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IDENTIFICATION OF A NOVEL HUMAN
RECEPTOR TYROSINE KINASE GENE

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FIELD OF THE INVENTION

This invention relates to the DNA sequence encoding a novel human growth factor receptor which is a type III receptor tyrosine kinase. The receptor is referred to as Kinase insert Domain containing Receptor (KDR) and binds specifically to the growth factor vascular endothelial cell growth factor (VEGF). This invention also relates to the amino acid sequence of the receptor.

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BACKGROUND OF THE INVENTION

Growth factors are small molecules which regulate normal cell growth and development through interaction with cell surface receptors. The receptors for a number of growth factors are referred to as tyrosine kinases; that is, binding of growth factor to the receptor stimulates an increased phosphorylation of tyrosine amino acids within the receptor; this in turn leads to cellular activation (Bibliography 1).

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There is increasing evidence that genetic alterations affecting the expression of receptor tyrosine kinases (RTK) can contribute to the altered cell growth associated with cancer. This conclusion is

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supported by the frequent identification of RTK as products of the oncogenes for many of the acutely transforming retroviruses (e.g., 2,3,4) and the overexpression of RTK in certain cancers (5). The identification of a novel RTK may lead to a better understanding of cell growth under both normal and transforming circumstances.

The amino acid sequence in the catalytic domain of all tyrosine kinases has been conserved (6). Detailed analysis of the amino acid sequences within the catalytic and noncatalytic domains of RTK indicates the existence of distinct structural subtypes. One group of RTK (designated type III) includes the ckit proto-oncogene and the receptors for platelet derived growth factor (PDGF) and colony stimulating factor-1 (CSF-1).

The most unusual feature of this subtype is that its catalytic (kinase) domain is interrupted by a long insertion sequence of 12-102 amino acids (the kinase insert domain). The two peptides constituting the kinase domain are conserved between the receptors, while the sequence of the kinase insert domain is unique for each receptor.

Several approaches have been tried in order to identify novel RTK, including low-stringency screening of cDNA libraries with previously characterized DNA probes (7). More recently, a technique has been developed that is capable of greatly facilitating the identification of novel genes for which some sequence data are known. The polymerase chain reaction (PCR) has been used to identify novel members of several gene families including those of guanine nucleotide regulatory proteins (8) and protein phosphatases (9). PCR has been used to identify novel tyrosine kinase genes (10), though the primers used in

that study were designed from DNA segments contained in all tyrosine kinases, rather than being specifically directed against RTK. It is a continuing goal to identify receptors for growth factors.

5 The elucidation of the growth factors, as well as their receptors, involved in regulating endothelial cell function is critical for the understanding of how new blood vessels are formed (angiogenesis). Angiogenesis plays a significant role
10 in both normal and pathological events such as embryogenesis, progression of ocular diseases, and wound healing (11). In particular, angiogenesis is an important process for the growth of tumors (11). Angiogenesis is a complex process involving endothelial
15 cell proliferation, migration, and tissue infiltration. These events are stimulated by growth factors which either (i) act directly on endothelial cells (12,13), or (ii) act indirectly by inducing host cells to release specific endothelial cell growth factors (11).
20 One member of the first group is vascular endothelial cell growth factor (VEGF), also known as vascular permeability factor (14-16). Besides its angiogenic activity, VEGF displays the physiological function of increasing the permeability of capillary vessels to
25 different macromolecules (14).

SUMMARY OF THE INVENTION

30 The present invention relates to novel DNA segments which together comprise a gene which encodes type III RTK. The type III RTK encoded by the gene is designated the KDR protein (which stands for Kinase insert Domain containing Receptor). The KDR protein
35 binds specifically to the growth factor VEGF (vascular endothelial cell growth factor).

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The DNA segments are identified and isolated through the use of PCR technology. The overall strategy is summarized as follows:

5 PCR is used to amplify the DNA segments
corresponding to the kinase insert domains of type III
receptor tyrosine kinase genes in an endothelial cell
library designated HL10246 (Clontech Laboratories,
Inc., Palo Alto, CA). Degenerate oligonucleotide
primers are designed which are complementary to
10 conserved tyrosine kinase domains flanking the kinase
insert domains of known type III receptor tyrosine
kinases. These primers are used in the PCR procedure.
DNA probes, designed from the DNA sequence of the PCR
product, are then used to identify cDNA clones of the
15 receptor gene from the original cDNA library.

In particular, the present invention relates
to specific oligonucleotides which, when used as
primers for PCR, allow for the amplification of DNA
segments corresponding to the kinase insert domains of
20 type III RTK genes.

In a principal embodiment, the present
invention is directed to three overlapping DNA segments
(designated BTIII081.8, BTIII129.5 and BTIV169) which
comprise the entire coding region of this novel gene,
25 namely, 4,068 nucleotides extending to the 3' end.

These DNA segments are isolated from a human
endothelial cell cDNA library and together comprise
the gene coding for a novel type III receptor tyrosine
kinase. The human gene containing these DNA segments
30 is referred to hereinafter as KDR (which stands for
Kinase insert Domain containing Receptor) or,
alternatively, as kdp (which stands for Kinase insert
Domain containing Protein). The use of the term KDR is
intended to include any DNA segments which form the
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human gene which encodes the novel type III RTK of this application.

5 The DNA segments embodied in this invention are isolated from human sources. The present invention comprises DNA segments, and methods for using these DNA segments, which allow for the identification of a closely related gene in mouse DNA. The methods developed in this invention can be readily used by those skilled in the art for the identification and isolation of closely-related homologues in other species. Therefore, the present invention also embodies all DNA segments from species other than human which encode proteins having substantially the same amino acid sequence as that encoded by the kdp gene.

10 The present invention further relates to methods developed for the detection of mRNA's produced as a result of transcription of the sense strands of the DNA segments of this invention. Messenger RNA prepared from bovine endothelial cells are used in developing these methods. The ability to detect mRNA for a novel RTK may ultimately have medical benefit, especially in light of recent observations that the mRNA for certain RTKs are overexpressed in some cancers (5).

15 The methods developed in the present invention for detecting mRNA expressed by the kdp gene can be readily used by those of ordinary skill in the art for the detection of mRNA species related to the kdp gene in any cell type and from any species. For this reason, the present invention embodies all mRNA segments which are the result of transcription of the kdp gene.

20 The present invention relates to methods for expression of the receptor protein, for example, in CMT-3 cells of monkey kidney origin. The receptor

protein, portions thereof, and mutated forms of the receptor protein may be expressed in many other cells by those skilled in the art using methods similar to those described in this application. For this reason, the present invention embodies all proteins encoded by the human KDR gene and proteins encoded by related genes found in other species.

The present invention further relates to methods for studying the interaction of VEGF to the expressed KDR protein. Recent work in the literature (17) indicates that VEGF is one member of a family of related proteins, and the interaction of growth factors similar to VEGF with the KDR protein can readily be studied by those skilled in the art using methods similar to those described in this application. These methods can readily be modified to study the interaction of candidate pharmaceuticals with the KDR protein towards the goal of developing an antagonist or agonist of VEGF action. For this reason, the present invention embodies methods for studying the interaction of VEGF and VEGF-related growth factors with the KDR protein.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 depicts a schematic representation of three receptor tyrosine kinase subclasses (6). KI is kinase insert domain; PTK is kinase domain; cys is cysteine rich region.

Figure 2 depicts the two sets of primers used for PCR (SEQ ID No: 1 and 2). The nucleotide sequences in appropriate regions of the four known type III receptor tyrosine kinase cDNAs are aligned and degenerate oligonucleotide primers are designed based upon the consensus sequences.

Figure 3 depicts the amplification of the kinase insert domains using PCR. DNA segments encoding the kinase insert domains of type III receptor tyrosine kinases are amplified by PCR. A sample (5 μ l) is run on a 1.0% agarose gel which is stained with ethidium bromide. DNA size standards (123 bp ladder; Bethesda Research Laboratories, Bethesda, MD) are run as well.

Figure 4 depicts the DNA sequence of the two PCR products (Panel A: 363 bp segment derived from the 420 bp product (SEQ ID NO: 3); Panel B: 251 bp product (SEQ ID NO: 4)). The two products are purified by agarose gel electrophoresis, digested with Sall and EcoRI, and cloned into the plasmid vector pBlueScribe(+) (Stratagene; San Diego, CA). The 420 bp PCR product is digested to 363 bp during this procedure. The DNA sequences for the primers used in the amplification are underlined.

Figure 5A depicts a computer assisted comparison of the DNA sequence for the 363 bp DNA segment derived from the 420 bp PCR product with the sequence of a DNA segment of the PDGF receptor (SEQ ID NO: 5) (18). A region of strong homology between the 363 bp segment derived from the 420 bp PCR product and the PDGF receptor is contained in a box. Figure 5B depicts a computer assisted comparison of the DNA sequence for the 251 bp PCR product with the sequence of a DNA segment of the FGF receptor (SEQ ID NO: 6) (7).

Figure 6 depicts the strategy used for sequencing the insert portions of clones BTIII081.8 and BTIII129.5 and BTIV169. The sequencing reaction uses either synthetic oligonucleotides (represented by boxes at the start of an arrow), or the M13 universal primer (no box) to initiate the reaction. In some cases, portions of these DNA segments are isolated using the

restriction enzymes indicated in the figure, and subcloned back into the plasmid vector pUC118, so that the M13 universal primer can be used. The position of the stop codon in BTIII129.5 is indicated. The coding portions of these DNA segments are shown at the bottom of the figure. The relative positions of the 1) membrane spanning portion, 2) kinase domains, and 3) kinase insert domain are indicated. The position of these structural features within the KDR derived DNA segments is compared in relation to their position in the PDGF-receptor ("PDGF-R").

Figure 7 depicts the DNA and predicted amino acid sequence of KDR, plus the stop codon (nucleotides 1-4071 of SEQ ID NO. 7). The sequence of the DNA segment amplified by PCR is underlined (nucleotides 2749-3105 of SEQ ID NO. 7). Cysteine residues in the putative extracellular domain are circled. Potential N-linked glycosylation sites are indicated by an asterisk. The putative membrane spanning region is enclosed in a box (nucleotides 2293-2367 of SEQ ID NO. 7).

Figure 8 depicts a hydropathy plot of the predicted amino acid sequence for the KDR protein.

Figure 9 depicts a comparison of the predicted amino acid sequence in the putative intracellular portion of the KDR protein to the ckit proto-oncogene (SEQ ID No: 8) (3), the CSF-1 receptor (SEQ ID NO: 9) (4), and the PDGF receptor (SEQ ID NO: 10) (18). Exact matches are indicated by an asterisk. Gaps are introduced to achieve maximum alignment. The putative ATP recognition site is indicated by three asterisks.

Figure 10 depicts the identification of kdp receptor mRNA by Northern blot analysis. Five micrograms of bovine aortic endothelial cell polyA+ RNA

are used. A nick-translated [^{32}P] CTP-labelled EcoRI/BamHI DNA segment (nucleotides 1510-2417 of SEQ ID NO. 7) is used as a probe. Autoradiography is for 36 hours.

5 Figure 11 depicts the *kdp* gene in human and mouse DNA by Southern blot analysis. A nick translated [^{32}P]CTP-labelled EcoRI/BamHI DNA segment (nucleotides 1510-2417 of SEQ ID NO. 7) is used as the probe. The probe is hybridized to Southern blots containing EcoRI digested DNA from human (lane 1), mouse (lane 2), and human-mouse hybrid cells (19) (lanes 3 and 4). The DNA used in lane 3 lacks the *kdp* locus, while DNA used in lane 4 contains the *kdp* locus.

10 Figure 12 depicts a Western blot analysis of CMT-3 cells which express the KDR protein. Cells are transfected with either the pcDNA1tkpASP vector alone (lane 1) or with that vector modified to contain the KDR gene (lane 2). 2×10^5 cells and 1 microgram of DNA are used for each transfection. Forty-eight hours later, Western blot analysis is performed on the samples using the anti-KDR.PS23 polyclonal antibody at a dilution of 1:1000. Detection of reacting proteins is performed using an ECL system (Amersham, Chicago, IL).

20 Figure 13 depicts the results of [^{125}I] VEGF binding to CMT-3 cells which express the KDR protein. Cells are transfected with either the vector alone (bars 1 and 2) or with the vector containing the KDR gene (bars 3 and 4). Forty-eight hours later, the samples are washed with phosphate buffered saline (PBS), and incubated with serum-free media containing 50 pM [^{125}I] VEGF (specific activity equal to 4,000 cpm per fmol), for 90 minutes. Nonradioactive VEGF, 5 nM, is added to some samples (bars 2 and 4) to define

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specific binding sites. The samples are washed with ice cold PBS, and the cells are transferred to gamma-counting tubes using 0.1% lubrol.

Figure 14 depicts the results of affinity cross-linking of [125 I] VEGF to CMT-3 cells which express the KDR protein. CMT-3 cells are transfected with either the vector alone (lane 1) or with the vector containing the KDR gene (lane 2). Forty-eight hours later, the cells are washed in PBS, and serum free media containing 200 pM [125 I] VEGF is added. After 90 minutes at room temperature, an affinity cross-linker disuccinimidyl suberate, 0.5 mM, is added for 15 minutes. The samples are then prepared for SDS-PAGE autoradiography.

DETAILED DESCRIPTION OF THE INVENTION

The strategy used to discover the DNA segments for the novel type III RTK gene begins with the design of two degenerate oligonucleotide primers based upon their homology to specific regions of the kinase domains of known RTK genes (Fig. 2) (3,4,7,18). In one embodiment, the polymerase chain reaction is then used to amplify DNA segments from a human endothelial cell cDNA library (designated HL 10246). The cDNA products from this step are each cloned into a plasmid vector designated pBlueScribe+ (Stratagene, San Diego, CA) and sequenced. Oligonucleotide probes are designed from potentially interesting sequences in order to screen the cDNA library for more full length clones of the novel cDNA.

The strategy just described provides several novel elements: 1) the DNA sequences of the oligonucleotide primers used during PCR; 2) the DNA sequence of the products generated by the polymerase chain

reaction; and 3) the DNA sequence of the final cloned DNA segments. Each of these elements of the invention described in this application will now be discussed in detail.

5 Figure 2 shows the rationale for choosing the oligonucleotide primers used in the PCR. The primers are designed to allow for the PCR amplification of the kinase insert domain of type III RTK genes. In order to design the primers, the DNA sequences of known type III
10 RTK genes are aligned in specific regions of their catalytic domains, and a consensus sequence is chosen. The regions of the catalytic domains chosen in designing the primers flank the kinase insert domains of the receptor genes.

15 Primer 1 (SEQ ID No: 1) is designed from a region of the kinase domain 5' to the kinase insert domain, and consists of a mixture of four different 21mers. Primer 2 (SEQ ID NO: 2) is designed from a region of the kinase domain 3' to the kinase insert
20 domain, and consists of a mixture of sixteen different 29mers with one inosine, indicated in SEQ ID NO: 2 by "N".

SalI and EcoRI restriction sites are included at the 5' end of primers 1 and 2, respectively, to
25 facilitate the subcloning of the amplified PCR products into plasmid vectors. Those skilled in the art may use other restriction sites; other minor modifications in the protocol above permits the design of primers without the inclusion of restriction sites.

30 The selection of these specific primers constitutes a novel approach towards identifying novel type III RTK genes. It had previously been shown (10) that primers designed from DNA sequences common to all tyrosine kinases allows for the identification of novel
35 proteins. The present invention is the first to

contemplate the use of PCR to specifically target type III RTK.

The protocol used for PCR is as follows:
Human endothelial cell cDNA (designated HL10246) is
5 denatured by boiling and submitted to 30 cycles of PCR
using 1 nmol of both primers in a final volume of 100
 μ l. The timing is 1.5 minutes at 92°C, 2 minutes at
50°C, and 2 minutes at 74°C. DNA from 5 μ l of sample is
10 separated on a 1% agarose gel and stained with ethidium
bromide.

Figure 3 shows the results of the PCR
amplification. Two DNA products, with sizes 251 bp
(SEQ ID NO: 4) and 420 bp, are visible when a sample of
the reaction is electrophoresed on a 1.0% agarose gel
15 and stained with ethidium bromide. The sizes of the
two products are within the range expected for type III
RTK genes (products derived from the FGF and PDGF
receptor genes, which have the smallest and largest
known kinase insert domains, would be 230 and 510 bp,
20 respectively (20, 21).

The DNA from four contiguous lanes with
sizes ranging from 200 to 600 bp is electrophoresed
onto DEAE filter paper, eluted from the paper with
salt, and ethanol precipitated. The samples are
25 incubated with 5 units of EcoRI and SalI. The
restriction enzymes digest the 420 bp DNA segment to a
363 bp DNA segment (SEQ ID NO: 3), due to the presence
of an EcoRI site within the 420 bp DNA segment
(nucleotide 2749, SEQ ID NO. 7). The restriction
30 enzyme digested PCR products are then subcloned into
the plasmid vector pBlueScribe(+). The recombinant
clones are analyzed by sequencing using the
dideoxy-method (22) using a United States Biochemical
(Cleveland, Ohio) Sequenase Version 2.0 sequencing kit.
35 Figure 4 shows the DNA sequences for the 251 bp PCR

product and the 363 bp DNA segment derived from the 420 bp PCR product.

5 Computer assisted comparison of the DNA sequence for the 363 bp segment of the 420 bp PCR product to databases of known DNA sequences reveals that the sequence is novel, because it shares strong sequence identity with the flanking catalytic domain of known type III RTK genes, but not their kinase insert domains. Figure 5A compares the DNA sequence for the 10 363 DNA segment with that for the PDGF receptor gene (SEQ ID No: 5). Similar results are obtained using other type III RTK genes.

DNA sequencing of the 251 bp PCR product reveals a novel sequence containing both primers used 15 for the amplification, but the sequence shows little homology to known tyrosine kinases. This is depicted in Figure 5B, which compares the DNA sequence for the 251 bp DNA segment with that for the FGF receptor (SEQ ID NO: 6). For this reason, further analysis of 20 Product 1 is not pursued.

The protocols used during the PCR do not allow for amplification of the kinase insert domains of known receptor tyrosine kinases in the endothelial cell library used because of the low copy number of the 25 message present in the library. There have been many studies on the effect of FGF on endothelial cell function (23,24) although there is evidence that the expression of the FGF receptor is developmentally regulated (7) and it is likely that the library used 30 contains little or no cDNA for the FGF receptor.

An oligonucleotide probe, designed from the DNA sequence of the 363 bp segment, is synthesized (using an ABI 380 DNA Synthesizer) in order to screen the human endothelial cell cDNA library (HL10246) for 35 the isolation of more full length clones containing the

363 bp DNA segment. The probe sequence is chosen from the region of the 363 bp DNA segment which shares little sequence homology with known RTK.

5 The screening of the endothelial cell cDNA library is conducted as follows: Lambda gt11 phage, 10^6 , are adsorbed to *E. coli* LE392 for 15 minutes at 37°C prior to plating onto agar plates at a density of 5×10^5 phage per plate. After allowing the phage
10 plaques to develop at 37°C , plaque lifts are made using nitrocellulose filters, denatured in 0.4 N NaCl for 1 minute, and neutralized in 0.5 M Tris.HCl, pH 7.3, plus 1.5 M NaCl. The filters are washed with 2 x standard saline citrate (SSC) and then baked for 1.5 hour in a vacuum oven at 80°C . The filters are probed with an
15 [^{32}P] ATP end labeled synthetic oligonucleotide, 5' - TTTCCCTTGACGGAATCGTGCCCTTTGGT-3', which is the reverse complement of a DNA sequence contained in the PCR amplified product (Fig. 3). Hybridization is performed at 50°C in 5 x SSPE (167 mM NaCl, 10 mM sodium
20 phosphate, pH 7.4, 1 mM EDTA), 2.5 x Denhardts, 0.5% sodium dodecyl sulfate (SDS), 100 $\mu\text{g}/\text{ml}$ salmon sperm DNA. The filters are washed twice, 20 minutes per wash, with 2 x SSC plus 0.1% SDS at room temperature, followed by washing twice at 50°C with 0.1 X SSC plus
25 0.1% SDS; 20 minutes per wash. Positive clones are identified, picked and plaque purified.

Forty-five positive clones are obtained. Three of these positive clones are plaque purified and their phage DNA isolated. Digestion of the DNA with
30 *Eco*RI and electrophoresis in agarose indicates that one clone, designated BTIII081.8, contains the largest insert, and subsequent analysis indicates that the DNA insert of this clone overlaps that of the inserts contained in other two purified clones (designated
35 BTIII079.11 and BTIII079.47A).

Digestion of the purified phage DNA of the clone designated BTIII081.8 with EcoRI results in DNA segments of 250 bp, 600 bp, and 1000 bp. Each of these three products is subcloned into the plasmid vector pUC118 and sequenced (Figure 6 shows the strategy used for sequencing). The orientation of the three fragments is determined by subcloning from the insert a BglII/BglII fragment into pUC118 and sequencing across the EcoRI junctions using a synthetic oligonucleotide to prime the sequencing reaction.

A restriction map is determined for each fragment (Figure 6). Various restriction site pieces are removed from the plasmids and recloned into pUC118 so that sequencing the resulting plasmids with the universal primer allows for sequencing most of the entire original fragments in both directions. Three oligonucleotide primers are required to sequence the entire cDNA in both directions. For the purposes of this application, this insert contains nucleotides numbered 1510-3406 (SEQ ID NO. 7).

A [³²P]CTP-labelled, nick-translated EcoRI-BamHI DNA segment derived from clone BTIII081.8 (nucleotides 1510-2417 of SEQ ID NO. 7) is used as a probe to rescreen the original endothelial cell cDNA library for more 5' full length DNA segments of the gene from which the insert portion of BTIII081.8 is derived. The protocols used to isolate the overlapping clones are identical to that used to isolate BTIII081.8.

A synthetic oligonucleotide probe is designed with 29 nucleotides corresponding to part of the DNA sequence of the insert portion of the clone BTIII081.8 (nucleotides 3297-3325 of SEQ ID NO. 7) in order to rescreen the original endothelial cell cDNA library for more full 3' length DNA segments of the gene from which

the insert portion of BTIII081.8 is derived. The protocols used to isolate the overlapping clones are identical to that used to isolate BTIII081.8. Several positive clones for each of the 5' and 3' ends are identified and plaque purified.

One of the clones is designated BTIII200.2. The DNA from BTIII200.2 contains a 3.4 kb insert as determined by EcoRI digestion of the isolated phage DNA. EcoRI digestion of BTIII200.2 results in three DNA fragments. One of these fragments (2.5 kb) is cloned into pUC119 and is designated BTIV006. The clone BTIV006 contains nucleotides numbered 7-2482. As described below, BTIV006 plus nucleotides 1-6 is designated BTIV169. DNA sequencing of the 2.5 kb DNA insert (BTIV169) indicates that it overlaps over one thousand nucleotides of the DNA sequence of the insert portion of the clone BTIII081.8 (Figure 6) at the 5' end.

A second clone isolated from the cDNA library is designated BTIII129.5. The DNA from BTIII129.5 contains a 2.2 kb insert as determined by EcoRI digestion of the isolated phage DNA. DNA sequencing of the 2.2 kb DNA insert indicates that it overlaps over five hundred nucleotides of the DNA sequence of the insert portion of the clone BTIII081.8 (Figure 6). The clone BTIII129.5 contains nucleotides numbered 2848-4236 (SEQ ID NO. 7). The DNA sequence for BTIII129.5 contains the stop codon TAA, defining the position of the 3' end of an open reading frame for the novel gene. Except for the first six nucleotides of the gene which are discussed below, these three clones define a gene encoding a growth factor receptor. These three clones define a 4,062 nucleotide sequence of the open reading frame of the gene extending to the 3' end, followed by a 168 nucleotide non-coding region (SEQ ID

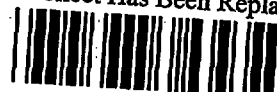
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NO. 7). A sample of a lambda gt11 phage harboring the clone BTIII081.8 has been deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, Maryland 20852, U.S.A., and has been assigned ATCC accession number 40,931. A sample of a lambda gt11 phage harboring the clone BTIII129.5 has been deposited with the American Type Culture Collection and has been assigned ATCC accession number 40,975. For reasons discussed below, a sample of the clone BTIV006 was not deposited.

The aforementioned DNA segments (BTIII081.8, BTIII129.5, and BTIII200.2 (or BTIV006) encode 4062 nucleotides of the coding portion of a novel gene. The cDNA clones are incomplete in that a transcription initiation coding for methionine is missing. After the isolation of these clones, Matthews et al. (25) reported the cloning of a gene homologue of KDR in mouse, which was referred to as Flk-1. Analysis of the nucleic acid and amino acid sequence of Flk-1 indicated that the addition of six nucleotides to the 5' end of the isolated KDR clones would provide for a complete coding region.

To achieve this, an EcoRI-BamHI restriction fragment of BTIV200.2 is cloned into the plasmid pBlueScript KS (Strategene, La Jolla, CA). The 5' end of the inserted DNA is blunt ended with Klenow polymerase and Mung Bean nuclease. Next, the synthetic oligonucleotide TCGACGCGCG ATG GAG (SEQ ID NO. 11) is cloned into this vector. The oligonucleotide contains the sequence ATG GAG in frame with the downstream DNA insert. These nucleotides (ATG GAG) encode the amino acids methionine and glutamic acid, the first two amino acids encoded by the KDR gene. The resulting plasmid vector is designated BTIV140. This plasmid is purified on a CsCl gradient.

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The purified plasmid is designated BTIV169. The insert of BTIV169 contains nucleotides 1-2400 (SEQ ID NO. 7) of the KDR gene. A sample of the plasmid pBlueScript KS which contains the clone BTIV169 has been deposited with the American Type Culture Collection and has been assigned ATCC accession number 75200.

Thus, together the clones BTIII081.8, BTIII129.5 and BTIV169 comprise the entire open reading frame of 4,068 nucleotides for the novel KDR gene. As will be discussed below, the KDR gene expresses the novel KDR receptor which binds specifically to the growth factor VEGF.

DNA sequencing of BTIII081.8, BTIII129.5 and BTIV169 (SEQ ID NO. 7) shows that the newly isolated gene is similar to, but distinct from, previously identified type III RTK. The predicted amino acid sequence (SEQ ID NO. 7) contains several structural features which demonstrate that the novel gene is a type III RTK. These structural features are summarized as follows:

1) A hydropathy plot of the predicted amino acid sequence indicates a single membrane spanning region (see Figure 8). This is characteristic of a type III RTK (Figure 7).

2) The putative amino-terminal 762 amino acid portion of the receptor has structural features of extracellular receptor ligand binding domains (1), including regularly spaced cysteines and 18 potential N-linked glycosylation sites (Figure 7).

3) The predicted amino acid sequence of the carboxy-terminal 530 amino acid portion contains an ATP-binding site at lysine 868, 22 amino acids downstream from the consensus ATP recognition sequence Gly-X-Gly-X-X-Gly (26) (Figure 8).



4) Within the kinase domain there is a 55-60% identical match in amino acid sequence to three other type III receptor tyrosine kinases: ckit proto-oncogene (SEQ ID NO: 8), CSF-1 (SEQ ID NO: 9) and PDGF (SEQ ID NO: 10) (Figure 9).

5) The predicted kinase domain contains a kinase insert domain of approximately 71 amino acids. As indicated in Figure 9, this portion of the amino acid sequence shares little sequence homology with other type III RTK.

The endothelial cell library can be further screened to isolate the 5' untranslated region and genomic clones can be generated so as to isolate the promoter region for the KDR gene.

In addition to the DNA sequence described for the KDR gene (SEQ ID NO. 7), the present invention further comprises DNA sequences which, by virtue of the redundancy of the genetic code, are biologically equivalent to the sequences which encode for the receptor, that is, these other DNA sequences are characterized by nucleotide sequences which differ from those set forth herein, but which encode a receptor having the same amino acid sequences as those encoded by the DNA sequences set forth herein.

In particular, the invention contemplates those DNA sequences which are sufficiently duplicative of the sequence of SEQ ID NO. 7 so as to permit hybridization therewith under standard high stringency Southern hybridization conditions, such as those described in Sambrook et al. (27), as well as the biologically active proteins produced thereby.

This invention also comprises DNA sequences which encode amino acid sequences which differ from those of the novel receptor, but which are the biological equivalent to those described for the

receptor. Such amino acid sequences may be said to be biologically equivalent to those of the receptor if their sequences differ only by minor deletions from or conservative substitutions to the receptor sequence, such that the tertiary configurations of the sequences are essentially unchanged from those of the receptor.

For example, a codon for the amino acid alanine, a hydrophobic amino acid, may be substituted by a codon encoding another less hydrophobic residue, such as glycine, or a more hydrophobic residue, such as valine, leucine, or isoleucine. Similarly, changes which result in substitution of one negatively charged residue for another, such as aspartic acid for glutamic acid, or one positively charged residue for another, such as lysine for arginine, as well as changes based on similarities of residues in their hydropathic index, can also be expected to produce a biologically equivalent product. Nucleotide changes which result in alteration of the N-terminal or C-terminal portions of the protein molecule would also not be expected to alter the activity of the protein. It may also be desirable to eliminate one or more of the cysteines present in the sequence, as the presence of cysteines may result in the undesirable formation of multimers when the protein is produced recombinantly, thereby complicating the purification and crystallization processes. Each of the proposed modifications is well within the routine skill in the art, as is determination of retention of biological activity of the encoded products. Therefore, where the terms "KDR gene" or "KDR protein" are used in either the specification or the claims, each will be understood to encompass all such modifications and variations which result in the production of a biologically equivalent protein.

In addition to the full length gene and protein, the invention encompasses biologically active fragments of each. By "biologically active" is meant a protein fragment which qualitatively retains the receptor activity of the larger KDR protein, or, in the case of a nucleotide sequence, which encodes such a protein fragment. It also refers, for purposes of antibody production, to fragments which are capable of eliciting production of antibodies capable of binding to the receptor protein.

To determine the size of the mRNA transcribed from the kdp gene, Northern blot hybridization experiments are carried out using an EcoRI/BamHI DNA segment (nucleotides 1510-2417, SEQ ID NO. 7) as a hybridization probe. The DNA used for the probe does not contain any portion of the putative kinase domain, and shares little sequence homology to other tyrosine kinases. The Northern blot analysis (Figure 10) shows that a 7 kb band is visualized in cytoplasmic poly(A)+ RNA of ABAE bovine aortic endothelial cells. This transcript differs in size from previously reported transcripts for known type III RTK (7,18).

The isolated cDNA is significant for several reasons. The cDNA encodes a novel type III receptor tyrosine kinase. The homology between the sequence of this cDNA and that of other receptors, as well as structural properties implied by the predicted amino acid sequence confirm the relationship. Receptors for growth factors should have tremendous utility in drug development as they face the outside of the cell and thus are among the best targets for drugs. In addition, the cellular levels of some receptors, in particular the neu proto-oncogene, increase during some cancers. This has been taken advantage of in designing diagnostic tests for these cancers.

Southern analysis demonstrates that the kdp gene is present in mouse as well as human DNA. Mouse and human (Hela cell) DNA, 15 μ g of each, are digested with 10 units of EcoRI and electrophoresed on a 0.7% agarose gel. The DNA is transferred onto nitrocellulose. The filter is hybridized to a [³²P]CTP-labelled cDNA probe made by nick translating an EcoRI/BamHI fragment from the 5' end of the kdp cDNA (nucleotides 1510-2417, SEQ ID NO. 7). Hybridization is conducted at 30°C in 5 X SSPE, 50% formamide, 0.1% SDS, plus 150 μ g/ml salmon sperm DNA. The DNA probe hybridizes to Southern blots containing EcoRI digested DNA. After 48 hours, the filter is washed at room temperature in 2 X SSC plus 0.1% SDS for 20 minutes, followed by two 20 minute washes at 40°C with 0.1 X SSC plus 0.1% SDS. Autoradiography is then performed for 48 hours. As shown in Figure 11, radioactively labelled DNA is present in both human and mouse samples. This indicates that the kdp gene is present in both species.

An experiment is conducted to ascertain the genetic locus of kdp on human chromosomes. Thirty-eight cell hybrids from 18 unrelated human cell lines and four mouse cell lines are examined (19). A DNA probe hybridizes to Southern blots which contain EcoRI digested DNA from the human-mouse hybrids (using the procedure and DNA probe for human and mouse tissue described in relation to Figure 11). Table I sets forth the results of the segregation of kdp with human chromosomes in EcoRI digested human-mouse somatic cell hybrid DNA:

Table I

5	<u>Chromosome</u>	Concordant # of Hybrids		Discordant # of Hybrids		<u>% Discordancy</u>
		<u>(+ / +)</u>	<u>(- / -)</u>	<u>(+ / -)</u>	<u>(- / +)</u>	
	1	4	19	8	4	34
	2	8	18	5	6	30
	3	11	12	3	9	34
10	4	14	24	0	0	0
	5	7	14	7	10	45
	6	7	19	7	5	32
	7	11	14	3	8	31
	8	8	11	6	13	50
15	9	3	20	10	4	38
	10	12	9	2	14	43
	11	9	13	4	11	41
	12	9	10	5	14	50
	13	7	18	7	6	34
20	14	11	8	3	16	50
	15	9	15	5	8	35
	16	7	19	7	5	32
	17	12	7	2	16	49
	18	11	14	3	10	34
25	19	7	18	7	6	34
	20	9	10	5	14	50
	21	11	9	3	15	47
	22	3	16	10	7	47
	X	8	10	3	8	38
30						

The scoring is determined by the presence(+) or absence (-) of human bands in the hybrids on Southern blots prepared in a similar to those shown in Figure 11. The scoring is compared to the presence or absence of human chromosomes in each hybrid. A 0%

discordancy indicates a matched segregation of the DNA probe with a chromosome. Three fragments, approximately 6.5 kb, 3.1 kb, and 0.7 kb in size are detected in digests of human DNA (Figure 11), and in all hybrids which had retained human chromosome 4 (Table I). All other chromosomes are excluded in at least 11 discordant hybrids (Table I). The results of Figure 11 and Table I demonstrate that the genetic locus of kdp is on human chromosome 4.

It is noteworthy that both the ckit (3) and the type A PDGF (28) receptor genes map to human chromosome 4. The finding that the genetic locus of kdp is on human chromosome 4 provides further evidence that the novel receptor of this invention is a type III receptor tyrosine kinase.

The next step after identifying the entire coding portion of the kdp gene is to express the receptor protein encoded by that gene. The receptor protein is then utilized so as to identify the growth factor which binds specifically to the receptor.

The receptor protein is expressed using established recombinant DNA methods. Suitable host organisms include bacteria, viruses, yeast, insect or mammalian cell lines, as well as other conventional organisms. For example, CMT-3 monkey kidney cells are transfected with a vector containing the complete coding region of the KDR gene.

The complete coding portion of the KDR gene is assembled by sequentially cloning into pUC119 three DNA fragments derived from BTIII081.8, BTIII129.5, and BTIV169. First, a SmaI-EcoRI fragment of clone BTIII129.5 (nucleotides 3152-4236, SEQ ID NO. 7) is blunt ended with Klenow polymerase and introduced into a SmaI site in pUC119. Next, a BamHI-SmaI fragment of clone BTIII081.8 (nucleotides 2418-3151, SEQ ID NO. 7)

is introduced at a BamHI-SmaI site. Finally, a SaII-BamHI fragment of clone BTIV169 (nucleotides 1-2417, SEQ ID NO. 7) is introduced at a SaII-BamHI site. Part of the cloning site of pUC119 is contained..
5 in the SaII-BamHI fragment, 5' to the KDR gene. In order to clone the complete coding portion into an expression vector, the assembled DNA (in pUC119) is digested with SaII and Asp118 and recloned into the eukaryotic expression vector pcDNA1tkpASP.

10 This vector is a modification of the vector pcDNA1 (Invitrogen; San Diego, CA). Specifically, the ampicillin resistance gene is cloned from pBR322 into pcDNA1. A small SV40 T splice and the SV40 polyadenylation signal are then removed and are replaced with a
15 Herpes Simplex Virus-1 polyadenylation signal. Finally, a cytomegalovirus intermediate early splice is inserted 5' to the cloning site to yield pcDNA1tkpASP.

Transfection of CMT-3 cells is done using DEAE-dextran. Forty-eight hours after transfection,
20 expression of the novel receptor is monitored using Western blot analysis as follows.

An antibody is used to assay the expressed receptor protein. The predicted amino acid sequence of the receptor is used to generate peptide-derived
25 antibodies to the receptor by conventional techniques. The presence of the novel receptor protein is confirmed by Western blot hybridization.

Specifically, a synthetic peptide with 13 residues is synthesized based on the 12 residues
30 corresponding to amino acids 986-997 of the putative amino acid sequence of the KDR protein (SEQ ID NO. 7), with a cysteine residue linked to the lysine (amino acid 997). The cysteine facilitates coupling of the peptide to a macromolecule which functions as a carrier
35 for the peptide. For example, the peptide is coupled

to keyhole limpet haemocyanin (KLH) using m-maleimido-benzoyl-N-hydroxysuccinimide ester. Other conventional carriers may be used such as human and bovine serum albumins, myoglobins, β -galactosidase, penicillinase and bacterial toxoids, as well as synthetic molecules such as multi-poly-DL-alanyl-poly-L-lysine and poly-L-lysine.

Rabbits are immunized with the peptide-KLH conjugate to raise polyclonal antibodies. After different periods of time, serum is collected from the rabbits. The IgG fraction of the serum is then purified using a protein A Sepharose column (Pharmacia LKB, Uppsala, Sweden) to obtain the antibody which is designated anti-KDR.PS23.

A sample of the expressed KDR protein is subjected to SDS-PAGE using a 7% acrylamide gel under standard conditions. The protein band is then transferred on to nitrocellulose paper for Western blot analysis and the anti-KDR.PS23 antibody is added at a dilution of 1:1,000 to allow the antibody to react with the protein present. A second antibody, goat anti-rabbit antibody to rabbit IgG, which binds to anti-KDR.PS23, is then added. The detection of proteins which react with the antibodies is performed by autoradiography of bands using an ECL system (Amersham, Chicago, IL). The results are depicted in Figure 12.

Figure 12 shows that a 190 kD protein is present in the cells transfected with the vector containing the KDR gene, but is absent in cells transfected with vector alone. The size of this protein is consistent with it being encoded by the KDR gene, in that the predicted amino acid sequence for the unglycosylated KDR protein is 156 kD, and that sequence contains 18 putative extracellular glycosylation sites

which would account for the balance of the size seen in the 190 kD band.

The expressed receptor is then used to identify the growth factor which interacts with the receptor. In order to test the hypothesis that the KDR protein is a receptor for VEGF, radioligand binding studies are performed. VEGF (provided by D. Gospodarowicz) is radiolabelled with ^{125}I . Cells are transfected with either the vector pcDNA1tkpASP alone (bars 1 and 2 of Figure 13) or with the vector containing the KDR gene (bars 3 and 4). Forty-eight hours later, the transfected cell samples are washed with PBS and then incubated for 90 minutes with serum-free media containing 50 pM [^{125}I]VEGF (specific activity equal to 4,000 cpm per fmol). Excess nonradioactive VEGF, 5 nM, is added to some samples (bars 2 and 4) to define specific binding sites. The samples are washed with ice cold PBS, and the cells are transferred to gamma-counting tubes using a detergent, 0.1% lubrol.

The results of the radioligand binding studies are depicted in Figure 13. Figure 13 shows that CMT-3 cells transfected with vector containing the KDR gene contain specific binding sites for [^{125}I]VEGF (compare bars 3 and 4), while cells transfected with vector alone do not (compare bars 1 and 2).

Further evidence that the KDR gene encodes a receptor for VEGF is demonstrated by affinity cross-linking studies (Figure 14). Figure 14 depicts the results of affinity cross-linking of [^{125}I]VEGF to CMT-3 cells which express the KDR protein. CMT-3 cells are transfected with either the pcDNA1tkpASP vector alone (lane 1 of Figure 14) or with the vector containing the KDR gene (lane 2). Forty-eight hours later, the cells are washed in PBS, and serum free

media containing 200 pM [¹²⁵I]VEGF is added. After 90 minutes at room temperature, an affinity cross-linker disuccinimidyl suberate (Pierce Biochemicals, Rockford, IL), 0.5mM, is added for 15 minutes. The samples are then subjected to SDS-PAGE autoradiography.

Three protein bands are seen in SDS-PAGE autoradiograms from samples of CMT-3 cells transfected with the KDR gene and cross-linked to [¹²⁵I]VEGF (lane 1). The size of band 1 (235 kD) is consistent with it being the 190 kD protein seen by Western blot analysis (Figure 12), because a 45 kD [¹²⁵I] VEGF dimer plus 190 kD would migrate in a manner identical to band 1. The origin of band 2 is not clear, but may represent an altered glycosylation form of band 1. Band 3 (22.5 kD) is most likely VEGF itself, and can be seen faintly in cells transfected with vector alone (lane 2).

The novel KDR gene of this invention is significant for several reasons. Studies of the cellular mechanisms by which receptors function in signal transduction have led in the past to a better understanding of how cells grow in both normal and diseased states. Receptor tyrosine kinases, in particular, have received a great deal of attention because of the observation that a number of RTK are the cellular counterparts for viral oncogenes, implying a direct correlation between changes in the expression of RTK and cancer. In view of this, it is likely that pharmaceuticals targeted at RTK will inhibit the changes in cell growth associated with cancer. In addition, it is likely that monitoring the levels of expression of RTK will prove valuable in diagnosing the onset of cancer.

The described cDNA is isolated from a human endothelial cell library. Endothelial cells participate in angiogenesis, the formation of new blood

capillaries. Previous work directed towards identifying the growth factors which regulate angiogenesis have primarily focused upon FGF (13), although recent evidence has indicated that other growth factors may be involved as well (12,15,29). This evidence consists of the observations that: 1) FGF does not contain a signal sequence (24) and thus may not be secreted from cells in a manner consistent with the tight regulation of angiogenesis, and 2) endothelial cells synthesize FGF and yet are normally resting (15). Our discovery, then, of a novel growth factor receptor may ultimately clarify these inconsistencies and lead to a better understanding of endothelial cell function.

The teachings of this invention can be readily used by those skilled the art for the purpose of testing pharmaceuticals targeted at the KDR protein. Two examples of approaches which can be used for this purpose are now given.

First, the methods described in this invention for studying the interaction of VEGF with KDR protein can be used to test for pharmaceuticals which will antagonize that interaction. For these studies, cells expressing the KDR protein are incubated with [¹²⁵I]VEGF, together with a candidate pharmaceutical. Inhibition of radioligand binding is tested for; significant inhibition indicates the candidate is an antagonist. Permanent expression of the KDR protein in a cell type such as NIH3T3 cells would make these studies less laborious. This can be easily achieved by those skilled in the art using the described methods.

Second, using the teachings of this invention, those skilled in the art can study structural properties of the KDR protein involved in receptor function. This structural information can

then be used to more rationally design pharmaceuticals
which inhibit that function. Mutagenesis of the KDR
gene by well established protocols is one approach,
crystallization of the receptor binding site is
another.

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(A) TELEPHONE: 203 321 2719

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(2) INFORMATION FOR SEQ ID NO: 1:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GTCGAC AAY CTG TTG GGR GCC TGC AAC 27

(2) INFORMATION FOR SEQ ID NO: 2 :

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GAATTC AG CAC KTT NCT RGC YGC CAG GTC TGY GTC 35

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 363 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

	GAA TTC TGC AAA TTT GGA AAC CTG TCC ACT TAC CTG	36
	AGG ACG AAG AGA AAT GAA TTT GTC CCC TAC AAG ACC	72
20	AAA GGG GCA CGA TTC CGT CAA GGG AAA GAC TAC GTT	108
	GGA GCA ATC CCT GTG GAT CTG AAA CGG CGC TTG GAC	144
25	ACG CAT CAC CAG TAG CCA GAG CTC AGC CAG CTC TGG	180
	ATT TGT GGA GGA GAA GTC CCT CAG TGA TGT AGA AGA	216
	AGA GGA AGC TCC TGA AGA TCT GTA TAA GGA CTT CCT	252
30	GAC CTT GGA GCA TCT CAT CTG TTA CAG TTT CCA AGT	288
	GGC TAA GGG CAT GGA GTT CTT GGC ATC GCG AAA GTG	324
35	TAT CCA CAG AGA CCT GGC AGC CAG GAA CGT GCT GAA	360

TTC

363

(2) INFORMATION FOR SEQ ID NO: 4 :

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 base pairs

10

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

20

GTC GAC AAT CTG TTG GGG GCC TGC ACC ATC CCA ACA 36

TCC TGC TGC TCT ACA ACT ATT TTT ATG ACC GGA GGA 72

GGA TCT ACT TGA TTC TAG AGT ATG CCC CCC GCG GAG 108

25

CTC TAC AAG GAG CTG CAG AAG AGC TGC ACA TTT GAC 144

GAG CAG CGA ACA GCC ACG ATC ATG GAG GAG TTG GCA 180

30

GAT GCT CTA ATG TAC TGC CGT GGG AAG AAG GTG ATT 216

CAC AGA GAC CTG GCA GCC AGC AAC GTG CTG AAT TC 251

35

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 510 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: PDGF Receptor DNA

(B) LOCATION: Internal sequence

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Gronwald, R., et al.

(B) JOURNAL: Proc. Natl. Acad. Sci.

(C) VOLUME: 85

(D) PAGES: 3435-3439

(E) DATE: 1988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AAC CTG TGG GGG CCT GCA CCA AAG GAG GAC CAT CTA 36

	TAT CAT CTA TAT CAT CAC TGA GTA CTG CCG CTA CGG	72
	AGA CCT GGT GGA CTA CCT GCA CCG CAA CAA ACA CAC	108
5	CTT CCT GCA GCA CCA CTC CGA CAA GCG CCG CCC GCC	144
	CAG CGC GGA GCT CTA CAG CAA TGC TCT GCC CGT TGG	180
	GCT CCC CCT GCC CAG CCA TGT GTC CTT GAC CGG GGG	216
10	AGA GCG ACG GTG GCT ACA TGG ACA TGA GCA AGG ACG	252
	AGT CGG TGG ACT ATG TGC CCA TGC TGG ACA TGA AAG	288
15	GAG ACG TCA AAT AGC AGA CAT CGA GTC CTC CAA CTA	324
	CAT GGC CCC TTA CGA TAA CTA CGT TCC CTC TGC CCC	360
	TGA GAG GAC CTG CCG AGC AAC TTT GAT CAA CGA GTC	396
20	TCC AGT GCT AAG CTA CAT GGA CCT CGT GGG CTT CAG	432
	CTA CCA GGT GGC CAA TGG CAT GGA GTT CTG GCC TCC	468
25	AAG AAC TGC GTC CAC AGA GAC CTG GCG GCT AGG AAC	504
	GTC CTT	510

30 (2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 base pairs

35

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

5 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

10

(A) NAME/KEY: FGF Receptor DNA

(B) LOCATION: Internal sequence

15

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Ruta, M., et al.

(B) JOURNAL: Oncogene

20

(C) VOLUME: 3

(D) PAGES: 9-15

25

(E) DATE: 1988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

30

AAC CTG CTG GGG GCC TGC ACG CAG GAT GGT CCC TTG 36

TAT GTC ATC GTG GAG TAT GCC TCC AAG GGC AAC CTG 72

CGG GAG TAC CTG CAG ACC CGG AGG CCC CCA GGG CTG 108

35

GAA TAC TGC TAT AAC CCC AGC CAC AAC CCA GAG GAG 144

CAG CTC TCC TCC AAG GAC CTG GTG TCC TGC GCC TAC 180

CAG GAG GCC CGA GGC ATG GAG TAT CTG GCC TCC AAG 216

5 AAG TGC ATA CAC CGA GAC CTG GCA GCC AGG AAT GTC 252

CTG 255

(2) INFORMATION FOR SEQ ID NO: 7:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4236 base pairs

15

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

25 ATG GAG AGC AAG GTG CTG CTG GCC GTC GCC CTG 33

Met Glu Ser Lys Val Leu Leu Ala Val Ala Leu

1 5 10

TGG CTC TGC GTG GAG ACC CGG GCC GCC TCT GTG GGT 69

30

Trp Leu Cys Val Glu Thr Arg Ala Ala Ser Val Gly

15 20

TTG CCT AGT GTT TCT CTT GAT CTG CCC AGG CTC AGC 105

Leu Pro Ser Val Ser Leu Asp Leu Pro Arg Leu Ser

35

25 30 35

	ATA CAA AAA GAC ATA CTT ACA ATT AAG GCT AAT ACA	141
	Ile Gln Lys Asp Ile Leu Thr Ile Lys Ala Asn Thr	
	40 45	
5	ACT CTT CAA ATT ACT TGC AGG GGA CAG AGG GAC TTG	177
	Thr Leu Gln Ile Thr Cys Arg Gly Gln Arg Asp Leu	
	50 55	
10	GAC TGG CTT TGG CCC AAT AAT CAG AGT GGC AGT GAG	213
	Asp Trp Leu Trp Pro Asn Asn Gln Ser Gly Ser Glu	
	60 65 70	
15	CAA AGG GTG GAG GTG ACT GAG TGC AGC GAT GGC CTC	249
	Gln Arg Val Glu Val Thr Glu Cys Ser Asp Gly Leu	
	75 80	
20	TTC TGT AAG ACA CTC ACA ATT CCA AAA GTG ATC GGA	285
	Phe Cys Lys Thr Leu Thr Ile Pro Lys Val Ile Gly	
	85 90 95	
25	AAT GAC ACT GGA GCC TAC AAG TGC TTC TAC CGG GAA	321
	Asn Asp Thr Gly Ala Tyr Lys Cys Phe Tyr Arg Glu	
	100 105	
30	ACT GAC TTG GCC TCG GTC ATT TAT GTC TAT GTT CAA	357
	Thr Asp Leu Ala Ser Val Ile Tyr Val Tyr Val Gln	
	110 115	
35	GAT TAC AGA TCT CCA TTT ATT GCT TCT GTT AGT GAC	393
	Asp Tyr Arg Ser Pro Phe Ile Ala Ser Val Ser Asp	
	120 125 130	
40	CAA CAT GGA GTC GTG TAC ATT ACT GAG AAC AAA AAC	429
	Gln His Gly Val Val Tyr Ile Thr Glu Asn Lys Asn	
	135 140	

	AAA ACT GTG GTG ATT CCA TGT CTC GGG TCC ATT TCA	465
	Lys Thr Val Val Ile Pro Cys Leu Gly Ser Ile Ser	
	145 150 155	
5	AAT CTC AAC GTG TCA CTT TGT GCA AGA TAC CCA GAA	501
	Asn Leu Asn Val Ser Leu Cys Ala Arg Tyr Pro Glu	
	160 165	
10	AAG AGA TTT GTT CCT GAT GGT AAC AGA ATT TCC TGG	537
	Lys Arg Phe Val Pro Asp Gly Asn Arg Ile Ser Trp	
	170 175	
15	GAC AGC AAG AAG GGC TTT ACT ATT CCC AGC TAC ATG	573
	Asp Ser Lys Lys Gly Phe Thr Ile Pro Ser Tyr Met	
	180 185 190	
20	ATC AGC TAT GCT GGC ATG GTC TTC TGT GAA GCA AAA	609
	Ile Ser Tyr Ala Gly Met Val Phe Cys Glu Ala Lys	
	195 200	
25	ATT AAT GAT GAA AGT TAC CAG TCT ATT ATG TAC ATA	645
	Ile Asn Asp Glu Ser Tyr Gln Ser Ile Met Tyr Ile	
	205 210 215	
30	GTT GTC GTT GTA GGG TAT AGG ATT TAT GAT GTG GTT	681
	Val Val Val Val Gly Tyr Arg Ile Tyr Asp Val Val	
	220 225	
35	CTG AGT CCG TCT CAT GGA ATT GAA CTA TCT GTT GGA	717
	Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly	
	230 235	
40	GAA AAG CTT GTC TTA AAT TGT ACA GCA AGA ACT GAA	753
	Glu Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu	
	240 245 250	

	CTA AAT GTG GGG ATT GAC TTC AAC TGG GAA TAC CCT	789
	Leu Asn Val Gly Ile Asp Phe Asn Trp Glu Tyr Pro	
	255 260	
5	TCT TCG AAG CAT CAG CAT AAG AAA CTT GTA AAC CGA	825
	Ser Ser Lys His Gln His Lys Lys Leu Val Asn Arg	
	265 270 275	
10	GAC CTA AAA ACC CAG TCT GGG AGT GAG ATG AAG AAA	861
	Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys	
	280 285	
15	TTT TTG AGC ACC TTA ACT ATA GAT GGT GTA ACC CGG	897
	Phe Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg	
	290 295	
20	AGT GAC CAA GGA TTG TAC ACC TGT GCA GCA TCC AGT	933
	Ser Asp Gln Gly Leu Tyr Thr Cys Ala Ala Ser Ser	
	300 305 310	
25	GGG CTG ATG ACC AAG AAG AAC AGC ACA TTT GTC AGG	969
	Gly Leu Met Thr Lys Lys Asn Ser Thr Phe Val Arg	
	315 320	
30	GTC CAT GAA AAA CCT TTT GTT GCT TTT GGA AGT GGC	1005
	Val His Glu Lys Pro Phe Val Ala Phe Gly Ser Gly	
	325 330 335	
35	ATG GAA TCT CTG GTG GAA GCC ACG GTG GGG GAG CGT	1041
	Met Glu Ser Leu Val Glu Ala Thr Val Gly Glu Arg	
	340 345	
35	GTC AGA ATC CCT GCG AAG TAC CTT GGT TAC CCA CCC	1077
	Val Arg Ile Pro Ala Lys Tyr Leu Gly Tyr Pro Pro	
	350 355	

	CCA GAA ATA AAA TGG TAT AAA AAT GGA ATA CCC CTT	1113
	Pro Glu Ile Lys Trp Tyr Lys Asn Gly Ile Pro Leu	
	360 365 370	
5	GAG TCC AAT CAC ACA ATT AAA GCG GGG CAT GTA CTG	1149
	Glu Ser Asn His Thr Ile Lys Ala Gly His Val Leu	
	375 380	
10	ACG ATT ATG GAA GTG AGT GAA AGA GAC ACA GGA AAT	1185
	Thr Ile Met Glu Val Ser Glu Arg Asp Thr Gly Asn	
	385 390 395	
15	TAC ACT GTC ATC CTT ACC AAT CCC ATT TCA AAG GAG	1221
	Tyr Thr Val Ile Leu Thr Asn Pro Ile Ser Lys Glu	
	400 405	
20	AAG CAG AGC CAT GTG GTC TCT CTG GTT GTG TAT GTC	1257
	Lys Gln Ser His Val Val Ser Leu Val Val Tyr Val	
	410 415	
25	CCA CCC CAG ATT GGT GAG AAA TCT CTA ATC TCT CCT	1293
	Pro Pro Gln Ile Gly Glu Lys Ser Leu Ile Ser Pro	
	420 425 430	
30	GTG GAT TCC TAC CAG TAC GGC ACC ACT CAA ACG CTG	1329
	Val Asp Ser Tyr Gln Tyr Gly Thr Thr Gln Thr Leu	
	435 440	
35	ACA TGT ACG GTC TAT GCC ATT CCT CCC CCG CAT CAC	1365
	Thr Cys Thr Val Tyr Ala Ile Pro Pro Pro His His	
	445 450 455	
40	ATC CAC TGG TAT TGG CAG TTG GAG GAA GAG TGC GCC	1401
	Ile His Trp Tyr Trp Gln Leu Glu Glu Glu Cys Ala	
	460 465	

	AAC GAG CCC AGC CAA GCT GTC TCA GTG ACA AAC CCA	1437
	Asn Glu Pro Ser Gln Ala Val Ser Val Thr Asn Pro	
	470 475	
5	TAC CCT TGT GAA GAA TGG AGA AGT GTG GAG GAC TTC	1473
	Tyr Pro Cys Glu Glu Trp Arg Ser Val Glu Asp Phe	
	480 485 490	
10	CAG GGA GGA AAT AAA ATT GAA GTT AAT AAA AAT CAA	1509
	Gln Gly Gly Asn Lys Ile Glu Val Asn Lys Asn Gln	
	495 500	
15	TTT GCT CTA ATT GAA GGA AAA AAC AAA ACT GTA AGT	1545
	Phe Ala Leu Ile Glu Gly Lys Asn Lys Thr Val Ser	
	505 510 515	
20	ACC CTT GTT ATC CAA GCG GCA AAT GTG TCA GCT TTG	1581
	Thr Leu Val Ile Gln Ala Ala Asn Val Ser Ala Leu	
	520 525	
25	TAC AAA TGT GAA GCG GTC AAC AAA GTC GGG AGA GGA	1617
	Tyr Lys Cys Glu Ala Val Asn Lys Val Gly Arg Gly	
	530 535	
30	GAG AGG GTG ATC TCC TTC CAC GTG ACC AGG GGT CCT	1653
	Glu Arg Val Ile Ser Phe His Val Thr Arg Gly Pro	
	540 545 550	
35	GAA ATT ACT TTG CAA CCT GAC ATG CAG CCC ACT GAG	1689
	Glu Ile Thr Leu Gln Pro Asp Met Gln Pro Thr Glu	
	555 560	
40	CAG GAG AGC GTG TCT TTG TGG TGC ACT GCA GAC AGA	1725
	Gln Glu Ser Val Ser Leu Trp Cys Thr Ala Asp Arg	
	565 570 575	

	TCT ACG TTT GAG AAC CTC ACA TGG TAC AAG CTT GGC	1761
	Ser Thr Phe Glu Asn Leu Thr Trp Tyr Lys Leu Gly	
	580 585	
5	CCA CAG CCT CTG CCA ATC CAT GTG GGA GAG TTG CCC	1797
	Pro Gln Pro Leu Pro Ile His Val Gly Glu Leu Pro	
	590 595	
10	ACA CCT GTT TGC AAG AAC TTG GAT ACT CTT TGG AAA	1833
	Thr Pro Val Cys Lys Asn Leu Asp Thr Leu Trp Lys	
	600 605 610	
15	TTG AAT GCC ACC ATG TTC TCT AAT AGC ACA AAT GAC	1869
	Leu Asn Ala Thr Met Phe Ser Asn Ser Thr Asn Asp	
	615 620	
20	ATT TTG ATC ATG GAG CTT AAG AAT GCA TCC TTG CAG	1905
	Ile Leu Ile Met Glu Leu Lys Asn Ala Ser Leu Gln	
	625 630 635	
25	GAC CAA GGA GAC TAT GTC TGC CTT GCT CAA GAC AGG	1941
	Asp Gln Gly Asp Tyr Val Cys Leu Ala Gln Asp Arg	
	640 645	
30	AAG ACC AAG AAA AGA CAT TGC GTG GTC AGG CAG CTC	1977
	Lys Thr Lys Lys Arg His Cys Val Val Arg Gln Leu	
	650 655	
35	ACA GTC CTA GAG CGT GTG GCA CCC ACG ATC ACA GGA	2013
	Thr Val Leu Glu Arg Val Ala Pro Thr Ile Thr Gly	
	660 665 670	
35	AAC CTG GAG AAT CAG ACG ACA AGT ATT GGG GAA AGC	2049
	Asn Leu Glu Asn Gln Thr Thr Ser Ile Gly Glu Ser	
	675 680	

	ATC GAA GTC TCA TGC ACG GCA TCT GGG AAT CCC CCT	2085
	Ile Glu Val Ser Cys Thr Ala Ser Gly Asn Pro Pro	
	685 690 695	
5	CCA CAG ATC ATG TGG TTT AAA GAT AAT GAG ACC CTT	2121
	Pro Gln Ile Met Trp Phe Lys Asp Asn Glu Thr Leu	
	700 705	
10	GTA GAA GAC TCA GGC ATT GTA TTG AAG GAT GGG AAC	2157
	Val Glu Asp Ser Gly Ile Val Leu Lys Asp Gly Asn	
	710 715	
15	CGG AAC CTC ACT ATC CGC AGA GTG AGG AAG GAG GAC	2193
	Arg Asn Leu Thr Ile Arg Arg Val Arg Lys Glu Asp	
	720 725 730	
20	GAA GGC CTC TAC ACC TGC CAG GCA TGC AGT GTT CTT	2229
	Glu Gly Leu Tyr Thr Cys Gln Ala Cys Ser Val Leu	
	735 740	
25	GGC TGT GCA AAA GTG GAG GCA TTT TTC ATA ATA GAA	2265
	Gly Cys Ala Lys Val Glu Ala Phe Phe Ile Ile Glu	
	745 750 755	
30	GGT GCC CAG GAA AAG ACG AAC TTG GAA ATC ATT ATT	2301
	Gly Ala Gln Glu Lys Thr Asn Leu Glu Ile Ile Ile	
	760 765	
35	CTA GTA GGC ACG ACG GTG ATT GCC ATG TTC TTC TGG	2337
	Leu Val Gly Thr Thr Val Ile Ala Met Phe Phe Trp	
	770 775	
40	CTA CTT CTT GTC ATC ATC CTA GGG ACC GTT AAG CGG	2373
	Leu Leu Leu Val Ile Ile Leu Gly Thr Val Lys Arg	
	780 785 790	

	GCC AAT GGA GGG GAA CTG AAG ACA GGC TAC TTG TCC	2409
	Ala Asn Gly Gly Glu Leu Lys Thr Gly Tyr Leu Ser	
	795 800	
5	ATC GTC ATG GAT CCA GAT GAA CTC CCA TTG GAT GAA	2445
	Ile Val Met Asp Pro Asp Glu Leu Pro Leu Asp Glu	
	805 810 815	
10	CAT TGT GAA CGA CTG CCT TAT GAT GCC AGC AAA TGG	2481
	His Cys Glu Arg Leu Pro Tyr Asp Ala Ser Lys Trp	
	820 825	
15	GAA TTC CCC AGA GAC CGG CTG AAC CTA GGT AAG CCT	2517
	Glu Phe Pro Arg Asp Arg Leu Asn Leu Gly Lys Pro	
	830 835	
20	CTT GGC CGT GGT GCC TTT GGC CAA GAG ATT GAA GCA	2553
	Leu Gly Arg Gly Ala Phe Gly Gln Glu Ile Glu Ala	
	840 845 850	
	GAT GCC TTT GGA ATT GAC AAG ACA GCA ACT TGC AGG	2589
	Asp Ala Phe Gly Ile Asp Lys Thr Ala Thr Cys Arg	
	855 860	
25	ACA GTA GCA GTC AAA ATG TTG AAA GAA GGA GCA ACA	2625
	Thr Val Ala Val Lys Met Leu Lys Glu Gly Ala Thr	
	865 870 875	
30	CAC AGT GAG CAT CGA GCT CTC ATG TCT GAA CTC AAG	2661
	His Ser Glu His Arg Ala Leu Met Ser Glu Leu Lys	
	880 885	
35	ATC CTC ATT CAT ATT GGT CAC CAT CTC AAT GTG GTC	2697
	Ile Leu Ile His Ile Gly His His Leu Asn Val Val	
	890 895	

	AAC CTT CTA GGT GCC TGT ACC AAG CCA GGA GGG CCA	2733
	Asn Leu Leu Gly Ala Cys Thr Lys Pro Gly Gly Pro	
	900 905 910	
5	CTC ATG GTG ATT GTG GAA TTC TGC AAA TTT GGA AAC	2769
	Leu Met Val Ile Val Glu Phe Cys Lys Phe Gly Asn	
	915 920	
10	CTG TCC ACT TAC CTG AGG AGC AAG AGA AAT GAA TTT	2805
	Leu Ser Thr Tyr Leu Arg Ser Lys Arg Asn Glu Phe	
	925 930 935	
15	GTC CCC TAC AAG ACC AAA GGG GCA CGA TTC CGT CAA	2841
	Val Pro Tyr Lys Thr Lys Gly Ala Arg Phe Arg Gln	
	940 945	
20	GGG AAA GAC TAC GTT GGA GCA ATC CCT GTG GAT CTG	2877
	Gly Lys Asp Tyr Val Gly Ala Ile Pro Val Asp Leu	
	950 955	
25	AAA CGG CGC TTG GAC AGC ATC ACC AGT AGC CAG AGC	2913
	Lys Arg Arg Leu Asp Ser Ile Thr Ser Ser Gln Ser	
	960 965 970	
30	TCA GCC AGC TCT GGA TTT GTG GAG GAG AAG TCC CTC	2949
	Ser Ala Ser Ser Gly Phe Val Glu Glu Lys Ser Leu	
	975 980	
35	AGT GAT GTA GAA GAA GAG GAA GCT CCT GAA GAT CTG	2985
	Ser Asp Val Glu Glu Glu Glu Ala Pro Glu Asp Leu	
	985 990 995	
35	TAT AAG GAC TTC CTG ACC TTG GAG CAT CTC ATC TGT	3021
	Tyr Lys Asp Phe Leu Thr Leu Glu His Leu Ile Cys	
	1000 1005	

	TAC AGC TTC CAA GTG GCT AAG GGC ATG GAG TTC TTG	3057
	Tyr Ser Phe Gln Val Ala Lys Gly Met Glu Phe Leu	
	1010 1015	
5	GCA TCG CGA AAG TGT ATC CAC AGG GAC CTG GCG GCA	3093
	Ala Ser Arg Lys Cys Ile His Arg Asp Leu Ala Ala	
	1020 1025 1030	
10	CGA AAT ATC CTC TTA TCG GAG AAG AAC GTG GTT AAA	3129
	Arg Asn Ile Leu Leu Ser Glu Lys Asn Val Val Lys	
	1035 1040	
15	ATC TGT GAC TTT GGC TTG GCC CGG GAT ATT TAT AAA	3165
	Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Tyr Lys	
	1045 1050 1055	
20	GAT CCA GAT TAT GTC AGA AAA GGA GAT GCT CGC CTC	3201
	Asp Pro Asp Tyr Val Arg Lys Gly Asp Ala Arg Leu	
	1060 1065	
25	CCT TTG AAA TGG ATG GCC CCA GAA ACA ATT TTT GAC	3237
	Pro Leu Lys Trp Met Ala Pro Glu Thr Ile Phe Asp	
	1070 1075	
30	AGA GTG TAC ACA ATC CAG AGT GAC GTC TGG TCT TTT	3273
	Arg Val Tyr Thr Ile Gln Ser Asp Val Trp Ser Phe	
	1080 1085 1090	
35	GGT GTT TTG CTG TGG GAA ATA TTT TCC TTA GGT GCT	3309
	Gly Val Leu Leu Trp Glu Ile Phe Ser Leu Gly Ala	
	1095 1100	
35	TCT CCA TAT CCT GGG GTA AAG ATT GAT GAA GAA TTT	3345
	Ser Pro Tyr Pro Gly Val Lys Ile Asp Glu Glu Phe	
	1105 1110 1115	

	TGT AGG CGA TTG AAA GAA GGA ACT AGA ATG AGG GCC	3381
	Cys Arg Arg Leu Lys Glu Gly Thr Arg Met Arg Ala	
	1120 1125	
5	CCT GAT TAT ACT ACA CCA GAA ATG TAC CAG ACC ATG	3417
	Pro Asp Tyr Thr Thr Pro Glu Met Tyr Gln Thr Met	
	1130 1135	
10	CTG GAC TGC TGG CAC GGG GAG CCC AGT CAG AGA CCC	3453
	Leu Asp Cys Trp His Gly Glu Pro Ser Gln Arg Pro	
	1140 1145 1150	
15	ACG TTT TCA GAG TTG GTG GAA CAT TTG GGA AAT CTC	3489
	Thr Phe Ser Glu Leu Val Glu His Leu Gly Asn Leu	
	1155 1160	
20	TTG CAA GCT AAT GCT CAG CAG GAT GGC AAA GAC TAC	3525
	Leu Gln Ala Asn Ala Gln Gln Asp Gly Lys Asp Tyr	
	1165 1170 1175	
25	ATT GTT CTT CCG ATA TCA GAG ACT TTG AGC ATG GAA	3561
	Ile Val Leu Pro Ile Ser Glu Thr Leu Ser Met Glu	
	1180 1185	
30	GAG GAT TCT GGA CTC TCT CTG CCT ACC TCA CCT GTT	3597
	Glu Asp Ser Gly Leu Ser Leu Pro Thr Ser Pro Val	
	1190 1195	
35	TCC TGT ATG GAG GAG GAG GAA GTA TGT GAC CCC AAA	3633
	Ser Cys Met Glu Glu Glu Glu Val Cys Asp Pro Lys	
	1200 1205 1210	
35	TTC CAT TAT GAC AAC ACA GCA GGA ATC AGT CAG TAT	3669
	Phe His Tyr Asp Asn Thr Ala Gly Ile Ser Gln Tyr	
	1215 1220	

	CTG CAG AAC AGT AAG CGA AAG AGC CGG CCT GTG AGT	3705
	Leu Gln Asn Ser Lys Arg Lys Ser Arg Pro Val Ser	
	1225 1230 1235	
5	GTA AAA ACA TTT GAA GAT ATC CCG TTA GAA GAA CCA	3741
	Val Lys Thr Phe Glu Asp Ile Pro Leu Glu Glu Pro	
	1240 1245	
10	GAA GTA AAA GTA ATC CCA GAT GAC AAC CAG ACG GAC	3777
	Glu Val Lys Val Ile Pro Asp Asp Asn Gln Thr Asp	
	1250 1255	
15	AGT GGT ATG GTT CTT GCC TCA GAA GAG CTG AAA ACT	3813
	Ser Gly Met Val Leu Ala Ser Glu Glu Leu Lys Thr	
	1260 1265 1270	
20	TTG GAA GAC AGA ACC AAA TTA TCT CCA TCT TTT GGT	3849
	Leu Glu Asp Arg Thr Lys Leu Ser Pro Ser Phe Gly	
	1275 1280	
	GGA ATG GTG CCC AGC AAA AGC AGG GAG TCT GTG GCA	3885
	Gly Met Val Pro Ser Lys Ser Arg Glu Ser Val Ala	
	1285 1290 1295	
25	TCT GAA GGC TCA AAC CAG ACA AGC GGC TAC CAG TCC	3921
	Ser Glu Gly Ser Asn Gln Thr Ser Gly Tyr Gln Ser	
	1300 1305	
30	GGA TAT CAC TCC GAT GAC ACA GAC ACC ACC GTG TAC	3957
	Gly Tyr His Ser Asp Asp Thr Asp Thr Thr Val Tyr	
	1310 1315	
35	TCC AGT GAG GAA GCA GAA CTT TTA AAG CTG ATA GAG	3993
	Ser Ser Glu Glu Ala Glu Leu Leu Lys Leu Ile Glu	
	1320 1325 1330	

ATT GGA GTG CAA ACC GGT AGC ACA GCC CAG ATT CTC 4029
Ile Gly Val Gln Thr Gly Ser Thr Ala Gln Ile Leu
1335 1340

5 CAG CCT GAC ACG GGG ACC ACA CTG AGC TCT CCT CCT 4065
Gln Pro Asp Thr Gly Thr Thr Leu Ser Ser Pro Pro
1345 1350 1355

10 GTT TAAAAGGAAG CATCCACACC CCAACTCCCG GACATCACAT 4108
Val
1356

GAGAGGTCTG CTCAGATTTT GAAGTGTGT TCTTTCCACC 4148

15 AGCAGGAAGT AGCCGCATTT GATTTTCATT TCGACAACAG 4188

AAAAAGGACC TCGGACTGCA GGGAGCCAGC TCTTCTAGGC 4228

20 TTGTGACC 4236

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 433 amino acids

(B) TYPE: amino acid

30 (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

35 (ix) FEATURE:

(A) NAME/KEY: ckit proto-oncogene receptor

(B) LOCATION: Amino acids 543-975

5

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Yarden, Y., et al.

10

(B) JOURNAL: EMBO J.

(C) VOLUME: 6

(D) PAGES: 3341-3351

15

(E) DATE: 1987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

20

Leu Thr Tyr Lys Tyr Leu Gln Lys Pro Met Tyr Glu Val Gln
543 545 550 555

Trp Lys Val Val Glu Glu Ile Asn Gly Asn Asn Tyr Val Tyr
560 565 570

25

Ile Asp Pro Thr Gln Leu Pro Tyr Asp His Lys Trp Glu Phe
575 580

30

Pro Arg Asn Arg Leu Ser Phe Gly Lys Thr Leu Gly Ala Gly
585 590 595

Ala Phe Gly Lys Val Val Ala Glu Thr Ala Tyr Gly Leu Ile
600 605 610

35

Lys Ser Asp Ala Ala Met Thr Val Ala Val Lys Met Leu Lys

	615		620		625
	Pro Ser Ala His Leu Thr Glu Arg Glu Ala Leu Met Ser Glu				
	630		635		640
5	Leu Lys Val Leu Ser Tyr Leu Gly Asn His Met Asn Ile Val				
	645		650		
	Asn Leu Leu Gly Ala Cys Thr Ile Gly Gly Pro Thr Leu Val				
10	655		660		665
	Ile Thr Glu Tyr Cys Cys Tyr Gly Asp Leu Leu Asn Phe Leu				
	670		675		680
15	Arg Arg Lys Arg Asp Ser Phe Ile Cys Ser Lys Gln Glu Asp				
	685		690		695
	His Ala Glu Ala Ala Leu Tyr Lys Asn Leu Leu His Ser Lys				
	700		705		710
20	Glu Ser Ser Cys Ser Asp Ser Thr Asn Glu Tyr Met Asp Met				
	715		720		
	Lys Pro Gly Val Ser Tyr Val Val Pro Thr Lys Ala Asp Lys				
25	725		730		735
	Arg Arg Ser Val Arg Ile Gly Ser Tyr Ile Glu Arg Asp Val				
	740		745		750
30	Thr Pro Ala Ile Met Glu Asp Asp Glu Leu Ala Leu Asp Leu				
	755		760		765
	Glu Asp Leu Leu Ser Phe Ser Tyr Gln Val Lys Gly Met Ala				
	770		775		780
35					

	Phe	Leu	Ala	Ser	Lys	Asn	Cys	Ile	His	Arg	Asp	Leu	Ala	Ala
						785						790		
5	Arg	Asn	Ile	Leu	Leu	Thr	His	Gly	Arg	Ile	Thr	Lys	Ile	Cys
	795					800						805		
	Asp	Phe	Gly	Leu	Ala	Arg	Asp	Ile	Lys	Asn	Asp	Ser	Asn	Tyr
		810					815					820		
10	Val	Val	Lys	Gly	Asn	Ala	Arg	Leu	Pro	Val	Lys	Val	Met	Ala
			825					830					835	
	Pro	Glu	Ser	Ile	Phe	Asn	Cys	Val	Tyr	Thr	Glu	Glu	Ser	Asp
				840					845					850
15	Val	Trp	Ser	Tyr	Gly	Ile	Phe	Leu	Trp	Glu	Leu	Phe	Ser	Leu
					855					860				
	Gly	Ser	Ser	Pro	Tyr	Pro	Gly	Met	Pro	Val	Lys	Ser	Lys	Phe
20	865					870					875			
	Tyr	Lys	Met	Ile	Lys	Glu	Gly	Phe	Arg	Met	Leu	Ser	Pro	Glu
		880					885					890		
25	His	Ala	Pro	Ala	Glu	Met	Tyr	Asp	Ile	Met	Lys	Thr	Cys	Trp
			895					900					905	
	Asp	Ala	Asp	Pro	Leu	Lys	Arg	Pro	Thr	Phe	Lys	Gln	Ile	Val
				910					915				920	
30	Gln	Leu	Ile	Glu	Lys	Gln	Ile	Ser	Glu	Ser	Thr	Asn	His	Ile
					925					930				
	Tyr	Ser	Asn	Leu	Ala	Asn	Cys	Ser	Pro	Asn	Arg	Gln	Lys	Pro
35	935					940					945			

Val Val Asp His Ser Val Arg Ile Asn Ser Val Gly Ser Thr
950 955 960

5 Ala Ser Ser Ser Gln Pro Leu Leu Val His Asp Asp Val
965 970 975

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 437 amino acids

(B) TYPE: amino acid

15

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

20

(ix) FEATURE:

(A) NAME/KEY: CSF-1 receptor

25

(B) LOCATION: Amino acids 536-972

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Coussens, L., et al.

30

(B) JOURNAL: Nature

(C) VOLUME: 320

35

(D) PAGES: 277-280

(E) DATE: 1986

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

	Leu	Leu	Tyr	Lys	Tyr	Lys	Gln	Lys	Pro	Lys	Tyr	Gln	Val	Arg
	536				540					545				
10	Trp	Lys	Ile	Ile	Glu	Ser	Tyr	Glu	Gly	Asn	Ser	Tyr	Thr	Phe
	550					555					560			
	Ile	Asp	Pro	Thr	Gln	Leu	Pro	Tyr	Asn	Glu	Lys	Trp	Glu	Phe
		565					570					575		
15	Pro	Arg	Asn	Asn	Leu	Gln	Phe	Gly	Lys	Thr	Leu	Gly	Ala	Gly
			580					585					590	
	Ala	Phe	Gly	Lys	Val	Val	Glu	Ala	Thr	Ala	Phe	Gly	Leu	Gly
20				595					600					605
	Lys	Glu	Asp	Ala	Val	Leu	Lys	Val	Ala	Val	Lys	Met	Leu	Lys
					610						615			
25	Ser	Thr	Ala	His	Ala	Asp	Glu	Lys	Glu	Ala	Leu	Met	Ser	Glu
	620					625					630			
	Leu	Lys	Ile	Met	Ser	His	Leu	Gly	Gln	His	Glu	Asn	Ile	Val
		635					640					645		
30	Asn	Leu	Leu	Gly	Ala	Cys	Thr	His	Gly	Gly	Pro	Val	Leu	Val
			650					655					660	
	Ile	Thr	Glu	Tyr	Cys	Cys	Tyr	Gly	Asp	Leu	Leu	Asn	Phe	Leu
35				665					670					675

	Arg Arg Lys Ala Glu Ala Met Leu Gly Pro Ser Leu Ser Pro	
	680	685
5	Gly Gln Asp Pro Glu Gly Gly Val Asp Tyr Lys Asn Ile His	
	690	700
	Leu Glu Lys Lys Tyr Val Arg Arg Asp Ser Gly Phe Ser Ser	
	705	715
10	Gln Gly Val Asp Thr Tyr Val Glu Met Arg Pro Val Ser Thr	
	720	730
	Ser Ser Asn Asp Ser Phe Ser Glu Gln Asp Leu Asp Lys Glu	
	735	745
15	Asp Gly Arg Pro Leu Glu Leu Arg Asp Leu Leu His Phe Ser	
	750	755
	Ser Gln Val Ala Gln Gly Met Ala Phe Leu Ala Ser Lys Asn	
20	760	770
	Cys Ile His Arg Asp Val Ala Ala Arg Asn Val Leu Leu Thr	
	775	785
25	Asn Gly His Val Ala Lys Ile Gly Asp Phe Gly Leu Ala Arg	
	790	800
	Asp Ile Met Asn Asp Ser Asn Tyr Ile Val Lys Gly Asn Ala	
	805	815
30	Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ser Ile Phe Asp	
	820	825
	Cys Val Tyr Thr Val Gln Ser Asp Val Trp Ser Tyr Gly Ile	
35	830	840

	Leu	Leu	Trp	Glu	Ile	Phe	Ser	Leu	Gly	Leu	Asn	Pro	Tyr	Pro
	845						850				855			
5	Gly	Ile	Leu	Val	Asn	Ser	Lys	Phe	Tyr	Lys	Leu	Val	Lys	Asp
	860						865				870			
	Gly	Tyr	Gln	Met	Ala	Gln	Pro	Ala	Phe	Ala	Pro	Lys	Asn	Ile
				875					880				885	
10	Tyr	Ser	Ile	Met	Gln	Ala	Cys	Trp	Ala	Leu	Glu	Pro	Thr	His
				890					895					
	Arg	Pro	Thr	Phe	Gln	Gln	Ile	Cys	Ser	Phe	Leu	Gln	Glu	Gln
15	900				905						910			
	Ala	Gln	Glu	Asp	Arg	Arg	Glu	Arg	Asp	Tyr	Thr	Asn	Leu	Pro
	915						920				925			
20	Ser	Ser	Ser	Arg	Ser	Gly	Gly	Ser	Gly	Ser	Ser	Ser	Ser	Glu
	930						935				940			
	Leu	Glu	Glu	Glu	Ser	Ser	Ser	Glu	His	Leu	Thr	Cys	Cys	Glu
				945					950				955	
25	Gln	Gly	Asp	Ile	Ala	Gln	Pro	Leu	Leu	Gln	Pro	Asn	Asn	Tyr
				960					965					
	Gln	Phe	Cys											
30	970													

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 566 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: PDGF receptor

(B) LOCATION: Amino acids 522-1087

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Gronwald, R., et al.

(B) JOURNAL: Proc. Natl. Acad. Sci.

(C) VOLUME: 85

(D) PAGES: 3435-3439

(E) DATE: 1988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met	Leu	Trp	Gln	Lys	Lys	Pro	Arg	Tyr	Glu	Ile	Arg	Trp	Lys
522			525					530					535

Val	Ile	Glu	Ser	Val	Ser	Ser	Asp	Gly	His	Glu	Tyr	Ile	Tyr
				540					545				

	Val Asp Pro Val Gln Leu Pro Tyr Asp Ser Thr Trp Glu Leu	
	550	555 560
5	Pro Arg Asp Gln Leu Val Leu Gly Arg Thr Leu Gly Ser Gly	
	565	570 575
	Ala Phe Gly Gln Val Val Glu Ala Thr Ala His Gly Leu Ser	
	580	585 590
10	His Ser Gln Ala Thr Met Lys Val Ala Val Lys Met Leu Lys	
	595	600 605
	Ser Thr Ala Arg Ser Ser Glu Lys Gln Ser Leu Met Ser Glu	
	610	615
15	Leu Lys Ile Met Ser His Leu Gly Pro His Leu Asn Val Val	
	620	625 630
	Asn Leu Leu Gly Ala Cys Thr Lys Gly Gly Pro Ile Tyr Ile	
20	635	640 645
	Ile Thr Glu Tyr Cys Arg Tyr Gly Asp Leu Val Asp Tyr Leu	
	650	655 660
25	His Arg Asn Lys His Thr Phe Leu Gln Arg His Ser Asn Lys	
	665	670 675
	His Cys Pro Pro Ser Ala Glu Leu Tyr Ser Asn Ala Leu Pro	
	680	685
30	Val Gly Phe Ser Leu Pro Ser His Leu Asn Leu Thr Gly Glu	
	690	695 700
	Ser Asp Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Ile	
35	705	710 715

	Asp Tyr Val Pro Met Leu Asp Met Lys Gly Asp Ile Lys Tyr	
	720	725 730
5	Ala Asp Ile Glu Ser Pro Ser Tyr Met Ala Pro Tyr Asp Asn	
	735	740 745
	Tyr Val Pro Ser Ala Pro Glu Arg Thr Tyr Arg Ala Thr Leu	
	750	755
10	Ile Asn Asp Ser Pro Val Leu Ser Tyr Thr Asp Leu Val Gly	
	760	765 770
	Phe Ser Tyr Gln Val Ala Asn Gly Met Asp Phe Leu Ala Ser	
	775	780 785
15	Lys Asn Cys Val His Arg Asp Leu Ala Ala Arg Asn Val Leu	
	790	795 800
	Ile Cys Glu Gly Lys Leu Val Lys Ile Cys Asp Phe Gly Phe	
20	805	810 815
	Ala Arg Asp Ile Met Arg Asp Ser Asn Tyr Ile Ser Lys Gly	
	820	825
25	Ser Thr Tyr Leu Pro Leu Lys Trp Met Ala Pro Glu Ser Ile	
	830	835 840
	Phe Asn Ser Leu Tyr Thr Thr Leu Ser Asp Val Trp Ser Phe	
	845	850 855
30	Gly Ile Leu Leu Trp Glu Ile Phe Thr Leu Gly Gly Thr Pro	
	860	865 870
	Tyr Pro Glu Leu Pro Met Asn Asp Gln Phe Tyr Asn Ala Ile	
35	875	880 885

	Lys Arg Gly Tyr Arg Met Ala Gln Pro Ala His Ala Ser Asp	
	890	895
5	Glu Ile Tyr Glu Ile Met Gln Lys Cys Trp Glu Glu Lys Phe	
	900	910
	Glu Thr Arg Pro Pro Phe Ser Gln Leu Val Leu Leu Leu Glu	
	915	925
10	Arg Leu Leu Gly Glu Gly Tyr Lys Lys Lys Tyr Gln Gln Val	
	930	940
	Asp Glu Glu Phe Leu Arg Ser Asp His Pro Ala Ile Leu Arg	
	945	955
15	Ser Gln Ala Arg Phe Pro Gly Ile His Ser Leu Arg Ser Pro	
	960	965
	Leu Asp Thr Ser Ser Val Leu Tyr Thr Ala Val Gln Pro Asn	
20	970	980
	Glu Ser Asp Asn Asp Tyr Ile Ile Pro Leu Pro Asp Pro Lys	
	985	995
25	Pro Asp Val Ala Asp Glu Gly Leu Pro Glu Gly Ser Pro Ser	
	1000	1010
	Leu Ala Ser Ser Thr Leu Asn Glu Val Asn Thr Ser Ser Thr	
	1015	1025
30	Ile Ser Cys Asp Ser Pro Leu Glu Leu Gln Glu Glu Pro Gln	
	1030	1035
	Gln Ala Glu Pro Glu Ala Gln Leu Glu Gln Pro Gln Asp Ser	
35	1040	1050

Gly Cys Pro Gly Pro Leu Ala Glu Ala Glu Asp Ser Phe Leu
1055 1060 1065

5 Glu Gln Pro Gln Asp Ser Gly Cys Pro Gly Pro Leu Ala Glu
1070 1075 1080

Ala Glu Asp Ser Phe Leu
1085

10 (2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TCGACGCGCG ATG GAG

16

30

35



We claim:

1. An isolated DNA sequence encoding the Kinase insert Domain containing Receptor.

5 2. The DNA sequence of Claim 1 wherein said sequence is a human gene.

3. An isolated DNA sequence comprising a DNA sequence capable of hybridizing with a DNA sequence encoding the amino acid sequence of Figure 7.

10 4. A method for the production of a growth factor receptor which comprises transforming a host cell with the DNA sequence of Claim 3 and culturing the host cell under conditions which result in expression of the gene by an expression vector.

15 5. The method of Claim 4 wherein the host cell is a bacteria, virus, yeast, insect or mammalian cell line.

20 6. The method of Claim 5 wherein the host cell is a COS-1 cell, NIH3T3 fibroblast or CMT-3 monkey kidney cell.

7. The method of Claim 5 where the expression vector is pcDNA1tkpASP expression vector.

25 8. A lambda gt11 phage harboring the clone BTIII081.8 (ATCC accession number 40,931) or the clone BTIII129.5 (ATCC Accession number 40,975).

9. A plasmid pBlueScript KS which contains the clone BTIV169 (ATCC accession number 75200).

30 10. An isolated growth factor receptor designated the Kinase insert Domain containing Receptor.

11. The receptor of Claim 10 comprising the amino acid sequence of Figure 7.

35 12. The receptor of Claim 10 encoded by an isolated DNA sequence comprising a DNA sequence capable

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of hybridizing with a DNA sequence encoding the amino acid sequence of Figure 7.

13. A biologically active protein fragment which retains the receptor activity of the receptor of Claim 10.

14. An isolated DNA sequence encoding a biologically active protein fragment which retains the receptor activity of an isolated growth factor receptor designated the Kinase insert Domain containing Receptor.

15. An oligonucleotide primer consisting of an oligonucleotide primer having 21 bases and having a sequence depicted for Primer 1 in Figure 2.

16. An oligonucleotide primer consisting of an oligonucleotide primer having 29 bases and having a sequence depicted for Primer 2 in Figure 2.

17. The 363 base pair product having the sequence depicted in Figure 4, or a biological equivalent of said sequence.

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Abstract of the Disclosure

5 A DNA sequence encoding a novel human growth
factor receptor referred to as a type III receptor
tyrosine kinase is described. The amino acid sequence
of the receptor is also described. The receptor has a
sequence which is similar to that of the kinase domains
10 of known type III receptor tyrosine kinases, but which
is unique in its kinase insert domain sequence. The
receptor binds specifically to the vascular endothelial
cell growth factor.

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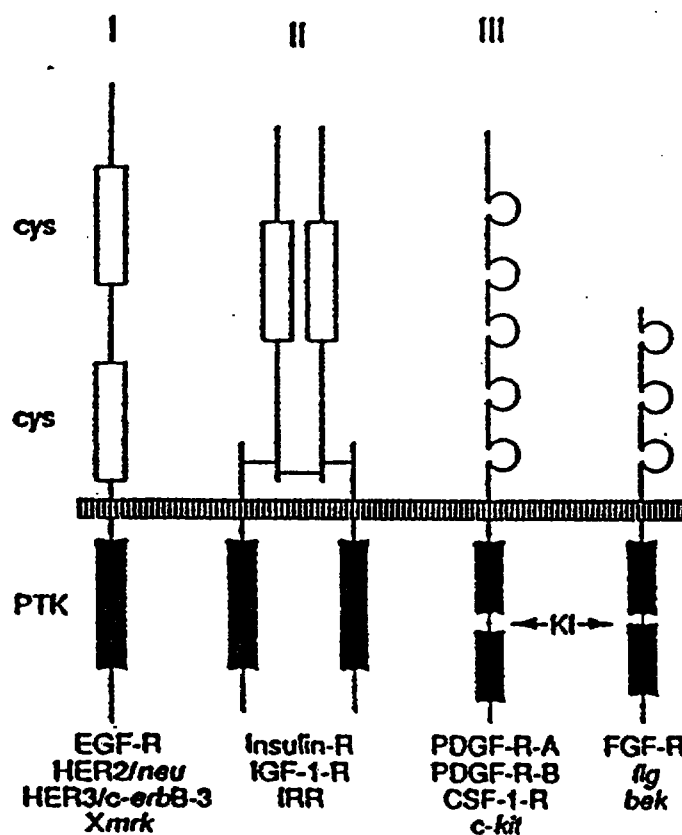


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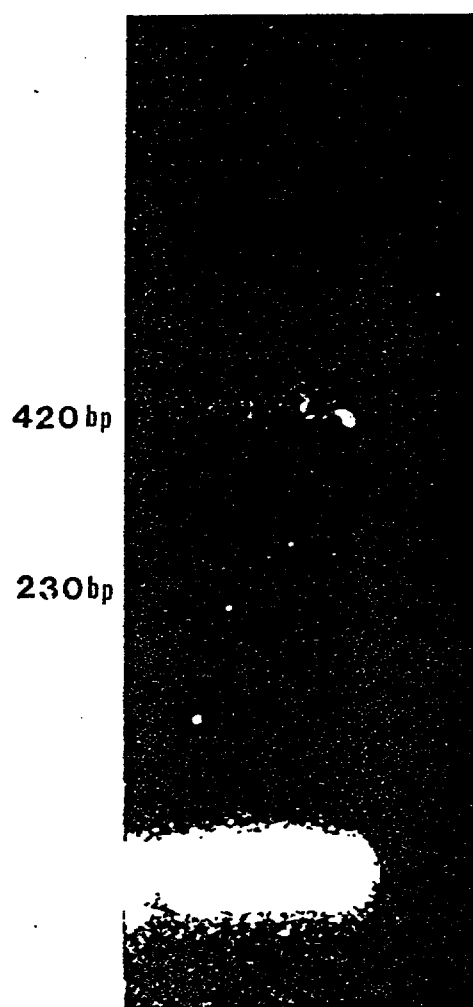
FIGURE 1



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FIGURE 3



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FIGURE 4

A. DNA sequence of the 360 bp segment derived from the 420 bp PCR product

G A A T T C T G C A A A T T T G G A A A C C T G T C C A C T T
A C C T G A G G A C G A A G A G A A A T G A A T T T G T C C C
C T A C A A G A C C A A A G G G G C A C G A T T C C G T C A A
G G G A A A G A C T A C G T T G G A G C A A T C C C T G T G G
A T C T G A A A C G G C G C T T G G A C A C G C A T C A C C A
G T A G C C A G A G C T C A G C C A G C T C T G G A T T T G T
G G A G G A G A A G T C C C T C A G T G A T G T A G A A G A A
G A G G A A G C T C C T G A A G A T C T G T A T A A G G A C T
T C C T G A C C T T G G A G C A T C T C A T C T G T T A C A G
T T T C C A A G T G G C T A A G G G C A T G G A G T T C T T G
G C A T C G C G A A A G T G T A T C C A C A G A G A C C T G G
C A G C C A G G A A C G T G C T G A A T T C

B. DNA sequence of the 230 bp PCR product

G T C G A C A A T C T G T T G G G G G C C T G C A C C A T C C
C A A C A T C C T G C T G C T C T A C A A C T A T T T T T A T
G A C C G G A G G A G G A T C T A C T T G A T T C T A G A G T
A T G C C C C C G C G G A G C T C T A C A A G G A G C T G C
A G A A G A G C T G C A C A T T T G A C G A G C A G C G A A C
A G C C A C G A T C A T G G A G G A G T T G G C A G A T G C T
C T A A T G T A C T G C C G T G G G A A G A A G G T G A T T C
A C A G A G A C C T G G C A G C C A G C A A C G T G C T G A A
T T C

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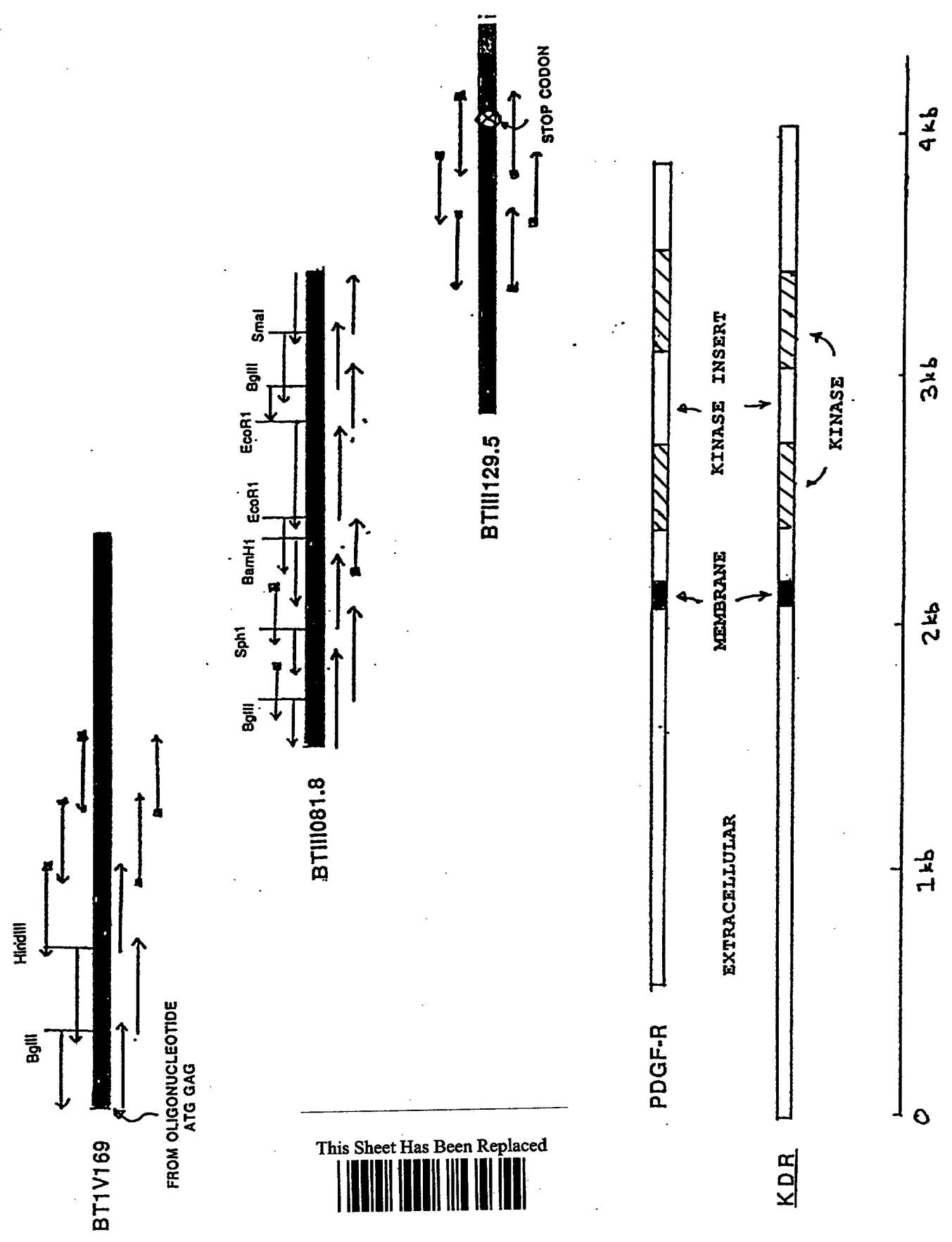
FIGURE 5A. COMPARISON OF THE DNA SEQUENCE OF THE 360 bp SEGMENT OF THE 420 bp PCR PRODUCT WITH THE PDGF-R

	10v	20v	30v	40v	50v	60v	70v	80v	90v	100v
PDGF	AACCTGTGGGGCCTGCACCAAGGAGGACCATCTATATCATCTATATCATCACTGAGTACTGCCGTACGGAGACCTGGTGGACTACCTGCACCGCAACA									
360 bp							TGC T GGA ACCTG	TACCTG	GCAA A	
							TGCAAAATTTGGAAACCTGTCCACTTACCTGAGGAGCAAGA			
							10"	20"	30"	40"
PDGF	A-----ACAC-ACCTTCTGCAGCACCCTCCGACAAGCGCCGCCCGCCGCGGAGCT-CTAC-----AGCAATGCTCTGCCCGT									
360 bp		ACA ACC	G GCAC A TCCG CAAG				GGA CTAC	AGCAAT	CCC	
	GAAATGAATTTGTCCCTACAAGACCAAGGG--GCACGATTCCTCAAG-----GGAAAGACTACGTTGGAGCAAT-----CCCTG									
	50"	60"	70"	80"			90"	100"	110"	
PDGF	TGGGCTCCCCCTGCCAGCCATGTGTCTTGACCGGGGAGAGCGACGGTGGCTACATGGACATGAGCAAGGACGAGTCGGTGGACTATGTGCCCATGCT									
360 bp	TGG	G C	G	G AGAGC G	GCT	TGGA TG G	AGGA	AGTC T	ATGT	
	TGGATCTGAAACGGCGCTTGGACAGCATCACCAGTAGCCAGAGCTCAGCCAGCTC--TGGATTGTGG-AGGAGAAGTCCCTCAGTGATGTAGAAGAAGA									
	120"	130"	140"	150"	160"	170"	180"	190"	200"	210"
PDGF	GGACATGAAAGGAGACGTCAAATAGCAGACATCGAGTCCTCCAACTACATGCCCCCTTACGATAACTACGTTCCCTCTGCCCTGAGAGGACCTGCCGAG									
360 bp	GGA	G AGA							CTG A	
	GGAAGCTCCTGAAGAT-----								CTGTATAA	
	220"								230"	
PDGF	CAACTTTGATCAACGAGTCTCCAGTGCTAAGCTACATGGAC--CTCGTGGGCTTCAGCTACCAGGTGGCCAATGGCATGGAGTTCTGGCCTCCAAGAAC									
360 bp	ACTT		TGGA							
	GGACTTCCTGACCT-----TGGAGCATCTCATCTGTTACAGCTTCCAAGTGGAAG-GGCATGGAGTTCTTGGCATCGCGAAA									
	240"	250"			260"	270"	280"	290"	300"	310"
PDGF	TCCG-TCCACAGAGACCTGGCGGCTAGGAACGTGCT									
360 bp	TCCACAGAGACCTGGC GC AGGAACGTGCT									
	GTGTATCCACAGAGACCTGGCAGCCAGGAACGTGCT									
	320"	330"	340"							

FIGURE 5B. COMPARISON OF THE DNA SEQUENCE OF THE 230 bp PCR PRODUCT WITH THE FGF-R

	10v	20v	30v	40v	50v	60v	70v	80v
FGF	AACCTGCTGGGGCCTGCACGCAGGATGGTCCCTTGTATGTGCATCGTGGAGTATGCCCTCCAAGGGCAACCTGCGGGAGTACCTGC-----							
230 bp	AA CTG TGGGGCCTGCAC		CCT	CGT	CTC A	CAAC	A ACC G	
	AATCTGTTGGGGCCTGCACCATCCCAACATCCTG-----CGT-----CTCTA-----CAACTATTTTATGACCGGAGGAGGATCTACTTGAT							
	10"	20"	30"					
FGFI	---AGACCCGAGGCCCCAGGGCTGGAATACTGCTATAACCCAGCCACAACCCAGAGGAGCAGCTCTCCTCCAAGGACCTGGTGTCTGCGCCTACCA							
230 bp	AGA G	CCC C G GCT A A	A AGC CA	GA GAGCAGC	C CCA G C TGG			
	TCTAGAGTATGCCCCCGCGGAGCTCTACAAGGAGCTGCAGAAGAGCTGCACATTTGACGAGCAGCGAAGCCAGCATG-----A							
	90"	100"	110"	120"	130"	140"	150"	160"
FGF	GGA---GGCCCGAGGCATGGAGTATCTGGCCTCCAAGAAGTGCATACACCGAGACCTGGCAGCCAGGAATGTCCTG							
230 bp	GGA GGC	G T GTA	AAGAAG	AT CAC	GAGACCTGGCAGCCAG	AA GT CT		
	GGAGTTGGCAGATGCTCTAATGTACTGCCGTGGGAAGAAGGTGATTACAGAGACCTGGCAGCCAGCAACGTGCT							
	170"	180"	190"	200"	210"	220"	230"	

FIGURE 6



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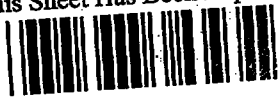


Figure 7

10	20	30	40	50
*	*	*	*	*
ATG GAG AGC AAG GTG CTG CTG GCC GTC GCC CTG TGG CTC TGC GTG GAG ACC CGG				
Met Glu Ser Lys Val Leu Leu Ala Val Ala Leu Trp Leu(Cys) Val Glu Thr Arg>				
60	70	80	90	100
*	*	*	*	*
GCC GCC TCT GTG GGT TTG CCT AGT GTT TCT CTT GAT CTG CCC AGG CTC AGC ATA				
Ala Ala Ser Val Gly Leu Pro Ser Val Ser Leu Asp Leu Pro Arg Leu Ser Ile>				
110	120	130	140	150
*	*	*	*	*
CAA AAA GAC ATA CTT ACA ATT AAG GCT AAT ACA ACT CTT CAA ATT ACT TGC AGG				
Gln Lys Asp Ile Leu Thr Ile Lys Ala Asn Thr Thr Leu Gln Ile Thr(Cys) Arg>				
170	180	190	200	210
*	*	*	*	*
GGA CAG AGG GAC TTG GAC TGG CTT TGG CCC AAT AAT CAG AGT GGC AGT GAG CAA				
Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro Asn Asn Gln Ser Gly Ser Glu Gln>				
220	230	240	250	260
*	*	*	*	*
AGG GTG GAG GTG ACT GAG TGC AGC GAT GGC CTC TTC TGT AAG ACA CTC ACA ATT				
Arg Val Glu Val Thr Glu(Cys) Ser Asp Gly Leu Phe(Cys) Lys Thr Leu Thr Ile>				
280	290	300	310	320
*	*	*	*	*
CCA AAA GTG ATC GGA AAT GAC ACT GGA GCC TAC AAG TGC TTC TAC CGG GAA ACT				
Pro Lys Val Ile Gly Asn Asp Thr Gly Ala Tyr Lys(Cys) Phe Tyr Arg Glu Thr>				
330	340	350	360	370
*	*	*	*	*
GAC TTG GCC TCG GTC ATT TAT GTC TAT GTT CAA GAT TAC AGA TCT CCA TTT ATT				
Asp Leu Ala Ser Val Ile Tyr Val Tyr Val Gln Asp Tyr Arg Ser Pro Phe Ile>				
380	390	400	410	420
*	*	*	*	*
GCT TCT GTT AGT GAC CAA CAT GGA GTC GTG TAC ATT ACT GAG AAC AAA AAC AAA				
Ala Ser Val Ser Asp Gln His Gly Val Val Tyr Ile Thr Glu Asn Lys Asn Lys>				
440	450	460	470	480
*	*	*	*	*
ACT GTG GTG ATT CCA TGT CTC GGG TCC ATT TCA AAT CTC AAC GTG TCA CTT TGT				
Thr Val Val Ile Pro(Cys) Leu Gly Ser Ile Ser Asn Leu Asn Val Ser Leu(Cys)				
490	500	510	520	530
*	*	*	*	*
GCA AGA TAC CCA GAA AAG AGA TTT GTT CCT GAT GGT AAC AGA ATT TCC TGG GAC				
Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg Ile Ser Trp Asp>				
550	560	570	580	590
*	*	*	*	*
AGC AAG AAG GGC TTT ACT ATT CCC AGC TAC ATG ATC AGC TAT GCT GGC ATG GTC				
Ser Lys Lys Gly Phe Thr Ile Pro Ser Tyr Met Ile Ser Tyr Ala Gly Met Val>				
600	610	620	630	640
*	*	*	*	*
TTC TGT GAA GCA AAA ATT AAT GAT GAA AGT TAC CAG TCT ATT ATG TAC ATA GTT				
Phe(Cys) Glu Ala Lys Ile Asn Asp Glu Ser Tyr Gln Ser Ile Met Tyr Ile Val>				



Figure 7 (Page 2)

650 660 670 680 690 700
 * * * * * *
 GTC GTT GTA GGG TAT AGG ATT TAT GAT GTG GTT CTG AGT CCG TCT CAT GGA ATT
 Val Val Val Gly Tyr Arg Ile Tyr Asp Val Val Leu Ser Pro Ser His Gly Ile>

710 720 730 740 750
 * * * * *
 GAA CTA TCT GTT GGA GAA AAG CTT GTC TTA AAT TGT ACA GCA AGA ACT GAA CTA
 Glu Leu Ser Val Gly Glu Lys Leu Val Leu Asn (Cys) Thr Ala Arg Thr Glu Leu>

760 770 780 790 800 810
 * * * * * *
 AAT GTG GGG ATT GAC TTC AAC TGG GAA TAC CCT TCT TCG AAG CAT CAG CAT AAG
 Asn Val Gly Ile Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys>

820 830 840 850 860
 * * * * *
 AAA CTT GTA AAC CGA GAC CTA AAA ACC CAG TCT GGG AGT GAG ATG AAG AAA TTT
 Lys Leu Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe>

870 880 890 900 910
 * * * * *
 TTG AGC ACC TTA ACT ATA GAT GGT GTA ACC CGG AGT GAC CAA GGA TTG TAC ACC
 Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu Tyr Thr>

920 930 940 950 960 970
 * * * * * *
 TGT GCA GCA TCC AGT GGG CTG ATG ACC AAG AAC AGC ACA TTT GTC AGG GTC
 (Cys) Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr Phe Val Arg Val>

980 990 1000 1010 1020
 * * * * *
 CAT GAA AAA CCT TTT GTT GCT TTT GGA AGT GGC ATG GAA TCT CTG GTG GAA GCC
 His Glu Lys Pro Phe Val Ala Phe Gly Ser Gly Met Glu Ser Leu Val Glu Ala>

1030 1040 1050 1060 1070 1080
 * * * * * *
 ACG GTG GGG GAG CGT GTC AGA ATC CCT GCG AAG TAC CTT GGT TAC CCA CCC CCA
 Thr Val Gly Glu Arg Val Arg Ile Pro Ala Lys Tyr Leu Gly Tyr Pro Pro Pro>

1090 1100 1110 1120 1130
 * * * * *
 GAA ATA AAA TGG TAT AAA AAT GGA ATA CCC CTT GAG TCC AAT CAC ACA ATT AAA
 Glu Ile Lys Trp Tyr Lys Asn Gly Ile Pro Leu Glu Ser Asn His Thr Ile Lys>

1140 1150 1160 1170 1180
 * * * * *
 GCG GGG CAT GTA CTG ACG ATT ATG GAA GTG AGT GAA AGA GAC ACA GGA AAT TAC
 Ala Gly His Val Leu Thr Ile Met Glu Val Ser Glu Arg Asp Thr Gly Asn Tyr>

1190 1200 1210 1220 1230 1240
 * * * * * *
 ACT GTC ATC CTT ACC AAT CCC ATT TCA AAG GAG AAG CAG AGC CAT GTG GTC TCT
 Thr Val Ile Leu Thr Asn Pro Ile Ser Lys Glu Lys Gln Ser His Val Val Ser>

1250 1260 1270 1280 1290
 * * * * *
 CTG GTT GTG TAT GTC CCA CCC CAG ATT GGT GAG AAA TCT CTA ATC TCT CCT GTG
 Leu Val Val Tyr Val Pro Pro Gln Ile Gly Glu Lys Ser Leu Ile Ser Pro Val>

1300 1310 1320 1330 1340 1350
 * * * * * *



Figure 7 (page 3)

GAT TCC TAC CAG TAC GGC ACC ACT CAA ACG CTG ACA TGT ACG GTC TAT GCC ATT
 Asp Ser Tyr Gln Tyr Gly Thr Thr Gln Thr Leu Thr (Cys) Thr Val Tyr Ala Ile>

1360 1370 1380 1390 1400
 * * * * *

CCT CCC CCG CAT CAC ATC CAC TGG TAT TGG CAG TTG GAG GAA GAG TGC GCC AAC
 Pro Pro Pro His His Ile His Trp Tyr Trp Gln Leu Glu Glu Glu (Cys) Ala Asn>

1410 1420 1430 1440 1450
 * * * * *

GAG CCC AGC CAA GCT GTC TCA GTG ACA AAC CCA TAC CCT TGT GAA GAA TGG AGA
 Glu Pro Ser Gln Ala Val Ser Val Thr Asn Pro Tyr Pro (Cys) Glu Glu Trp Arg>

1460 1470 1480 1490 1500 1510
 * * * * * *

AGT GTG GAG GAC TTC CAG GGA GGA AAT AAA ATT GAA GTT AAT AAA AAT CAA TTT
 Ser Val Glu Asp Phe Gln Gly Gly Asn Lys Ile Glu Val Asn Lys Asn Gln Phe>

1520 1530 1540 1550 1560
 * * * * *

GCT CTA ATT GAA GGA AAA AAC AAA ACT GTA AGT ACC CTT GTT ATC CAA GCG GCA
 Ala Leu Ile Glu Gly Lys Asn Lys Thr Val Ser Thr Leu Val Ile Gln Ala Ala>

1570 1580 1590 1600 1610 1620
 * * * * * *

AAT GTG TCA GCT TTG TAC AAA TGT GAA GCG GTC AAC AAA GTC GGG AGA GGA GAG
 Asn Val Ser Ala Leu Tyr Lys (Cys) Glu Ala Val Asn Lys Val Gly Arg Gly Glu>

1630 1640 1650 1660 1670
 * * * * *

AGG GTG ATC TCC TTC CAC GTG ACC AGG GGT CCT GAA ATT ACT TTG CAA CCT GAC
 Arg Val Ile Ser Phe His Val Thr Arg Gly Pro Glu Ile Thr Leu Gln Pro Asp>

1680 1690 1700 1710 1720
 * * * * *

ATG CAG CCC ACT GAG CAG GAG AGC GTG TCT TTG TGG TGC ACT GCA GAC AGA TCT
 Met Gln Pro Thr Glu Gln Glu Ser Val Ser Leu Trp (Cys) Thr Ala Asp Arg Ser>

1730 1740 1750 1760 1770 1780
 * * * * * *

ACG TTT GAG AAC CTC ACA TGG TAC AAG CTT GGC CCA CAG CCT CTG CCA ATC CAT
 Thr Phe Glu Asn Leu Thr Trp Tyr Lys Leu Gly Pro Gln Pro Leu Pro Ile His>

1790 1800 1810 1820 1830
 * * * * *

GTG GGA GAG TTG CCC ACA CCT GTT TGC AAG AAC TTG GAT ACT CTT TGG AAA TTG
 Val Gly Glu Leu Pro Thr Pro Val (Cys) Lys Asn Leu Asp Thr Leu Trp Lys Leu>

1840 1850 1860 1870 1880 1890
 * * * * * *

AAT GCC ACC ATG TTC TCT AAT AGC ACA AAT GAC ATT TTG ATC ATG GAG CTT AAG
 Asn Ala Thr Met Phe Ser Asn Ser Thr Asn Asp Ile Leu Ile Met Glu Leu Lys>

1900 1910 1920 1930 1940
 * * * * *

AAT GCA TCC TTG CAG GAC CAA GGA GAC TAT GTC TGC CTT GCT CAA GAC AGG AAG
 Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr Val Cys Leu Ala Gln Asp Arg Lys>

1950 1960 1970 1980 1990
 * * * * *

ACC AAG AAA AGA CAT TGC GTG GTC AGG CAG CTC ACA GTC CTA GAG CGT GTG GCA
 Thr Lys Lys Arg His (Cys) Val Val Arg Gln Leu Thr Val Leu Glu Arg Val Ala>

Figure 7 (page 4)

2000 2010 2020 2030 2040 2050
 * * * * * *
 CCC ACG ATC ACA GGA AAC CTG GAG AAT CAG ACG ACA AGT ATT GGG GAA AGC ATC
 Pro Thr Ile Thr Gly Asn Leu Glu Asn Gln Thr Thr Ser Ile Gly Glu Ser Ile>

 2060 2070 2080 2090 2100
 * * * * *
 GAA GTC TCA TGC ACG GCA TCT GGG AAT CCC CCT CCA CAG ATC ATG TGG TTT AAA
 Glu Val Ser (Cys) Thr Ala Ser Gly Asn Pro Pro Pro Gln Ile Met Trp Phe Lys>

 2110 2120 2130 2140 2150 2160
 * * * * * *
 GAT AAT GAG ACC CTT GTA GAA GAC TCA GGC ATT GTA TTG AAG GAT GGG AAC CGG
 Asp Asn Glu Thr Leu Val Glu Asp Ser Gly Ile Val Leu Lys Asp Gly Asn Arg>

 2170 2180 2190 2200 2210
 * * * * *
 AAC CTC ACT ATC CGC AGA GTG AGG AAG GAG GAC GAA GGC CTC TAC ACC TGC CAG
 Asn Leu Thr Ile Arg Arg Val Arg Lys Glu Asp Glu Gly Leu Tyr Thr (Cys) Gln>

 2220 2230 2240 2250 2260
 * * * * *
 GCA TGC AGT GTT CTT GGC TGT GCA AAA GTG GAG GCA TTT TTC ATA ATA GAA GGT
 Ala (Cys) Ser Val Leu Gly (Cys) Ala Lys Val Glu Ala Phe Phe Ile Ile Glu Gly>

 2270 2280 2290 2300 2310 2320
 * * * * * *
 GCC CAG GAA AAG ACG AAC TTG GAA ATC ATT ATT CTA GTA GGC ACG ACG GTG ATT
 Ala Gln Glu Lys Thr Asn Leu Glu Ile Ile Ile Leu Val Gly Thr Thr Val Ile>

 2330 2340 2350 2360 2370
 * * * * *
 GCC ATG TTC TTC TGG CTA CTT CTT GTC ATC ATC CTA GGC ACC GTT AAG CGG GCC
 Ala Met Phe Phe Trp Leu Leu Leu Val Ile Ile Leu Gly Thr Val Lys Arg Ala>

 2380 2390 2400 2410 2420 2430
 * * * * * *
 AAT GGA GGG GAA CTG AAG ACA GGC TAC TTG TCC ATC GTC ATG GAT CCA GAT GAA
 Asn Gly Gly Glu Leu Lys Thr Gly Tyr Leu Ser Ile Val Met Asp Pro Asp Glu>

 2440 2450 2460 2470 2480
 * * * * *
 CTC CCA TTG GAT GAA CAT TGT GAA CGA CTG CCT TAT GAT GCC AGC AAA TGG GAA
 Leu Pro Leu Asp Glu His Cys Glu Arg Leu Pro Tyr Asp Ala Ser Lys Trp Glu>

 2490 2500 2510 2520 2530
 * * * * *
 TTC CCC AGA GAC CGG CTG AAC CTA GGT AAG CCT CTT GGC CGT GGT GCC TTT GGC
 Phe Pro Arg Asp Arg Leu Asn Leu Gly Lys Pro Leu Gly Arg Gly Ala Phe Gly>

 2540 2550 2560 2570 2580 2590
 * * * * * *
 CAA GAG ATT GAA GCA GAT GCC TTT GGA ATT GAC AAG ACA GCA ACT TGC AGG ACA
 Gln Glu Ile Glu Ala Asp Ala Phe Gly Ile Asp Lys Thr Ala Thr Cys Arg Thr>

 2600 2610 2620 2630 2640
 * * * * *
 GTA GCA GTC AAA ATG TTG AAA GAA GGA GCA ACA CAC AGT GAG CAT CGA GCT CTC
 Val Ala Val Lys Met Leu Lys Glu Gly Ala Thr His Ser Glu His Arg Ala Leu>

 2650 2660 2670 2680 2690 2700



* * * * *
 ATG TCT GAA CTC AAG ATC CTC ATT CAT ATT GGT CAC CAT CTC AAT GTG GTC AAC
 Met Ser Glu Leu Lys Ile Leu Ile His Ile Gly His His Leu Asn Val Val Asn>
 2710 2720 2730 2740 2750
 * * * * *
 CTT CTA GGT GCC TGT ACC AAG CCA GGA GGG CCA CTC ATG GTG ATT GTG GAA TTC
 Leu Leu Gly Ala Cys Thr Lys Pro Gly Gly Pro Leu Met Val Ile Val Glu Phe>
 2760 2770 2780 2790 2800
 * * * * *
 TGC AAA TTT GGA AAC CTG TCC ACT TAC CTG AGG AGC AAG AGA AAT GAA TTT GTC
 Cys Lys Phe Gly Asn Leu Ser Thr Tyr Leu Arg Ser Lys Arg Asn Glu Phe Val>
 2810 2820 2830 2840 2850 2860
 * * * * *
 CCC TAC AAG ACC AAA GGG GCA CGA TTC CGT CAA GGG AAA GAC TAC GTT GGA GCA
 Pro Tyr Lys Thr Lys Gly Ala Arg Phe Arg Gln Gly Lys Asp Tyr Val Gly Ala>
 2870 2880 2890 2900 2910
 * * * * *
 ATC CCT GTG GAT CTG AAA CGG CGC TTG GAC AGC ATC ACC AGT AGC CAG AGC TCA
 Ile Pro Val Asp Leu Lys Arg Arg Leu Asp Ser Ile Thr Ser Ser Gln Ser Ser>
 2920 2930 2940 2950 2960 2970
 * * * * *
 GCC AGC TCT GGA TTT GTG GAG GAG AAG TCC CTC AGT GAT GTA GAA GAA GAG GAA
 Ala Ser Ser Gly Phe Val Glu Glu Lys Ser Leu Ser Asp Val Glu Glu Glu Glu>
 2980 2990 3000 3010 3020
 * * * * *
 GCT CCT GAA GAT CTG TAT AAG GAC TTC CTG ACC TTG GAG CAT CTC ATC TGT TAC
 Ala Pro Glu Asp Leu Tyr Lys Asp Phe Leu Thr Leu Glu His Leu Ile Cys Tyr>
 3030 3040 3050 3060 3070
 * * * * *
 AGC TTC CAA GTG GCT AAG GGC ATG GAG TTC TTG GCA TCG CGA AAG TGT ATC CAC
 Ser Phe Gln Val Ala Lys Gly Met Glu Phe Leu Ala Ser Arg Lys Cys Ile His>
 3080 3090 3100 3110 3120 3130
 * * * * *
 AGG GAC CTG GCG GCA CGA AAT ATC CTC TTA TCG GAG AAG AAC GTG GTT AAA ATC
 Arg Asp Leu Ala Ala Arg Asn Ile Leu Leu Ser Glu Lys Asn Val Val Lys Ile>
 3140 3150 3160 3170 3180
 * * * * *
 TGT GAC TTT GGC TTG GCC CGG GAT ATT TAT AAA GAT CCA GAT TAT GTC AGA AAA
 Cys Asp Phe Gly Leu Ala Arg Asp Ile Tyr Lys Asp Pro Asp Tyr Val Arg Lys>
 3190 3200 3210 3220 3230 3240
 * * * * *
 GGA GAT GCT CGC CTC CCT TTG AAA TGG ATG GCC CCA GAA ACA ATT TTT GAC AGA
 Gly Asp Ala Arg Leu Pro Leu Lys Trp Met Ala Pro Glu Thr Ile Phe Asp Arg>
 3250 3260 3270 3280 3290
 * * * * *
 GTG TAC ACA ATC CAG AGT GAC GTC TGG TCT TTT GGT GTT TTG CTG TGG GAA ATA
 Val Tyr Thr Ile Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile>
 3300 3310 3320 3330 3340
 * * * * *
 TTT TCC TTA GGT GCT TCT CCA TAT CCT GGG GTA AAG ATT GAT GAA GAA TTT TGT

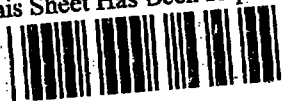


Figure 7 (page 6)

Phe Ser Leu Gly Ala Ser Pro Tyr Pro Gly Val Lys Ile Asp Glu Glu Phe Cys>
 3350 3360 3370 3380 3390 3400
 * * * * * *
 AGG CGA TTG AAA GAA GGA ACT AGA ATG AGG GCC CCT GAT TAT ACT ACA CCA GAA
 Arg Arg Leu Lys Glu Gly Thr Arg Met Arg Ala Pro Asp Tyr Thr Thr Pro Glu>
 3410 3420 3430 3440 3450
 * * * * *
 ATG TAC CAG ACC ATG CTG GAC TGC TGG CAC GGG GAG CCC AGT CAG AGA CCC ACG
 Met Tyr Gln Thr Met Leu Asp Cys Trp His Gly Glu Pro Ser Gln Arg Pro Thr>
 3460 3470 3480 3490 3500 3510
 * * * * * *
 TTT TCA GAG TTG GTG GAA CAT TTG GGA AAT CTC TTG CAA GCT AAT GCT CAG CAG
 Phe Ser Glu Leu Val Glu His Leu Gly Asn Leu Leu Gln Ala Asn Ala Gln Gln>
 3520 3530 3540 3550 3560
 * * * * *
 GAT GGC AAA GAC TAC ATT GTT CTT CCG ATA TCA GAG ACT TTG AGC ATG GAA GAG
 Asp Gly Lys Asp Tyr Ile Val Leu Pro Ile Ser Glu Thr Leu Ser Met Glu Glu>
 3570 3580 3590 3600 3610
 * * * * *
 GAT TCT GGA CTC TCT CTG CCT ACC TCA CCT GTT TCC TGT ATG GAG GAG GAG GAA
 Asp Ser Gly Leu Ser Leu Pro Thr Ser Pro Val Ser Cys Met Glu Glu Glu Glu>
 3620 3630 3640 3650 3660 3670
 * * * * * *
 GTA TGT GAC CCC AAA TTC CAT TAT GAC AAC ACA GCA GGA ATC AGT CAG TAT CTG
 Val Cys Asp Pro Lys Phe His Tyr Asp Asn Thr Ala Gly Ile Ser Gln Tyr Leu>
 3680 3690 3700 3710 3720
 * * * * *
 CAG AAC AGT AAG CGA AAG AGC CGG CCT GTG AGT GTA AAA ACA TTT GAA GAT ATC
 Gln Asn Ser Lys Arg Lys Ser Arg Pro Val Ser Val Lys Thr Phe Glu Asp Ile>
 3730 3740 3750 3760 3770 3780
 * * * * * *
 CCG TTA GAA GAA CCA GAA GTA AAA GTA ATC CCA GAT GAC AAC CAG ACG GAC AGT
 Pro Leu Glu Glu Pro Glu Val Lys Val Ile Pro Asp Asp Asn Gln Thr Asp Ser>
 3790 3800 3810 3820 3830
 * * * * *
 GGT ATG GTT CTT GCC TCA GAA GAG CTG AAA ACT TTG GAA GAC AGA ACC AAA TTA
 Gly Met Val Leu Ala Ser Glu Glu Leu Lys Thr Leu Glu Asp Arg Thr Lys Leu>
 3840 3850 3860 3870 3880
 * * * * *
 TCT CCA TCT TTT GGT GGA ATG GTG CCC AGC AAA AGC AGG GAG TCT GTG GCA TCT
 Ser Pro Ser Phe Gly Gly Met Val Pro Ser Lys Ser Arg Glu Ser Val Ala Ser>
 3890 3900 3910 3920 3930 3940
 * * * * * *
 GAA GGC TCA AAC CAG ACA AGC GGC TAC CAG TCC GGA TAT CAC TCC GAT GAC ACA
 Glu Gly Ser Asn Gln Thr Ser Gly Tyr Gln Ser Gly Tyr His Ser Asp Asp Thr>
 3950 3960 3970 3980 3990
 * * * * *
 GAC ACC ACC GTG TAC TCC AGT GAG GAA GCA GAA CTT TTA AAG CTG ATA GAG ATT
 Asp Thr Thr Val Tyr Ser Ser Glu Glu Ala Glu Leu Leu Lys Leu Ile Glu Ile>

Figure 7 (page 7)

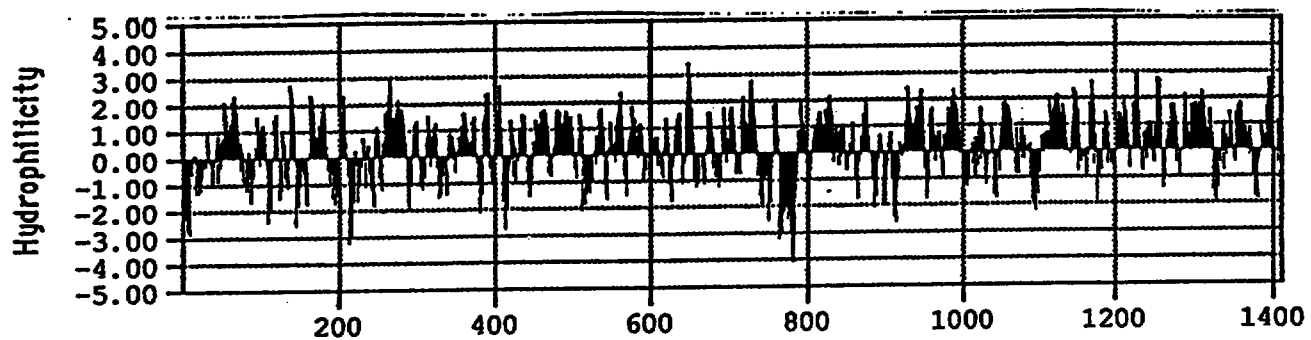
4000	4010	4020	4030	4040	4050
*	*	*	*	*	*
GGA GTG CAA ACC GGT AGC ACA GCC CAG ATT CTC CAG CCT GAC ACG GGG ACC ACA					
Gly Val Gln Thr Gly Ser Thr Ala Gln Ile Leu Gln Pro Asp Thr Gly Thr Thr>					
4060	4070				
*	*				
CTG AGC TCT CCT CCT GTT TAA					
Leu Ser Ser Pro Pro Val ***					

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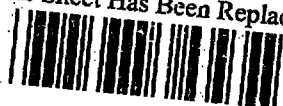


FIGURE 8

HYDROPHATHY PLOT OF PREDICTED AMINO ACID SEQUENCE



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KDR 787 GTVKRANGGELKTGYLSIVMDPDELPLDEHCERLPYDASKWEFFPRDRI.NI.GK
ckit 543 L***YLQKPMYEVQWKVVEEINGNNYVYIDPTQ****H-*****N**SF**
CSF1 536 LLY*YKQKPKYQVRWKIIESYEGNSYTFIDPTQ****NE-*****NN*QF**
PDGF 522 MLWQKKPRYEIRWKVIESVSSDGHEYIYVDPVQ****-ST*****QLV**R

* * *

KDR 839 PLGRGAFGQEIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILI
ckit 594 T**A****KVVAET*Y*LI*SDAAM*****PS*HLT*RE*****V*S
CSF1 587 T**A****KVV**T***LG*EDAVLK*****ST*HAD*KE*****MS
PDGF 573 T**S*****VV**T*H*LSHSQATMK*****ST*RSS*KQS*****MS

KDR 891 HIGHHLNVVNLLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVVPYKTKG
ckit 646 YL*N*M*I*****I-***TL**T*Y*CY*D*LNF**R**DS*ICS*QED
CSF1 639 *L*Q*E*I*****H-***VL**T*Y*CY*D*LNF**R*AEAMLGPSLSLSP
PDGF 625 *L*P*****I*YI*T*Y*RY*D*VD**HRNKHT*LQRHSNK

KDR 943 ARFRQ GKDYVGAIPVDLKRRLDSIT-SSQSSASSGFVEEKSL-----SDV
ckit 697 HAEA-A-L*KNLLHSKESSCS-DS*N-E----YMDMKPGVS--YVVPT--KA
CSF1 690 GQDPE*GVDYKN*HLEK*YVRD SGF***GVD TYVEMRPVSTSS-ND SF*EQ
PDGF 676 HCPPSAEL*SN*LP*GFSLP SHLNL TGESDGGYMDMSKDESIDYVPM LDMKG

KDR 987 EEEEAPEDLYKDF-----LTLEHLICYSFQV
ckit 737 D-KRRSVRIGSYI-----ERDVT PAIMEDDELA*D**D*LSF*Y**
CSF1 741 DLDKEDGRPL-----E*RD*LHF*S**
PDGF 728 DIKY*DIESPSYMAPYDNYVPSAPERTYRATLINDSPV-*SYTD*VGF*Y**

KDR 1013 AKGMEFLASRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGD
ckit 777 -***A*****N*****THGRIT*****KN*SN**V**N
CSF1 762 *Q**A*****N*****V**TNGHVA**G*****MN*SN*IV**N
PDGF 779 *N**D*****N*****V*ICEGKL*****MR*SN*IS**S

KDR 1065 ARLPLKWMAPETIFDRVYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFC
ckit 828 ****V*****S**NC***EE*****Y*IF*****S*****MPVKSK*Y
CSF1 814 ****V*****S***C***VQ*****Y*I*****LN****ILVNSK*Y
PDGF 831 ****V*****S**NS***TL*****I*****GT***ELPMNDQ*Y

KDR 1117 RRLKEGTRMRAPDYTTPEMYQTMLDCWHGEP SQRPTFSELVEHLGNLLQANA
ckit 880 KMI***F**LS*EHAPA***DI*KT**DAD*LK****KQIVQLIEKQISEST
CSF1 862 KLV*D*YQ*AQ*AFAPKNI*SI*QA**AL*TH****QQICSF*QEQAQEDR
PDGF 883 NAI*R*Y**AQ*AHASD*I*EI*QK**EEKFET**P**Q**LL*ER**GEGY

KDR 1169 QQDGKDYIVLP ISETLSMEEDSGLSLPTSPVSCMEEEEEVCDPKFHYDNTAGI
ckit 932 NHIYSNLANCSPNRQKPVVDHSVRINSVGSTASSSQPLL VHDDV
CSF1 914 RERDYTNLPSSSRSGG*GSSS*E*EEESSSEHLTCC*QGDIAQPLLQPNNYQ
PDGF 934 KKKYQQVDEEFLRSDHPAILR*QARF*GIHSLRSP LDTSSVLYTAVQPNESD

KDR 1213 SQYLQNSKRKSRPVS VKTFEDIPLEEPEVKVIPDDNQTDSGMVLASEELKTL
CSF1 966 FC
PDGF 987 ND*I IPLPDPKPD*ADEGLPEGSPSLASSTLNEVNTSSTISCDSP L*LQEEP

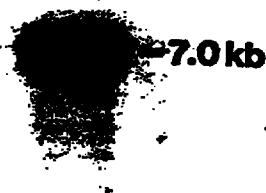
KDR 1273 EDRTKLSPSFGGMVPSKSRRESVASEGSNQTSGYQSGYHSDDTDTTVYSSEEA
PDGF1039 QQAEPEAQLEQPQDSGCPGLAEA*DSFLEQPQD**CPGLAEAEDSFL

KDR 1325 ELLKLIEIGVQTGSTAQILQPDGTGTTLSPPV

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FIGURE 10

IDENTIFICATION OF *kdp* mRNA



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FIGURE 11

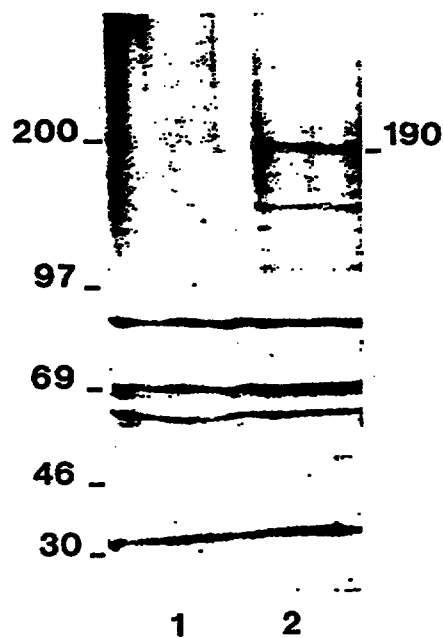
**IDENTIFICATION OF *kdp* GENE
BY SOUTHERN ANALYSIS**



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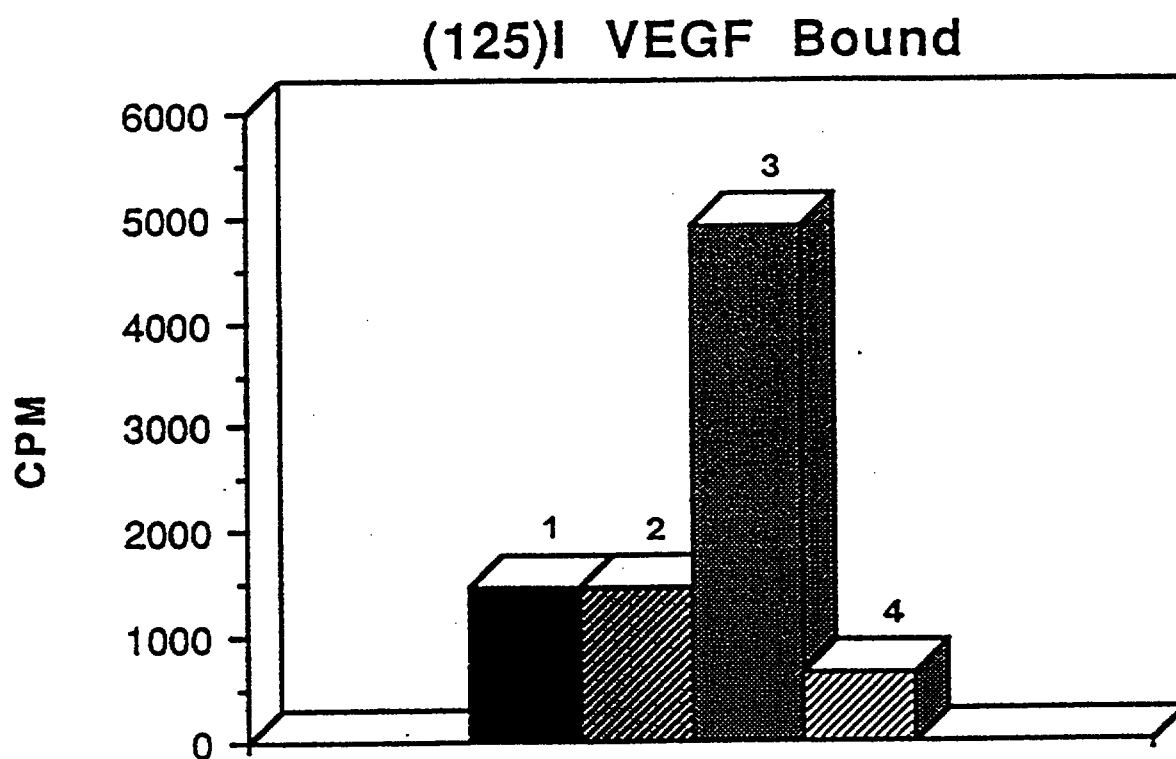
FIGURE 12



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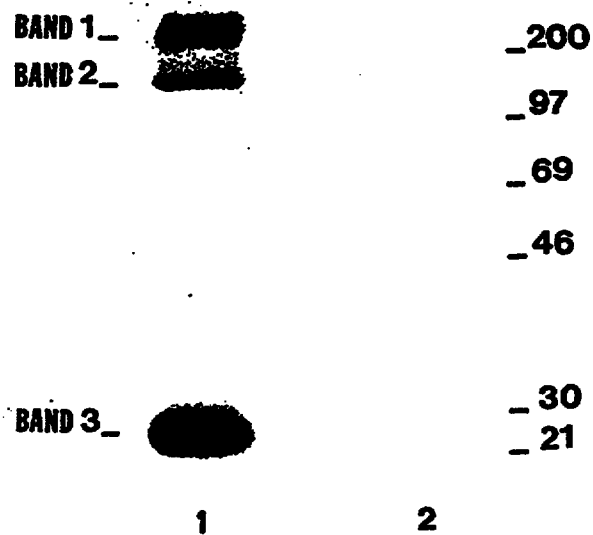
FIGURE 13



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FIGURE 14



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IDENTIFICATION OF A NOVEL HUMAN
RECEPTOR TYROSINE KINASE GENE

Abstract of the Disclosure

5 A DNA sequence encoding a novel human growth
factor receptor referred to as a type III receptor
tyrosine kinase is described. The amino acid sequence
of the receptor is also described. The receptor has a
sequence which is similar to that of the kinase domains
10 of known type III receptor tyrosine kinases, but which
is unique in its kinase insert domain sequence. The
receptor binds specifically to the vascular endothelial
cell growth factor.

15

No Figure

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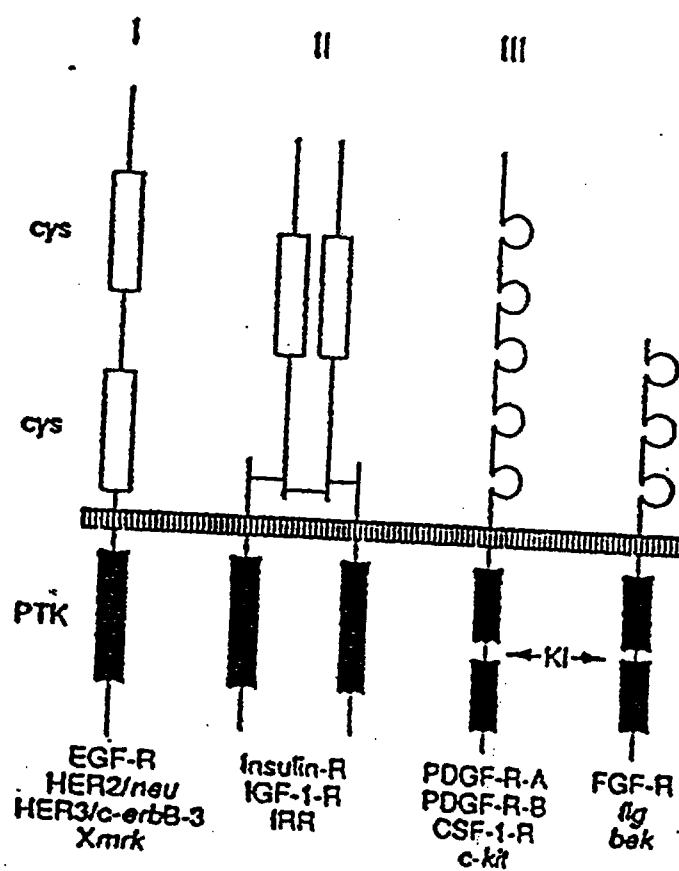
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FIGURE 1



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FIGURE 2

DESIGN OF PRIMERSPRIMER 1RECEPTOR

PDGF	AAC	CTG	TTG	GGG	GCC	TGC	ACC
ckit	T	A	T	A			
CSF	T			A			
FGF			C				G

PRIMER 1	GTCGAC	AAC	CTG	TTG	GGG	GCC	TGC	AAC
		T			A			

PRIMER 2RECEPTOR

PDGF	CAC	AGA	GAC	CTG	GCG	GCT	AGG	AAC	GTG	CT
ckit				T	GA	C	A	T		A
CSF		C	G	G	A	GC	C	T		
FGF		C			C	C		T		C

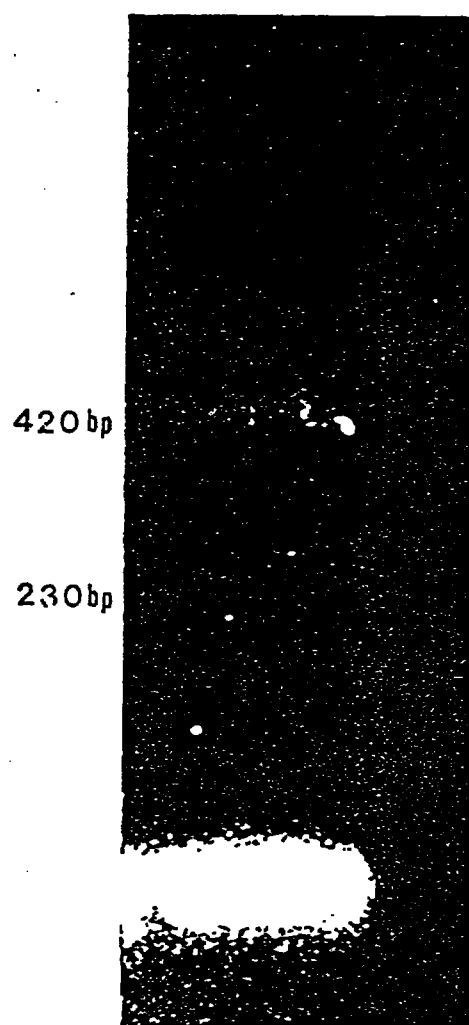
CONSENSUS	CAC	AGA	GAC	CTG	GCC	GCT	AGI	AAC	GTG	CT
		C				T	C		T	

PRIMER 2	GAATTC	AG	CAC	GTT	ICT	AGC	CGC	CAG	GTC	TCT	GTG
			T		G	T					G

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FIGURE 3



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FIGURE 4

A. DNA sequence of the 360 bp segment derived from the 420 bp PCR product

G A A T T C T G C A A A T T T G G A A A C C T G T C C A C T T
A C C T G A G G A C G A A G A G A A A T G A A T T T G T C C C
C T A C A A G A C C A A A G G G G C A C G A T T C C G T C A A
G G G A A A G A C T A C G T T G G A G C A A T C C C T G T G G
A T C T G A A A C G G C G C T T G G A C A C G C A T C A C C A
G T A G C C A G A G C T C A G C C A G C T C T G G A T T T G T
G G A G G A G A A G T C C C T C A G T G A T G T A G A A G A A
G A G G A A G C T C C T G A A G A T C T G T A T A A G G A C T
T C C T G A C C T T G G A G C A T C T C A T C T G T T A C A G
T T T C C A A G T G G C T A A G G G C A T G G A G T T C T T G
G C A T C G C G A A A G T G T A T C C A C A G A G A C C T G G
C A G C C A G G A A C G T G C T G A A T T C

B. DNA sequence of the 230 bp PCR product

G T C G A C A A T C T G T T G G G G G C C T G C A C C A T C C
C A A C A T C C T G C T G C T C T A C A A C T A T T T T T A T
G A C C G G A G G A G G A T C T A C T T G A T T C T A G A G T
A T G C C C C C G C G G A G C T C T A C A A G G A G C T G C
A G A A G A G C T G C A C A T T T G A C G A G C A G C G A A C
A G C C A C G A T C A T G G A G G A G T T G G C A G A T G C T
C T A A T G T A C T G C C G T G G G A A G A A G G T G A T T C
A C A G A G A C C T G G C A G C C A G C A A C G T G C T G A A
T T C

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FIGURE 5A. COMPARISON OF THE DNA SEQUENCE OF THE
360 bp SEGMENT OF THE 420 bp PCR PRODUCT
WITH THE PDGF-R

	10v	20v	30v	40v	50v	60v	70v	80v	90v	100v
PDGF	AACCTGTGGGGCCCTGCACCAAGGAGGACCATCTATATCATCTATATCATCACTGAGTACTGCCGCTACGGAGACCTGGTGGACTACCTGCACCGCAACA									
360 bp	TGC T GGA ACCTG TACCTG GCAA A TGCAATTTGGAAACCTGTCCACITACCTGAGGAGCAACA									
			110v	120v	130v	140v	150v	160v	170v	
PDGF	A-----ACAC-ACCTTCTGCAGCACCCTCCGACAAGCGCCGCCAGCGCGGAGCT-CTAC-----AGCAATGCCITGCCCGT									
360 bp	ACA ACC G GCAC A TCCG CAAG GGA CTAC AGCAAT CCC									
	50v	60v	70v	80v	90v	100v	110v			
PDGF	GAAATGAATTTGTCCCTACAAGACCAAGGG--GCACGATTCGGTCAAG-----GGAAGACTACGTTGGAGCAAT-----CCCTG									
360 bp	v 190v 200v 210v 220v 230v 240v 250v 260v 270v									
	TGGGCTCCCTCCCTGCCAGCCATGTGTCTTACCGGGGAGAGCGACGGTGGCTACATGCACATGAGCAAGCAGGAGTGGTGGACTATGTGCCCATGCT									
PDGF	TGG TGG TGG TGG TGG TGG TGG TGG TGG TGG TGG									
360 bp	TGGATCTGAAACGGCGCTTGGACAGCATCACCAGTAGCCAGAGCTCAGCCAGCTC--TGGATTTGTGG-AGGAGAAGTCCCTCAGTGATGTAGAAGAAGA									
	120v	130v	140v	150v	160v	170v	180v	190v	200v	210v
PDGF	GGACATGAAAGGAGAGCTCAAATAGCAGACATCGAGTCTCCAACTACATGGCCCCCTTACGATAACTACGTTCCCTCTGCCCTGAGAGGACCTGCCGAG									
360 bp	GGA G AGA CTG A									
	220v	230v	240v	250v	260v	270v	280v	290v	300v	310v
PDGF	GGAAGCTCCTGAAGAT-----CTGTATAA									
360 bp	v 390v 400v 410v 420v 430v 440v 450v 460v 470v									
	CAACTTTGATCAACGAGTCTCCAGTGTAAAGTACATGGAC--CTCGTGGGCTTCAGCTACCAGGTGGCCAATGGCATGGAGTTCTGGCCTCCAAGAAC									
PDGF	ACTT TGGG									
360 bp	GGACTTCCTGACCT-----TGGAGCATCTCATCTGTTACAGCTTCCAAGTGGTAAG-GGCATGGAGTTCTTGGCATCGCGAAA									
	240v	250v	260v	270v	280v	290v	300v	310v		
PDGF	TCCG-TCCACAGAGACCTGGCGGTAGGAACGTGCT									
360 bp	TCCACAGAGACCTGGC GC AGGAACGTGCT									
	320v	330v	340v							
PDGF	GTGTATCCACAGAGACCTGGCAGCCAGGAACGTGCT									

FIGURE 5B. COMPARISON OF THE DNA SEQUENCE OF THE
230 bp PCR PRODUCT WITH THE FGF-R

	10v	20v	30v	40v	50v	60v	70v	80v
FGF	AACCTGCTGGGGCCCTGCACGCAGGATGGTCCCTGTATGTATCGTGGAGTATGCCTCCAAGGGCAACCTGCGGGAGTACCTGC-----							
230 bp	AA CTG TGGGGCCCTGCAC CCT CGT CTC A CAAC A ACC G							
	10v	20v	30v	40v	50v	60v	70v	80v
FGF	AATCTGTTGGGGCCCTGCACCATCCCAACATCCTG-----CGT-----CTCTA-----CAACTATTTTATGACCGGAGGAGGATCTACTTGAT							
230 bp	90v 100v 110v 120v 130v 140v 150v 160v 170v 180v							
	---AGACCGGAGGCGCCAGGGCTGGAATACTGCTATAACCCAGGCACAAACCCAGGAGCAGCTCTCCTCCAAGGACCTGGTCTCTGCCCTACCA							
FGF	AGA G CCC G G GCT A A A AGC CA GA GAGCAG C CCA G C TGG							
230 bp	TCTAGAGTATGCCCGCCGAGCTCTACAAGGAGCTGCAGAGAGCTGCACATTTGACGAGCAGGGAACAGCCAGATCATGG-----A							
	90v	100v	110v	120v	130v	140v	150v	160v
FGF	GGA---GGCCCGAGGCATGGAGTATCTGGCCTCCAAGAAGTGCATACACCGAGACCTGGCAGCCAGGAATGTCCTG							
230 bp	GGA GGC G T GTA AAGAAG AT CAC GAGACCTGGCAGCCAG AA GT CT							
	170v	180v	190v	200v	210v	220v	230v	
FGF	GGAGTTGGCAGATGCTCTAATGTACTGCCGTGGGAAGAAGGTGATTACAGAGACCTGGCAGCCAGCAACGTGCT							

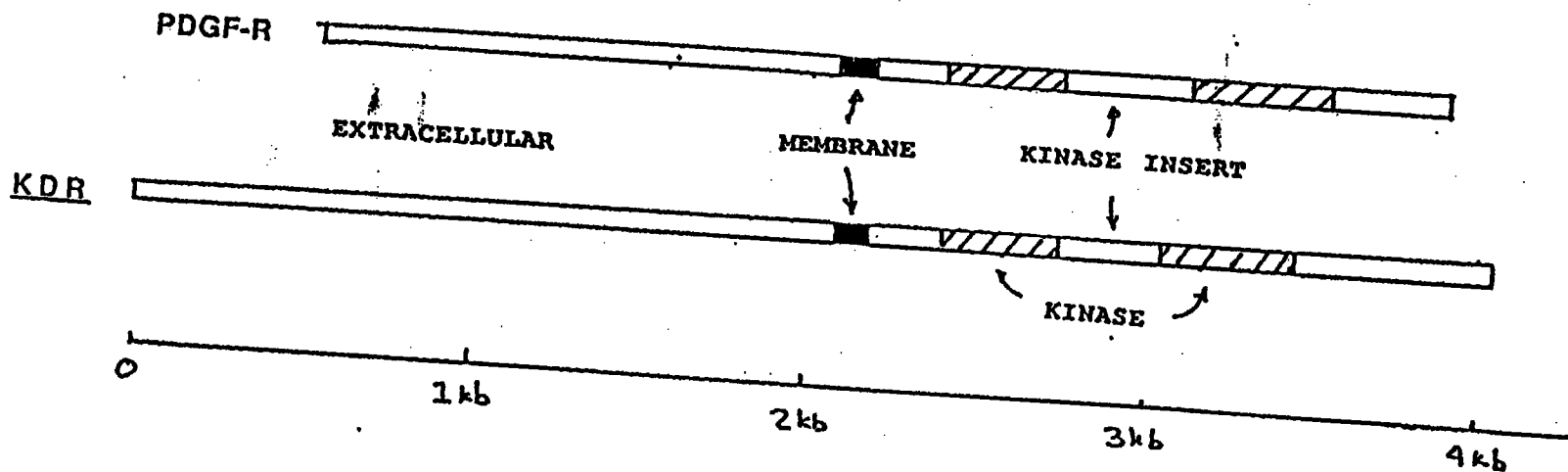
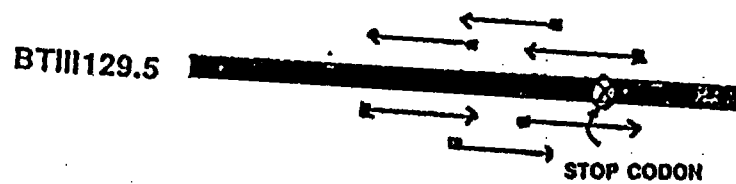
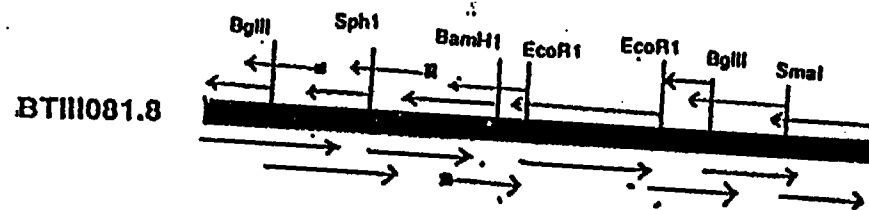
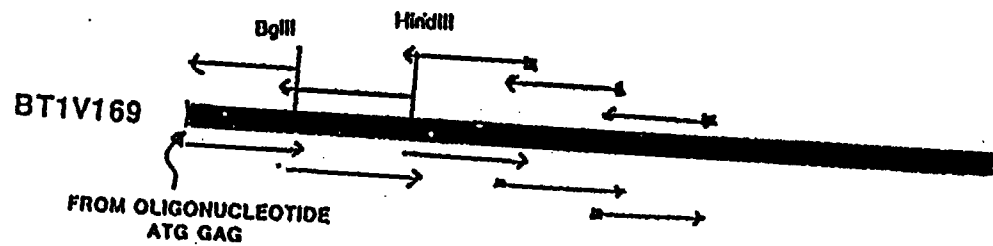


FIGURE 6

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Figure 7

10	20	30	40	50
ATG GAG AGC AAG GTG CTG CTG GCC GTC GCC CTG TGG CTC TGC GTG GAG ACC CGG				
Met Glu Ser Lys Val Leu Leu Ala Val Ala Leu Trp Leu (Cys) Val Glu Thr Arg>				
60	70	80	90	100
GCC GCC TCT GTG GGT TTG CCT AGT GTT TCT CTT GAT CTG CCC AGG CTC AGC ATA				
Ala Ala Ser Val Gly Leu Pro Ser Val Ser Leu Asp Leu Pro Arg Leu Ser Ile>				
110	120	130	140	150
CAA AAA GAC ATA CTT ACA ATT AAG GCT AAT ACA ACT CTT CAA ATT ACT TGC AGG				
Gln Lys Asp Ile Leu Thr Ile Lys Ala Asn Thr Thr Leu Gln Ile Thr (Cys) Arg>				
170	180	190	200	210
GGA CAG AGG GAC TTG GAC TGG CTT TGG CCC AAT AAT CAG AGT GGC AGT GAG CAA				
Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro Asn Asn Gln Ser Gly Ser Glu Gln>				
220	230	240	250	260
AGG GTG GAG GTG ACT GAG TGC AGC GAT GGC CTC TTC TGT AAG ACA CTC ACA ATT				
Arg Val Glu Val Thr Glu (Cys) Ser Asp Gly Leu Phe (Cys) Lys Thr Leu Thr Ile>				
280	290	300	310	320
CCA AAA GTG ATC GGA AAT GAC ACT GGA GCC TAC AAG TGC TTC TAC CGG GAA ACT				
Pro Lys Val Ile Gly Asn Asp Thr Gly Ala Tyr Lys (Cys) Phe Tyr Arg Glu Thr>				
330	340	350	360	370
GAC TTG GCC TCG GTC ATT TAT GTC TAT GTT CAA GAT TAC AGA TCT CCA TTT ATT				
Asp Leu Ala Ser Val Ile Tyr Val Tyr Val Gln Asp Tyr Arg Ser Pro Phe Ile>				
380	390	400	410	420
GCT TCT GTT AGT GAC CAA CAT GGA GTC GTG TAC ATT ACT GAG AAC AAA AAC AAA				
Ala Ser Val Ser Asp Gln His Gly Val Val Tyr Ile Thr Glu Asn Lys Asn Lys>				
440	450	460	470	480
ACT GTG GTG ATT CCA TGT CTC GGG TCC AAT TCA AAT CTC AAC GTG TCA CTT TGT				
Thr Val Val Ile Pro (Cys) Leu Gly Ser Ile Ser Asn Leu Asn Val Ser Leu (Cys)>				
490	500	510	520	530
GCA AGA TAC CCA GAA AAG AGA TTT GTT CCT GAT GGT AAC AGA ATT TCC TGG GAC				
Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg Ile Ser Trp Asp>				
550	560	570	580	590
AGC AAG AAG GGC TTT ACT ATT CCC AGC TAC ATG ATC AGC TAT GCT GGC ATG GTC				
Ser Lys Lys Gly Phe Thr Ile Pro Ser Tyr Met Ile Ser Tyr Ala Gly Met Val>				
600	610	620	630	640
TTC TGT GAA GCA AAA ATT AAT GAT GAA AGT TAC CAG TCT ATT ATG TAC ATA GTT				
Phe (Cys) Glu Ala Lys Ile Asn Asp Glu Ser Tyr Gln Ser Ile Met Tyr Ile Val>				

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Figure 7 (Page 2)

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650      660      670      680      690      700
*      *      *      *      *      *
GTC GTT GTA GGG TAT AGG ATT TAT GAT GTG GTT CTG AGT CCG TCT CAT GGA ATT
Val Val Val Gly Tyr Arg Ile Tyr Asp Val Val Leu Ser Pro Ser His Gly Ile>

      710      720      730      740      750
*      *      *      *      *
GAA CTA TCT GTT GGA GAA AAG CTT GTC TTA AAT TGT ACA GCA AGA ACT GAA CTA
Glu Leu Ser Val Gly Glu Lys Leu Val Leu Asn (Cys) Thr Ala Arg Thr Glu Leu>

      760      770      780      790      800      810
*      *      *      *      *      *
AAT GTG GGG ATT GAC TTC AAC TGG GAA TAC CCT TCT TCG AAG CAT CAG CAT AAG
Asn Val Gly Ile Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys>

      820      830      840      850      860
*      *      *      *      *
AAA CTT GTA AAC CGA GAC CTA AAA ACC CAG TCT GGG AGT GAG ATG AAG AAA TTT
Lys Leu Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe>

      870      880      890      900      910
*      *      *      *      *
TTG AGC ACC TTA ACT ATA GAT GGT GTA ACC CGG AGT GAC CAA GGA TTG TAC ACC
Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu Tyr Thr>

920      930      940      950      960      970
*      *      *      *      *      *
TGT GCA GCA TCC AGT GGG CTG ATG ACC AAG AAG AAC AGC ACA TTT GTC AGG GTC
(Cys) Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr Phe Val Arg Val>

      980      990      1000      1010      1020
*      *      *      *      *
CAT GAA AAA CCT TTT GTT GCT TTT GGA AGT GGC ATG GAA TCT CTG GTG GAA GCC
His Glu Lys Pro Phe Val Ala Phe Gly Ser Gly Met Glu Ser Leu Val Glu Ala>

      1030      1040      1050      1060      1070      1080
*      *      *      *      *      *
ACG GTG GGG GAG CGT GTC AGA ATC CCT GCG AAG TAC CTT GGT TAC CCA CCC CCA
Thr Val Gly Glu Arg Val Arg Ile Pro Ala Lys Tyr Leu Gly Tyr Pro Pro Pro>

      1090      1100      1110      1120      1130
*      *      *      *      *
GAA ATA AAA TGG TAT AAA AAT GGA ATA CCC CTT GAG TCC AAT CAC ACA ATT AAA
Glu Ile Lys Trp Tyr Lys Asn Gly Ile Pro Leu Glu Ser Asn His Thr Ile Lys>

      1140      1150      1160      1170      1180
*      *      *      *      *
GCG GGG CAT GTA CTG ACG ATT ATG GAA GTG AGT GAA AGA GAC ACA GGA AAT TAC
Ala Gly His Val Leu Thr Ile Met Glu Val Ser Glu Arg Asp Thr Gly Asn Tyr>

1190      1200      1210      1220      1230      1240
*      *      *      *      *      *
ACT GTC ATC CTT ACC AAT CCC ATT TCA AAG GAG AAG CAG AGC CAT GTG GTC TCT
Thr Val Ile Leu Thr Asn Pro Ile Ser Lys Glu Lys Gln Ser His Val Val Ser>

      1250      1260      1270      1280      1290
*      *      *      *      *
CTG GTT GTG TAT GTC CCA CCC CAG ATT GGT GAG AAA TCT CTA ATC TCT CCT GTG
Leu Val Val Tyr Val Pro Pro Gln Ile Gly Glu Lys Ser Leu Ile Ser Pro Val>

      1300      1310      1320      1330      1340      1350
*      *      *      *      *      *

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Figure 7 (page 3)

GAT TCC TAC CAG TAC GGC ACC ACT CAA ACG CTG ACA TGT ACG GTC TAT GCC ATT
 Asp Ser Tyr Gln Tyr Gly Thr Thr Gln Thr Leu Thr (Cys) Thr Val Tyr Ala Ile>

1360 1370 1380 1390 1400
 * * * * *
 CCT CCC CCG CAT CAC ATC CAC TGG TAT TGG CAG TTG GAG GAA GAG TGC GCC AAC
 Pro Pro Pro His His Ile His Trp Tyr Trp Gln Leu Glu Glu (Cys) Ala Asn>

1410 1420 1430 1440 1450
 * * * * *
 GAG CCC AGC CAA GCT GTC TCA GTG ACA AAC CCA TAC CCT TGT GAA GAA TGG AGA
 Glu Pro Ser Gln Ala Val Ser Val Thr Asn Pro Tyr Pro (Cys) Glu Glu Trp Arg>

1460 1470 1480 1490 1500 1510
 * * * * *
 AGT GTG GAG GAC TTC CAG GGA GGA AAT AAA ATT GAA GTT AAT AAA AAT CAA TTT
 Ser Val Glu Asp Phe Gln Gly Gly Asn Lys Ile Glu Val Asn Lys Asn Gln Phe>

1520 1530 1540 1550 1560
 * * * * *
 GCT CTA ATT GAA GGA AAA AAC AAA ACT GTA AGT ACC CTT GTT ATC CAA GCG GCA
 Ala Leu Ile Glu Gly Lys Asn Lys Thr Val Ser Thr Leu Val Ile Gln Ala Ala>

1570 1580 1590 1600 1610 1620
 * * * * *
 AAT GTG TCA GCT TTG TAC AAA TGT GAA GCG GTC AAC AAA GTC GGG AGA GGA GAG
 Asn Val Ser Ala Leu Tyr Lys (Cys) Glu Ala Val Asn Lys Val Gly Arg Gly Glu>

1630 1640 1650 1660 1670
 * * * * *
 AGG GTG ATC TCC TTC CAC GTG ACC AGG GGT CCT GAA ATT ACT TTG CAA CCT GAC
 Arg Val Ile Ser Phe His Val Thr Arg Gly Pro Glu Ile Thr Leu Gln Pro Asp>

1680 1690 1700 1710 1720
 * * * * *
 ATG CAG CCC ACT GAG CAG GAG AGC GTG TCT TTG TGG TGC ACT GCA GAC AGA TCT
 Met Gln Pro Thr Glu Gln Glu Ser Val Ser Leu Trp (Cys) Thr Ala Asp Arg Ser>

1730 1740 1750 1760 1770 1780
 * * * * *
 ACG TTT GAG AAC CTC ACA TGG TAC AAG CTT GGC CCA CAG CCT CTG CCA ATC CAT
 Thr Phe Glu Asn Leu Thr Trp Tyr Lys Leu Gly Pro Gln Pro Leu Pro Ile His>

1790 1800 1810 1820 1830
 * * * * *
 GTG GGA GAG TTG CCC ACA CCT GTT TGC AAG AAC TTG GAT ACT CTT TGG AAA TTG
 Val Gly Glu Leu Pro Thr Pro Val (Cys) Lys Asn Leu Asp Thr Leu Trp Lys Leu>

1840 1850 1860 1870 1880 1890
 * * * * *
 AAT GCC ACC ATG TTC TCT AAT AGC ACA AAT GAC ATT TTG ATC ATG GAG CTT AAG
 Asn Ala Thr Met Phe Ser Asn Ser Thr Asn Asp Ile Leu Ile Met Glu Leu Lys>

1900 1910 1920 1930 1940
 * * * * *
 AAT GCA TCC TTG CAG GAC CAA GGA GAC TAT GTC TGC CTT GCT CAA GAC AGG AAG
 Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr Val Cys Leu Ala Gln Asp Arg Lys>

1950 1960 1970 1980 1990
 * * * * *
 ACC AAG AAA AGA CAT TGC GTG GTC AGG CAG CTC ACA GTC CTA GAG CGT GTG GCA
 Thr Lys Lys Arg His (Cys) Val Val Arg Gln Leu Thr Val Leu Glu Arg Val Ala>

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Figure 7 (page 4)

2000 2010 2020 2030 2040 2050
 * * * * * *
 CCC ACC ATC ACA GGA AAC CTG GAG AAT CAG ACG ACA AGT ATT GGG GAA AGC ATC
 Pro Thr Ile Thr Gly Asn Leu Glu Asn Gln Thr Thr Ser Ile Gly Glu Ser Ile>

 2060 2070 2080 2090 2100
 * * * * *
 GAA GTC TCA TGC ACG GCA TCT GGG AAT CCC CCT CCA CAG ATC ATG TGG TTT AAA
 Glu Val Ser (Cys) Thr Ala Ser Gly Asn Pro Pro Pro Gln Ile Met Trp Phe Lys>

 2110 2120 2130 2140 2150 2160
 * * * * * *
 GAT AAT GAG ACC CTT GTA GAA GAC TCA GGC ATT GTA TTG AAG GAT GGG AAC CGG
 Asp Asn Glu Thr Leu Val Glu Asp Ser Gly Ile Val Leu Lys Asp Gly Asn Arg>

 * 2170 2180 2190 2200 2210
 * * * * * *
 AAC CTC ACT ATC CGC AGA GTG AGG AAG GAG GAC GAA GGC CTC TAC ACC TGC CAG
 Asn Leu Thr Ile Arg Arg Val Arg Lys Glu Asp Glu Gly Leu Tyr Thr (Cys) Gln>

 2220 2230 2240 2250 2260
 * * * * *
 GCA TGC AGT GTT CTT GGC TGT GCA AAA GTG GAG GCA TTT TTC ATA ATA GAA GGT
 Ala (Cys) Ser Val Leu Gly (Cys) Ala Lys Val Glu Ala Phe Phe Ile Ile Glu Gly>

 2270 2280 2290 2300 2310 2320
 * * * * * *
 GCC CAG GAA AAG ACG AAC TTG GAA ATC ATT ATT CTA GTA GGC ACG ACG GTG ATT
 Ala Gln Glu Lys Thr Asn Leu Glu Ile Ile Ile Leu Val Gly Thr Thr Val Ile>

 2330 2340 2350 2360 2370
 * * * * *
 GCC ATG TTC TTC TGG CTA CTT CTT GTC ATC ATC CTA GGG ACC GTT AAG CGG GCC
 Ala Met Phe Phe Trp Leu Leu Leu Val Ile Ile Leu Gly Thr Val Lys Arg Ala>

 2380 2390 2400 2410 2420 2430
 * * * * * *
 AAT GGA GGG GAA CTG AAG ACA GGC TAC TTG TCC ATC GTC ATG GAT CCA GAT GAA
 Asn Gly Gly Glu Leu Lys Thr Gly Tyr Leu Ser Ile Val Met Asp Pro Asp Glu>

 2440 2450 2460 2470 2480
 * * * * *
 CTC CCA TTG GAT GAA CAT TGT GAA CGA CTG CCT TAT GAT GCC AGC AAA TGG GAA
 Leu Pro Leu Asp Glu His Cys Glu Arg Leu Pro Tyr Asp Ala Ser Lys Trp Glu>

 2490 2500 2510 2520 2530
 * * * * *
 TTC CCC AGA GAC CGG CTG AAC CTA GGT AAG CCT CTT GGC CGT GGT GCC TTT GGC
 Phe Pro Arg Asp Arg Leu Asn Leu Gly Lys Pro Leu Gly Arg Gly Ala Phe Gly>

 2540 2550 2560 2570 2580 2590
 * * * * * *
 CAA GAG ATT GAA GCA GAT GCC TTT GGA ATT GAC AAG ACA GCA ACT TGC AGG ACA
 Gln Glu Ile Glu Ala Asp Ala Phe Gly Ile Asp Lys Thr Ala Thr Cys Arg Thr>

 2600 2610 2620 2630 2640
 * * * * *
 GTA GCA GTC AAA ATG TTG AAA GAA GGA GCA ACA CAC AGT GAG CAT CGA GCT CTC
 Val Ala Val Lys Met Leu Lys Glu Gly Ala Thr His Ser Glu His Arg Ala Leu>

 2650 2660 2670 2680 2690 2700

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Figure 7 (page 5)

* * * * *
 ATG TCT GAA CTC AAG ATC CTC ATT CAT ATT GGT CAC CAT CTC AAT GTG GTC AAC
 Met Ser Glu Leu Lys Ile Leu Ile His Ile Gly His His Leu Asn Val Val Asn>
 2710 2720 2730 2740 2750
 * * * * *
 CTT CTA GGT GCC TGT ACC AAG CCA GGA GGG CCA CTC ATG GTG ATT GTG GAA TTC
 Leu Leu Gly Ala Cys Thr Lys Pro Gly Gly Pro Leu Met Val Ile Val Glu Phe>
 2760 2770 2780 2790 2800
 * * * * *
 TGC AAA TTT GGA AAC CTG TCC ACT TAC CTG AGG AGC AAG AGA AAT GAA TTT GTC
 Cys Lys Phe Gly Asn Leu Ser Thr Tyr Leu Arg Ser Lys Arg Asn Glu Phe Val>
 2810 2820 2830 2840 2850 2860
 * * * * *
 CCC TAC AAG ACC AAA GGG GCA CGA TTC CGT CAA GGG AAA GAC TAC GTT GGA GCA
 Pro Tyr Lys Thr Lys Gly Ala Arg Phe Arg Gln Gly Lys Asp Tyr Val Gly Ala>
 2870 2880 2890 2900 2910
 * * * * *
 ATC CCT GTG GAT CTG AAA CGG CGC TTG GAC AGC ATC ACC AGT AGC CAG AGC TCA
 Ile Pro Val Asp Leu Lys Arg Arg Leu Asp Ser Ile Thr Ser Ser Gln Ser Ser>
 2920 2930 2940 2950 2960 2970
 * * * * *
 GCC AGC TCT GGA TTT GTG GAG GAG AAG TCC CTC AGT GAT GTA GAA GAA GAG GAA
 Ala Ser Ser Gly Phe Val Glu Glu Lys Ser Leu Ser Asp Val Glu Glu Glu Glu>
 2980 2990 3000 3010 3020
 * * * * *
 GCT CCT GAA GAT CTG TAT AAG GAC TTC CTG ACC TTG GAG CAT CTC ATC TGT TAC
 Ala Pro Glu Asp Leu Tyr Lys Asp Phe Leu Thr Leu Glu His Leu Ile Cys Tyr>
 3030 3040 3050 3060 3070
 * * * * *
 AGC TTC CAA GTG GCT AAG GGC ATG GAG TTC TTG GCA TCG CGA AAG TGT ATC CAC
 Ser Phe Gln Val Ala Lys Gly Met Glu Phe Leu Ala Ser Arg Lys Cys Ile His>
 3080 3090 3100 3110 3120 3130
 * * * * *
 AGG GAC CTG GCG GCA CGA AAT ATC CTC TTA TCG GAG AAG AAC GTG GTT AAA ATC
 Arg Asp Leu Ala Ala Arg Asn Ile Leu Leu Ser Glu Lys Asn Val Val Lys Ile>
 3140 3150 3160 3170 3180
 * * * * *
 TGT GAC TTT GGC TTG GCC CGG GAT ATT TAT AAA GAT CCA GAT TAT GTC AGA AAA
 Cys Asp Phe Gly Leu Ala Arg Asp Ile Tyr Lys Asp Pro Asp Tyr Val Arg Lys>
 3190 3200 3210 3220 3230 3240
 * * * * *
 GGA GAT GCT CGC CTC CCT TTG AAA TGG ATG GCC CCA GAA ACA ATT TTT GAC AGA
 Gly Asp Ala Arg Leu Pro Leu Lys Trp Met Ala Pro Glu Thr Ile Phe Asp Arg>
 3250 3260 3270 3280 3290
 * * * * *
 GTG TAC ACA ATC CAG AGT GAC GTC TGG TCT TTT GGT GTT TTG CTG TGG GAA ATA
 Val Tyr Thr Ile Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile>
 3300 3310 3320 3330 3340
 * * * * *
 TTT TCC TTA GGT GCT TCT CCA TAT CCT GGG GTA AAG ATT GAT GAA GAA TTT TGT

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Figure 7 (page 6)

Phe Ser Leu Gly Ala Ser Pro Tyr Pro Gly Val Lys Ile Asp Glu Glu Phe Cys>

3350 3360 3370 3380 3390 3400
* * * * * *
AGG CGA TTG AAA GAA GGA ACT AGA ATG AGG GCC CCT GAT TAT ACT ACA CCA GAA
Arg Arg Leu Lys Glu Gly Thr Arg Met Arg Ala Pro Asp Tyr Thr Thr Pro Glu>

3410 3420 3430 3440 3450
* * * * *
ATG TAC CAG ACC ATG CTG GAC TGC TGG CAC GGG GAG CCC AGT CAG AGA CCC ACG
Met Tyr Gln Thr Met Leu Asp Cys Trp His Gly Glu Pro Ser Gln Arg Pro Thr>

3460 3470 3480 3490 3500 3510
* * * * * *
TTT TCA GAG TTG GTG GAA CAT TTG GGA AAT CTC TTG CAA GCT AAT GCT CAG CAG
Phe Ser Glu Leu Val Glu His Leu Gly Asn Leu Leu Gln Ala Asn Ala Gln Gln>

3520 3530 3540 3550 3560
* * * * *
GAT GGC AAA GAC TAC ATT GTT CTT CCG ATA TCA GAG ACT TTG AGC ATG GAA GAG
Asp Gly Lys Asp Tyr Ile Val Leu Pro Ile Ser Glu Thr Leu Ser Met Glu Glu>

3570 3580 3590 3600 3610
* * * * *
GAT TCT GGA CTC TCT CTG CCT ACC TCA CCT GTT TCC TGT ATG GAG GAG GAG GAA
Asp Ser Gly Leu Ser Leu Pro Thr Ser Pro Val Ser Cys Met Glu Glu Glu Glu>

3620 3630 3640 3650 3660 3670
* * * * * *
GTA TGT GAC CCC AAA TTC CAT TAT GAC AAC ACA GCA GGA ATC AGT CAG TAT CTG
Val Cys Asp Pro Lys Phe His Tyr Asp Asn Thr Ala Gly Ile Ser Gln Tyr Leu>

3680 3690 3700 3710 3720
* * * * *
CAG AAC AGT AAG CGA AAG AGC CGG CCT GTG AGT GTA AAA ACA TTT GAA GAT ATC
Gln Asn Ser Lys Arg Lys Ser Arg Pro Val Ser Val Lys Thr Phe Glu Asp Ile>

3730 3740 3750 3760 3770 3780
* * * * * *
CCG TTA GAA GAA CCA GAA GTA AAA GTA ATC CCA GAT GAC AAC CAG ACG GAC AGT
Pro Leu Glu Glu Pro Glu Val Lys Val Ile Pro Asp Asp Asn Gln Thr Asp Ser>

3790 3800 3810 3820 3830
* * * * *
GGT ATG GTT CTT GCC TCA GAA GAG CTG AAA ACT TTG GAA GAC AGA ACC AAA TTA
Gly Met Val Leu Ala Ser Glu Glu Leu Lys Thr Leu Glu Asp Arg Thr Lys Leu>

3840 3850 3860 3870 3880
* * * * *
TCT CCA TCT TTT GGT GGA ATG GTG CCC AGC AAA AGC AGG GAG TCT GTG GCA TCT
Ser Pro Ser Phe Gly Gly Met Val Pro Ser Lys Ser Arg Glu Ser Val Ala Ser>

3890 3900 3910 3920 3930 3940
* * * * * *
GAA GGC TCA AAC CAG ACA AGC GGC TAC CAG TCC GGA TAT CAC TCC GAT GAC ACA
Glu Gly Ser Asn Gln Thr Ser Gly Tyr Gln Ser Gly Tyr His Ser Asp Asp Thr>

3950 3960 3970 3980 3990
* * * * *
GAC ACC ACC GTG TAC TCC AGT GAG GAA GCA GAA CTT TTA AAG CTG ATA GAG ATT
Asp Thr Thr Val Tyr Ser Ser Glu Glu Ala Glu Leu Leu Lys Leu Ile Glu Ile>

Figure 7 (page 7)

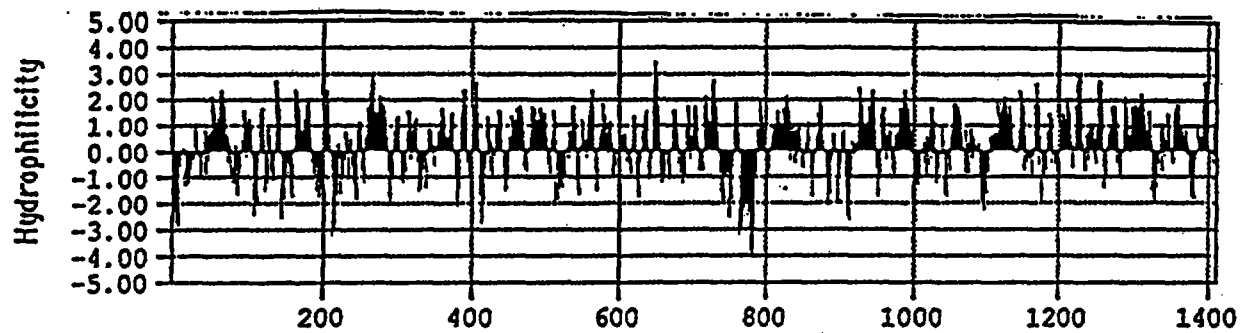
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* * * * * *
GGA GTG CAA ACC GGT AGC ACA GCC CAG ATT CTC CAG CCT GAC ACG GGG ACC ACA
Gly Val Gln Thr Gly Ser Thr Ala Gln Ile Leu Gln Pro Asp Thr Gly Thr Thr>

4060 4070
* *
CTG AGC TCT CCT CCT GTT TAA
Leu Ser Ser Pro Pro Val ***

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FIGURE 8

HYDROPHATHY PLOT OF PREDICTED AMINO ACID SEQUENCE



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FIGURE 9

KDR 787 GTVKRANGGELKTGYLSIVMDPDELPLDEHCERLPYDASKWEFPRDRINI.GK
ckit 543 L***YLOKPMYEVQWKVVEEINGNNYVYIDPTQ***H-*****N**SF**
CSF1 536 LLY*YKQKPKYQVRWKIIESYEGNSYTFIDPTQ***NE-*****NN*QF**
PDGF 522 MLWQKKPRYEIRWKVIESVSSDGHEYIYVDPVQ****-ST*****QLV**R

* * *
KDR 839 PLGRGAFGQEIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILI
ckit 594 T**A****KVVAET*Y*LI*SDAAM*****PS*HLT*RE*****V*S
CSF1 587 T**A****KV**T***LG*EDAVLK*****ST*HAD*KE*****MS
PDGF 573 T**S*****V**T*H*LSHSQATMK*****ST*RSS*KQS*****MS

KDR 891 HIGHHLNVVNLLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKTKG
ckit 646 YL*N*M*I*****I-****TL**T*Y*CY*D*LNF**R**DS*ICS*QED
CSF1 639 *L*Q*E*I*****H-****VL**T*Y*CY*D*LNF**R*AEAMLGPSLS
PDGF 625 *L*P*****I*****IYI*T*Y*RY*D*VD**HRNKHT*LQRHSNK

KDR 943 ARFRQGDYVGAIPVDLKRRLDSIT-SSQSSASSGFVEEKSL-----SDV
ckit 697 HAEA-A-L*KNLLHSKESSCS-DS*N-E----YMDMKPGVS--YVVPT--KA
CSF1 690 GQDPE*GVDYKN*HLEK*YVRDSGF***GVDYVEMRPVSTSS-NDSE*EQ
PDGF 676 HCPPSAEL*SN*LP*GFSLPSHLNLTGESDGGYMDMSKDESIDYVPMLOMKG

KDR 987 EEEEAPEDLYKDF-----LTLEHLICYSFQV
ckit 737 D-KRRSVRIGSYI-----ERDVTPAIMEDELA*D**D*LSF*Y**
CSF1 741 DLDKEDGRPL-----E*RD*LHF*S**
PDGF 728 DIKY*DIESPSYMAPYDNYVPSAPERTYRATLINDSPV-*SYTD*VGF*Y**

KDR 1013 AKGMEFLASRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGD
ckit 777 -***A*****N*****THGRIT*****KN*SN**V**N
CSF1 762 *Q**A*****N*****V**TNGHVA**G*****MN*SN*IV**N
PDGF 779 *N**D*****N*****V*ICEGKL*****MR*SN*IS**S

KDR 1065 ARLPLKWMAPETIFDRVYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEFEFC
ckit 828 *****V*****S**NC***EE*****Y*IF*****S*****MPVKSK*Y
CSF1 814 *****V*****S***C***VQ*****Y*I*****LN*****ILVNSK*Y
PDGF 831 *****S**NS***TL*****I*****GT***ELPMNDQ*Y

KDR 1117 RRLKEGTRMRAPDYTTPEMYQTMLDCHWGEPSQRPTFSELVEHLGNLLQANA
ckit 880 KMI***F**LS*EHAPA***DI*KT**DAD*LK****KQIVQLIEKQISEST
CSF1 862 KLV*D*YQ*AQ*AFAPKNI*SI*QA**AL*TH****QQICSF*QEQAQEDR
PDGF 883 NAI*R*Y**AQ*AHASD*I*EI*QK**EEKFET**P**Q**LL*ER**GEGY

KDR 1169 QQDGKDYIVLP ISETLSMEEDSGLSLPTSPVSCMEEEVCDPKFHYDNTAGI
ckit 932 NHIYSNLANCSPNRQKPVVDHSVRINSVGSTASSSQPLLVDHDDV
CSF1 914 RERDYTNLPSSSRSGG*GSSS*E*EESSSEHLTCC*QGDIAQPLLQPNNYQ
PDGF 934 KKKYQQVDEEFLLRSDHPAILR*QARF*GIHSLRSPLODTSSVLYTAVQPNESD

KDR 1213 SQYLQNSKRKSRPVSVKTFEDIPLLEEPEVKVIPDDNQTDSGMVLASEELKTL
CSF1 966 FC
PDGF 987 ND*I IPLPDPKPD*ADEGLPEGSPSLASSTLNEVNTSSTISCDSP*LQEEP

KDR 1273 EDRTKLSPSFSGGMVPSKSRRESVASEGSNQTSGYQSGYHSDDTDTTVYSSEEA
PDGF1039 QQAPEPAQLEQPQDSGCPGLAEA*DSFLEQPQD**CPGFLAEAE DSFL

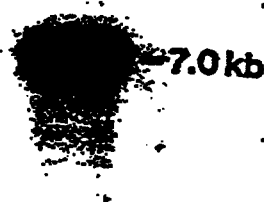
KDR 1325 ELLKLIEIGVQTGSTAQILQPDGTGTTLSSPPV

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FIGURE 10

IDENTIFICATION OF *kdp* mRNA

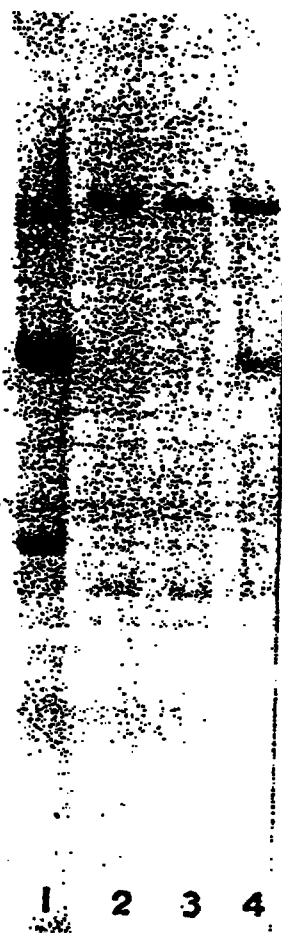


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FIGURE 11

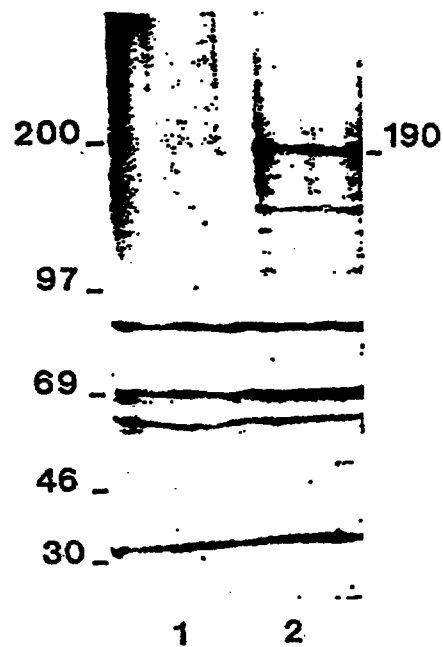
**IDENTIFICATION OF *kdp* GENE
BY SOUTHERN ANALYSIS**



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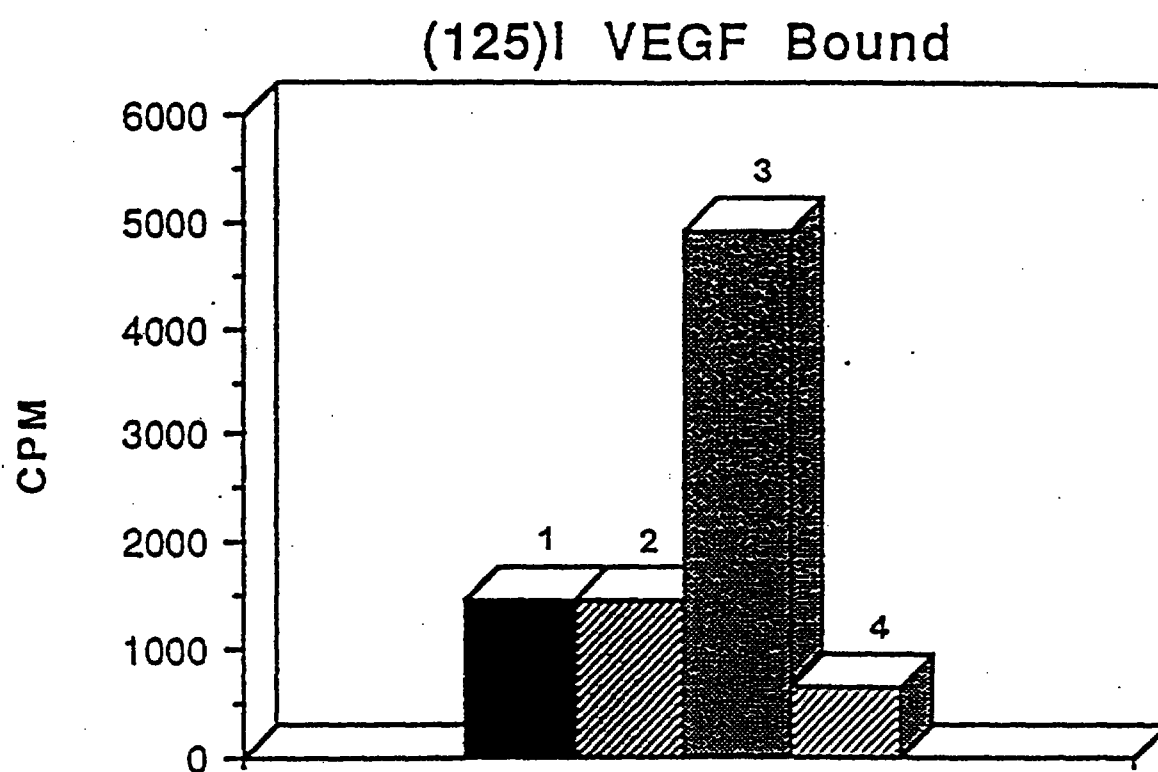
FIGURE 12



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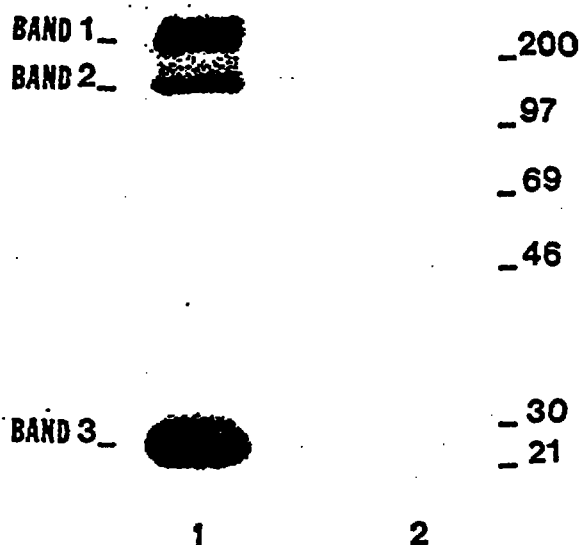
FIGURE 13



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FIGURE 14



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REPLACEMENT SHEET

21 AUG 1998

- 3a -

In accordance with a first aspect of the present invention, there is provided a recombinant human DNA sequence encoding a Kinase insert Domain containing Receptor, said DNA comprising the nucleotide sequence of SEQ ID NO:7.

In accordance with a second aspect of the present invention, there is provided a lambda gt11 phage harboring the clone BTIII081.8 deposited under ATCC accession number 40,931 or the clone BTIII129.5 deposited under ATCC Accession number 40,975.

In accordance with a third aspect of the present invention, there is provided a plasmid which contains the clone BTIV169 deposited under ATCC accession number 75200.

In accordance with a fourth aspect of the present invention, there is provided a recombinant human Kinase insert Domain containing Receptor comprising the amino acid sequence of SEQ ID NO: 8.

In accordance with a fifth aspect of the present invention, there is provided an oligonucleotide primer consisting of 27 bases and having the sequence of SEQ ID NO:1.

In accordance with a sixth aspect of the present invention, there is provided an oligonucleotide primer consisting of 35 bases and having the sequence of SEQ ID NO:2.

In accordance with a seventh aspect of the present invention, there is provided a 363 base pair nucleic acid having the sequence of SEQ ID NO:3.

This Sheet Has Been Replaced



THIS SHEET HAS BEEN
REPLACED

REPLACEMENT SHEET

21 AUG 1998

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In accordance with an eighth aspect of the present invention, there is provided an expression vector comprising the nucleotide sequence of SEQ ID NO:7, wherein the expression vector is capable of expressing a Kinase insert Domain containing Receptor having the amino acid sequence of SEQ ID NO:8 in a transformed host cell.

In accordance with a ninth aspect of the present invention, there is provided a screening method to identify compounds that inhibit the action of vascular endothelial cell growth factor (VEGF) on a human Kinase insert Domain containing Receptor (KDR) encoded by a nucleic acid sequence comprising SEQ ID NO:7, comprising the steps of.

- (a) incubating cells which have been transformed or transfected to express the KDR with [125 I]VEGF and a compound;
- (b) measuring the emitted radioactivity to determine the amount of inhibition of binding of VEGF to the KDR by the compound.

In accordance with a tenth aspect of the present invention, there is provided a method for the expression of a human Kinase insert Domain containing Receptor (KDR) which comprises transforming a host cell with an expression vector comprising a recombinant human DNA sequence encoding the human KDR and culturing the transformed host cell under conditions which result in expression of the human KDR by the expression vector.

In accordance with an eleventh aspect of the present invention, there is provided a recombinant human KDR comprising an endothelial cell receptor tyrosine kinase which binds to vascular endothelial cell growth factor and has a single membrane spanning region.

In accordance with a twelfth aspect of the present invention, there is provided a recombinant human DNA sequence encoding a human Kinase insert Domain containing Receptor (KDR), wherein the KDR is an endothelial cell receptor tyrosine kinase which binds to vascular endothelial cell growth factor and has a single membrane spanning region.

This Sheet Has Been Replaced



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REPLACEMENT SHEET

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NO. 7). A sample of a lambda gt11 phage harboring the clone BTIII081.8 has been deposited on 4 December 1990 with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, Maryland 20852, U.S.A., and has been assigned ATCC accession number 40,931. A sample of a lambda gt11 phage harboring the clone BTIII129.5 has been deposited on 13 February 1991 with the American Type Culture Collection and has been assigned ATCC accession number 40,975. For reasons discussed below, a sample of the clone BTIV006 was not deposited.

The aforementioned DNA segments (BTIII081.8, BTIII129.5, and BTIII200.2 (or BTIV006) encode 4062 nucleotides of the coding portion of a novel gene. The cDNA clones are incomplete in that a transcription initiation coding for methionine is missing. After the isolation of these clones, Matthews et al. (25) reported the cloning of a gene homologue of KDR in mouse, which was referred to as Flk-1. Analysis of the nucleic acid and amino acid sequence of Flk-1 indicated that the addition of six nucleotides to the 5' end of the isolated KDR clones would provide for a complete coding region.

To achieve this, an EcoRI-BamHI restriction fragment of BTIV200.2 is cloned into the plasmid pBlueScript KS (Stratagene, La Jolla, CA). The 5' end of the inserted DNA is blunt ended with Klenow polymerase and Mung Bean nuclease. Next, the synthetic oligonucleotide TCGACGCGCG ATG GAG (SEQ ID NO. 11) is cloned into this vector. The oligonucleotide contains the sequence ATG GAG in frame with the downstream DNA insert. These nucleotides (ATG GAG) encode the amino acids methionine and glutamic acid, the first two amino acids encoded by the KDR gene. The resulting plasmid vector is designated BTIV140. This plasmid is purified on a CsCl gradient.



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The purified plasmid is designated BTIV169. The insert of BTIV169 contains nucleotides 1-2400 (SEQ ID NO. 7) of the KDR gene. A sample of the plasmid pBlueScript KS which contains the clone BTIV169 has been deposited on 7 February 1992 with the American Type Culture Collection and has been assigned ATCC accession number 75200.

Thus, together the clones BTIII081.8, BTIII129.5 and BTIV169 comprise the entire open reading frame of 4,068 nucleotides for the novel KDR gene. As will be discussed below, the KDR gene expresses the novel KDR receptor which binds specifically to the growth factor VEGF.

DNA sequencing of BTIII081.8, BTIII129.5 and BTIV169 (SEQ ID NO. 7) shows that the newly isolated gene is similar to, but distinct from, previously identified type III RTK. The predicted amino acid sequence (SEQ ID NO. 7) contains several structural features which demonstrate that the novel gene is a type III RTK. These structural features are summarized as follows:

1) A hydropathy plot of the predicted amino acid sequence indicates a single membrane spanning region (see Figure 8). This is characteristic of a type III RTK (Figure 7).

2) The putative amino-terminal 762 amino acid portion of the receptor has structural features of extracellular receptor ligand binding domains (1), including regularly spaced cysteines and 18 potential N-linked glycosylation sites (Figure 7).

3) The predicted amino acid sequence of the carboxy-terminal 530 amino acid portion contains an ATP-binding site at lysine 868, 22 amino acids downstream from the consensus ATP recognition sequence Gly-X-Gly-X-X-Gly (26) (Figure 8).

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CLAIMS

1. A recombinant human DNA sequence encoding a Kinase insert Domain containing Receptor, said DNA comprising the nucleotide sequence of SEQ ID NO:7.
2. A lambda gt11 phage harboring the clone BTIII081.8 deposited under ATCC accession number 40,931 or the clone BTIII129.5 deposited under ATCC Accession number 40,975.
3. A plasmid which contains the clone BTIV169 deposited under ATCC accession number 75200.
4. A recombinant human Kinase insert Domain containing Receptor comprising the amino acid sequence of SEQ ID NO:8.
5. A biologically active protein fragment of the recombinant human Kinase insert Domain containing Receptor of claim 4 which binds to vascular endothelial cell growth factor.
6. An oligonucleotide primer consisting of 27 bases and having the sequence of SEQ ID NO: 1.
7. An oligonucleotide primer consisting of 35 bases and having the sequence of SEQ ID NO: 2.
8. A 363 base pair nucleic acid having the sequence of SEQ ID NO: 3.

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9. An expression vector comprising the nucleotide sequence of SEQ ID NO: 7, wherein the expression vector is capable of expressing a Kinase insert Domain containing Receptor having the amino acid sequence of SEQ ID NO:8 in a transformed host cell.

10. A screening method to identify compounds that inhibit the action of vascular endothelial cell growth factor (VEGF) on a human Kinase insert Domain containing Receptor (KDR) encoded by a nucleic acid sequence comprising SEQ ID NO: 7, comprising the steps of:

(a) incubating cells which have been transformed or transfected to express the KDR with [125 I]VEGF and a compound;

(b) measuring the emitted radioactivity to determine the amount of inhibition of binding of VEGF to the KDR by the compound.

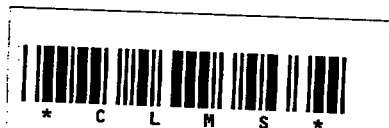
11. A method for the expression of a human Kinase insert Domain containing Receptor (KDR) which comprises transforming a host cell with an expression vector comprising a recombinant human DNA sequence encoding the human KDR and culturing the transformed host cell under conditions which result in expression of the human KDR by the expression vector.

12. The method of claim 11, wherein the expression vector comprises the nucleotide sequence of SEQ ID NO: 7.

13. The method of claim 11, wherein the host cell is a bacteria, virus, yeast, insect or mammalian cell line.

14. The method of claim 13, wherein the host cell is a COS-1 cell, NIH3T3 fibroblast or CMT-3 monkey kidney cell.





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15. A recombinant human KDR comprising an endothelial cell receptor tyrosine kinase which binds to vascular endothelial cell growth factor and has a single membrane spanning region.

16. The recombinant human KDR of claim 15, wherein the recombinant human KDR is encoded by an isolated DNA sequence comprising a DNA sequence which hybridizes under high stringency conditions with a DNA sequence encoding the amino acid sequence of SEQ ID NO: 7.

17. An isolated DNA sequence encoding a biologically active protein fragment of the recombinant human KDR of claim 15 which retains the receptor activity of the recombinant human KDR of Claim 15.

18. A recombinant human DNA sequence encoding a human Kinase insert Domain containing Receptor (KDR), wherein the KDR is an endothelial cell receptor tyrosine kinase which binds to vascular endothelial cell growth factor and has a single membrane spanning region.

19. An expression vector comprising the recombinant human DNA sequence of claim 18, wherein the expression vector is capable of expressing a human KDR in a transformed host cell.

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In accordance with an eighth aspect of the present invention, there is provided an expression vector comprising the nucleotide sequence of SEQ ID NO:7, wherein the expression vector is capable of expressing a Kinase insert Domain containing Receptor having the amino acid sequence of SEQ ID NO:8 in a transformed host cell.

In accordance with a ninth aspect of the present invention, there is provided a screening method to identify compounds that inhibit the action of vascular endothelial cell growth factor (VEGF) on a human Kinase insert Domain containing Receptor (KDR) encoded by a nucleic acid sequence comprising SEQ ID NO:7, comprising the steps of.

- (a) incubating cells which have been transformed or transfected to express the KDR with [125 I]VEGF and a compound;
- (b) measuring the emitted radioactivity to determine the amount of inhibition of binding of VEGF to the KDR by the compound.

In accordance with a tenth aspect of the present invention, there is provided a method for the expression of a human Kinase insert Domain containing Receptor (KDR) which comprises transforming a host cell with an expression vector comprising a recombinant human DNA sequence encoding the human KDR in accordance with the eleventh aspect of the invention and culturing the transformed host cell under conditions which result in expression of the human KDR by the expression vector.

In accordance with an eleventh aspect of the present invention, there is provided a recombinant human KDR comprising an endothelial cell receptor tyrosine kinase which binds to vascular endothelial cell growth factor and has a single membrane spanning region.

In accordance with a twelfth aspect of the present invention, there is provided a recombinant human DNA sequence encoding a human Kinase insert Domain containing Receptor (KDR), wherein the KDR is an endothelial cell receptor tyrosine kinase which binds to vascular endothelial cell growth factor and has a single membrane spanning region.



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9. An expression vector comprising the nucleotide sequence of SEQ ID NO: 7, wherein the expression vector is capable of expressing a Kinase insert Domain containing Receptor having the amino acid sequence of SEQ ID NO:8 in a transformed host cell.
10. A screening method to identify compounds that inhibit the action of vascular endothelial cell growth factor (VEGF) on a human Kinase insert Domain containing Receptor (KDR) encoded by a nucleic acid sequence comprising SEQ ID NO: 7, comprising the steps of:
- (a) incubating cells which have been transformed or transfected to express the KDR with [125 I]VEGF and a compound;
 - (b) measuring the emitted radioactivity to determine the amount of inhibition of binding of VEGF to the KDR by the compound.
11. A method for the expression of a human Kinase insert Domain containing Receptor (KDR) which comprises transforming a host cell with an expression vector comprising a recombinant human DNA sequence encoding the human KDR of claim 15 and culturing the transformed host cell under conditions which result in expression of the human KDR by the expression vector.
12. The method of claim 11, wherein the expression vector comprises the nucleotide sequence of SEQ ID NO: 7.
13. The method of claim 11, wherein the host cell is a bacteria, virus, yeast, insect or mammalian cell line.
14. The method of claim 13, wherein the host cell is a COS-1 cell, NIH3T3 fibroblast or CMT-3 monkey kidney cell.