CGT	TGC	ATG	TTT	CTT	TAT	CCC	GAA	GAC			
Trp	Asp	Ser	Arg	Lys	Gly	Phe	Ile	Ile	Ser	Asn	Ala	Thr	Tyr	Lys	Glu	Ile	Gly	Leu	Leu	>		
			310				320				330				340				350			360
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
ACC	TGT	GAA	GCA	ACA	GTC	AAT	GGG	CAT	TTG	TAT	AAG	ACA	AAC	TAT	CTC	ACA	CAT	CGA	CAA			
TGG	ACA	CTT	CGT	TGT	CAG	TTA	CCC	GTA	AAC	ATA	TTC	TGT	TTG	ATA	GAG	TGT	GTA	GCT	GTT			
Thr	Cys	Glu	Ala	Thr	Val	Asn	Gly	His	Leu	Tyr	Lys	Thr	Asn	Tyr	Leu	Thr	His	Arg	Gln	>		
			370				380				390				400				410			420
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
ACC	AAT	ACA	ATC	ATA	GAT	GTC	CAA	ATA	AGC	ACA	CCA	CGC	CCA	GTC	AAA	TTA	CTT	AGA	GGC			
TGG	TTA	TGT	TAG	TAT	CTA	CAG	GTT	TAT	TCG	TGT	GGT	GCG	GGT	CAG	TTT	AAT	GAA	TCT	CCG			
Thr	Asn	Thr	Ile	Ile	Asp	Val	Gln	Ile	Ser	Thr	Pro	Arg	Pro	Val	Lys	Leu	Leu	Arg	Gly	>		
			430				440				450				460				470			480
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
CAT	ACT	CTT	GTC	CTC	AAT	TGT	ACT	GCT	ACC	ACT	CCC	TTG	AAC	ACG	AGA	GTT	CAA	ATG	ACC			
GTA	TGA	GAA	CAG	GAG	TTA	ACA	TGA	CGA	TGG	TGA	GGG	AAC	TTG	TGC	TCT	CAA	GTT	TAC	TGG			
His	Thr	Leu	Val	Leu	Asn	Cys	Thr	Ala	Thr	Thr	Pro	Leu	Asn	Thr	Arg	Val	Gln	Met	Thr	>		
			490				500				510				520				530			540
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
TGG	AGT	TAC	CCT	GAT	GAA	ATT	GAC	CAA	AGC	AAT	TCC	CAT	GCC	AAC	ATA	TTC	TAC	AGT	GTT			
ACC	TCA	ATG	GGA	CTA	CTT	TAA	CTG	GTT	TCG	TTA	AGG	GTA	CGG	TTG	TAT	AAG	ATG	TCA	CAA			
Trp	Ser	Tyr	Pro	Asp	Glu	Ile	Asp	Gln	Ser	Asn	Ser	His	Ala	Asn	Ile	Phe	Tyr	Ser	Val	>		

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Fig.14B.

			550				560				570				580				590			600
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
CTT	ACT	ATT	GAC	AAA	ATG	CAG	AAC	AAA	GAC	AAA	GGA	CTT	TAT	ACT	TGT	CGT	GTA	AGG	AGT			
GAA	TGA	TAA	CTG	TTT	TAC	GTC	TTG	TTT	CTG	TTT	CCT	GAA	ATA	TGA	ACA	GCA	CAT	TCC	TCA			
Leu	Thr	Ile	Asp	Lys	Met	Gln	Asn	Lys	Asp	Lys	Gly	Leu	Tyr	Thr	Cys	Arg	Val	Arg	Ser	>		
			610				620				630				640				650			660
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
GGA	CCA	TCA	TTC	AAA	TCT	GTT	AAC	ACC	TCA	GTG	CAT	ATA	TAT	GAT	AAA	GCA	GGC	CCG	GGC			
CCT	GGT	AGT	AAG	TTT	AGA	CAA	TTG	TGG	AGT	CAC	GTA	TAT	ATA	CTA	TTT	CGT	CCG	GGC	CCG			
Gly	Pro	Ser	Phe	Lys	Ser	Val	Asn	Thr	Ser	Val	His	Ile	Tyr	Asp	Lys	Ala	Gly	Pro	Gly	>		
			670				680				690				700				710			720
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	CCG	TGC	CCA	GCA	CCT	GAA	CTC	CTG			
CTC	GGG	TTT	AGA	ACA	CTG	TTT	TGA	GTG	TGT	ACG	GGT	GGC	ACG	GGT	CGT	GGA	CTT	GAG	GAC			
Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	>		
			730				740				750				760				770			780
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
GGG	GGA	CCG	TCA	GTC	TTC	CTC	TTC	CCC	CCA	AAA	CCC	AAG	GAC	ACC	CTC	ATG	ATC	TCC	CGG			
CCC	CCT	GGC	AGT	CAG	AAG	GAG	AAG	GGG	GGT	TTT	GGG	TTC	CTG	TGG	GAG	TAC	TAG	AGG	GCC			
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	>		
			790				800				810				820				830			840
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
ACC	CCT	GAG	GTC	ACA	TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAC	GAA	GAC	CCT	GAG	GTC	AAG	TTC			
TGG	GGA	CTC	CAG	TGT	ACG	CAC	CAC	CAC	CTG	CAC	TCG	GTG	CTT	CTG	GGA	CTC	CAG	TTC	AAG			
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	>		
			850				860				870				880				890			900
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
AAC	TGG	TAC	GTG	GAC	GGC	GTG	GAG	GTG	CAT	AAT	GCC	AAG	ACA	AAG	CCG	CGG	GAG	GAG	CAG			
TTG	ACC	ATG	CAC	CTG	CCG	CAC	CTC	CAC	GTA	TTA	CGG	TTC	TGT	TTC	GGC	GCC	CTC	CTC	GTC			
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	>		
			910				920				930				940				950			960
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
TAC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC	GTC	CTC	ACC	GTC	CTG	CAC	CAG	GAC	TGG	CTG	AAT			
ATG	TTG	TCG	TGC	ATG	GCA	CAC	CAG	TCG	CAG	GAG	TGG	CAG	GAC	GTG	GTC	CTG	ACC	GAC	TTA			
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	>		
			970				980				990				1000				1010			1020
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
GGC	AAG	GAG	TAC	AAG	TGC	AAG	GTC	TCC	AAC	AAA	GCC	CTC	CCA	GCC	CCC	ATC	GAG	AAA	ACC			
CCG	TTC	CTC	ATG	TTC	ACG	TTC	CAG	AGG	TTG	TTT	CGG	GAG	GGT	CGG	GGG	TAG	CTC	TTT	TGG			
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	>		
			1030				1040				1050				1060				1070			1080
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
ATC	TCC	AAA	GCC	AAA	GGG	CAG	CCC	CGA	GAA	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CGG			
TAG	AGG	TTT	CGG	TTT	CCC	GTC	GGG	GCT	CTT	GGT	GTC	CAC	ATG	TGG	GAC	GGG	GGT	AGG	GCC			
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	>		

Fig.14C.

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			1090				1100				1110				1120				1130				1140
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
GAT	GAG	CTG	ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GGC	TTC	TAT	CCC	AGC				
CTA	CTC	GAC	TGG	TTC	TTG	GTC	CAG	TCG	GAC	TGG	ACG	GAC	CAG	TTT	CCG	AAG	ATA	GGG	TCG				
Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	>			
			1150				1160				1170				1180				1190				1200
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
GAC	ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	CAG	CCG	GAG	AAC	AAC	TAC	AAG	ACC	ACG	CCT				
CTG	TAG	CGG	CAC	CTC	ACC	CTC	TCG	TTA	CCC	GTC	GGC	CTC	TTG	TTG	ATG	TTC	TGG	TGC	GGA				
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	>			
			1210				1220				1230				1240				1250				1260
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
CCC	GTG	CTG	GAC	TCC	GAC	GGC	TCC	TTC	TTC	CTC	TAC	AGC	AAG	CTC	ACC	GTG	GAC	AAG	AGC				
GGG	CAC	GAC	CTG	AGG	CTG	CCG	AGG	AAG	AAG	GAG	ATG	TCG	TTC	GAG	TGG	CAC	CTG	TTC	TCG				
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	>			
			1270				1280				1290				1300				1310				1320
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
AGG	TGG	CAG	CAG	GGG	AAC	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG	GCT	CTG	CAC	AAC	CAC				
TCC	ACC	GTC	GTC	CCC	TTG	CAG	AAG	AGT	ACG	AGG	CAC	TAC	GTA	CTC	CGA	GAC	GTG	TTG	GTG				
Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	>			
			1330				1340				1350												
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
TAC	ACG	CAG	AAG	AGC	CTC	TCC	CTG	TCT	CCG	GGT	AAA	TGA											
ATG	TGC	GTC	TTC	TCG	GAG	AGG	GAC	AGA	GGC	CCA	TTT	ACT											
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	***	>										

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Fig.15A.

10	20	30	40	50	60
* * *	* * *	* * *	* * *	* * *	* * *
ATG GTC AGC TAC TGG GAC ACC GGG GTC CTG CTG TGC GCG CTG CTC AGC TGT CTG CTT CTC					
TAC CAG TCG ATG ACC CTG TGG CCC CAG GAC GAC ACG CGC GAC GAG TCG ACA GAC GAA GAG					
Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser Cys Leu Leu Leu>					
70	80	90	100	110	120
* * *	* * *	* * *	* * *	* * *	* * *
ACA GGA TCT AGT TCC GGA GGT AGA CCT TTC GTA GAG ATG TAC AGT GAA ATC CCC GAA ATT					
TGT CCT AGA TCA AGG CCT CCA TCT GGA AAG CAT CTC TAC ATG TCA CTT TAG GGG CTT TAA					
Thr Gly Ser Ser Ser Gly Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu Ile>					
130	140	150	160	170	180
* * *	* * *	* * *	* * *	* * *	* * *
ATA CAC ATG ACT GAA GGA AGG GAG CTC GTC ATT CCC TGC CGG GTT ACG TCA CCT AAC ATC					
TAT GTG TAC TGA CTT CCT TCC CTC GAG CAG TAA GGG ACG GCC CAA TGC AGT GGA TTG TAG					
Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile>					
190	200	210	220	230	240
* * *	* * *	* * *	* * *	* * *	* * *
ACT GTT ACT TTA AAA AAG TTT CCA CTT GAC ACT TTG ATC CCT GAT GGA AAA CGC ATA ATC					
TGA CAA TGA AAT TTT TTC AAA GGT GAA CTG TGA AAC TAG GGA CTA CCT TTT GCG TAT TAG					
Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile>					
250	260	270	280	290	300
* * *	* * *	* * *	* * *	* * *	* * *
TGG GAC AGT AGA AAG GGC TTC ATC ATA TCA AAT GCA ACG TAC AAA GAA ATA GGG CTT CTG					
ACC CTG TCA TCT TTC CCG AAG TAG TAT AGT TTA CGT TGC ATG TTT CTT TAT CCC GAA GAC					
Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu>					
310	320	330	340	350	360
* * *	* * *	* * *	* * *	* * *	* * *
ACC TGT GAA GCA ACA GTC AAT GGG CAT TTG TAT AAG ACA AAC TAT CTC ACA CAT CGA CAA					
TGG ACA CTT CGT TGT CAG TTA CCC GTA AAC ATA TTC TGT TTG ATA GAG TGT GTA GCT GTT					
Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln>					
370	380	390	400	410	420
* * *	* * *	* * *	* * *	* * *	* * *
ACC AAT ACA ATC ATA GAT GTC CAA ATA AGC ACA CCA CGC CCA GTC AAA TTA CTT AGA GGC					
TGG TTA TGT TAG TAT CTA CAG GTT TAT TCG TGT GGT GCG GGT CAG TTT AAT GAA TCT CCG					
Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val Lys Leu Leu Arg Gly>					
430	440	450	460	470	480
* * *	* * *	* * *	* * *	* * *	* * *
CAT ACT CTT GTC CTC AAT TGT ACT GCT ACC ACT CCC TTG AAC ACG AGA GTT CAA ATG ACC					
GTA TGA GAA CAG GAG TTA ACA TGA CGA TGG TGA GGG AAC TTG TGC TCT CAA GTT TAC TGG					
His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr Arg Val Gln Met Thr>					
490	500	510	520	530	540
* * *	* * *	* * *	* * *	* * *	* * *
TGG AGT TAC CCT GAT GAA AAA AAT AAG AGA GCT TCC GTA AGG CGA CGA ATT GAC CAA AGC					
ACC TCA ATG GGA CTA CTT TTT TTA TTC TCT CGA AGG CAT TCC GCT GCT TAA CTG GTT TCG					
Trp Ser Tyr Pro Asp Glu Lys Asn Lys Arg Ala Ser Val Arg Arg Arg Ile Asp Gln Ser>					

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Fig.15B.

```

      550      560      570      580      590      600
      *      *      *      *      *      *
AAT TCC CAT GCC AAC ATA TTC TAC AGT GTT CTT ACT ATT GAC AAA ATG CAG AAC AAA GAC
TTA AGG GTA CGG TTG TAT AAG ATG TCA CAA GAA TGA TAA CTG TTT TAC GTC TTG TTT CTG
Asn Ser His Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys Asp>

      610      620      630      640      650      660
      *      *      *      *      *      *
AAA GGA CTT TAT ACT TGT CGT GTA AGG AGT GGA CCA TCA TTC AAA TCT GTT AAC ACC TCA
TTT CCT GAA ATA TGA ACA GCA CAT TCC TCA CCT GGT AGT AAG TTT AGA CAA TTG TGG AGT
Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys Ser Val Asn Thr Ser>

      670      680      690      700      710      720
      *      *      *      *      *      *
GTG CAT ATA TAT GAT AAA GCA GGC CCG GGC GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA
CAC GTA TAT ATA CTA TTT CGT CCG GGC CCG CTC GGG TTT AGA ACA CTG TTT TGA GTG TGT
Val His Ile Tyr Asp Lys Ala Gly Pro Gly Glu Pro Lys Ser Cys Asp Lys Thr His Thr>

      730      740      750      760      770      780
      *      *      *      *      *      *
TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA
ACG GGT GGC ACG GGT CGT GGA CTT GAG GAC CCC CCT GGC AGT CAG AAG GAG AAG GGG GGT
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro>

      790      800      810      820      830      840
      *      *      *      *      *      *
AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC
TTT GGG TTC CTG TGG GAG TAC TAG AGG GCC TGG GGA CTC CAG TGT ACG CAC CAC CAC CTG
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp>

      850      860      870      880      890      900
      *      *      *      *      *      *
GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT
CAC TCG GTG CTT CTG GGA CTC CAG TTC AAG TTG ACC ATG CAC CTG CCG CAC CTC CAC GTA
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His>

      910      920      930      940      950      960
      *      *      *      *      *      *
AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC GTC
TTA CGG TTC TGT TTC GGC GCC CTC CTC GTC ATG TTG TCG TGC ATG GCA CAC CAG TCG CAG
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val>

      970      980      990      1000      1010      1020
      *      *      *      *      *      *
CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC
GAG TGG CAG GAC GTG GTC CTG ACC GAC TTA CCG TTC CTC ATG TTC ACG TTC CAG AGG TTG
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn>

      1030      1040      1050      1060      1070      1080
      *      *      *      *      *      *
AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA
TTT CGG GAG GGT CGG GGG TAG CTC TTT TGG TAG AGG TTT CGG TTT CCC GTC GGG GCT CTT
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu>

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SUBSTITUTE SHEET (RULE 26)

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Fig.15C.

1090	1100	1110	1120	1130	1140
* * *	* *	* *	* *	* *	* *
CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG					
GGT GTC CAC ATG TGG GAC GGG GGT AGG GCC CTA CTC GAC TGG TTC TTG GTC CAG TCG GAC					
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu>					

1150	1160	1170	1180	1190	1200
* * *	* *	* *	* *	* *	* *
ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG					
TGG ACG GAC CAG TTT CCG AAG ATA GGG TCG CTG TAG CGG CAC CTC ACC CTC TCG TTA CCC					
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly>					

1210	1220	1230	1240	1250	1260
* * *	* *	* *	* *	* *	* *
CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC					
GTC GGC CTC TTG TTG ATG TTC TGG TGC GGA GGG CAC GAC CTG AGG CTG CCG AGG AAG AAG					
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe>					

1270	1280	1290	1300	1310	1320
* * *	* *	* *	* *	* *	* *
CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC					
GAG ATG TCG TTC GAG TGG CAC CTG TTC TCG TCC ACC GTC GTC CCC TTG CAG AAG AGT ACG					
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys>					

1330	1340	1350	1360	1370	1380
* * *	* *	* *	* *	* *	* *
TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG					
AGG CAC TAC GTA CTC CGA GAC GTG TTG GTG ATG TGC GTC TTC TCG GAG AGG GAC AGA GGC					
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro>					

*
GGT AAA TGA
CCA TTT ACT
Gly Lys ***>

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Fig.16A.

	10		20		30		40		50		60								
*	*	*	*	*	*	*	*	*	*	*	*								
ATG	GTC	AGC	TAC	TGG	GAC	ACC	GGG	GTC	CTG	CTG	TGC	GCG	CTG	CTC	AGC	TGT	CTG	CTT	CTC
TAC	CAG	TCG	ATG	ACC	CTG	TGG	CCC	CAG	GAC	GAC	ACG	CGC	GAC	GAG	TCG	ACA	GAC	GAA	GAG
Met	Val	Ser	Tyr	Trp	Asp	Thr	Gly	Val	Leu	Leu	Cys	Ala	Leu	Leu	Ser	Cys	Leu	Leu	Leu>

	70		80		90		100		110		120								
*	*	*	*	*	*	*	*	*	*	*	*								
ACA	GGA	TCT	AGT	TCA	GGT	TCA	AAA	TTA	AAA	GAT	CCT	GAA	CTG	AGT	TTA	AAA	GGC	ACC	CAG
TGT	CCT	AGA	TCA	AGT	CCA	AGT	TTT	AAT	TTT	CTA	GGA	CTT	GAC	TCA	AAT	TTT	CCG	TGG	GTC
Thr	Gly	Ser	Ser	Ser	Gly	Ser	Lys	Leu	Lys	Asp	Pro	Glu	Leu	Ser	Leu	Lys	Gly	Thr	Gln>

	130		140		150		160		170		180								
*	*	*	*	*	*	*	*	*	*	*	*								
CAC	ATC	ATG	CAA	GCA	GGC	CAG	ACA	CTG	CAT	CTC	CAA	TGC	AGG	GGG	GAA	GCA	GCC	CAT	AAA
GTG	TAG	TAC	GTT	CGT	CCG	GTC	TGT	GAC	GTA	GAG	GTT	ACG	TCC	CCC	CTT	CGT	CGG	GTA	TTT
His	Ile	Met	Gln	Ala	Gly	Gln	Thr	Leu	His	Leu	Gln	Cys	Arg	Gly	Glu	Ala	Ala	His	Lys>

	190		200		210		220		230		240								
*	*	*	*	*	*	*	*	*	*	*	*								
TGG	TCT	TTG	CCT	GAA	ATG	GTG	AGT	AAG	GAA	AGC	GAA	AGG	CTG	AGC	ATA	ACT	AAA	TCT	GCC
ACC	AGA	AAC	GGA	CTT	TAC	CAC	TCA	TTC	CTT	TCG	CTT	TCC	GAC	TCG	TAT	TGA	TTT	AGA	CGG
Trp	Ser	Leu	Pro	Glu	Met	Val	Ser	Lys	Glu	Ser	Glu	Arg	Leu	Ser	Ile	Thr	Lys	Ser	Ala>

	250		260		270		280		290		300								
*	*	*	*	*	*	*	*	*	*	*	*								
TGT	GGA	AGA	AAT	GGC	AAA	CAA	TTC	TGC	AGT	ACT	TTA	ACC	TTG	AAC	ACA	GCT	CAA	GCA	AAC
ACA	CCT	TCT	TTA	CCG	TTT	GTT	AAG	ACG	TCA	TGA	AAT	TGG	AAC	TTG	TGT	CGA	GTT	CGT	TTG
Cys	Gly	Arg	Asn	Gly	Lys	Gln	Phe	Cys	Ser	Thr	Leu	Thr	Leu	Asn	Thr	Ala	Gln	Ala	Asn>

	310		320		330		340		350		360								
*	*	*	*	*	*	*	*	*	*	*	*								
CAC	ACT	GGC	TTC	TAC	AGC	TGC	AAA	TAT	CTA	GCT	GTA	CCT	ACT	TCA	AAG	AAG	AAG	GAA	ACA
GTG	TGA	CCG	AAG	ATG	TCG	ACG	TTT	ATA	GAT	CGA	CAT	GGA	TGA	AGT	TTC	TTC	TTC	CTT	TGT
His	Thr	Gly	Phe	Tyr	Ser	Cys	Lys	Tyr	Leu	Ala	Val	Pro	Thr	Ser	Lys	Lys	Lys	Glu	Thr>

	370		380		390		400		410		420								
*	*	*	*	*	*	*	*	*	*	*	*								
GAA	TCT	GCA	ATC	TAT	ATA	TTT	ATT	AGT	GAT	ACA	GGT	AGA	CCT	TTC	GTA	GAG	ATG	TAC	AGT
CTT	AGA	CGT	TAG	ATA	TAT	AAA	TAA	TCA	CTA	TGT	CCA	TCT	GGA	AAG	CAT	CTC	TAC	ATG	TCA
Glu	Ser	Ala	Ile	Tyr	Ile	Phe	Ile	Ser	Asp	Thr	Gly	Arg	Pro	Phe	Val	Glu	Met	Tyr	Ser>

	430		440		450		460		470		480								
*	*	*	*	*	*	*	*	*	*	*	*								
GAA	ATC	CCC	GAA	ATT	ATA	CAC	ATG	ACT	GAA	GGA	AGG	GAG	CTC	GTC	ATT	CCC	TGC	CGG	GTT
CTT	TAG	GGG	CTT	TAA	TAT	GTG	TAC	TGA	CTT	CCT	TCC	CTC	GAG	CAG	TAA	GGG	ACG	GCC	CAA
Glu	Ile	Pro	Glu	Ile	Ile	His	Met	Thr	Glu	Gly	Arg	Glu	Leu	Val	Ile	Pro	Cys	Arg	Val>

	490		500		510		520		530		540								
*	*	*	*	*	*	*	*	*	*	*	*								
ACG	TCA	CCT	AAC	ATC	ACT	GTT	ACT	TTA	AAA	AAG	TTT	CCA	CTT	GAC	ACT	TTG	ATC	CCT	GAT
TGC	AGT	GGA	TTG	TAG	TGA	CAA	TGA	AAT	TTT	TTC	AAA	GGT	GAA	CTG	TGA	AAC	TAG	GGA	CTA
Thr	Ser	Pro	Asn	Ile	Thr	Val	Thr	Leu	Lys	Lys	Phe	Pro	Leu	Asp	Thr	Leu	Ile	Pro	Asp>

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Fig.16B.

```

      550      560      570      580      590      600
      *      *      *      *      *      *
GGA AAA CGC ATA ATC TGG GAC AGT AGA AAG GGC TTC ATC ATA TCA AAT GCA ACG TAC AAA
CCT TTT GCG TAT TAG ACC CTG TCA TCT TTC CCG AAG TAG TAT AGT TTA CGT TGC ATG TTT
Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys>

      610      620      630      640      650      660
      *      *      *      *      *      *
GAA ATA GGG CTT CTG ACC TGT GAA GCA ACA GTC AAT GGG CAT TTG TAT AAG ACA AAC TAT
CTT TAT CCC GAA GAC TGG ACA CTT CGT TGT CAG TTA CCC GTA AAC ATA TTC TGT TTG ATA
Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr>

      670      680      690      700      710      720
      *      *      *      *      *      *
CTC ACA CAT CGA CAA ACC AAT ACA ATC ATA GAT GTC CAA ATA AGC ACA CCA CGC CCA GTC
GAG TGT GTA GCT GTT TGG TTA TGT TAG TAT CTA CAG GTT TAT TCG TGT GGT GCG GGT CAG
Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val>

      730      740      750      760      770      780
      *      *      *      *      *      *
AAA TTA CTT AGA GGC CAT ACT CTT GTC CTC AAT TGT ACT GCT ACC ACT CCC TTG AAC ACG
TTT AAT GAA TCT CCG GTA TGA GAA CAG GAG TTA ACA TGA CGA TGG TGA GGG AAC TTG TGC
Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr>

      790      800      810      820      830      840
      *      *      *      *      *      *
AGA GTT CAA ATG ACC TGG AGT TAC CCT GAT GAA AAA AAT AAG AAC GCT TCC GTA AGG CGA
TCT CAA GTT TAC TGG ACC TCA ATG GGA CTA CTT TTT TTA TTC TTG CGA AGG CAT TCC GCT
Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys Asn Lys Asn Ala Ser Val Arg Arg>

      850      860      870      880      890      900
      *      *      *      *      *      *
CGA ATT GAC CAA AGC AAT TCC CAT GCC AAC ATA TTC TAC AGT GTT CTT ACT ATT GAC AAA
GCT TAA CTG GTT TCG TTA AGG GTA CGG TTG TAT AAG ATG TCA CAA GAA TGA TAA CTG TTT
Arg Ile Asp Gln Ser Asn Ser His Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys>

      910      920      930      940      950      960
      *      *      *      *      *      *
ATG CAG AAC AAA GAC AAA GGA CTT TAT ACT TGT CGT GTA AGG AGT GGA CCA TCA TTC AAA
TAC GTC TTG TTT CTG TTT CCT GAA ATA TGA ACA GCA CAT TCC TCA CCT GGT AGT AAG TTT
Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys>

      970      980      990      1000      1010      1020
      *      *      *      *      *      *
TCT GTT AAC ACC TCA GTG CAT ATA TAT GAT AAA GCA GGC CCG GGC GAG CCC AAA TCT TGT
AGA CAA TTG TGG AGT CAC GTA TAT ATA CTA TTT CGT CCG GGC CCG CTC GGG TTT AGA ACA
Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Gly Pro Gly Glu Pro Lys Ser Cys>

      1030      1040      1050      1060      1070      1080
      *      *      *      *      *      *
GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC
CTG TTT TGA GTG TGT ACG GGT GGC ACG GGT CGT GGA CTT GAG GAC CCC CCT GGC AGT CAG
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val>

```

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Fig.16C.

1090	1100	1110	1120	1130	1140
* * *	* * *	* * *	* * *	* * *	* * *
TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA	AAG GAG AAG GGG GGT TTT GGG TTC CTG TGG GAG TAC TAG AGG GCC TGG GGA CTC CAG TGT	Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr>			
1150	1160	1170	1180	1190	1200
* * *	* * *	* * *	* * *	* * *	* * *
TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC	ACG CAC CAC CAC CTG CAC TCG GTG CTT CTG GGA CTC CAG TTC AAG TTG ACC ATG CAC CTG	Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp>			
1210	1220	1230	1240	1250	1260
* * *	* * *	* * *	* * *	* * *	* * *
GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC	CCG CAC CTC CAC GTA TTA CGG TTC TGT TTC GGC GCC CTC CTC GTC ATG TTG TCG TGC ATG	Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr>			
1270	1280	1290	1300	1310	1320
* * *	* * *	* * *	* * *	* * *	* * *
CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG	GCA CAC CAG TCG CAG GAG TGG CAG GAC GTG GTC CTG ACC GAC TTA CCG TTC CTC ATG TTC	Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys>			
1330	1340	1350	1360	1370	1380
* * *	* * *	* * *	* * *	* * *	* * *
TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA	ACG TTC CAG AGG TTG TTT CGG GAG GGT CGG GGG TAG CTC TTT TGG TAG AGG TTT CGG TTT	Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys>			
1390	1400	1410	1420	1430	1440
* * *	* * *	* * *	* * *	* * *	* * *
GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG	CCC GTC GGG GCT CTT GGT GTC CAC ATG TGG GAC GGG GGT AGG GCC CTA CTC GAC TGG TTC	Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys>			
1450	1460	1470	1480	1490	1500
* * *	* * *	* * *	* * *	* * *	* * *
AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG	TTG GTC CAG TCG GAC TGG ACG GAC CAG TTT CCG AAG ATA GGG TCG CTG TAG CGG CAC CTC	Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu>			
1510	1520	1530	1540	1550	1560
* * *	* * *	* * *	* * *	* * *	* * *
TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC	ACC CTC TCG TTA CCC GTC GGC CTC TTG TTG ATG TTC TGG TGC GGA GGG CAC GAC CTG AGG	Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser>			
1570	1580	1590	1600	1610	1620
* * *	* * *	* * *	* * *	* * *	* * *
GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG	CTG CCG AGG AAG AAG GAG ATG TCG TTC GAG TGG CAC CTG TTC TCG TCC ACC GTC GTC CCC	Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly>			

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Fig.16D.

	1630		1640		1650		1660		1670		1680								
	*		*		*		*		*		*								
AAC	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG	GCT	CTG	CAC	AAC	CAC	TAC	ACG	CAG	AAG	AGC
TTG	CAG	AAG	AGT	ACG	AGG	CAC	TAC	GTA	CTC	CGA	GAC	GTG	TTG	GTG	ATG	TGC	GTC	TTC	TCG
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser>
	1690		1700																
	*		*		*		*												
CTC	TCC	CTG	TCT	CCG	GGT	AAA	TGA												
GAG	AGG	GAC	AGA	GGC	CCA	TTT	ACT												
Leu	Ser	Leu	Ser	Pro	Gly	Lys	***>												

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Fig.17.

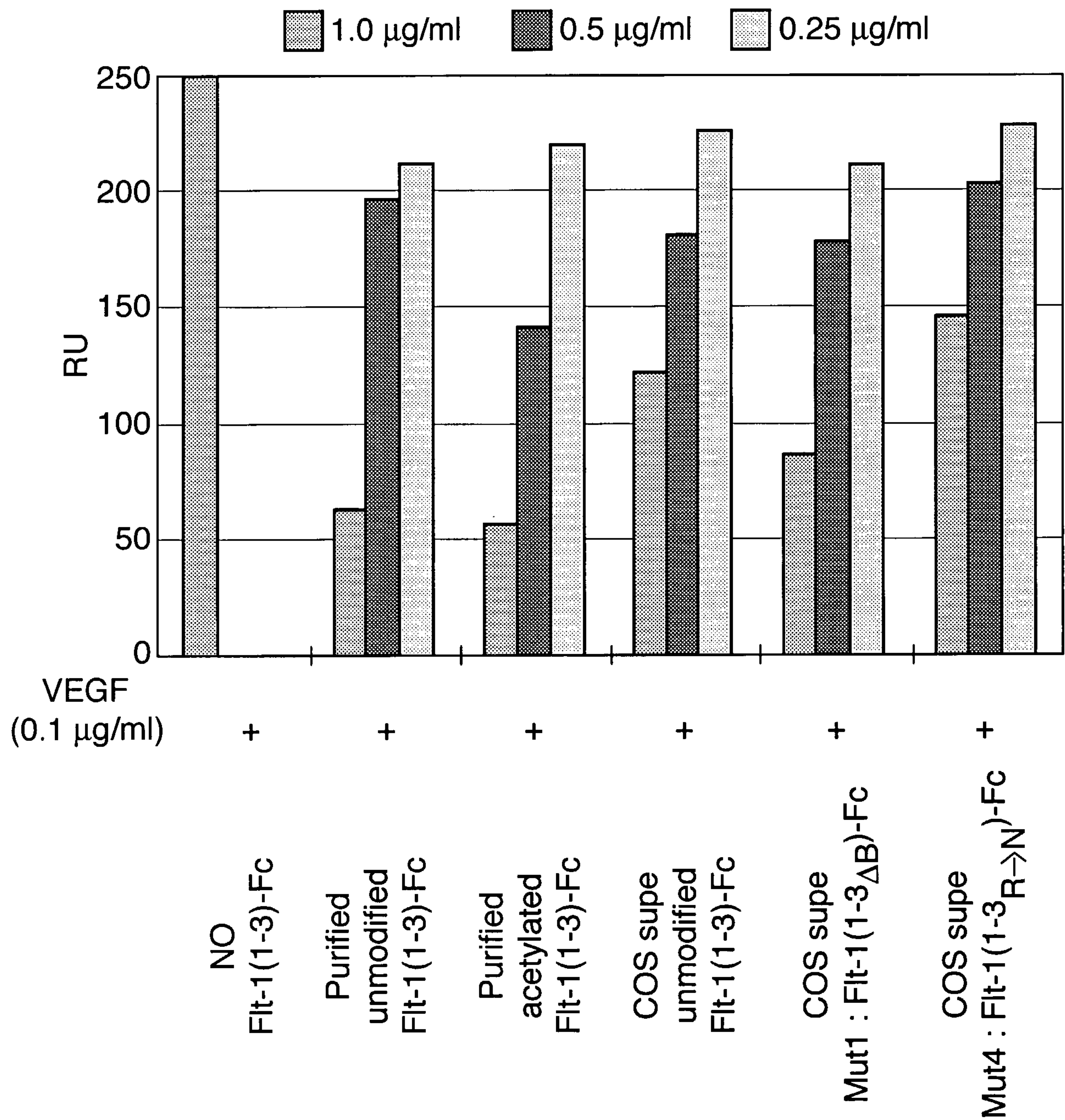
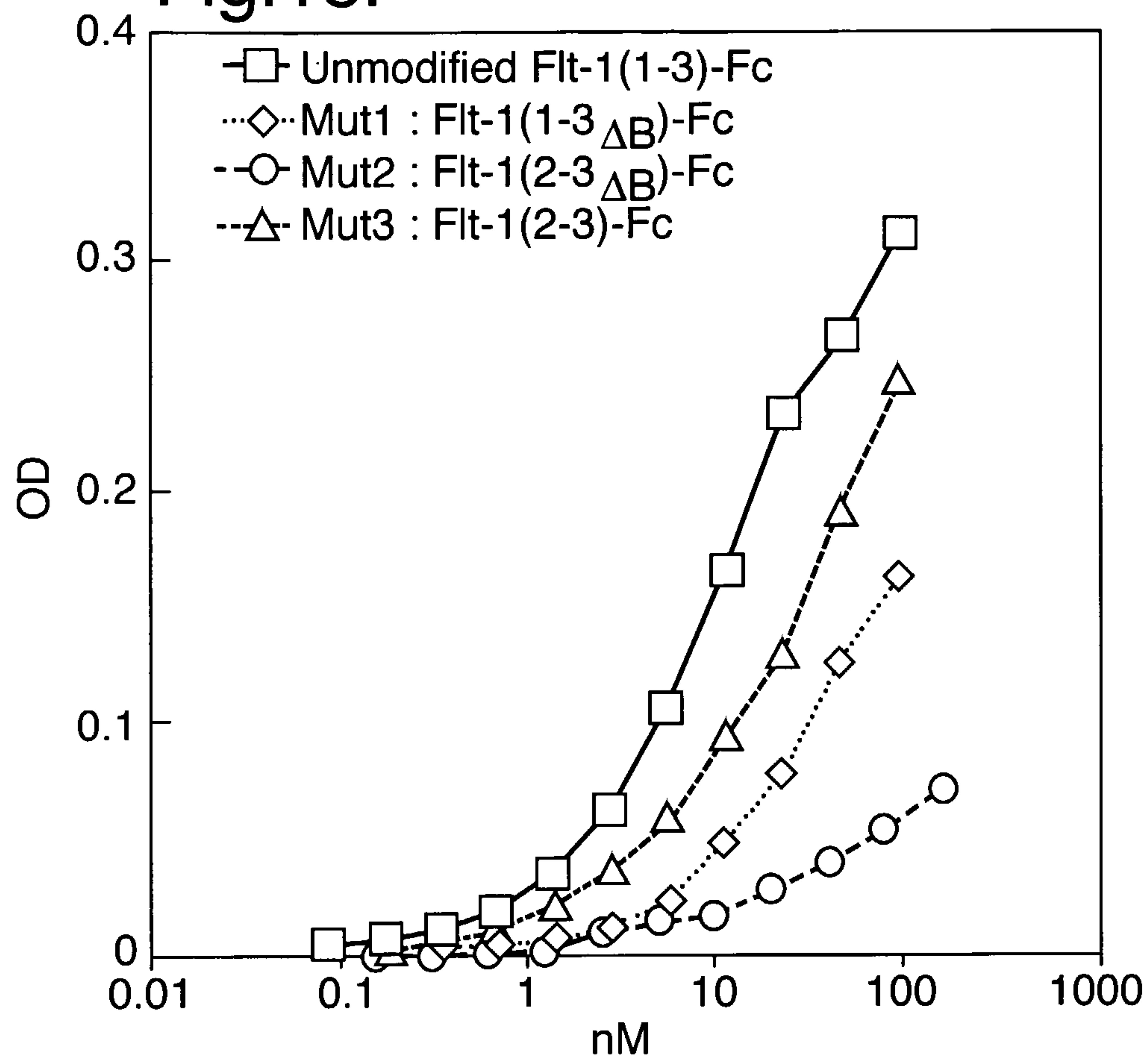
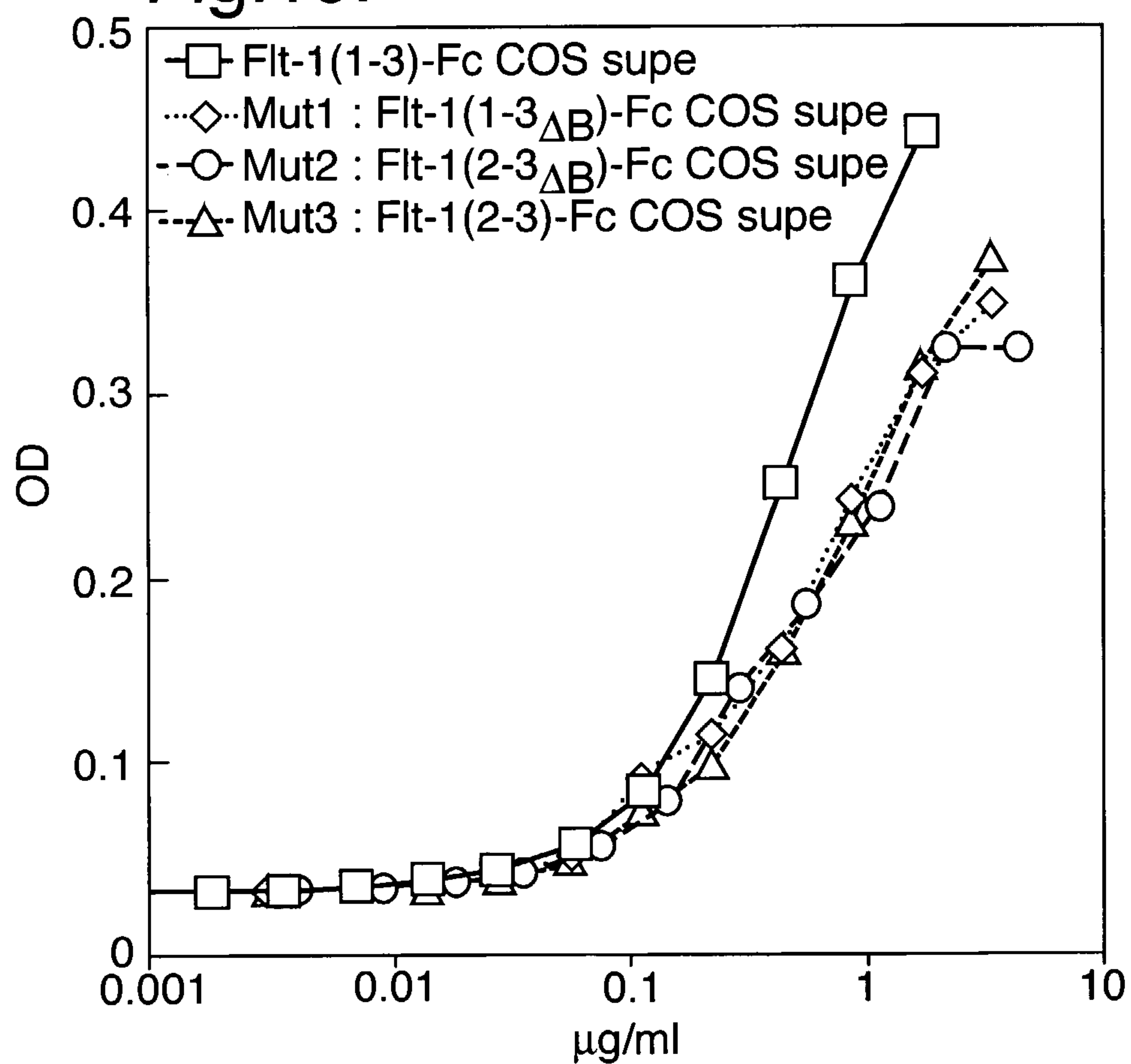
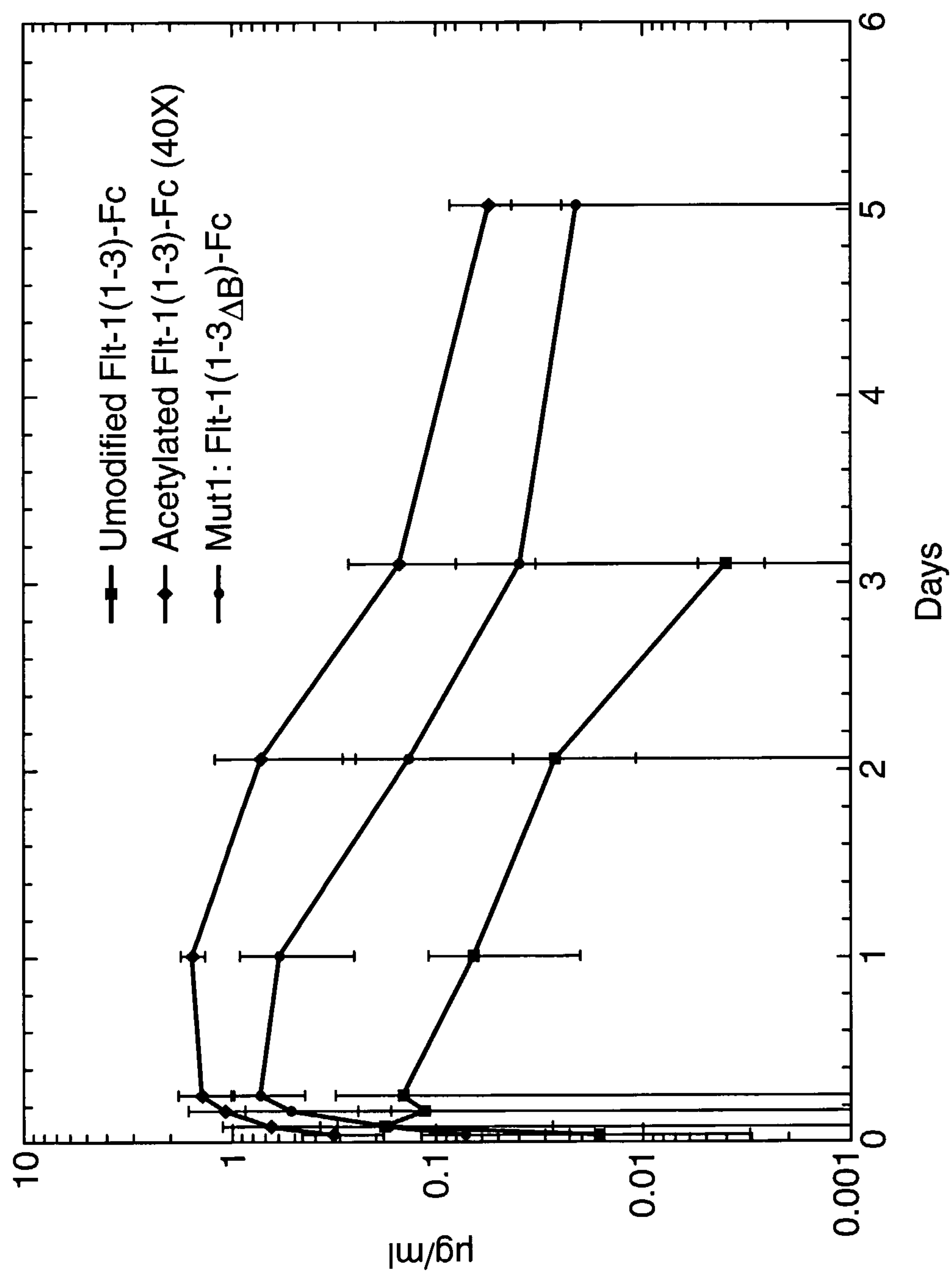


Fig.18. 30/55**Fig.19.**

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Fig.20.



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Fig.21A.

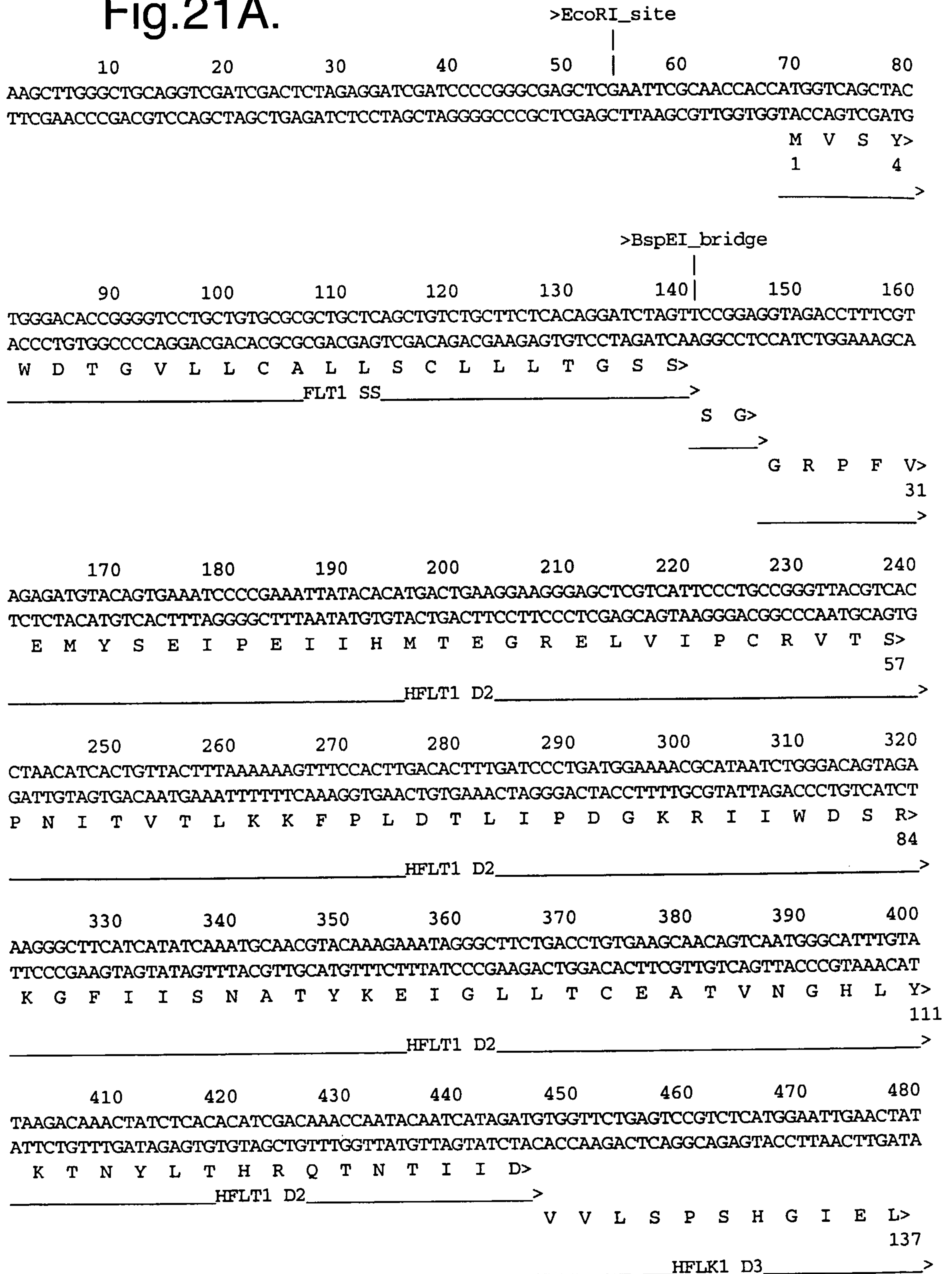


Fig.21B. 33/55

490 500 510 520 530 540 550 560
CTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATTGACTTCAACTGGGAATACCCCT
GACAACCTCTTTTCGAACAGAATTTAACATGTCGTTCTTGACTTGATTTACACCCCTAACTGAAGTTGACCCCTTATGGGA
S V G E K L V L N C T A R T E L N V G I D F N W E Y P>
164
_____HFLK1 D3_____>

570 580 590 600 610 620 630 640
TCTTCGAAGCATCAGCATAAGAACTTGTAAACCGAGACCTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTAG
AGAAGCTTCGTAGTCGTATTCTTTGAACATTTGGCTCTGGATTTTGGGTCAGACCCCTCACTCTACTTCTTTAAAAACTC
S S K H Q H K K L V N R D L K T Q S G S E M K K F L S>
191
_____HFLK1 D3_____>

650 660 670 680 690 700 710 720
CACCTTAACTATAGATGGTGTAAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAGA
GTGGAATTGATATCTACCACATTGGGCCTCACTGGTTCCTAACATGTGGACACGTCGTAGGTCACCCGACTACTGGTTCT
T L T I D G V T R S D Q G L Y T C A A S S G L M T K>
217
_____HFLK1 D3_____>

>Srf_Bridge_
|
730 740 750 760 770 780 790 800
AGAACAGCACATTTGTCAGGGTCCATGAAAAGGGCCCGGGCGACAAACTCACACATGCCACCGTGCCAGCACCTGAA
TCTTGTCTGTGTAACAGTCCCAGGTACTTTTCCCGGGCCCGCTGTTTGTAGTGTGTACGGGTGGCACGGGTCTGGACTT
K N S T F V R V H E K>
_____HFLK1 D3_____>
G P G>
_____>
D K T H T C P P C P A P E>
244
_____FCΔC1 (A)_____>

810 820 830 840 850 860 870 880
CTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCAC
GAGGACCCCTGGCAGTCAGAAGGAGAAGGGGGTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTG
L L G G P S V F L F P P K P K D T L M I S R T P E V T>
271
_____FCΔC1 (A)_____>

890 900 910 920 930 940 950 960
ATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG
TACGCACCACCACTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC
C V V V D V S H E D P E V K F N W Y V D G V E V H N>
297
_____FCΔC1 (A)_____>

970 980 990 1000 1010 1020 1030 1040
CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCCTCCTGCACCAGGACTGG
GGTTCCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTCTGACC
A K T K P R E E Q Y N S T Y R V V S V L T V L H Q D W>
324
_____FCΔC1 (A)_____>

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Fig.21C.

1050 1060 1070 1080 1090 1100 1110 1120
CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAA
GACTTACCGTTCCTCATGTTCACGTTCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTT
L N G K E Y K C K V S N K A L P A P I E K T I S K A K>
351
FCΔC1 (A) >

>A>C_A_allotype
|
>G>T_A_allotype
| |
1130 1140 1150 1160 1170 1180 1190 1200
AGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCT
TCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGA
G Q P R E P Q V Y T L P P S R D E L T K N Q V S L T>
377
FCΔC1 (A) >

1210 1220 1230 1240 1250 1260 1270 1280
GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACC
CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGG
C L V K G F Y P S D I A V E W E S N G Q P E N N Y K T>
404
FCΔC1 (A) >

>T>C
|
1290 1300 1310 1320 1330 1340 1350 1360
ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG
TGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATATCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCC
T P P V L D S D G S F F L Y S K L T V D K S R W Q Q G>
431
FCΔC1 (A) >

1370 1380 1390 1400 1410 1420 1430 1440
GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA
CTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCAT
N V F S C S V M H E A L H N H Y T Q K S L S L S P G>
457
FCΔC1 (A) >

>NotI_site
|
|1450
AATGAGCGGCCGC
T TACTCGCCGGCG
K *>
458
____>

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Fig.22A.

>EcoRI_site
|

10 20 30 40 50 60 70 80
AAGCTTGGGCTGCAGGTCGATCGACTCTAGAGGATCGATCCCCGGGCGAGCTCGAATTCGCAACCACCATGGTCAGCTAC
TTCGAACCCGACGTCCAGCTAGCTGAGATCTCCTAGCTAGGGGCCCGCTCGAGCTTAAGCGTTGGTGGTACCAGTCGATG
M V S Y>
1 4
_____>

>BspEI_bridge
|

90 100 110 120 130 140 150 160
TGGGACACCGGGGTCTGTGTGCGCGCTGCTCAGCTGTCTGCTTCTCACAGGATCTAGTTCCGGAGGTAGACCTTTTCGT
ACCCTGTGGCCCCAGGACGACACGCGCGACGAGTCGACAGACGAAGAGTGTCTAGATCAAGGCCTCCATCTGGAAAGCA
W D T G V L L C A L L S C L L L T G S S>
_____FLT1 SIGNAL SEQUENCE_____>
S G>
_____>
G R P F V>
31
_____>

170 180 190 200 210 220 230 240
AGAGATGTACAGTGAAATCCCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTTCATTTCCCTGCCGGGTACGTCAC
TCTCTACATGTCACTTTAGGGGCTTTAATATGTGTACTGACTTCCCTCCCTCGAGCAGTAAGGGACGGCCCAATGCAGTG
E M Y S E I P E I I H M T E G R E L V I P C R V T S>
57
_____FLT1 IG DOMAIN 2_____>

250 260 270 280 290 300 310 320
CTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTTGATCCCTGATGGAAAACGCATAATCTGGGACAGTAGA
GATTGTAGTGACAATGAAATTTTTTCAAAGGTGAACTGTGAAACTAGGGACTACCTTTTTCGTATTAGACCTGTCATCT
P N I T V T L K K F P L D T L I P D G K R I I W D S R>
84
_____FLT1 IG DOMAIN 2_____>

330 340 350 360 370 380 390 400
AAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTA
TTCCCGAAGTAGTATAGTTTACGTTGCATGTTTCTTTATCCCGAAGACTGGACACTTCGTTGTCAGTTACCCGTAAACAT
K G F I I S N A T Y K E I G L L T C E A T V N G H L Y>
111
_____FLT1 IG DOMAIN 2_____>

410 420 430 440 450 460 470 480
TAAGACAAACTATCTCACACATCGACAAACCAATACAATCATAGATATCCAGCTGTTGCCAGGAAGTCGCTGGAGCTGC
ATTCTGTTTGATAGAGTGTGTAGCTGTTTGGTTATGTTAGTATCTATAGGTCGACAACGGGTCCTTCAGCGACCTCGACG
K T N Y L T H R Q T N T I I D>
_____FLT1 IG DOMAIN 2_____>
I Q L L P R K S L E L>
137
_____VEGFR3 (FLT4) IG DOMAIN 3_____>

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Fig.22B.

490 500 510 520 530 540 550 560
TGGTAGGGGAGAAGCTGGTCCTCAACTGCACCGTGTGGGCTGAGTTTAACTCAGGTGTCACCTTTGACTGGGACTACCCA
ACCATCCCCCTCTTCGACCAGGAGTTGACGTGGCACACCCGACTCAAATTGAGTCCACAGTGGAAACTGACCCTGATGGGT
L V G E K L V L N C T V W A E F N S G V T F D W D Y P>
164
____VEGFR3 (FLT4) IG DOMAIN 3____>

570 580 590 600 610 620 630 640
GGGAAGCAGGCAGAGCGGGGTAAGTGGGTGCCCCGAGCGACGCTCCCAACAGACCCACACAGAACTCTCCAGCATCCTGAC
CCCTTCGTCCGTCTCGCCCCATTACCCACGGGCTCGCTGCGAGGGTTGTCTGGGTGTGTCTTGAGAGGTCGTAGGACTG
G K Q A E R G K W V P E R R S Q Q T H T E L S S I L T>
191
____VEGFR3 (FLT4) IG DOMAIN 3____>

650 660 670 680 690 700 710 720
CATCCACAACGTCAGCCAGCACGACCTGGGCTCGTATGTGTGCAAGGCCAACAACGGCATCCAGCGATTTCGGGAGAGCA
GTAGGTGTTGCAGTCGGTCGTGCTGGACCCGAGCATAACACGTTCCGGTTGTTGCCGTAGGTGCGCTAAAGCCCTCTCGT
I H N V S Q H D L G S Y V C K A N N G I Q R F R E S>
217
____VEGFR3 (FLT4) IG DOMAIN 3____>

730 740 750 760 770 780 790 800
CCGAGGTCATTGTGCATGAAAATGGCCCGGGCGACAAACTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGG
GGCTCCAGTAACACGTACTTTTACCGGGCCCGCTGTTTGTAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCC
T E V I V H E N>
____VEGFR3 (FLT4) IG____>
G P G>
____>
D K T H T C P P C P A P E L L G>
244
____FCΔC1 - A ALLOTYPE____>

810 820 830 840 850 860 870 880
GGACCGTCAGTCTTCCTCTTCCCCCAAACCCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGT
CCTGGCAGTCAGAAGGAGAAGGGGGGTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCA
G P S V F L F P P K P K D T L M I S R T P E V T C V V>
271
____FCΔC1 - A ALLOTYPE____>

890 900 910 920 930 940 950 960
GGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAA
CCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGT
V D V S H E D P E V K F N W Y V D G V E V H N A K T>
297
____FCΔC1 - A ALLOTYPE____>

970 980 990 1000 1010 1020 1030 1040
AGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGC
TCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCG
K P R E E Q Y N S T Y R V V S V L T V L H Q D W L N G>
324
____FCΔC1 - A ALLOTYPE____>

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Fig.22C.

1050 1060 1070 1080 1090 1100 1110 1120
AAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCC
TTCCTCATGTTACGTTCCAGAGGTTGTTTCGGGAGGGTTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGG
K E Y K C K V S N K A L P A P I E K T I S K A K G Q P>
351
FCΔC1 - A ALLOTYPED

>A>C_A_allotype
|
>G>T_A_allotype
| |
1130 1140 1150 1160 1170 1180 1190 1200
CCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCA
GGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGT
R E P Q V Y T L P P S R D E L T K N Q V S L T C L V>
377
FCΔC1 - A ALLOTYPED

1210 1220 1230 1240 1250 1260 1270 1280
AAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCC
TTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGTGATGTTCTGGTGGCGAGGG
K G F Y P S D I A V E W E S N G Q P E N N Y K T T P P>
404
FCΔC1 - A ALLOTYPED

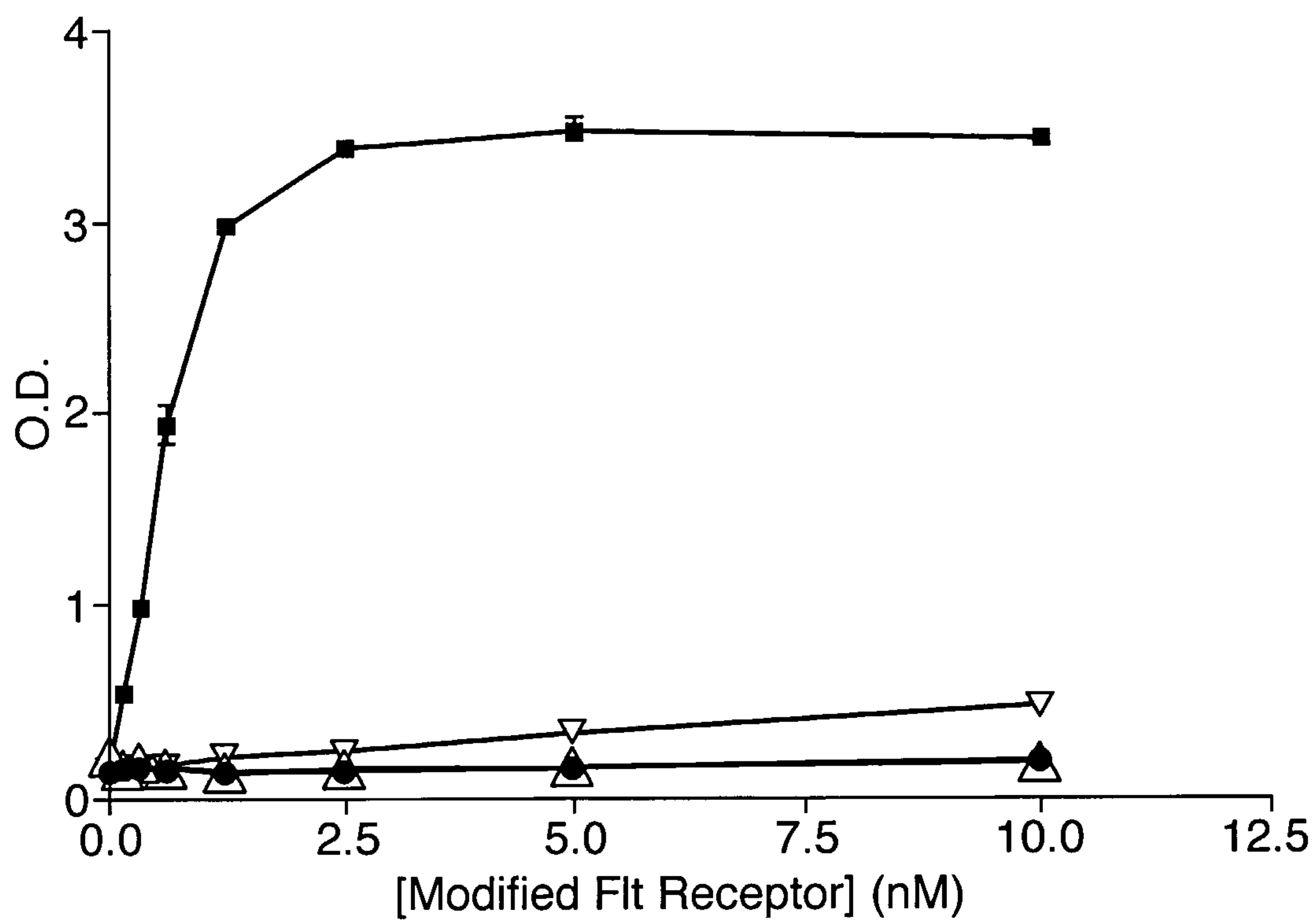
>T>C
|
1290 1300 1310 1320 1330 1340 1350 1360
GTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTT
CACGACCTGAGGCTGCCGAGGAAGAAGGAGATATCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAA
V L D S D G S F F L Y S K L T V D K S R W Q Q G N V F>
431
FCΔC1 - A ALLOTYPED

>NotI_site
|
1370 1380 1390 1400 1410 1420 1430 1440
CTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAGCGG
GAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGTGTCGTCCTTCTCGGAGAGGGACAGAGGCCCATTTACTCGCC
S C S V M H E A L H N H Y T Q K S L S L S P G K *>
455
FCΔC1 - A ALLOTYPED

CCGC
GGCG

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Fig.23.



- Flt1D2Flk1D3.FcdeltaC1(a)
- △ Flt1D2VEGFR3D3.FcdeltaC1(a)
- ▽ TIE2-Fc
- Flt1(1-3)-Fc

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Fig.24A.

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      10      20      30      40      50      60
      *      *      *      *      *      *
ATG GTC AGC TAC TGG GAC ACC GGG GTC CTG CTG TGC GCG CTG CTC AGC TGT CTG CTT CTC
TAC CAG TCG ATG ACC CTG TGG CCC CAG GAC GAC ACG CGC GAC GAG TCG ACA GAC GAA GAG
M  V  S  Y  W  D  T  G  V  L  L  C  A  L  L  S  C  L  L  L>
_1_____5_____hFLT1 SIGNAL SEQUENCE_____15_____20>

      70      80      90     100     110     120
      *      *      *      *      *      *
ACA GGA TCT AGT TCC GGA AGT GAT ACC GGT AGA CCT TTC GTA GAG ATG TAC AGT GAA ATC
TGT CCT AGA TCA AGG CCT TCA CTA TGG CCA TCT GGA AAG CAT CTC TAC ATG TCA CTT TAG
T  G  S  S  S  G>
21_hFLT1 SIGNAL SEQ_26>

      S  D  T  G  R  P  F  V  E  M  Y  S  E  I>
     _27_____30_____hFLT1 IG DOMAIN 2_____40>

     130     140     150     160     170     180
     *      *      *      *      *      *
CCC GAA ATT ATA CAC ATG ACT GAA GGA AGG GAG CTC GTC ATT CCC TGC CGG GTT ACG TCA
GGG CTT TAA TAT GTG TAC TGA CTT CCT TCC CTC GAG CAG TAA GGG ACG GCC CAA TGC AGT
P  E  I  I  H  M  T  E  G  R  E  L  V  I  P  C  R  V  T  S>
41_____45_____hFLT1 IG DOMAIN 2_____55_____60>

     190     200     210     220     230     240
     *      *      *      *      *      *
CCT AAC ATC ACT GTT ACT TTA AAA AAG TTT CCA CTT GAC ACT TTG ATC CCT GAT GGA AAA
GGA TTG TAG TGA CAA TGA AAT TTT TTC AAA GGT GAA CTG TGA AAC TAG GGA CTA CCT TTT
P  N  I  T  V  T  L  K  K  F  P  L  D  T  L  I  P  D  G  K>
61_____65_____hFLT1 IG DOMAIN 2_____75_____80>

     250     260     270     280     290     300
     *      *      *      *      *      *
CGC ATA ATC TGG GAC AGT AGA AAG GGC TTC ATC ATA TCA AAT GCA ACG TAC AAA GAA ATA
GCG TAT TAG ACC CTG TCA TCT TTC CCG AAG TAG TAT AGT TTA CGT TGC ATG TTT CTT TAT
R  I  I  W  D  S  R  K  G  F  I  I  S  N  A  T  Y  K  E  I>
81_____85_____hFLT1 IG DOMAIN 2_____95_____100>

     310     320     330     340     350     360
     *      *      *      *      *      *
GGG CTT CTG ACC TGT GAA GCA ACA GTC AAT GGG CAT TTG TAT AAG ACA AAC TAT CTC ACA
CCC GAA GAC TGG ACA CTT CGT TGT CAG TTA CCC GTA AAC ATA TTC TGT TTG ATA GAG TGT
G  L  L  T  C  E  A  T  V  N  G  H  L  Y  K  T  N  Y  L  T>
101_____105_____hFLT1 IG DOMAIN 2_____115_____120>

     370     380     390     400     410     420
     *      *      *      *      *      *
CAT CGA CAA ACC AAT ACA ATC ATA GAT GTG GTT CTG AGT CCG TCT CAT GGA ATT GAA CTA
GTA GCT GTT TGG TTA TGT TAG TAT CTA CAC CAA GAC TCA GGC AGA GTA CCT TAA CTT GAT
H  R  Q  T  N  T  I  I  D>
121_____hFLT1 IG DOMAIN 2_____129>

      V  V  L  S  P  S  H  G  I  E  L>
     130_____hFLK1 IG DOMAIN 3_____140>

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Fig.24B.

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      430      440      450      460      470      480
      *        *        *        *        *        *
TCT GTT GGA GAA AAG CTT GTC TTA AAT TGT ACA GCA AGA ACT GAA CTA AAT GTG GGG ATT
AGA CAA CCT CTT TTC GAA CAG AAT TTA ACA TGT CGT TCT TGA CTT GAT TTA CAC CCC TAA
S V G E K L V L N C T A R T E L N V G I>
141_____145_____hFLK1 IG DOMAIN 3_____155_____160>

      490      500      510      520      530      540
      *        *        *        *        *        *
GAC TTC AAC TGG GAA TAC CCT TCT TCG AAG CAT CAG CAT AAG AAA CTT GTA AAC CGA GAC
CTG AAG TTG ACC CTT ATG GGA AGA AGC TTC GTA GTC GTA TTC TTT GAA CAT TTG GCT CTG
D F N W E Y P S S K H Q H K K L V N R D>
161_____165_____hFLK1 IG DOMAIN 3_____175_____180>

      550      560      570      580      590      600
      *        *        *        *        *        *
CTA AAA ACC CAG TCT GGG AGT GAG ATG AAG AAA TTT TTG AGC ACC TTA ACT ATA GAT GGT
GAT TTT TGG GTC AGA CCC TCA CTC TAC TTC TTT AAA AAC TCG TGG AAT TGA TAT CTA CCA
L K T Q S G S E M K K F L S T L T I D G>
181_____185_____hFLK1 IG DOMAIN 3_____195_____200>

      610      620      630      640      650      660
      *        *        *        *        *        *
GTA ACC CGG AGT GAC CAA GGA TTG TAC ACC TGT GCA GCA TCC AGT GGG CTG ATG ACC AAG
CAT TGG GCC TCA CTG GTT CCT AAC ATG TGG ACA CGT CGT AGG TCA CCC GAC TAC TGG TTC
V T R S D Q G L Y T C A A S S G L M T K>
201_____205_____hFLK1 IG DOMAIN 3_____215_____220>

      670      680      690      700      710      720
      *        *        *        *        *        *
AAG AAC AGC ACA TTT GTC AGG GTC CAT GAA AAG GAC AAA ACT CAC ACA TGC CCA CCG TGC
TTC TTG TCG TGT AAA CAG TCC CAG GTA CTT TTC CTG TTT TGA GTG TGT ACG GGT GGC ACG
K N S T F V R V H E K>
221_____hFLK1 IG DOMAIN 3_____231>
      D K T H T C P P C>
232_____hFCAC1 A _____240>

      730      740      750      760      770      780
      *        *        *        *        *        *
CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC
GGT CGT GGA CTT GAG GAC CCC CCT GGC AGT CAG AAG GAG AAG GGG GGT TTT GGG TTC CTG
P A P E L L G G P S V F L F P P K P K D>
241_____245_____hFCAC1 A _____255_____260>

      790      800      810      820      830      840
      *        *        *        *        *        *
ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC GAA
TGG GAG TAC TAG AGG GCC TGG GGA CTC CAG TGT ACG CAC CAC CAC CTG CAC TCG GTG CTT
T L M I S R T P E V T C V V V D V S H E>
261_____265_____hFCAC1 A _____275_____280>

      850      860      870      880      890      900
      *        *        *        *        *        *
GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA
CTG GGA CTC CAG TTC AAG TTG ACC ATG CAC CTG CCG CAC CTC CAC GTA TTA CGG TTC TGT
D P E V K F N W Y V D G V E V H N A K T>
281_____285_____hFCAC1 A _____295_____300>

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Fig.24C.

910	920	930	940	950	960
*	*	*	*	*	*
AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG					
TTC GGC GCC CTC CTC GTC ATG TTG TCG TGC ATG GCA CAC CAG TCG CAG GAG TGG CAG GAC					
K P R E E Q Y N S T Y R V V S V L T V L>					
301_____305_____hFCAC1 A _____315_____320>					
970	980	990	1000	1010	1020
*	*	*	*	*	*
CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA					
GTG GTC CTG ACC GAC TTA CCG TTC CTC ATG TTC ACG TTC CAG AGG TTG TTT CGG GAG GGT					
H Q D W L N G K E Y K C K V S N K A L P>					
321_____325_____hFCAC1 A _____335_____340>					
1030	1040	1050	1060	1070	1080
*	*	*	*	*	*
GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC					
CGG GGG TAG CTC TTT TGG TAG AGG TTT CGG TTT CCC GTC GGG GCT CTT GGT GTC CAC ATG					
A P I E K T I S K A K G Q P R E P Q V Y>					
341_____345_____hFCAC1 A _____355_____360>					
1090	1100	1110	1120	1130	1140
*	*	*	*	*	*
ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC					
TGG GAC GGG GGT AGG GCC CTA CTC GAC TGG TTC TTG GTC CAG TCG GAC TGG ACG GAC CAG					
T L P P S R D E L T K N Q V S L T C L V>					
361_____365_____hFCAC1 A _____375_____380>					
1150	1160	1170	1180	1190	1200
*	*	*	*	*	*
AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC					
TTT CCG AAG ATA GGG TCG CTG TAG CGG CAC CTC ACC CTC TCG TTA CCC GTC GGC CTC TTG					
K G F Y P S D I A V E W E S N G Q P E N>					
381_____385_____hFCAC1 A _____395_____400>					
1210	1220	1230	1240	1250	1260
*	*	*	*	*	*
AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG					
TTG ATG TTC TGG TGC GGA GGG CAC GAC CTG AGG CTG CCG AGG AAG AAG GAG ATG TCG TTC					
N Y K T T P P V L D S D G S F F L Y S K>					
401_____405_____hFCAC1 A _____415_____420>					
1270	1280	1290	1300	1310	1320
*	*	*	*	*	*
CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT					
GAG TGG CAC CTG TTC TCG TCC ACC GTC GTC CCC TTG CAG AAG AGT ACG AGG CAC TAC GTA					
L T V D K S R W Q Q G N V F S C S V M H>					
421_____425_____hFCAC1 A _____435_____440>					
1330	1340	1350	1360	1370	
*	*	*	*	*	
GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA TGA					
CTC CGA GAC GTG TTG GTG ATG TGC GTC TTC TCG GAG AGG GAC AGA GGC CCA TTT ACT					
E A L H N H Y T Q K S L S L S P G K *>					
441_____445_____hFCAC1 A _____455_____458_____>					

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Fig.25A.

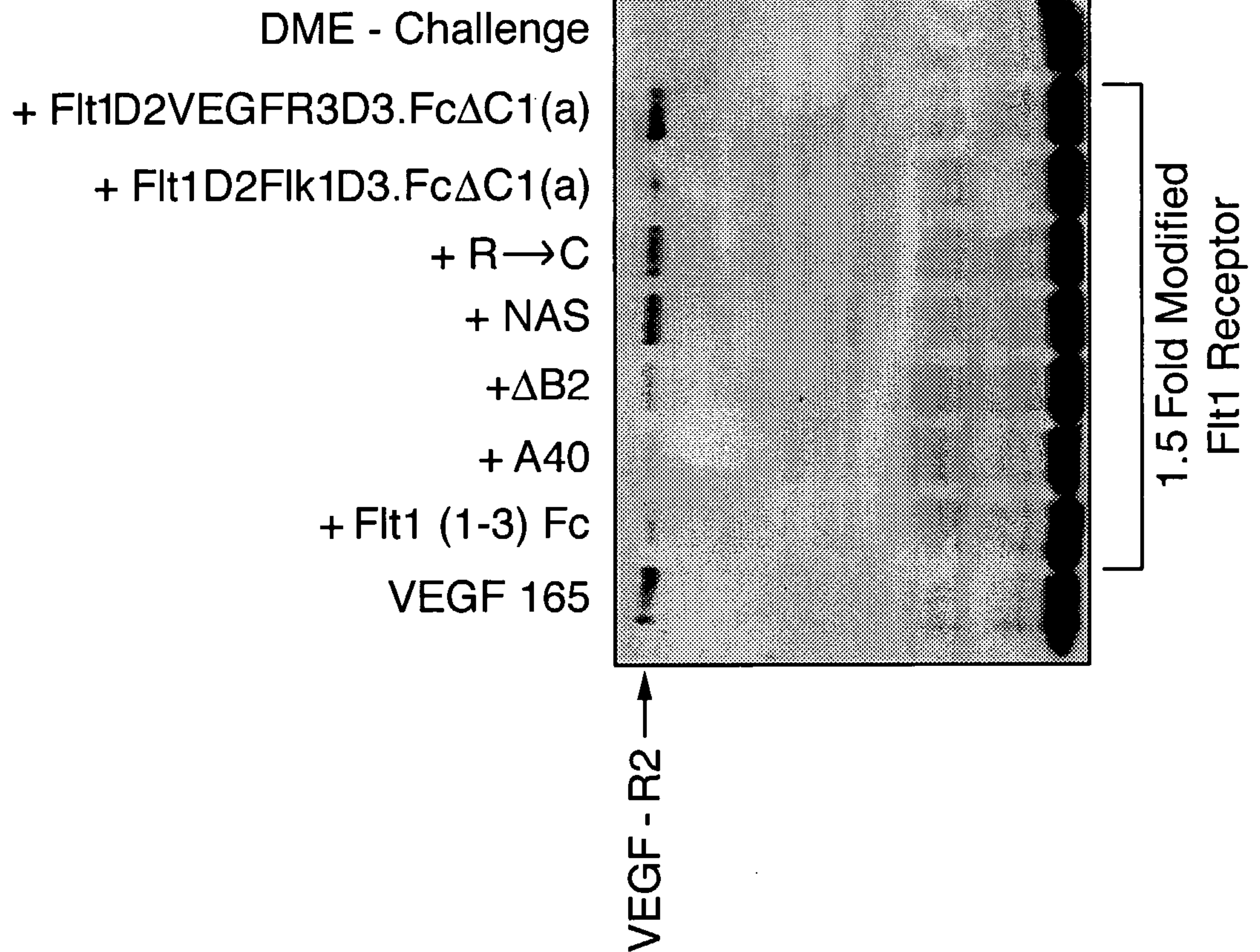


Fig.25B.

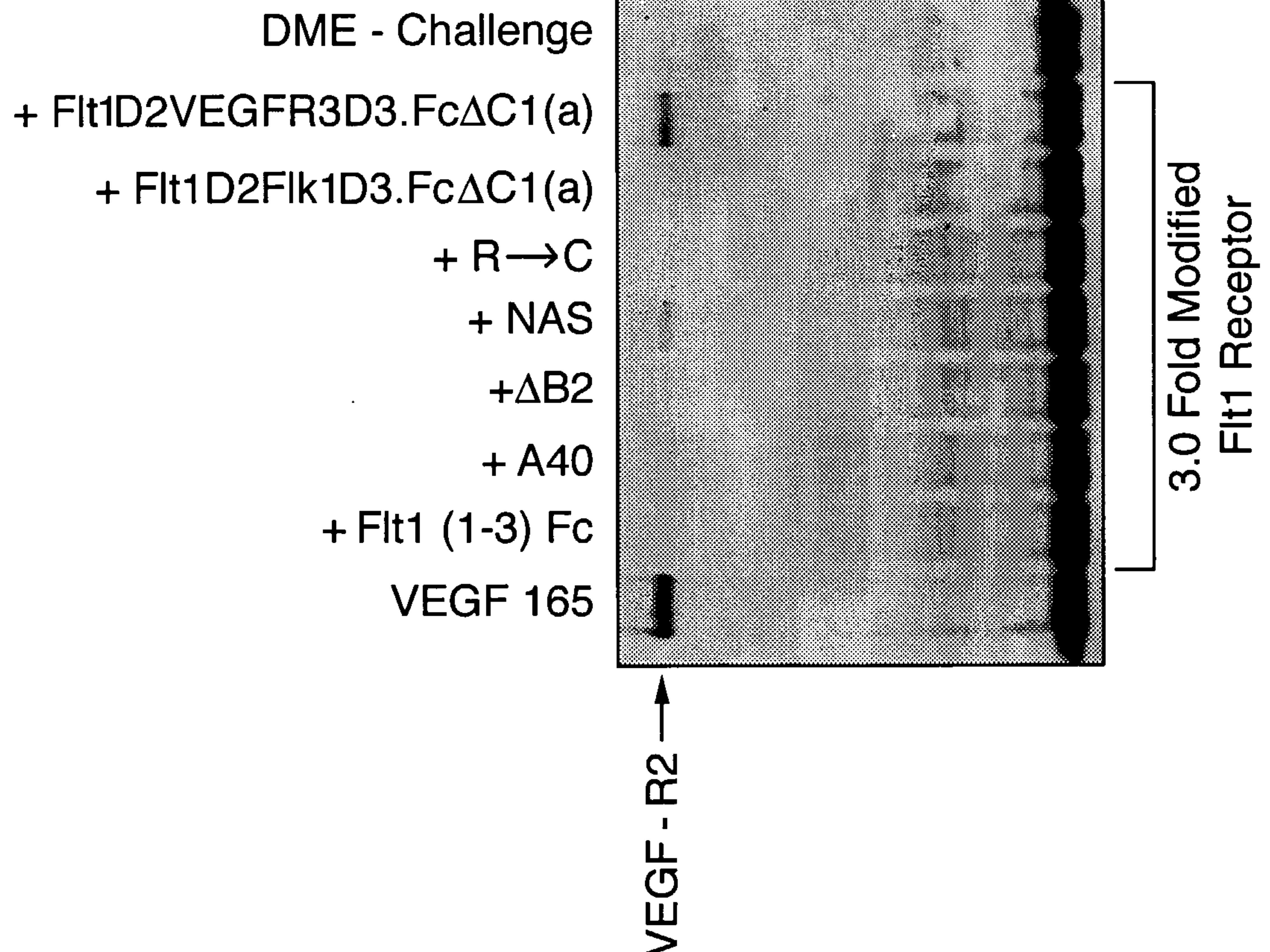


Fig.25C.

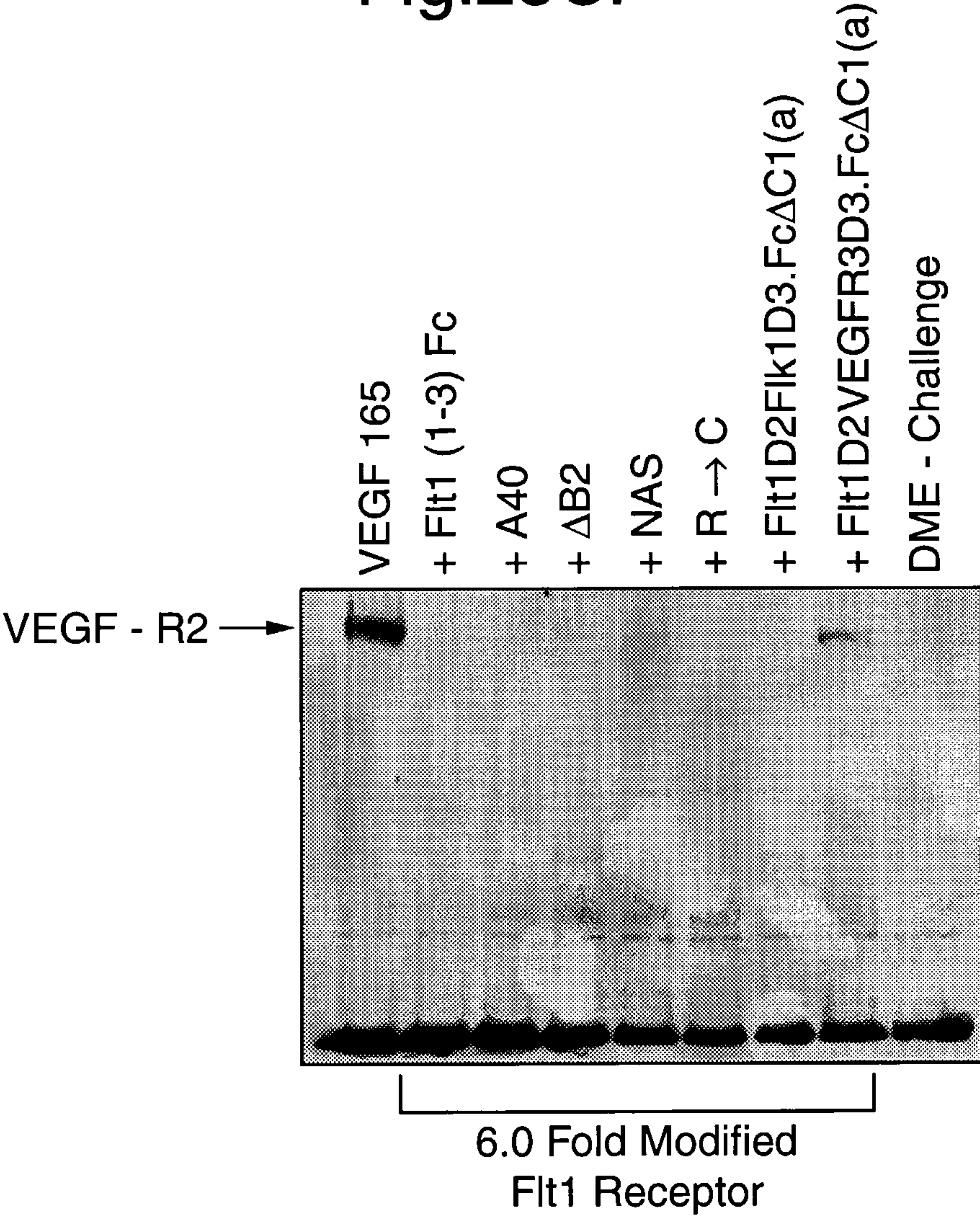


Fig.26A.

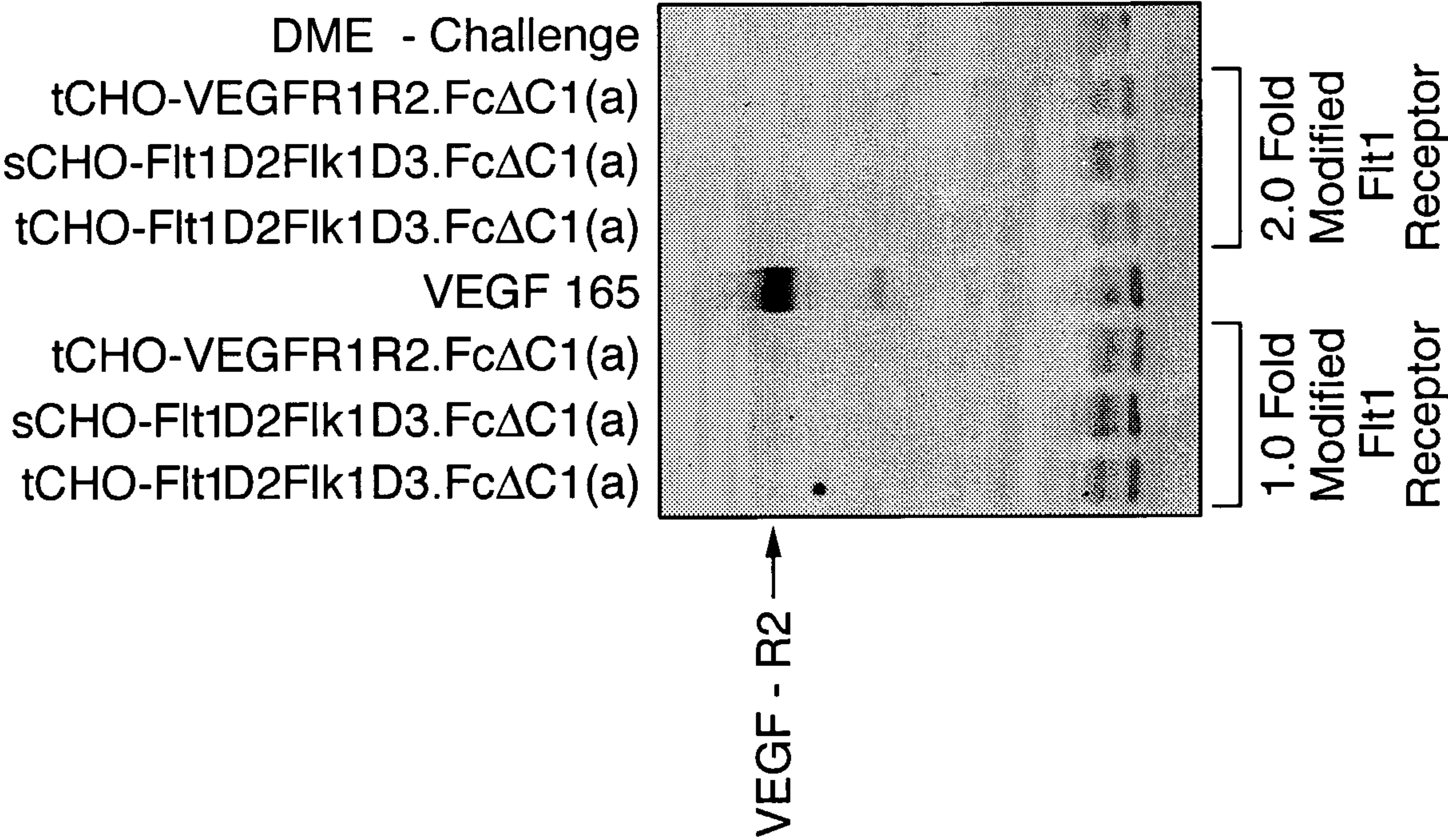
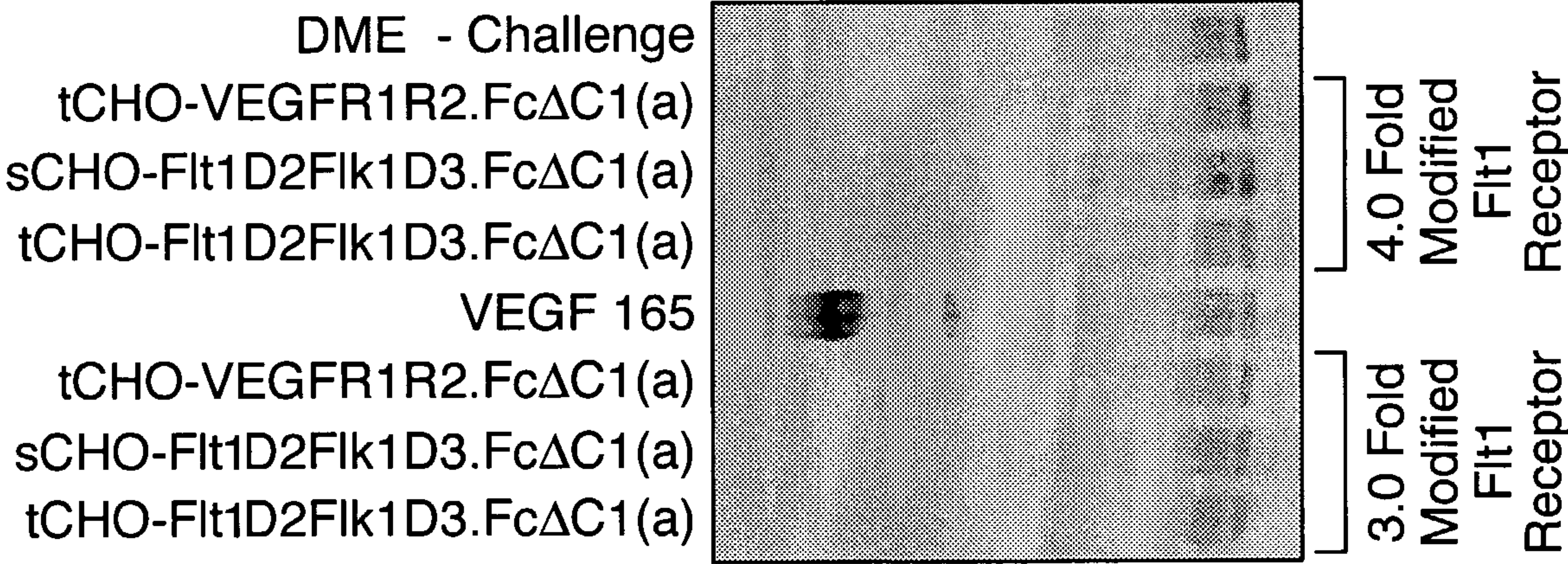


Fig.26B.



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Fig.27.

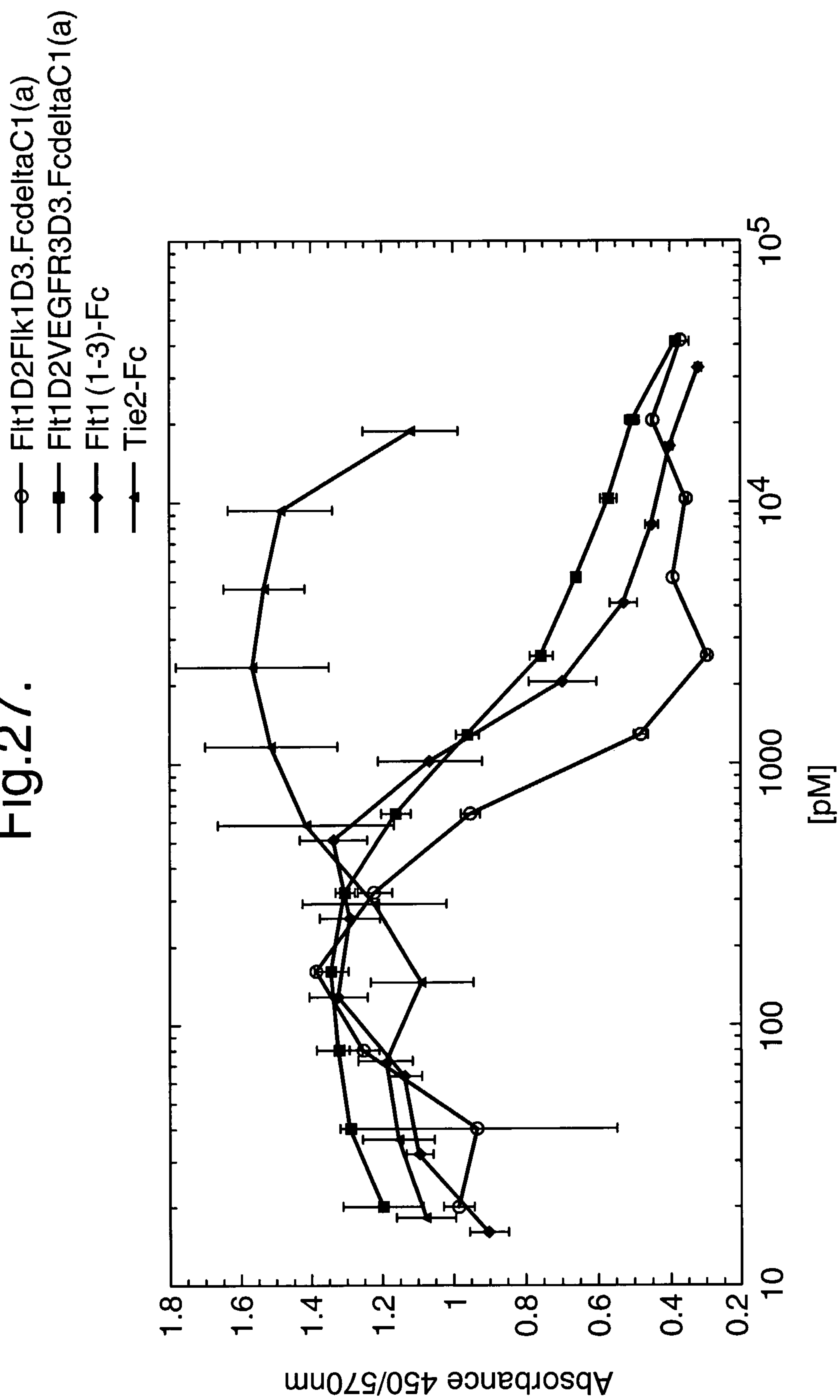


Fig.28.

Binding Stoichiometry of hVEGF165 to Flt1D2Flk1D3.FcΔC1(a) & VEGFR1R2-FcΔC1(a)		
hVEGF165 (nM)	VEGF/Flt1D2Flk1D3.FcΔC1(a)	VEGF/VEGFR1R2-FcΔC1(a)
1	0.93	0.98
10	0.97	0.94
50	1	0.99
Average ± StDev	0.96 ± 0.03	0.97 ± 0.02

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Fig.29.

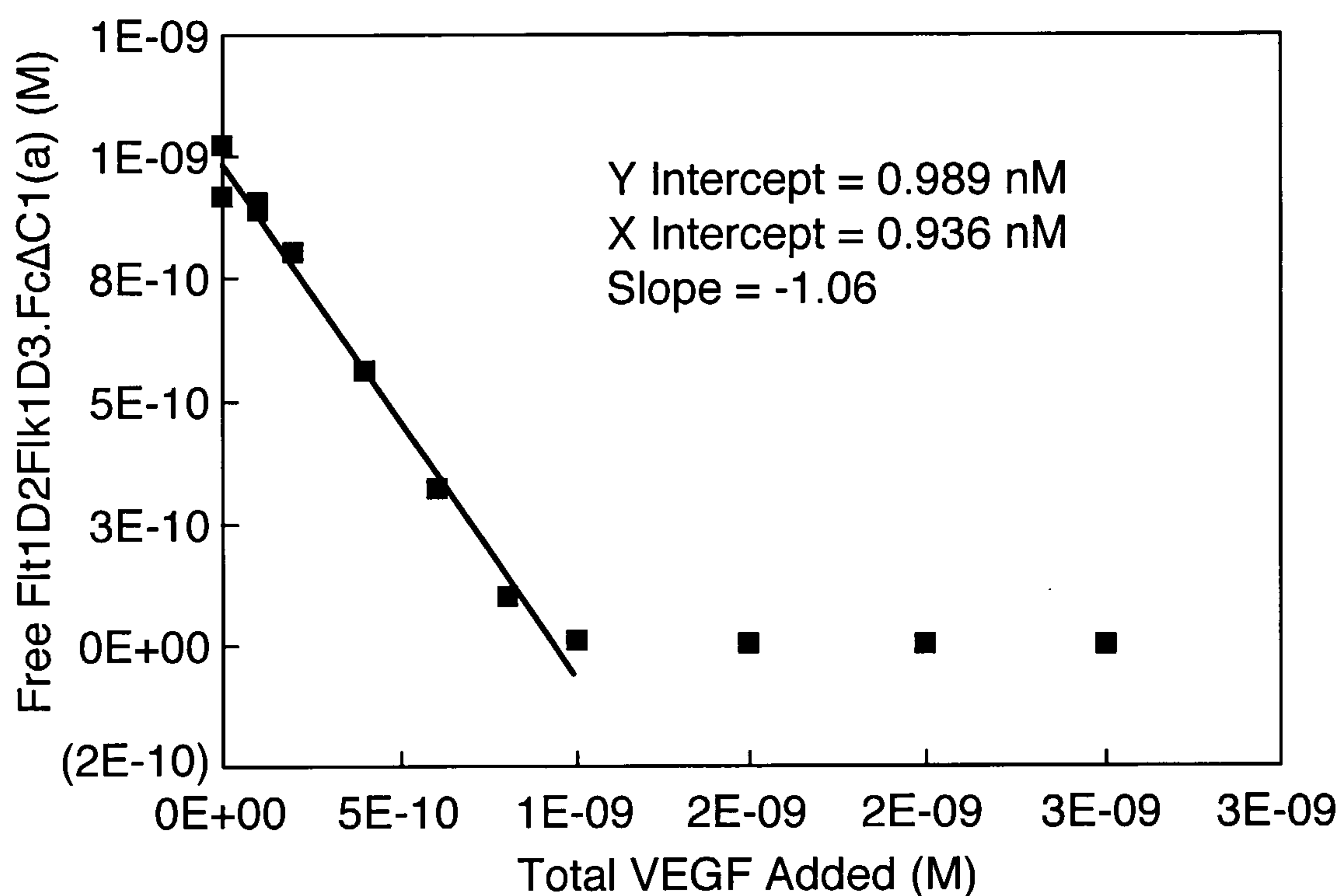
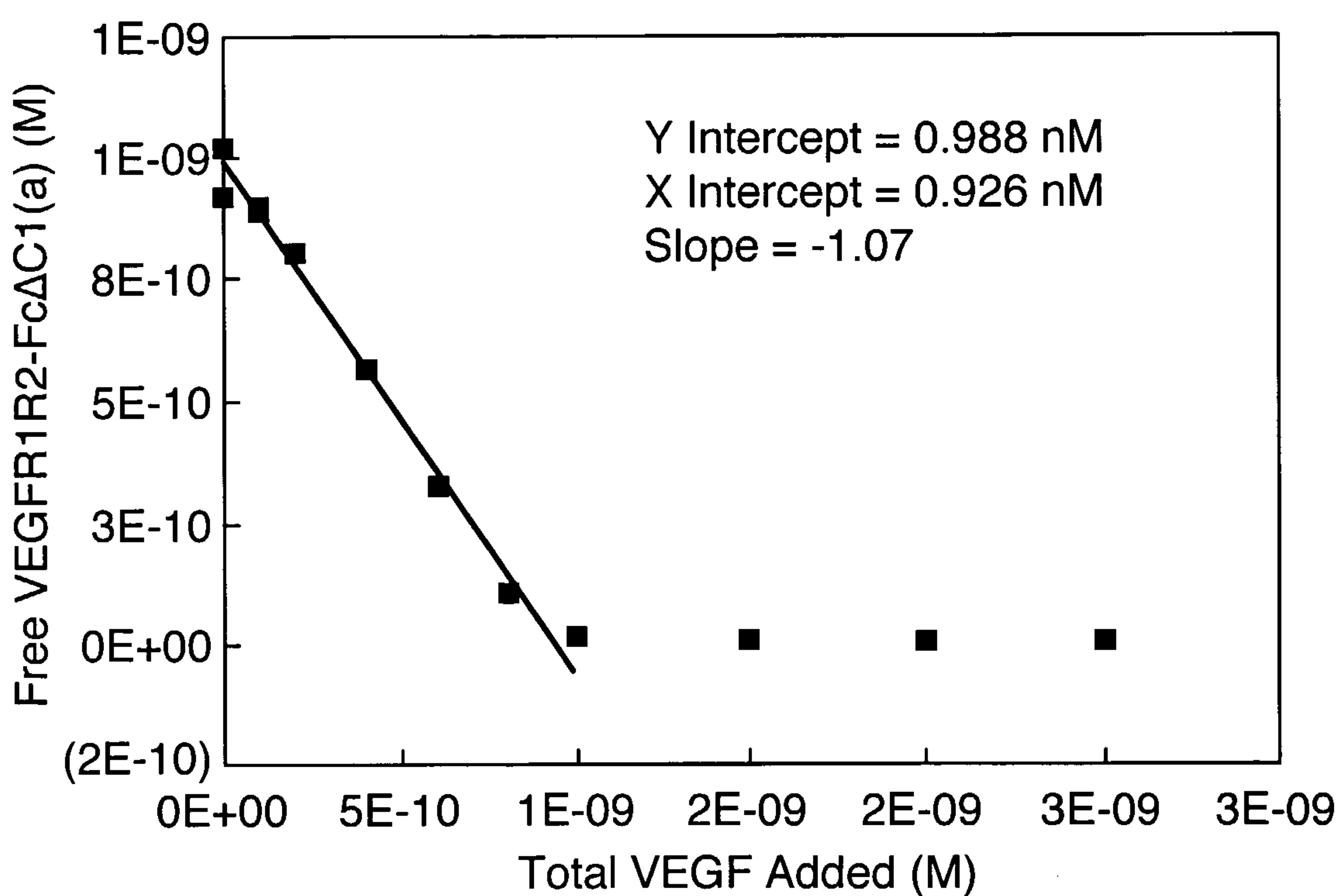
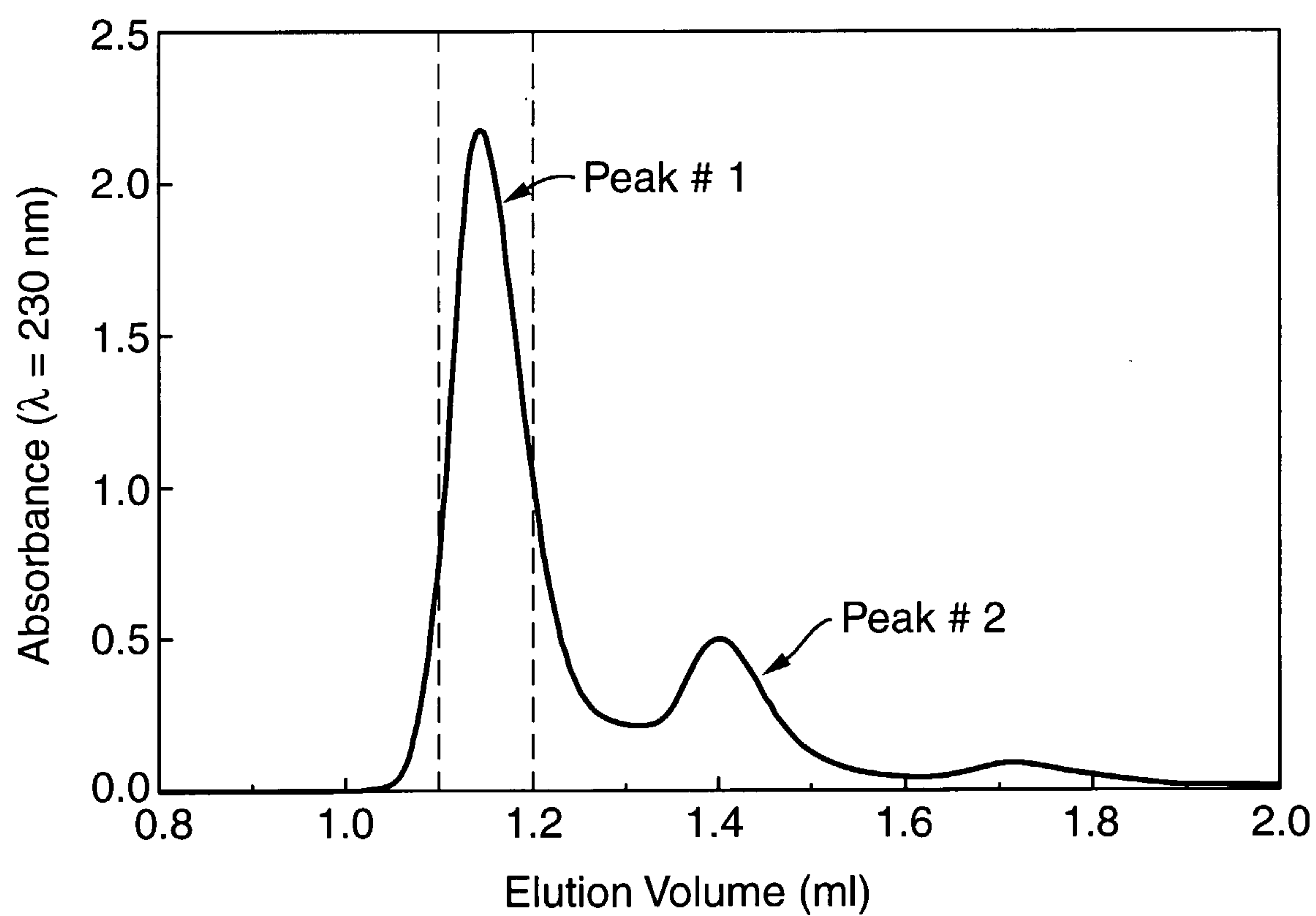


Fig.30.



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Fig.31.



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Fig.32.

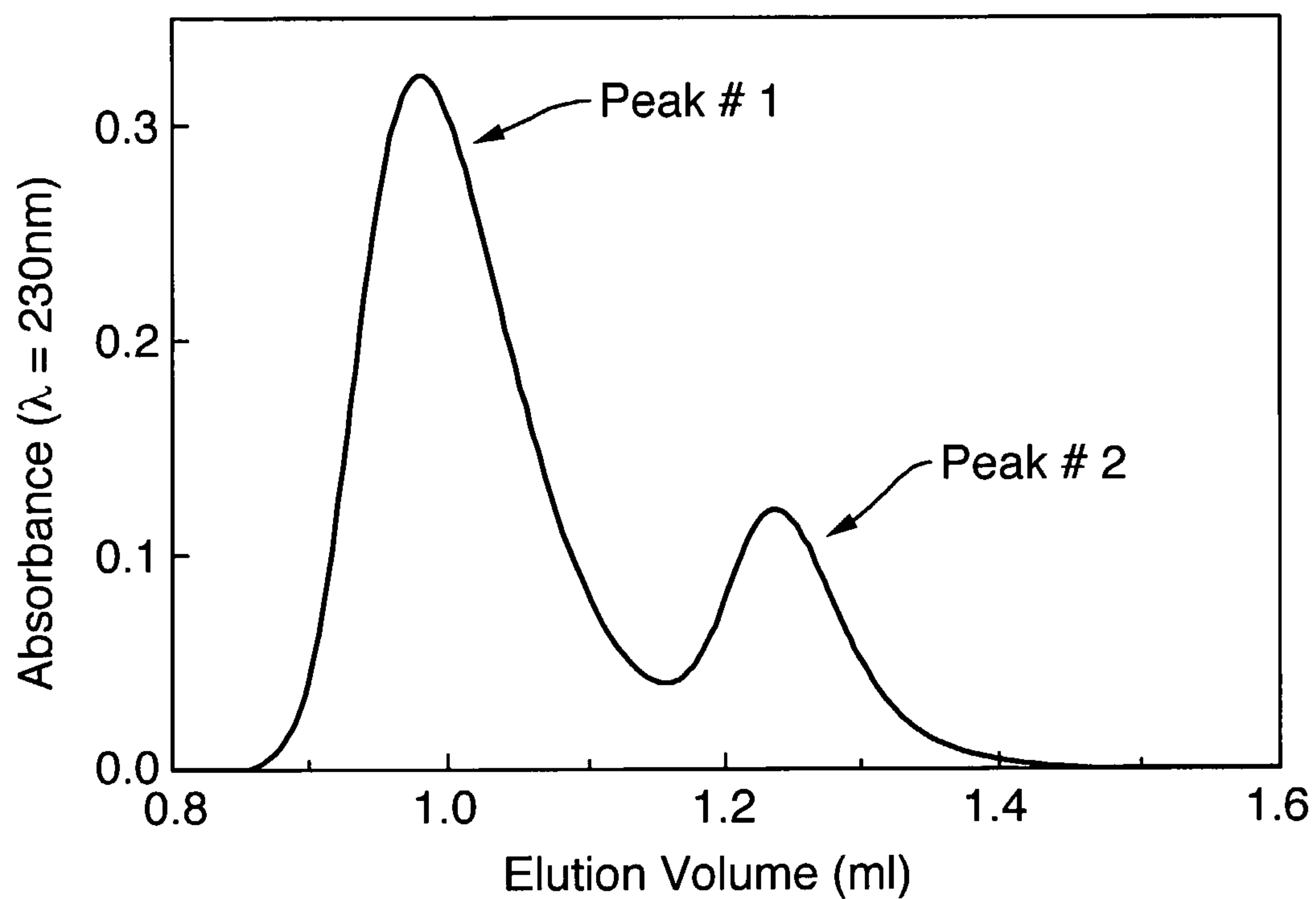
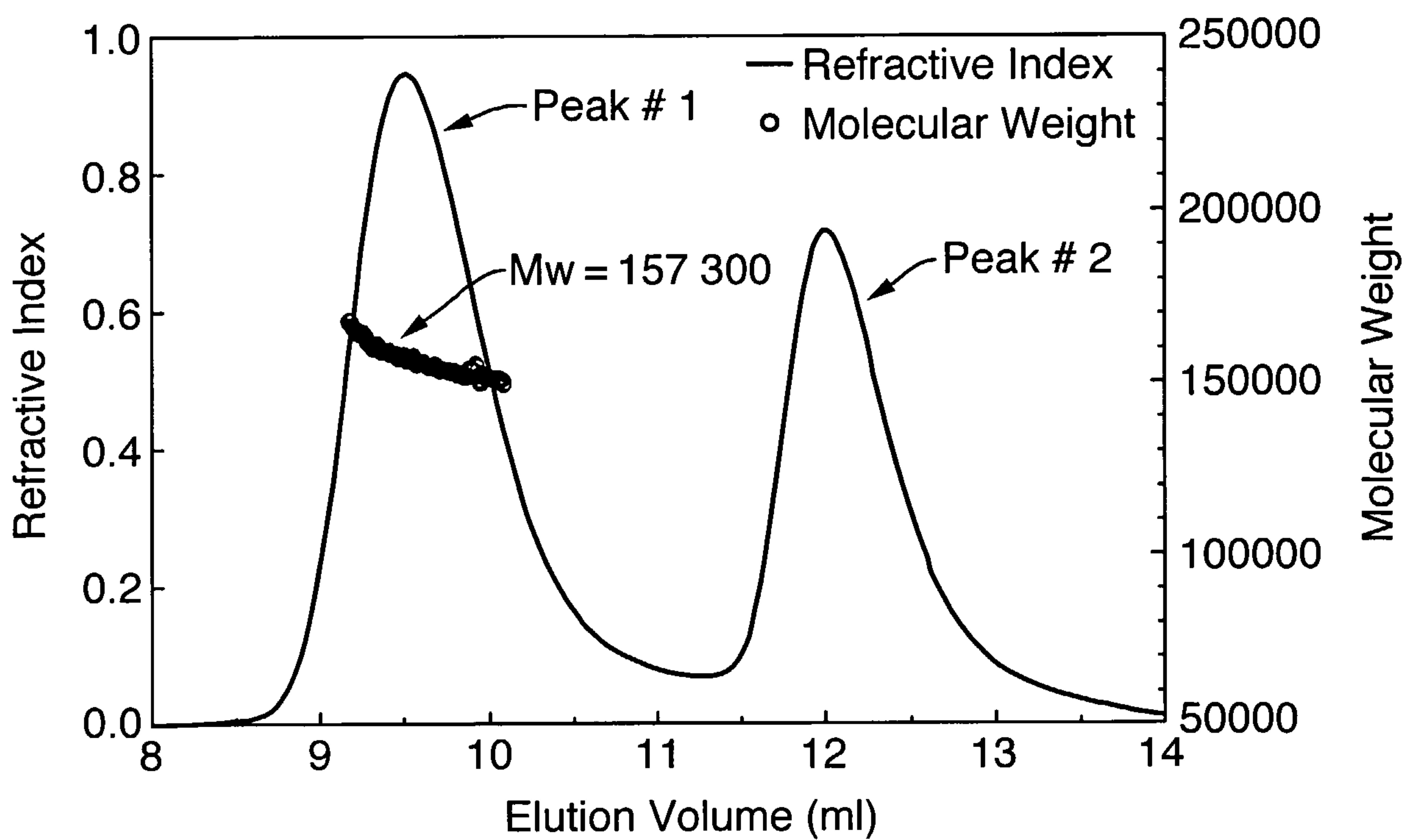


Fig.33.



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Fig.34.

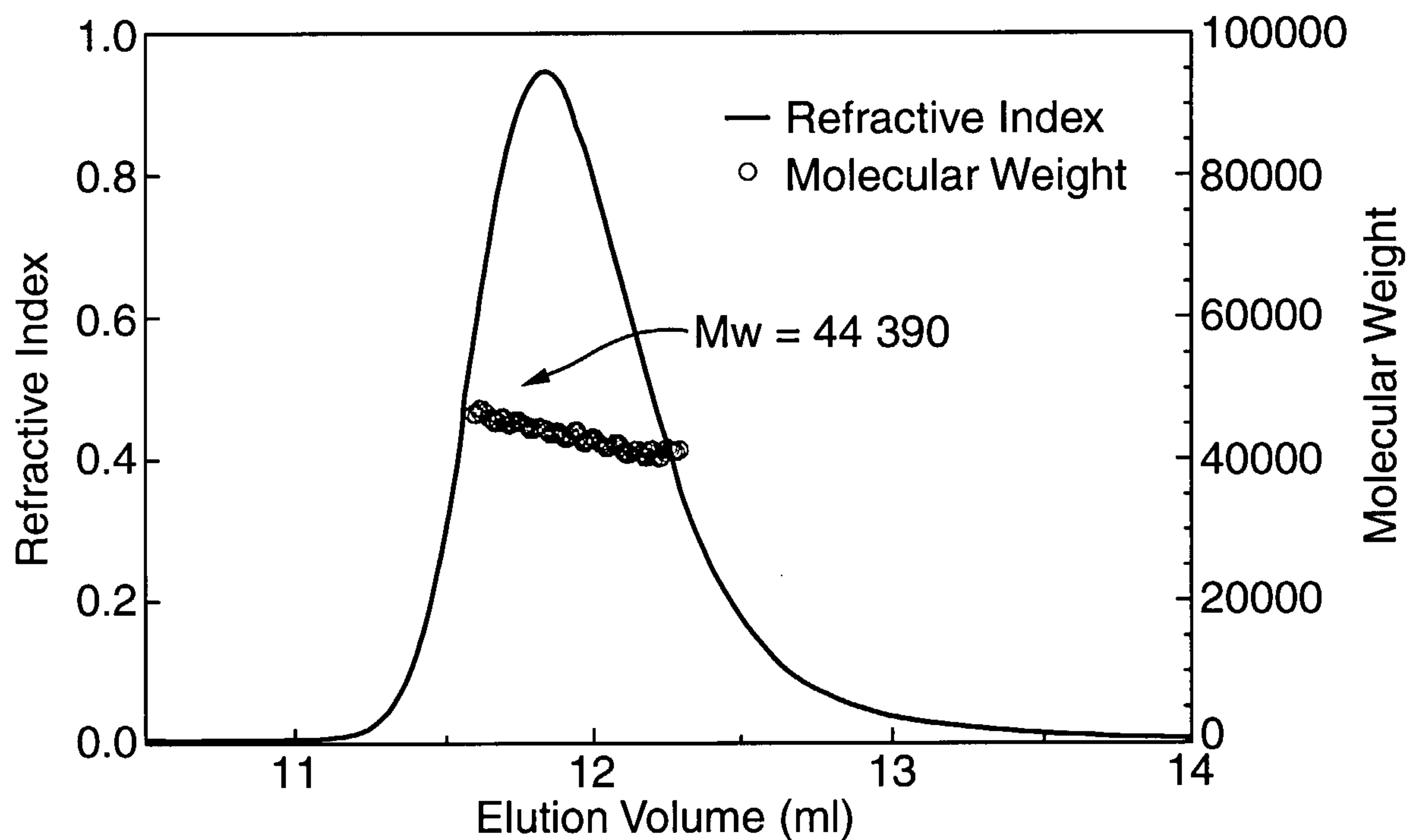


Fig.35.

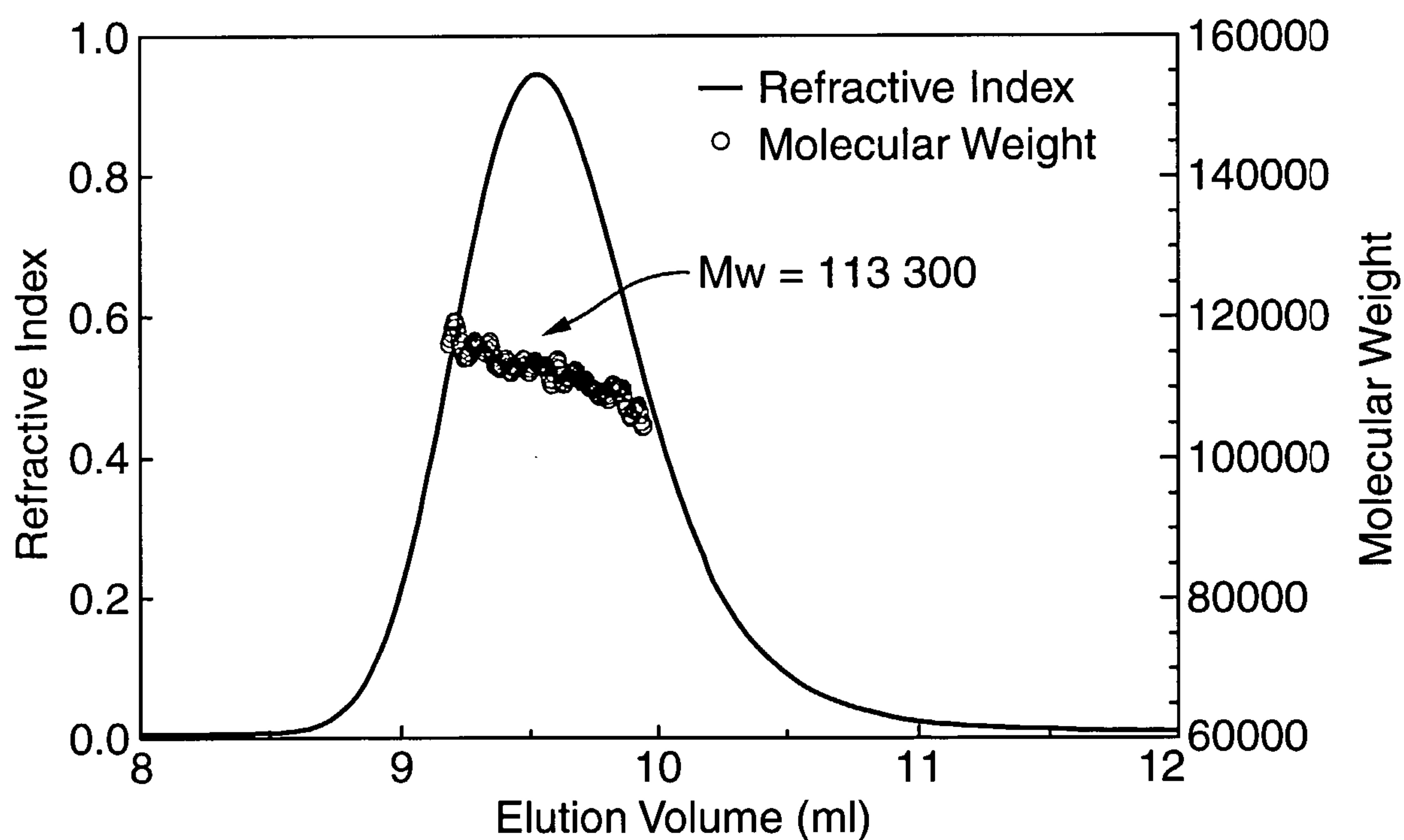


Fig.36.

50
GRPFVEMYSEIPEIIHMTEGREL VIPCRVTSPNITVTLKKFPLDTLIPDG
100
KRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIID
150
VVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNR
200
DLKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVH
250
EKGPGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD
300
VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN
350
GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSL
400
TCLVKGFYPSDIAVEWESNGQPENNNYKTTTPVLDSDGSFFLYSKLTVDKS
RWQQGNVFSQSVMEALHNHYTQKSLSLSPGK

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Fig.37.

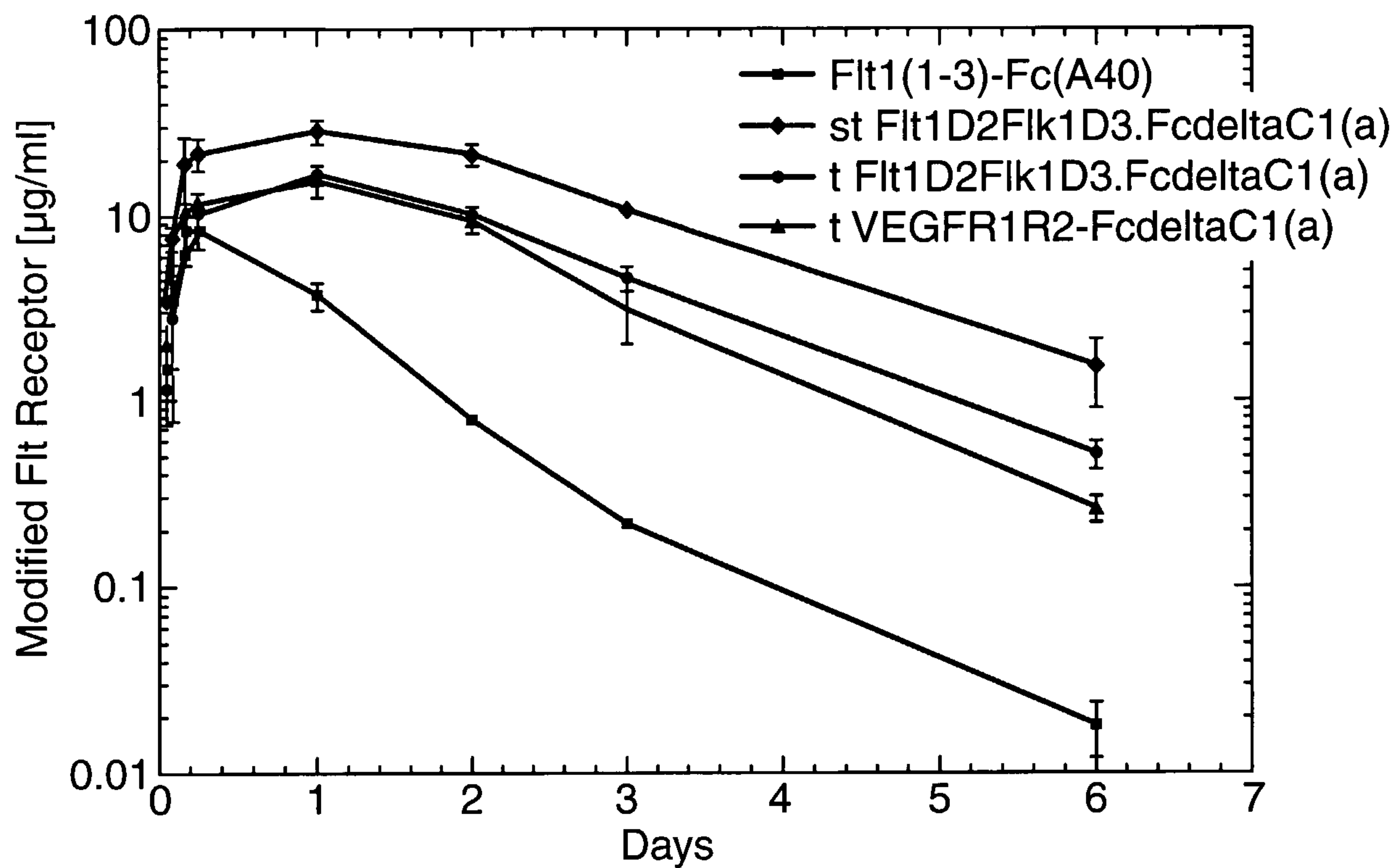
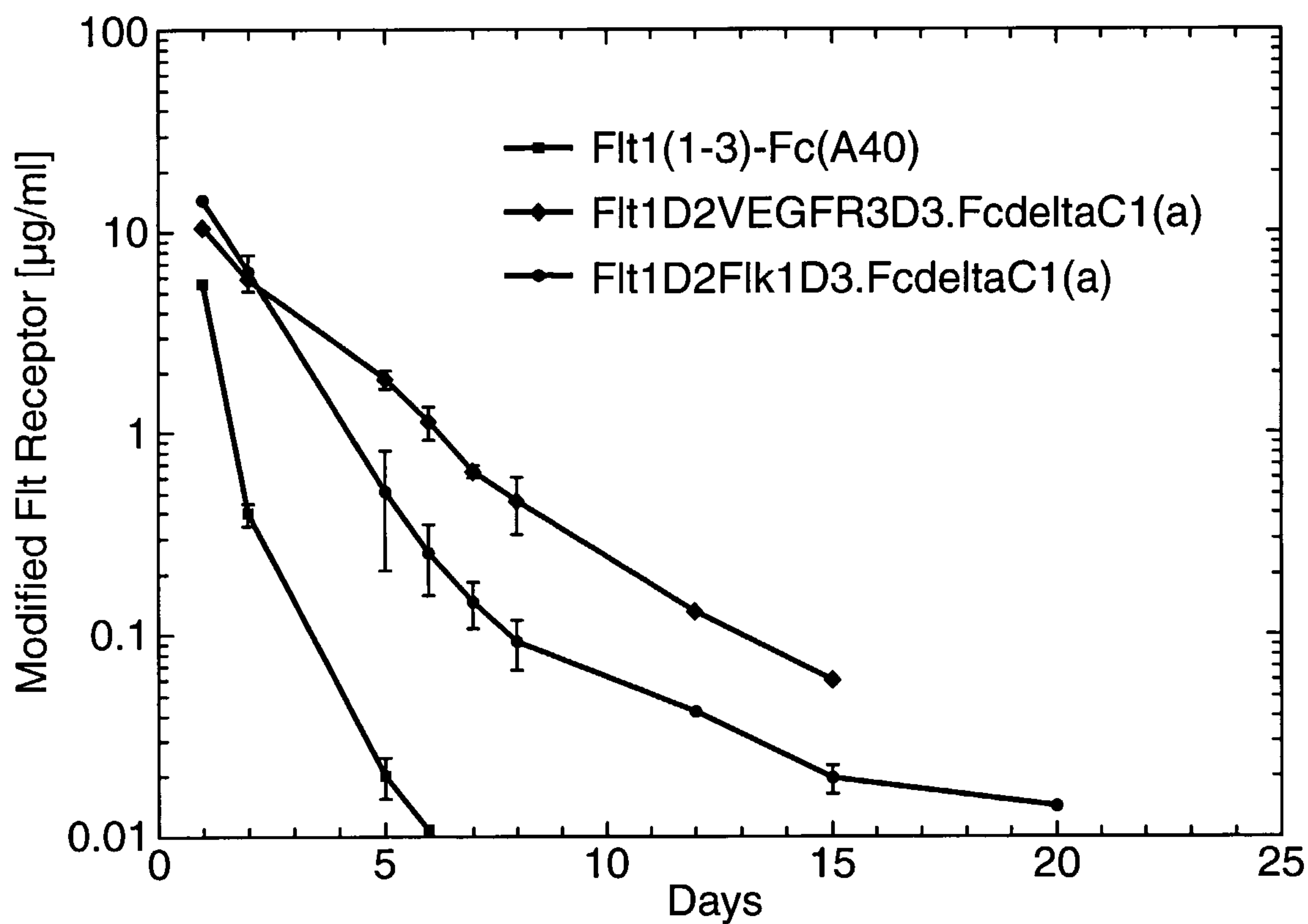


Fig.38.



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Fig.39.

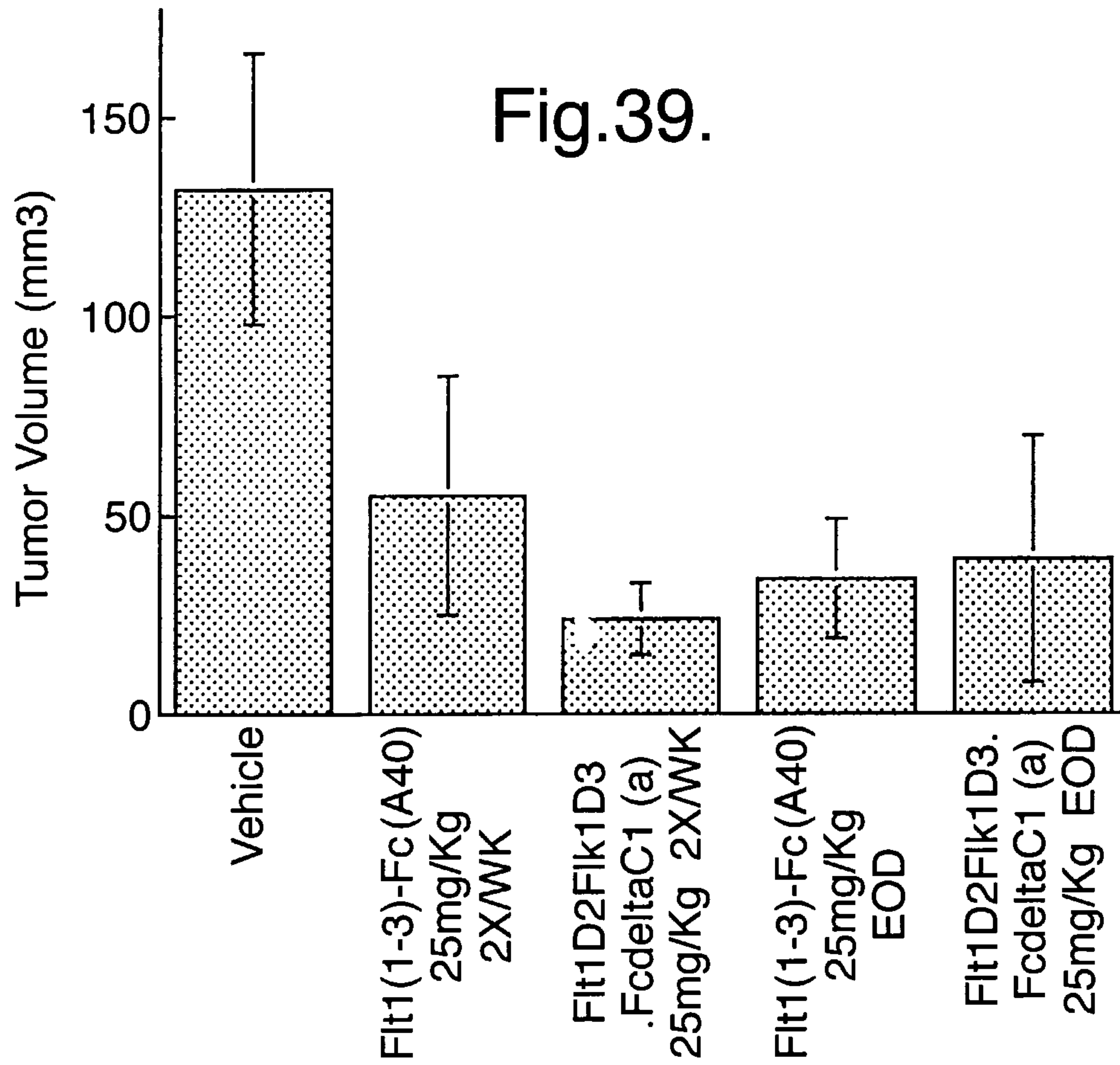


Fig.40.

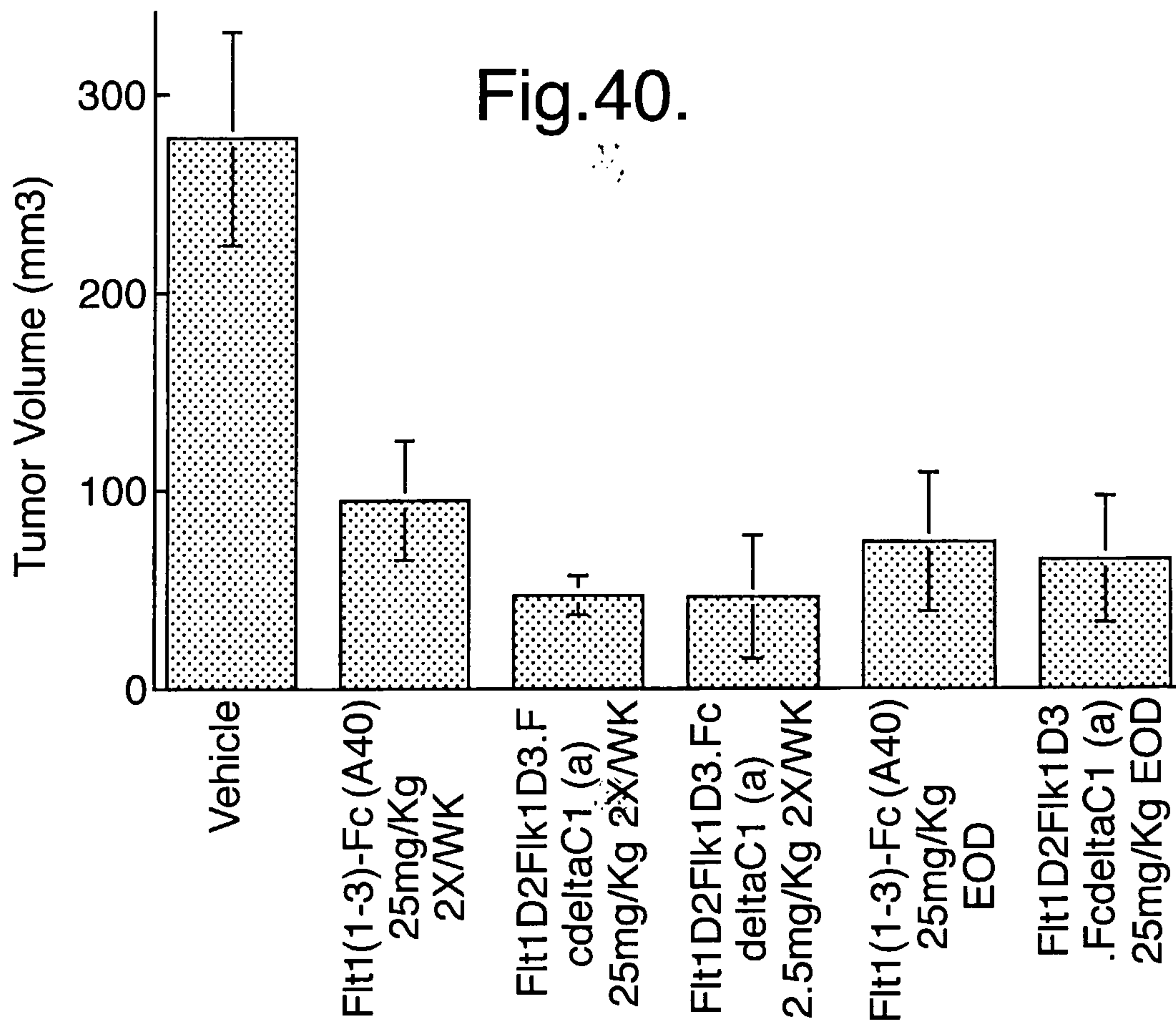
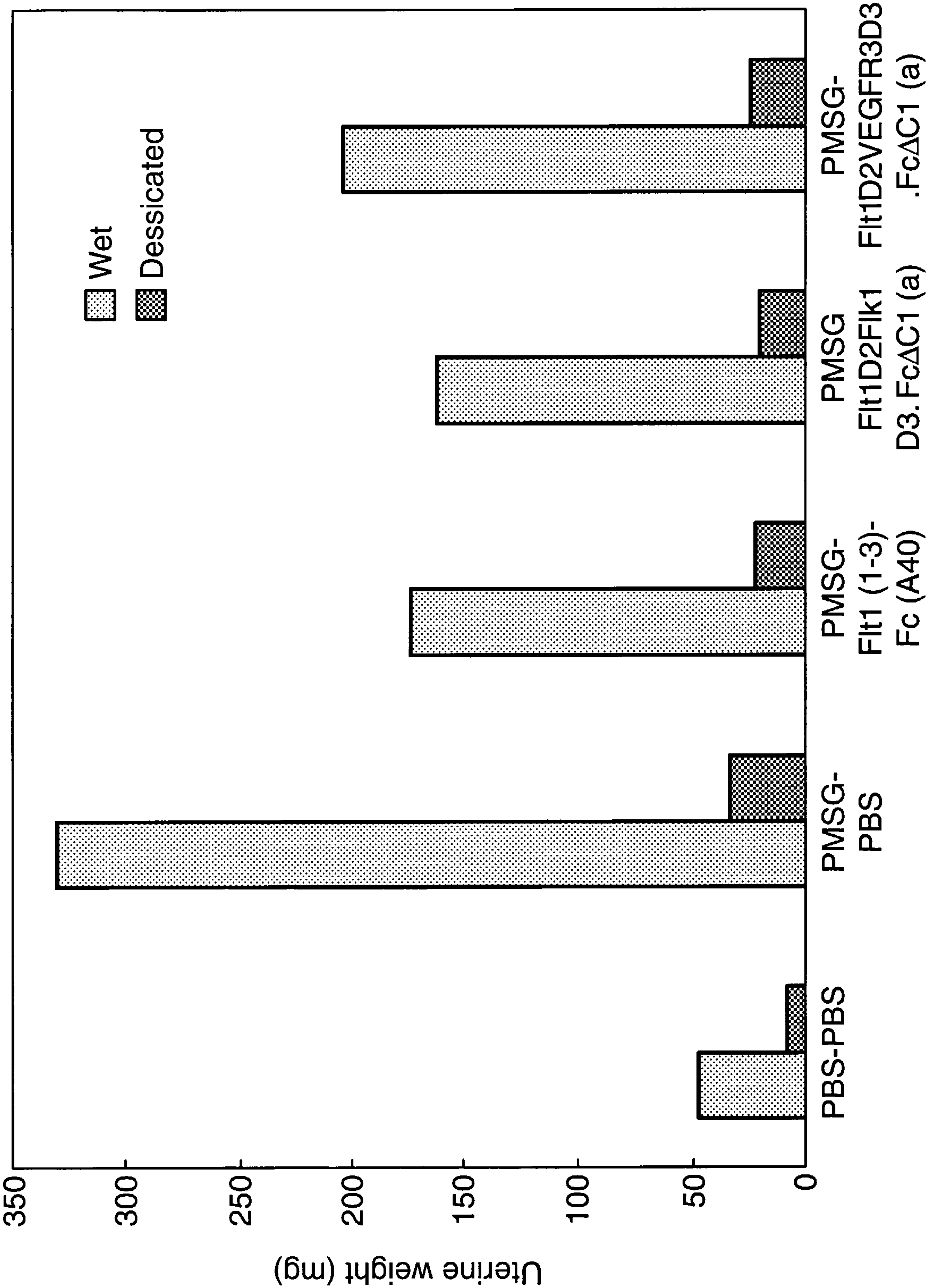


Fig.41.



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Fig.42A.

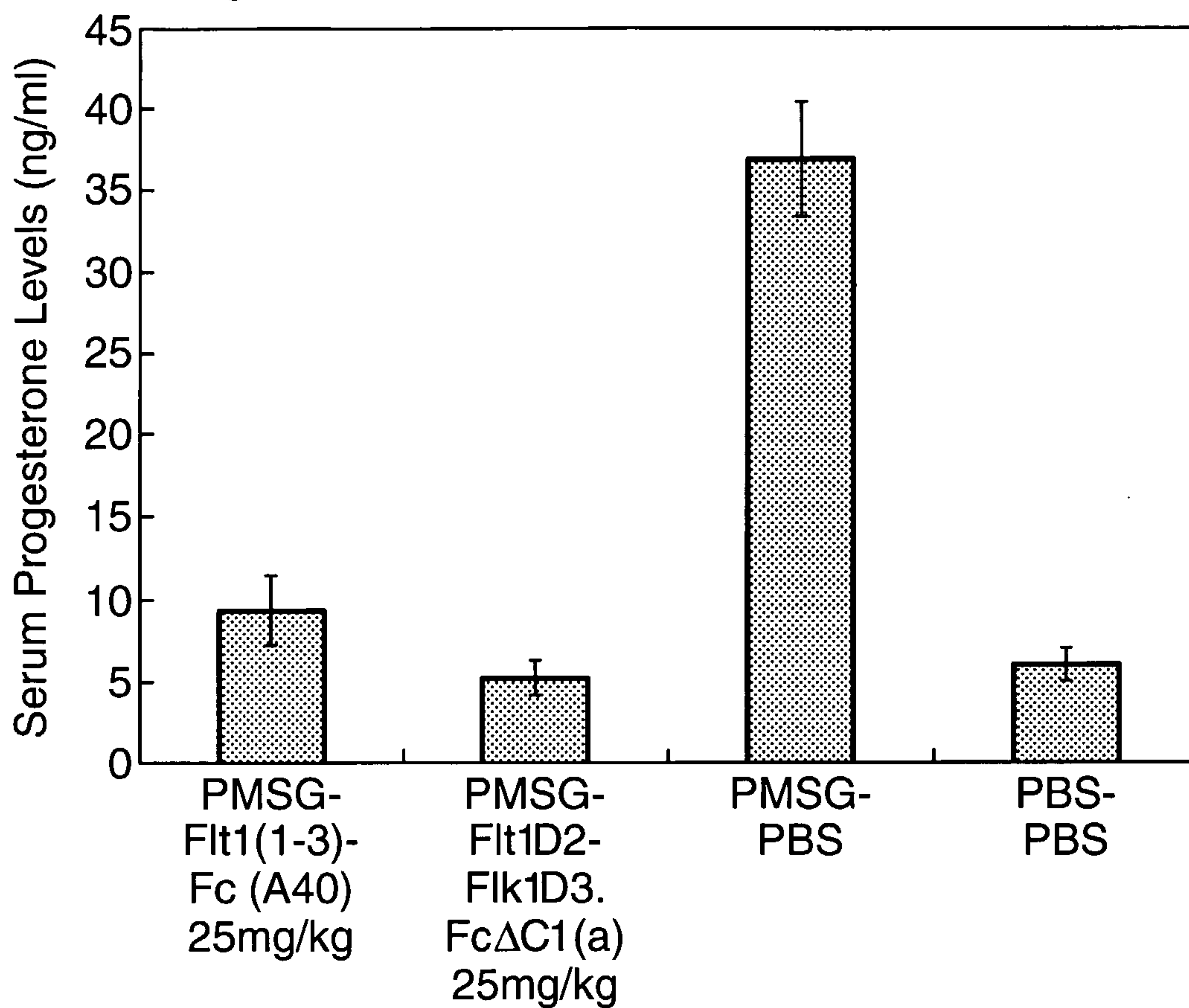


Fig.42B.

