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(57) **Abrégé/Abstract:**

DNA encoding a parathyroid hormone receptor; production and isolation of recombinant and synthetic parathyroid hormone receptor polypeptides and fragments; antibodies to parathyroid hormone receptors and receptor fragments; methods for screening candidate compounds for antagonistic or agonistic effects on parathyroid hormone receptor action ; and diagnostic and therapeutic methods of these compounds are disclosed.



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(54) Title: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME			
(57) Abstract DNA encoding a parathyroid hormone receptor; production and isolation of recombinant and synthetic parathyroid hormone receptor polypeptides and fragments; antibodies to parathyroid hormone receptors and receptor fragments; methods for screening candidate compounds for antagonistic or agonistic effects on parathyroid hormone receptor action; and diagnostic and therapeutic methods of these compounds are disclosed.			

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PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME

Background of the Invention

Partial funding of the work described herein was
5 provided by the U.S. Government, which has certain rights
to the invention.

The invention relates to endocrine receptors.

A crucial step in the expression of hormonal
action is the interaction of hormones with receptors on
10 the plasma membrane surface of target cells. The
formation of hormone-receptor complexes allows the
transduction of extracellular signals into the cell to
elicit a variety of biological responses. For example,
binding of a hormone such as follicle stimulating hormone
15 (FSH), luteinizing hormone (LH), thyroid stimulating
hormone (TSH), and chorionic gonadotropin (CG), to its
cell surface receptor induces a conformational change in
the receptor, resulting in the association of the
receptor with a transductor molecule, the stimulatory
20 guanine nucleotide (GTP) binding protein, a component of
which is (G_s). This association stimulates adenylate
cyclase activity which in turn triggers other cellular
processes such as protein phosphorylation, steroid
synthesis and secretion, and the modulation of ion flux.
25 Binding of other hormones, including arginine vasopressin
(VP), angiotensin II, and norepinephrine, to their cell
surface receptors results in the activation of other
types of GTP binding proteins components such as (G_p),
which in turn stimulates the activity of the enzyme
30 phospholipase C. The products of phospholipase C
hydrolysis initiate a complex cascade of cellular events,
including the mobilization of intracellular calcium and
protein phosphorylation.

Parathyroid hormone (PTH) is a major regulator of
35 calcium homeostasis whose principal target cells occur in

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bone and kidney. Regulation of calcium concentration is necessary for the normal function of the gastrointestinal, skeletal, neurologic, neuromuscular, and cardiovascular systems. PTH synthesis and release are controlled principally by the serum calcium level: a low level stimulates and a high level suppresses both the hormone synthesis and release. PTH, in turn, maintains the serum calcium level by directly or indirectly promoting calcium entry into the blood at three sites of calcium exchange: gut, bone and kidney. PTH contributes to net gastrointestinal absorption of calcium by favoring the renal synthesis of the active form of vitamin D. PTH promotes calcium resorption from bone by inhibiting osteoblasts and, indirectly, by stimulating differentiation of the bone-resorbing cells, osteoclasts. It also mediates at least three main effects on the kidney: stimulation of tubular calcium reabsorption, enhancement of phosphate clearance, and promotion of an increase in the enzyme that completes synthesis of the active form of vitamin D. PTH exerts these effects primarily through receptor-mediated activation of adenylate cyclase, although receptor-mediated activation of phospholipase C by PTH has also been reported (Hruska et al., J. Clin. Invest. 79:230, 1987).

Disruption of calcium homeostasis may produce many clinical disorders (e.g., severe bone disease, anemia, renal impairment, ulcers, myopathy, and neuropathy) and usually results from conditions which produce an alteration in the level of parathyroid hormone.

Hypercalcemia is a condition which is characterized by an elevation in the serum calcium level. It is often associated with primary hyperparathyroidism in which an excess of PTH production occurs as a result of a lesion (e.g., adenoma, hyperplasia or carcinoma) of the parathyroid glands. Another type of hypercalcemia,

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humoral hypercalcemia of malignancy (HHM), is the most common paraneoplastic syndrome. It appears to result in most instances from the production by tumors (e.g., squamous, renal, ovarian or bladder carcinomas) of a novel class of protein hormone which shares amino acid homology with PTH. These PTH-related proteins (PTHrP) appear to mimic certain of the renal and skeletal actions of PTH and are believed to interact with the PTH receptor in these tissues. PTHrP is normally found at low levels in many tissues, including keratinocytes, brain, pituitary, parathyroid, adrenal cortex, medulla, fetal liver, osteoblast-like cells and lactating mammary tissues. In many HHM malignancies, PTHrP is found in the circulatory system at high levels, thereby producing the elevated calcium levels associated with HHM.

Summary of the Invention

The invention features isolated DNA comprising a DNA sequence encoding a cell receptor, preferably a parathyroid hormone receptor, of a vertebrate animal, which receptor has an amino acid sequence with at least 30% (preferably at least 50%, even more preferably at least 60%, and most preferably at least 75%) identity to the amino acid sequence shown in FIG. 3 (SEQ ID NO.: 3): i.e., when the closest match is made between the two amino acid sequences (using standard methods), at least 30% of the amino acid residues of the former sequence are identical to the amino acid residues of the latter sequence. By "isolated" is meant that the DNA is free of the coding sequences of those genes that, in the naturally-occurring genome of the organism (if any) from which the DNA of the invention is derived, immediately flank the gene encoding the DNA of the invention. The isolated DNA may be single-stranded or double-stranded, and may be genomic DNA, cDNA, recombinant hybrid DNA, or

synthetic DNA. It may be identical to a naturally-occurring, cell receptor- (e.g. PTH receptor) encoding DNA sequence, or may differ from such sequence by the deletion, addition, or substitution of one or more nucleotides. Single-stranded DNAs of the invention are generally at least 8 nucleotides long, (preferably at least 18 nucleotides long, and more preferably at least 30 nucleotides long) ranging up to full length of the gene or cDNA; they preferably are detectably labelled for use as hybridization probes, and may be antisense. Preferably, the isolated DNA hybridizes under conditions of high stringency to all or part of the DNA sequence show in FIG. 1 (SEQ ID NO.:1), FIG. 2 (SEQ ID NO.:2), FIG. 3 (SEQ ID NO.:3), or FIG. 6 (SEQ ID NO.:4). By "high stringency" is meant, for example, conditions such as those described herein below for the isolation of human kidney PTH receptor cDNA (also see Current Protocols in Molecular Biology, John Wiley & Sons, New York, 1989). Most preferably, the animal is a mammal (such as an opossum, a rat, or a human), and the DNA sequence encodes substantially all of the amino acid sequence shown in FIG. 1 (SEQ ID NO.:1), FIG. 2 (SEQ ID NO.:2), FIG. 3 (SEQ ID NO.:3) or FIG. 6 (SEQ ID NO.:4); or is encoded by the coding sequence of one of the plasmids deposited with the American Type Culture Collection (ATCC) and designated ATCC Accession No. 68570 or 68571. The DNA of the invention may be incorporated into a vector [which may be provided as a purified preparation (e.g., a vector separated from the mixture of vectors which make up a library)] containing a DNA sequence encoding a cell receptor of the invention (e.g. parathyroid hormone receptor) or fragment of the receptor, and a cell or essentially homogenous population of cells (e.g., prokaryotic cells, or eukaryotic cells such as mammalian

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cells) which contain the vector (or the isolated DNA described above). By "essentially homogenous" is meant that at least 99% of the cells contain the vector of the invention (or the isolated DNA, as the case may be).

- 5 Preferably, this vector (e.g., R15B) is capable of directing expression of a parathyroid hormone receptor (for example, in a cell transfected or transformed with the vector).

In another aspect, the invention features a cell
10 receptor, preferably parathyroid hormone receptor, (or an essentially purified preparation thereof) produced by expression of a recombinant DNA molecule encoding the cell receptor. An "essentially purified preparation" is one which is substantially free of the proteins and
15 lipids with which it is naturally associated.

In a related aspect, the invention features a polypeptide which includes a fragment of a naturally-occurring cell receptor of the invention. Preferably, the polypeptide includes a fragment of a naturally-
20 occurring parathyroid hormone receptor which is capable of binding parathyroid hormone or parathyroid hormone-related protein. In preferred embodiments, this fragment is at least six amino acids long, and has a sequence selected from the group including:

- 25 (a) TNETREREVFDRLGMIYTVG; (SEQ ID NO.: 5).
(b) YLYSGFTLDEAERLTEEEL; (SEQ ID NO.: 6)
(c) VTFFLYFLATNYYWILVEG; (SEQ ID NO.: 7)
(d) Y-RATLANTGCWDLSSGHKKWIIQVP; (SEQ. ID NO.: 8)
(e) PYTEYSGTLWQIQMHYEM; (SEQ ID NO.: 9)
30 (f) DDVFTKEEQIFLLHRAQA; (SEQ ID NO.: 10)
(g) FFRLHCTRNY; (SEQ ID NO.: 11)
(h) EKKYLWGFTL; (SEQ ID NO.: 12)
(i) VLATKLRETNAGRCQYRKLLK; or (SEQ ID NO. 13)
(j) a fragment (i.e., a portion at least six
35 residues long, but less than all) or analog of (a) - (i)

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which is capable of binding parathyroid hormone or parathyroid hormone-related protein [wherein "analog" denotes a peptide having a sequence at least 50% (and preferably at least 70%) identical to the peptide of which it is an analog]. Preferably, the polypeptide of the invention is produced by expression of a recombinant DNA molecule or is synthetic (i.e., assembled by chemical rather than biological means). The invention provides a method for producing such a polypeptide, which method includes providing a cell containing isolated DNA encoding a cell receptor of the invention or receptor fragment and culturing this cell under conditions which permit expression of a polypeptide from the isolated DNA.

The invention also features an antibody (monoclonal or polyclonal), and a purified preparation of an antibody, which is capable of forming an immune complex with a cell receptor of the invention (preferably a parathyroid hormone receptor such as a human PTH receptor) such antibody being generated by using as antigen either (1) a polypeptide that includes a fragment of the cell receptor of the invention, or (2) a cell receptor of the invention which is on the surface of a cell. This antibody is preferably capable of neutralizing (i.e., partially or completely inhibiting) a biological activity of the cell receptor of the invention (i.e., a component of one of the cascades naturally triggered by the receptor when its ligand binds to it). In preferred embodiments, the antibody of the invention is capable of forming an immune complex with parathyroid hormone receptor and is capable of neutralizing a biological activity of the PTH receptor (i.e. adenylate cyclase activation or phospholipase C stimulation).

Also within the invention is a therapeutic composition including, in a pharmaceutically-acceptable carrier, (a) a cell receptor of the invention, (b) a

polypeptide containing a fragment of the cell receptor of the invention, or (c) an antibody to a cell receptor of the invention. These therapeutic compositions provide a means for treating various disorders characterized by overstimulation of the cell receptors of the invention by their ligand. In preferred embodiments, the polypeptides of the invention include the PTH receptor, fragments of the PTH receptor and antibodies which form immune complexes with the PTH receptor. These polypeptides and antibodies are useful as diagnostics, for distinguishing those cases of hypercalcemia related to PTH or PTHrP from those which are not.

The nucleic acid probes of the invention enable one of ordinary skill in the art of genetic engineering to identify and clone cell receptor homologs or cell receptors from any species which are related to the cell receptors of the invention, expanding the usefulness of the sequences of the invention.

Other features and advantages of the invention will be apparent from the following description of the preferred embodiments and from the claims.

Detailed Description

The drawings will first be briefly described.

DRAWINGS

FIG. 1 is a representation of the nucleic acid and amino acid sequence encoding the opossum kidney PTH/PTHrP receptor clone, OK-H. (nucleic acid SEQ ID NO.: 1; amino acid SEQ ID NO.: 18)

FIG. 2 is a representation of the nucleic acid and amino acid sequence encoding the opossum kidney PTH/PTHrP receptor clone; O.K-O. (nucleic acid SEQ ID NO.: 2; amino acid SEQ ID NO.: 19)

FIG. 3 is a representation of the nucleic acid and amino acid sequence encoding the rat bone PTH/PTHrP receptor clone, R15B. (nucleic acid SEQ ID NO.: 3; amino acid SEQ ID NO.: 20)

FIG. 4 is a comparison of the deduced amino acid sequences encoded by cDNAs from clones OK-O and R15B.

FIG. 5 is a comparison of the deduced amino acid sequences of OK-O, OK-H and R15B, lined up according to sequence homology.

5 FIG. 6 is a representation of the nucleic acid and amino acid sequence encoding the human PTH/PTHrP receptor. (nucleic acid SEQ ID NO.: 4; amino acid SEQ ID NO.: 21).

10 FIG. 7 is a schematic representation of the rat bone PTH/PTHrP receptor cDNA, the human genomic DNA clone HPG1 and two cDNA clones encoding the human PTH/PTHrP receptor.

FIG. 8 is a hydrophobicity plot of the deduced amino acid sequence of the human kidney PTH/PTHrP receptor. Predicted membrane-spanning domains I through VII are indicated; A, B and C indicate additional, hydrophobic regions.

15 FIG. 9 is a graph illustrating binding of PTHrP to COS cells transfected with OK-H.

FIG. 10 is a graph illustrating stimulation of intracellular free calcium by NlePTH in COS cells transfected with OK-H.

20 FIG. 11 is a graph illustrating binding of PTHrP to COS cells transfected with OK-O.

FIG. 12 is a graph illustrating stimulation of intracellular free calcium by NlePTH in COS cells transfected with OK-O.

FIG. 13 is a graph illustrating binding of PTHrP to COS cells transfected with R15B.

25 FIG. 14 is a graph illustrating stimulation of intracellular free calcium by NlePTH in COS cells transfected with R15H.

FIG. 15 is a graph illustrating stimulation of inositol phosphate metabolism by NlePTH in COS cells transfected with OK-H, OK-O, or R15B.

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FIG. 16 is a graph illustrating cyclic AMP accumulation in COS cells transfected with CDM-8, OK-H, R15B by NlePTH.

FIG. 17 are graphs illustrating binding of ^{125}I -labelled PTH(1-34) (A and B) and ^{125}I -labelled PTHrP(1-36) (C and D) to COS-7 cells transiently expressing the human kidney (A and C) and the rat bone (B and D) PTH/PTHrP receptor; competing ligands included PTH(1-34) ($\square$), PTHrP(1-36) (*), PTH(3-34) ($\blacksquare$), PTH(7-34) (+). Data are given as % specific binding and represent the mean $\pm$ SD of at least three independent experiments.

FIG. 18 is a bar graph illustrating stimulated accumulation of intracellular cAMP in COS-7 cells transiently expressing the human kidney receptor. Data show the mean $\pm$ SD, and are representative of at least three independent experiments.

FIG. 19 represents a Northern blot analysis of total RNA ($\sim 10 \mu\text{g}/\text{lane}$) prepared from human kidney (A) and SaOS-2 cells (B). The blot was hybridized with the full length cDNA encoding the human kidney PTH/PTHrP receptor; positions of 28S and 18S ribosomal RNA bands are indicated.

FIG. 20 represents a Southern blot analysis of human genomic DNA digested with SstI, HindIII, and XhoI ($\sim 10 \mu\text{g}/\text{lane}$). The blot was hybridized with the full length cDNA encoding the human kidney PTH/PTHrP receptor.

FIG. 21 is a schematic diagram of the proposed arrangement, in a cellular membrane, of PTH/PTHrP rat bone receptor encoded by R15B.

30

MATERIALS AND METHODS

GENERAL: [Nle^{8,18}, Tyr³⁴]bPTH(1-34)amide (PTH(1-34)), [Nle^{8,18}, Tyr³⁴]bPTH(3-34)amide (PTH(3-34)), and [Nle^{8,18}, Tyr³⁴]bPTH(7-34)amide (PTH(7-34)) were obtained from Bachem Fine Chemicals, Torrance, CA; [Tyr³⁶]PTHrP(1-

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36)amide (PTHrP(1-36)) was synthesized as described (Keutman et al., Endocrinology 117:1230, 1985) using an Applied Biosystems Synthesizer 420A. Dulbecco's modified Eagles medium (DMEM), EDTA/trypsin, and gentamycin were from GIBCO (Grand Island, NY); fetal bovine serum (FBS) was from Hyclone Laboratory, Logan, UT. Total RNA from human kidney was provided by Per Hellman, University Hospital, Uppsala, Sweden. Oligonucleotide primers were synthesized using an Applied Biosystems 380B DNA Synthesizer. Restriction enzymes, Klenow enzyme, T4 polynucleotide Kinase and T4 DNA ligase were from New England Biolabs, Beverly, MA. Calf alkaline phosphatase was from Boehringer Mannheim, Germany. All other reagents were of highest purity available.

15 CELLS

Cell lines used include COS cells, OK cells, SaOS-2 cells, CHO cells, AtT20 cells, LLC-PK1 cells, and UMR-106 cells, which are available from a variety of sources including the American Type Culture Collection (Rockland, Maryland), Accession Nos. CRL1650, CRL6551, HTB85, CCL61, CCL89, CL101, and CRL1161, respectively. ROS 17/2 and ROS 17/2.8 are available from a number of sources including Dr. Gideon Rodan (Merck Laboratories, West Point, PA). MC-3T3 cells are derived from mouse bone cells and are also available from a number of sources including Dr. Chohei Shigeno (Dept. of Biochem. Medicine, Hyoto Univ., Kyoto, Japan).

All cells were grown in a humidified 95% air, 5% CO₂ atmosphere and maintained in monolayer culture with Ham's

F-12 or DMEM medium (Grand Island Biological Co.), supplemented with 5% or 10% fetal calf serum (M.A. Bioproducts, Walkersville, MD). The medium was changed every 3 or 4 days, and the cells were subcultured every 2 or 3 weeks by

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trypsinization using standard methods.

CLONING

Isolation of cDNA clones encoding the rat and opossum PTH/PTHrP receptors: Total RNA was initially
5 isolated from rat osteosarcoma (ROS) cells (ROS 17/2.8) and opossum kidney (OK) cells, by standard methods using guanidium isothiocyanate (Ullrich et al., Science 196: 1313, 1977; Chirgwin et al. Biochemistry 24: 5294, 1979), and centrifugation through cesium chloride (Gilsen et
10 al., Biochemistry 13: 2633, 1974). Poly A+ RNAs (mRNAs) were then recovered after passage of the total RNAs over oligo dT columns (Pharmacia, Piscataway, NJ) by the method of Aviv and Leder (Proc. Natl. Acad Sci. USA 69: 14087, 1972). The cDNA library from the ROS 17/2.8 mRNA
15 was prepared from poly A+ RNA using the method of Gubler and Hoffman (Gene (Amst.) 25: 263, 1983). Oligo dT-primed and random-primed cDNAs were synthesized from poly A+ ROS 17/2.8 and OK cell mRNA, respectively (Aviv and Leder, supra). The cDNAs were ligated to BstX1 linkers
20 (Invitrogen, San Diego, CA) and size-selected by centrifugation (3 h, 55,000 xg) in a 5-20% potassium acetate gradient. The size-selected cDNA was then inserted into the plasmid vector, pCDNA I (Invitrogen), using the non-self annealing BstX1 restriction sites.
25 The resultant plasmid libraries were then used to transform E. coli (MC1061/P3, Invitrogen) containing a larger helper plasmid, p3. The p3 plasmid possesses amber mutations in two genes which code for ampicillin and
30 tetracycline resistance. Using ampicillin and tetracycline selection, only those cells containing both the p3 and a tRNA suppressor gene, which is contained within pCDNA I, were capable of growth. The transformed bacteria were then grown to confluence, and the plasmid
35 DNAs isolated using standard techniques (e.g., see

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Ausebel et al., Current Protocols in Molecular Biology, John Wiley
sons, New York, 1989). These DNAs were then taken up in a DEAE-dextran
solution, and used to transfect African Green Monkey kidney (COS)
cells, which had been grown to 75% confluence in "sideflasks™" (Nunc,
5 Denmark).

Screening for COS cells containing plasmids capable of expressing
functionally-intact ROS or OK cell parathyroid hormone/parathyroid
hormone related-protein (PTH/PTHrP) receptor proteins was performed
according to Gearing et al. (EMBO J. 8: 3676, 1989), with some minor
10 modifications including DEAF-Dextran transfection in sideflasks.
Forty-eight hours after transfection, the cells were tested for
binding of ^{125}I -labeled (Tyr ^{36}]PTHrp (1-36) amide, using methods
previously described (Yamamoto et al., Endocrinology 122: 1208, 1988),
with the following exceptions: the time and temperature of the
15 incubation were 2h and room temperature, respectively. After rinsing,
the cells were fixed with 1.25% glutaraldehyde, and rinsed with 1%
gelatin. After snapping off the top of the sideflask, the remaining
microscope slide was dipped into NTB-2™ photographic emulsion (Eastman
Kodak, Rochester, NY). After 3-4 days of exposure at 4°C, the slides
20 were developed, fixed, and stained with 0.03% toluidine blue. Screening
of each slide was performed under a light microscope (Olympus). One
pool of plasmid-DNA from ROS cells, and two pools of plasmid-DNA from
OK cells, (10,000 independent clones), each gave rise to 3-4
transfected COS cells expressing the PTH/PTHrP receptor. These pools
25 were subsequently subdivided. The subpools were used to transfect COS
cells, and single clones were identified that expressed receptor
protein capable of binding the radioligand.

Isolation of cDNA and genomic DNA clones encoding the human
PTH/PTHrP receptor: A human kidney oligo dT-

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primed cDNA library (1.7×10^6 independent clones) in lambda GT10 and a genomic library of human placental DNA (2.5×10^6 independent clones) in EMBL3 (Sp6/T7) (Clontech, Palo Alto, CA) were screened by the plaque hybridization technique (Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Ed. pp. 108-113, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1989) with the ^{32}P -labelled (Random primed labelling kitTM, Boehringer Mannheim, Germany) BamHI/NotI 1.8kb restriction enzyme fragment encoding most of the coding sequence of the rat bone PTH/PTHrp receptor (Fig. 3). The nitrocellulose filters were incubated at 42°C for 4 hrs in a prehybridization solution containing 50% formamide, 4x saline sodium citrate (SSC; $1 \times$ SSC: 300 mM NaCl, 30 mM NaCitrate, pH 7.0), 2x Denhardt's solution, 10% Dextran sulphate, 100 µg/ml salmon sperm DNA (final concentration). The hybridizations were carried out in the same solution at 42°C for 18-24h. Filters were washed with 2x SSC/0.1% SDS for 30 minutes at room temperature and then with $1 \times$ SSC/0.1% SDS for 30 minutes at 45°C. The films were exposed at -80°C for 18-24h using intensifying screens.

About 1,000,000 clones were screened from each library. Positive clones were plaque-purified and lambda phage DNA was isolated (Sambrook et al., supra). Cloned inserts were removed from phage DNA by digestion with restriction endonucleases HindIII and EcoRI (lambda GT10 library), or with XhoI and SstI (EMBL3 library), and were then subcloned into pcDNAITM (Invitrogen, San Diego, CA) using the appropriate, dephosphorylated restriction sites. Sequencing of the CsCl₂-purified subclones was performed according to Sanger et al. (Biochem 74:5463, 1977) by the dideoxy termination method (SequenaseTM version 2 sequencing kit, United States Biochemical Corporation, Cleveland, OH).

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Reverse transcription and polymerase chain

reaction (PCR): 3 μ g of poly (A)+ RNA from human kidney (Clontech, Palo Alto, CA) in 73.5 μ l of H₂O was incubated at 100°C for 30 seconds, quenched on ice, and then added to 20 μ l of 5x RT buffer (1x RT buffer: 40 mM Tris-HCl, pH 8.2, 40 mM KCl, 6.6 mM MgCl₂, 10 mM dithiothreitol, and dNTPs at 0.5 mM each), 2 μ l (4 units) RNasin (Promega Biotec, Madison, WI), 1 μ l (80 pmo/ μ l) of the human cDNA primer H12

10 (5'-AGATGAGGCTGTGCAGGT-3'; SEQ ID NO.: 14) and 80 units of avian myeloblastosis virus reverse transcriptase (Life Sciences, St. Petersburg, FL). The reaction mixture was incubated for 40 minutes at 42°C. One-tenth of the first strand synthesis reaction mixture was then amplified by
15 PCR in a final volume of 100 μ l containing 3 mM MgSO₄, 200 μ M dNTPs, 2 units of Vent polymerase (New England Biolab, Beverly, MA), and 2 μ M each of the forward and the reverse primers (PCR conditions: denaturing for 1 min at 94°C, annealing for 1 min at 50°C, and extension at
20 72°C for 3 minutes; 40 cycles).

Two independent PCRs were performed using two different forward primers: i) degenerate primer RK-1 (5'-GGAATTCCATGGGAGCGGCCCGGAT-3'; SEQ ID NO.: 15) based on

25 G CC
the 5' coding end of the two previously cloned PTH/PTHrP receptors (described above), and ii) primer RK-2 (5'-CGGGATCCCGCGGCCCTAGGCGGT-3'; SEQ ID NO.: 16) based on the 5' untranslated region of the human genomic clone
30 HPG1. Both PCR reactions used the reverse primer H26 (5'AGTATAGCGTCCTTGACGA-3'; SEQ ID NO.: 17) representing nucleotides 713 to 731 of the coding region of the human PTH/PTHrP receptor (Fig. 4). PCR products were blunt-ended using Klenow enzyme and cloned into
35 dephosphorylated pcDNAI cut with EcoRV.

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Northern blot analysis: Total RNA was extracted from SaOS-2 cells and from human kidney by the guanidine thiocyanate method (Chirgwin et al., Biochem. 18:5294, 1979). For Northern blot analysis, ~10 µg of total RNA was subjected to electrophoresis on a 1.5%/37% formaldehyde gel and blotted onto nitrocellulose filters (Schleicher and Schuell, Keene, NH). The hybridization conditions were the same as those for screening the phage libraries (see above). The filters were washed at a final stringency of 0.5x SSC/0.1% SDS for 30 min at 60°C and exposed for autoradiography.

Southern blot analysis: Human genomic DNA was prepared using the SDS/proteinase K method (Gross-Bellard et al., Eur. J. Biochem. 36:32, 1973). For Southern analysis, ~10 µg of DNA was digested with SstI, PvuII and XhoI; subjected to electrophoresis on a 0.8% agarose gel; and blotted onto nitrocellulose membranes (Schleicher and Schuell, Keene, NH). The hybridization conditions were the same as those for screening the phage libraries (see above). The filters were washed at a final stringency of 0.5x SSC/0.1% SDS for 30 min at 55°C and exposed for autoradiography.

FUNCTIONAL ASSAYS

Tests to characterize the functional properties of the cloned receptors expressed on COS cells included:

- I) binding of PTH and PTHrP fragments and analogues,
- II) stimulation of cyclic AMP accumulation by PTH and PTHrP fragments and analogues,
- III) increase of intracellular free calcium by PTH and PTHrP fragments and analogues, and
- IV) activation of inositol phosphate metabolism by PTH and PTHrP fragments and analogues. The methodologies are as follows:

Radioreceptor Assay

[Nle⁸, Nle¹⁸, Tyr³⁴] bPTH-(1-34) amide (NlePTH), and [Tyr³⁶] PTHrP (1-36) amide (PTHrP) were iodinated with Na¹²⁵I (carrier free, New England Nuclear, Boston, MA) as previously reported (Segre et al., J. Biol. Chem. 254: 6980, 1979), and purified by reverse-phase HPLC. In brief, the labeled peptide was dissolved in 0.1% trifluoroacetic acid. (TFA), applied to a C₁₈ Sep-pakTM cartridge (Waters Associates, Inc., Milford, MA) and eluted with a solution of 60% acetonitrile in 0.1% TFA. After lyophilization, the radioligand then was applied to C₁₈-
10 μ BondapakTM column (3.9 mm x 30 cm. Waters Associates) and eluted over 30 min with a linear gradient of 30-50% acetonitrile-0.1% TFA at a flow rate of 2 ml/min. The radioligand eluted in two peaks; the first peak, which eluted at approximately 38% acetonitrile, was used in these studies because it gave higher total and specific bindings. The
15 specific activity was 500 $\pm$ 75 mCi/mg, which corresponds to an average iodine-peptide ratio of 1.

COS-7 cells were grown in 15 cm plates in DMEM, 10% heat-inactivated FBS, 10 mg/L gentamycin until 80-90% confluent. Twenty-four hours after transfection by the DEAE/Dextran method (Sambrook et al., supra), with 1-2 μ g of plasmid DNA, the cells were trypsinized
20 and replated in multiwell plastic: dishes (16 or 35 mm diameter, Costar, Cambridge, MA) at a cell concentration of 5 x 10⁴ cells/cm²). Cell number increased only slightly after transfection. After, continuing culture for another 48 h, radioreceptor assays were
25 performed. The culture medium was replaced with buffer containing 50 mM Tris-HCL (pH 7.7), 100 mM NaCl, 2 mM CaCl₂, 5 mM KCL, 0.5% heat-inactivated fetal bovine serum (GIBCO), and 5% heat-inactivated horse

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serum (KC Biological Inc., Lenexa, KS) immediately before studies were initiated. Unless otherwise indicated, studies were conducted with cells incubated in this buffer at 15°C for 4 h with 4×10^5 cpm/ml (9.6×10^{-11} M) of ^{125}I -labeled NlePTH or PTHrP.

5 Incubations were terminated by aspirating the buffer, and repeatedly (x3) washing the culture dishes containing the adherent cells with chilled 0.9% NaCl solution, over a 15 sec period. Cell-bound radioactivity was recovered by the sequential addition (x3) of 1 N NaOH (200 μ) to each well. After 30 min at room temperature, the
10 NaOH was transferred to a glass tube. A second and third extraction with 1 N NaOH (200 μ l) were combined with the first, and the total radioactivity was counted in a γ -spectrometer (Packard Instruments, Downers Grove, IL). Tracer adherence to culture vessel without cells was negligible (<0.2% of total counts added), if vessels were
15 preincubated with culture medium. Determinations of cAMP accumulation

Intracellular cAMP accumulation was measured as described previously (Abou-Samra et al., J. Biol. Chem. 262:1129, 1986). Cells in 24-well plates were rinsed with culture medium containing 0.1% BSA and 2mM IBMX. The cells were then incubated with PTH or PTHrP for 15
20 min. at 37° C. The supernatant was removed and the cells immediately frozen by placing the whole plate in dry ice powder. Intracellular cAMP was extracted by thawing the cells in 1ml of 50 mM HCl and analyzed by a specific radioimmunoassay using an anti-cAMP antibody (e.g., Sigma, St. Louis, MO). A cAMP analog (2'-O-monosuccinyl-
25 adenosine 3':5'-cyclic monophosphate tyrosyl methyl ester, obtained from Sigma) which was used a tracer for cAMP was iodinated by the chloramine T method. Free iodine was removed by adsorbing the iodinated cAMP analog onto a C18 Sep-pak™ cartridge (Waters, Milford, MA).

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After washing with dH_2O , the iodinated cAMP analog was eluted from the Sep-pak™ Cartridge with 40% acetonitrille (ACN) and 0.1% trifluoroacetic acid (TFA). The iodinated cAMP analog was lyophilized, reconstituted in 1 ml 0.1% TFA, and injected into a C18 reverse phase HPLC column (Waters). The column was equilibrated with 10% ACN in 0.1% TFA, and eluted with gradient of 10-30% ACN in 0.1% TFA. This allows separation of the mono-iodinated cAMP analog from the non-iodinated cAMP analog. The tracer is stable for up to 4 months when stored at -20°C . The standard used for the assay, adenosine 3':5'-cyclic monophosphate, was purchased from Sigma. Samples (1-10 μl of HCl extracts) or standards (0.04-100 fmol/tube) were diluted in 50 mM Na-acetate (pH 5.5), and acetylated with 10 μl of mixture of triethylamine and acetic anhydride (2:1 vol:vol). After acetylation, cAMP antiserum (100 μl) was added from a stock solution (1:4000) made in PBS (pH 7.4), 5 mM EDTA and 1% normal rabbit serum. The tracer was diluted in PBS (pH 7.4) with 0.1% BSA, and added (20,000 cpm/tube). The assay was incubated at 4°C overnight. The bound tracer was precipitated by adding 100 μl of goat anti-rabbit antiserum (1:20 in PBS) and 1 ml of 7% polyethyleneglycol (MW 5000-6000), centrifuging at 2000 rpm for 30 min. at 4°C . The supernatant was removed and the bound radioactivity was counted in a γ -counter (Micromedic). Standard curves were calculated using the four-parameter RIA program supplied by Micromedic. Typically, the assay sensitivity is 0.1 fmol/ tube, and the standard concentration that displaces 50% of tracer is 5 fmol/tube.

In an alternative method for assaying cAMP accumulation, COS cells transfected with PTH/PTHrP receptor cDNA are harvested with a plastic policeman into a solution containing 10 mM Tris-HCl (pH 7.5), 0.2 mM

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MgCl₂, 0.5 mM ethyleneglycolbis (β -amino ethyl ether) N,N'-tetra-acetic acid (EGTA) (Sigma) and 1 mM dithiothreitol(Sigma). Cells are homogenated by 20 strokes of tightly-fitting Dounce homogenizer, and centrifuged at 13,000 x g for 15 min at 4°C (Eppendorf™, type 5412, Brinkmann Instruments, Inc., Westburg, NY). The pellet containing the plasma membranes is resuspended in the same buffer by several strokes with a Dounce homogenizer, and further diluted with the same buffer to a protein concentration of approximately 1.2 mg/ml, as determined by the method of Lowry et al. (Lowry et al., J. Biol. Chem 193: 265, 1951). Approximately 30 μ g (25 μ l) membrane are incubated with varying concentrations of hormone or vehicle alone for 10 min at 37°C (final volume, 100 μ l) in 50 mM Tris-HCl (pH 7.5), 0.8 mM ATP, 4 x 10⁶ cpm [α -³²P] ATP (New England Nuclear, Boston, MA), 9 mM theophylline, 4.2 mM MgCl₂, 26 mM KCl, 0.12% BSA, and an ATP-regenerating system containing 5 mM creatine phosphate (Schwartz/Mann Division, Becton-Dickenson & Co., Orangeburg, NY) and 0.1 mg/ml creatine phosphokinase (Shwartz/Mann). Incubations are initiated by addition of the membrane suspension and terminated by addition of 100 μ l of a solution containing 20 mM cAMP, approximately 50,000 cpm [³H]cAMP, and 80 mM ATP. The reaction mixture is boiled, and the [³²P] cAMP generated is purified by sequential chromatography on ion-exchange columns (Dowex 50 W-X4™, Biorad Lab, Richmond, CA) and alumina (Sigma). The [³²P]CAMP may be counted in a β -scintillation counter (Packard Instrument Co.), with correction for recovery of [³H] cAMP.

25 Determination of intracellular free calcium

Measurements of intracellular calcium levels in cells transfected with PTH/PTHrP receptor cDNAs were performed using Fura-2 AM™ (acetomethoxy ester of Fura-2™,

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Molecular Probes Inc., Eugene, OR) loaded cells. Details of the methodology are:

Coverslips plated with COS cells were incubated in Fura-2 AM loading buffer containing, in mM: HEPES (N-[2-Hydroxyethyl]piperazine-N'-[2-ethanesulfonic acid]), 20; CaCl_2 , 1; KCl 5; NaCl, 145; MgSO_4 , 0.5; NaHCO_3 , 25; K_2HPO_4 , 1.4; glucose, 10; and Fura-2 AM 91-(2-5'-carboxyoxazol-2'-yl)-6-aminobenzofuran-5oxy-(2'-amino-5'-methylphenoxy)ethane-N,N,N',N'-tetraacetic acid acetomethoxy ester), 0.5; at 37°C at pH7.4, aerated with 95% air and 5% CO_2 for 45 minutes. Cells loaded with Fura-2 AM were then washed with a modified Krebs-Heinseleit (KH) buffer containing, in mM: HEPES, 20; CaCl_2 , 1; KCl, 5; NaCl, 145; MgSO_4 , 0.5; Na_2HPO_4 , 1; glucose, 5; pH7.4. To check that cleavage of the ester occurred, the excitation spectra after different times of Fura-2 AM incubation were measured. At 5 min. after the start of incubation, the excitation spectrum peaked at approximately 360 nm, reflecting incomplete hydrolysis of Fura-2 AM, whereas beyond 30 min. the excitation spectrum peaked at 345 nm, characteristic of Fura-2.

To measure fluorescence of individual cells, the cover slips were placed in a microscope tissue chamber (Biophysica Technologies, Inc., MD). The chamber consisted of a shallow, sloped compartment made of Teflon with a silicone rubber seal. The cover slips served as the bottom of the chamber. A heater/cooler ring was encased in the silicone rubber which sealed the coverslip in place. Temperatures were varied between 22°C and 37°C by applying 0-7.4 V to the heater. If the temperature is not specifically stated, the experiment was performed at 37°C. The chamber was mounted on the stage of an inverted microscope (Zeiss IM-35, Thornwood, NY). Fura-2 fluorescence was excited with a 75 watt Xenon arc lamp placed at the focal point of a condenser (Photon

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Technologies International (PTI) Inc., NJ). Grating monochromators, alternated by a rotating chopper in which mirror vanes alternate with transmitting sectors, were used for selecting wavelengths. The monochromator outputs were combined to form a common optical path
5 which exited the source housing through an adjustable iris. The light then passed through quartz lenses and a dichroic mirror through a 100x Nikon Fluor objective. A photon-counting PMT device detection was used to measure the light output. Data analysis was performed using PTI software run on an IBM™-compatible AT/286 computer using the MS-DOS™
10 operating system. Data was retained and manipulated in a packed binary format.

Intracellular calcium concentrations were calculated according to the formula: $[Ca^{2+}]_i = K_d(R - R_{min}) / (R_{max} - R)B$, where R is the ratio of fluorescence of the cell at 340 and 380 nm; R_{max} and R_{min} represent
15 the ratios of Fura-2™ fluorescence intensity at 340 and 380 nm excitation wavelengths in the presence of a saturating amount of calcium and effectively zero calcium, respectively; B is the ratio of fluorescence of Fura-2™ at 380 nm in zero calcium to that in saturating amounts of calcium; and K_d is the dissociation constant of
20 Fura-2™ for calcium. To determine R_{max}, at the end of an experiment ionomycin was added to the Fura-2 AM™ loaded cells to equilibrate Ca²⁺ between the extracellular (1mM) and intracellular environments. To calculate R_{min}, 1mM EGTA was then added to the bathing solution. Different dissociation constants were used at the different
25 temperatures: 224 nM at 34-37°C and 135 nM at 24-27°C. Determination of inositol phosphate

The level of inositol phosphate metabolism was determined in COS cells transfected with PTH/PTHrP

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receptors using previously published methods (Bonventre, et al., J. Biol. Chem. 265: 4934, 1990).

RESULTS

Molecular characterization

5 Two independent clones (OK-H and OK-O), both of which were isolated from the OK cell cDNA library, had lengths of approximately 2 kilobases. The determined nucleotide sequence and predicted amino acid sequence of these clones are shown in Figs. 1 (SEQ ID NO.:1) and 2
10 (SEQ ID NO.:2) respectively. The R15B clone isolated from the ROS cell cDNA library had a length of approximately 4 kilobases. The determined nucleotide sequence and predicted amino acid sequence of the rat bone PTH/PTHrP receptor is depicted in Fig. 3 (SEQ ID
15 NO.:3).

The three cDNA clones appear to be full-length by the criteria of having codons encoding methionine residues that are predicted to be the likely candidates as initiator methionines. These methionine codons are
20 followed by amino acid sequences (deduced from the DNA) with properties suggesting that they are "signal-peptide" sequences. All three receptor cDNAs have stop codons at locations that permit these receptors to "fit" a putative seven-membrane spanning model, a model typical for G-
25 protein-linked receptors. Most importantly, all three cloned receptors bind ligands and, when activated, are capable of activating intracellular effectors. These properties suggest that all three of the isolated clones encode full-length cDNAs.

30 Fig. 4 demonstrates the high degree of homology between the amino acid sequences encoded by the cDNAs from OK-O and ROS 15B. There is an overall 87% homology and a 77.8% amino acid identity between these two receptors. This high level of identity over long

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stretches of amino acids demonstrates that the amino acid sequence of the PTH receptor is evolutionarily conserved to a high degree. This allows the data from both OK-O and R15B to be extrapolated to other species, including
5 human.

Fig. 5 shows the deduced amino acid sequences of all three cloned cDNAs lined up according to sequence homology. The OK-H sequence is identical to OK-O except in the C-terminus tail, where the OK-O sequence totals
10 585 amino acids whereas the OK-H sequence stops at 515 amino acids. This difference is attributable to a single nucleotide (G) deleted in the OK-H sequence compared to the OK-O sequence, causing a frame shift and early stop codon in the former. It is not known whether OK-O and
15 OK-H represent the products of two separate genes or of a laboratory artifact.

Some G-protein-coupled receptors are encoded by intronless genes (Kobilka et al., Nature 329:75, 1987); Kobilka et al., J. Biol. Chem. 262:7321, 1987; Heckert et
20 al., Mol. Endocrinol. 6:70, 1992; Kobilka et al., Science 238:650, 1987; Bonner et al., Science 237:527, 1987; Sunahara et al., Nature 347:80, 1990). To isolate a human PTH/PTHrP receptor cDNA, both a human cDNA library and a human genomic library were screened with a probe
25 (BamHI/NotI) representing most of the coding region of the rat bone PTH/PTHrP receptor (Fig. 3). Screening the human kidney cDNA library led to the isolation of the clone HK-1 (Fig. 6) [SEQ ID NO.: 6]. Since one of the two EcoRI cloning sites of lambda GT10 proved to be
30 eliminated as a result of the library construction, the HindIII/EcoRI phage fragment containing the cDNA insert and ~250 bp of the 37 kb (left) lambda arm was subcloned into the corresponding restriction sites in pCDNA1. DNA sequencing revealed that the cloned cDNA contained ~1000
35 bp of the 3' coding region and ~200 bp of the 3' non-

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coding region including an A-rich 3' end. The coding region 5' to the XhoI site was subsequently used to re-screen the library and led to the isolation of the clone HK-2 which, after subcloning into pCDNAI, proved to contain ~1400 bp of the coding region. For the third screening of the library, the PvuII/PstI fragment of HK-2 was used; the isolated clone HK-3 proved to be identical to HK-2.

The genomic library screening ($\sim 10^6$ pfu) resulted in the isolation of four independent clones. Comparison of Southern blot analyses of restriction enzyme digests of these clones with that of normal genomic DNA, revealed that one 15 kb genomic clone, HPG1 (also referred to as HG4A), contained a SstI/SstI fragment that had the same size as one hybridizing DNA species from normal human genomic DNA digested with SstI (see below). The hybridizing 2.3 kb SstI/SstI DNA fragment and an ~8 kb XhoI fragment which comprised the SstI/SstI fragment were both subcloned into pCDNAI. Further Southern blot analysis of the SstI/SstI DNA fragment revealed that an ~1000 bp BamHI/SstI fragment encoded a portion of the human PTH/PTHrP receptor which later proved to represent the exon encoding the putative signal peptide and the 5' non-translated region which is interrupted by an ~1000 bp intron (Fig. 7).

To isolate the remaining ~450 nucleotides of the coding region, poly (A)+ RNA from human kidney was reverse transcribed after priming with H12 (Fig. 7). After single strand synthesis, two independent PCRs were performed using two different forward primers: i) a degenerate primer RK-1 based on the 5' coding end of the two previously cloned PTH/PTHrP receptors, OK-0 and R15B; and ii) primer RK-2 based on the 5' non-coding region of HPG1. H-26 was used as the reverse primer for both reactions. Southern blot and restriction map analyses

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confirmed the expected size of the amplified DNA encoding the human PTH/PTHrP receptor. The blunt-ended PCR products encoding the 5' end of the human PTH/PTHrP were cloned into pCDNAI using the dephosphorylated EcoRV sites. Sequence analysis of each PCR clone confirmed their 5' nucleotide difference due to the difference in forward primer sequence, but revealed otherwise identical sequences. Nucleotide sequencing of both strands of the human PTH/PTHrP receptor cDNA revealed an open reading frame encoding a 593-amino acid protein (Fig. 6, SEQ ID NO.:4).

The full-length human kidney PTH/PTHrP receptor cDNA, HKrk, was constructed using the BamHI/PvuII fragment of PCR clone #2 and HK-2. Using the full-length cDNA encoding the human PTH/PTHrP receptor, Northern blot analysis of total RNA (~10 µg/lane) from human kidney and SaOS-2 cells revealed one major hybridizing DNA species of ~2.5 kb (Fig. 19). The XhoI digest of normal human genomic DNA, when probed with the same full-length cDNA (Fig. 20), revealed one major hybridizing species of about 5.5 kb, and two DNA species of 4 and 8 kb which weakly hybridized. These data suggest that the human PTH/PTHrP receptor is the product of a single gene. This full-length clone was then transiently expressed in COS-7 cells for functional and biological characterization by the methods cited above.

Comparison of the human receptor with the opossum kidney PTH/PTHrP receptor and the rat bone PTH/PTHrP receptor, revealed 81% and 91% amino acid sequence identity, respectively, and consequently a very similar hydrophobicity plot (Fig. 8). All extracellular cysteines including the two cysteine residues in the presumed signal peptide are conserved, as are all potential, extracellular

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N-glycosylation sites. A number of the amino acids which were not identical between the human kidney and rat bone PTH/PTHr receptors were found to be conserved between the human and the opossum receptors. These conserved amino acids include an Arg to Leu at 51, an Arg to Trp at 58, an Arg to His at 262, an Asp to His at 358, an Ile to Thr at 422, and a Thr to Leu at 427.

Biological Characterization

Functional characterization of the biological properties of the opossum and rat PTH/PTHrP receptors was performed in transiently transfected COS cells by a radioreceptor assay technique using both ^{125}I -PTHrP and ^{125}I -NlePTH as radioligands, and by bioassays that measure ligand-stimulated cAMP accumulation, increase in intracellular free calcium, and stimulation of inositol phosphate metabolism, by the methods cited above.

Fig. 9 demonstrates that COS cells expressing OK-H bind ^{125}I -PTHrP. These data also demonstrate that binding of PTHrP is inhibited when intact PTH (1-34) or PTH analogues which are shortened at their amino terminus (i.e. the 3-34 and 7-34 analogues, which contain Nle substitutions for methionine at positions 8 and 18 and a tyrosine substitution for phenylalanine at position 34) are used as competitors for binding. Similarly, binding of ^{125}I -NlePTH to COS cells expressing OK-H was inhibited when PTHrP or PTHrP fragments were used as competitors. These data indicate that PTH and PTHrP both bind to the receptor encoded by OK-H.

Fig. 10 demonstrates that COS cells expressing OK-H increase their concentration of intracellular free calcium when exposed to NlePTH, but to a smaller extent (mean = 39 nm), or not at all, when compared to COS cells expressing OK-0 or R15B receptors (Fig. 12 and Fig. 14) and stimulated with NlePTH. Unlike COS cells expressing

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OK-O or R15B, COS cells expressing OK-H do not show a detectable increase in metabolism of inositol phosphate when stimulated with NlePTH (Fig. 15).

Fig. 11 demonstrates that COS cells expressing OK-
5 O bind ^{125}I -PTHrP. These data also demonstrate that binding of PTHrP is inhibited when intact PTH (1-34) or PTH analogues which are shortened at their amino terminus (i.e. the 3-34 and 7-34 analogues, which contain Nle substitutions for methionine at positions 8 and 18 and a
10 tyrosine substitution for phenylalanine at position 34) are used as competitors for binding. Similarly, binding of ^{125}I -NlePTH to COS cells expressing OK-H was inhibited when PTHrP or PTHrP fragments were used as competitors. These data indicate that PTH and PTHrP both bind to the
15 receptor encoded by OK-O.

Fig. 12 demonstrates that COS cells expressing OK-O increase their concentration of intracellular free calcium and their rate of inositol phosphate metabolism after stimulation with NlePTH and PTHrP (Fig. 15).

Fig. 13 demonstrates that COS cells expressing
20 R15B bind ^{125}I -PTHrP. These data also demonstrate that binding of PTHrP is inhibited when intact PTH (1-34) or PTH analogues which are shortened at their amino terminus (i.e. the 3-34 and 7-34 analogues, which contain Nle
25 substitutions for methionine at positions 8 and 18 and a tyrosine substitution for phenylalanine at position 34) are used as competitors for binding. Similarly, binding of ^{125}I -NlePTH to COS cells expressing OK-H was inhibited when PTHrP or PTHrP fragments were used as competitors.
30 These data indicate that PTH and PTHrP both bind to the receptor encoded by R15B.

Fig. 14 demonstrates that COS cells expressing R15B increase their concentration of intracellular calcium to an extent similar to stimulated COS cells
35 expressing OK-O.

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Fig. 15 demonstrates that COS cells expressing R15B or OK-O increase their rate of phosphatidyl inositol hydrolysis, as evidenced by the rapid increase in inositol trisphosphate (IP_3) and inositol bisphosphate (IP_2) accumulation after stimulation of the cells with NlePTH or PTHrP. Conversely, COS cells expressing OK-H did not show any detectable increase in inositol trisphosphate and inositol bisphosphate accumulation after stimulation with NlePTH or PTHrP. These data suggest that the PTH receptor encoded by R15B and OK-O is coupled to phospholipase C, presumably through G_p . Since the only difference between OK-O and OK-H is in the cytoplasmic C-terminal tail, these data strongly suggest that the C-terminus of the PTH receptor encoded by OK-O and R15B is involved in the activation of phospholipase C.

Fig. 16 demonstrates that COS cells expressing R15B and OK-H increase cAMP accumulation after stimulation with NlePTH. Similar results were obtained in COS cells expressing OK-O. No cAMP stimulation was detected in COS cells transfected with the cDM8 vector alone. These data suggest that PTH receptor coupling to adenylate cyclase does not require the full length C-terminal cytoplasmic tail of the receptor.

These data demonstrate that all three PTH/PTHrP receptors cloned from both OK and ROS cell cDNA libraries bind the amino-terminal ligands of both peptides equivalently. Activation of all these receptors by ligand stimulates adenylate cyclase (as measured by increased intracellular cAMP), presumably through activation of one class of guanine nucleotide binding proteins (G-proteins). G-proteins have a trimeric peptide structure in which one of the subunits, alpha, is distinct, and the other two, beta and gamma, are identical or highly homologous. One of these G-proteins

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(G_s) contains G-alpha-"stimulatory" (G-alpha-s) which is involved in the activation of adenylate cyclase.

Binding of ligand to OK-O and R15B, but not to OK-H, also increases intracellular free calcium and stimulates metabolism of inositol phosphate. These properties strongly suggest that activation of both OK-O and R15B receptors by ligand results in stimulation of a second intracellular effector, phospholipase C. The coupling mechanism between these activated receptors and phospholipase C is likely to be a G-protein which is distinct from G_s. In contrast, the properties of the activated OK-H receptor which is truncated at the carboxy terminus, suggest that it may not activate phospholipase C, or that it activates phospholipase C inefficiently.

The biochemical role of the carboxy-terminal tail of the PTH/PTHrP receptor was further investigated by the construction of a carboxy-terminally-truncated rat receptor, R480, by standard PCR technology using R15B as a template and an upstream primer containing a stop codon inserted at position 481. Briefly, the upstream primer was a synthetic oligonucleotide based on nucleotides 1494-1513 of the rat cDNA sequence (see Fig. 3; SEQ ID NO.: 3) to which a stop codon and an XbaI cloning site were added. Thirty PCR cycles were carried out, each cycle consisting of 1 min at 92°C for denaturation, 1 min at 60°C for annealing, and 1 min at 72°C for extension. The product was cut with NsiI and XbaI and purified by gel electrophoresis. R15B was sequentially digested with XbaI and NsiI, and the purified PCR product was then ligated into the XbaI-NsiI cut R15B vector. The resulting plasmid, R480, was amplified in bacteria and sequenced.

R480 encodes 480 amino acids that are identical to those in the 591 amino acids receptor. This truncated cDNA was expressed in COS-7 cells (transient expression)

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and in CHO cells (stable expression). Both COS-7 and CHO cells expressing the truncated receptor, R480, and the wild type receptor, RB, bind PTH(1-34) with equivalent affinities. When activated, R480 stimulates cAMP accumulation in COS7 and CHO cells as efficiently as does the wild type receptor. In contrast to the wild type receptor, R480 did not mediate any increase in $[Ca^{2+}]_i$ when stimulated by PTH in either the COS-7 cells or the CHO cells. These data indicate that the molecular requirements for activation of phospholipase C and adenylate cyclase by PTH/PTHrP receptor are distinct from each other, and point to a major role of the carboxy-terminal tail of the PTH/PTHrP receptor in coupling to phospholipase C but not to adenylate cyclase. Of course, it is also possible that activated PTH/PTHrP receptors may activate additional G-proteins and/or intracellular effector molecules.

Analysis of COS-7 cells transfected with the cloned human PTH/PTHrP receptor demonstrated that radiolabelled PTH(1-34) and PTHrP(1-36) (~200,000 cpm) bound to the expressed receptors with similar efficiency (specific binding: $10.1 \pm 3.7\%$ and $7.6 \pm 6.0\%$, respectively) to that observed for COS-7 cells expressing R15B (specific binding: $8.1 \pm 3.5\%$ and $7.1 \pm 4.1\%$, respectively). The expressed human PTH/PTHrP receptors bound PTH(1-34) with 2-fold higher apparent K_d than did the rat bone PTH/PTHrP receptor: ~5 nM versus ~10 nM (Fig. 17). However, despite their high degree of amino acid homology, the two receptors showed significant differences in affinity for PTH(3-34) and PTH(7-34). PTHrP(1-36) displayed a 2- to 4-fold lower affinity for the human PTH/PTHrP receptor than for the rat receptor (~35 nM for HKrk versus ~10 nM for R15B) which appeared more pronounced when PTHrP(1-36) was used as radioligand. The affinities for PTH(3-34) and PTH(7-34) were 7- and

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35-fold higher with the expressed HKrK than with R15B (~7 nM versus ~45 nM for PTH(3-34), respectively; ~60 nM versus ~2000 nM for PTH(7-34), respectively). In COS-7 cells expressing either receptor, both PTH(1-34) and PTHrP(1-36) stimulated the increase in intracellular free calcium and cAMP accumulation to the same extent (Fig. 18).

Relationship of PTH/PTHrP receptors

The amino acid sequence of the human PTH/PTHrP receptor displays a very high degree of conservation compared to the bone PTH/PTHrP receptor from rat, a eutherian mammal, while its sequence identity with the PTH/PTHrP receptor with the opossum, a marsupial mammal, is less marked. Like the opossum kidney and the rat bone receptor, the human kidney receptor induces an increase in both intra-cellular cAMP and intracellular free calcium when challenged with either PTH or PTHrP. Despite the high degree of homology between the human PTH/PTHrP receptor and the opossum and rat homologs, the transiently expressed human receptor has some functional characteristics that are distinct from those of the rat bone receptor. These include a slightly higher affinity for PTH(1-34) and a significantly decreased affinity for PTHrP(1-36). Higher affinities were observed for PTH(3-34) and in particular for PTH(7-34), the affinity of which for the human receptor was about 35-fold higher in comparison to the rat bone receptor. These findings may have significant implications for the future development of PTH/PTHrP analogues, since they predict that species-specific tissues would be the appropriate tissues for testing the potency of antagonists (and agonists) in vitro.

Relationship of PTH/PTHrP receptors to other receptors

The biochemical properties of PTH and PTHrP receptors suggest that they are members of the class of

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membrane receptor molecules known as G-protein-linked membrane receptors. The structural features of well-characterized G-protein receptors indicate that they all have at least seven regions of several consecutive
5 hydrophobic amino acids, each of which regions is of sufficient length to span the plasma membrane.

One subfamily of G-protein-linked membrane receptors, termed the glycopeptide receptor subfamily, includes receptors that bind and are activated by
10 glycopeptide hormones (thyroid-stimulating hormone, luteinizing hormone, follicle-stimulating hormone, and chorionic gonadotropin). All of these receptors are characterized by (1) extensive putative amino-terminal extracellular domains (greater than 300 amino acids) that
15 are thought to contain some or all of the ligand-binding domains, and (2) considerable amino-acid homology, particularly in the seven putative transmembrane domains. A second subfamily, termed the adrenergic/muscarinic subfamily, includes receptors that are activated by small
20 ligands, such as the catecholamines, neuromuscular transmitters, and retinol. These receptors are all characterized by relatively short (25-75 amino acids) putative amino-terminal extracellular domains, as well as considerable amino acid homology, particularly in the
25 seven putative transmembrane domains. Activation of these receptors by their ligands appears to involve at least several of the multiple transmembrane domains, and does not appear to involve the amino-terminal portion of the receptors.

30 Several structural characteristics which can be deduced from the predicted amino acid sequence of the rat PTH/PTHrP receptor (Fig. 3) indicate that the PTH/PTHrP is a G-protein-linked receptor. The amino terminus shows characteristic features of a signal peptide, including a
35 hydrophobic domain and the presence of three consecutive

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leucine residues. This amino acid stretch of 20-28 amino acids may serve as a leader sequence, similar to the amino terminus preceding the extracellular domains of other glycoprotein receptors. There is also a cluster of
5 seven hydrophobic segments which represent putative membrane-spanning domains (Fig. 19).

The predicted amino acid sequences of the opossum kidney, rat bone and human kidney PTH/PTHrP receptors indicate that they do not fit comfortably into either of
10 these G-protein linked receptor subfamilies. Overall homology of the rat and human PTH/PTHrP receptors with the glycopeptide receptor and adrenergic/muscarinic subfamilies is approximately 10 to 20%, with a somewhat higher degree of homology within the transmembrane
15 domains. The latter is to be expected because of the limited menu of hydrophobic amino acids that could occur in those regions. Twenty percent homology is far less than that found among the receptors generally accepted to be members of each of these subfamilies. Additionally,
20 there are no portions of these sequences that have what could be characterized as intense homology (i.e., exactly matching amino acid sequences), even over limited regions.

Recent comparison with the newly characterized
25 secretin and calcitonin receptors (Ishihara et al., EMBO J 10:1635, 1991; Lin et al., Science 254:1022, 1991) has revealed between 30 and 40% identity between these receptors and the PTH/PTHrP receptor. Although the PTH/PTHrP receptor is more than 100 amino acids longer
30 than the calcitonin receptor, there is an ~32% identify between the amino acid sequences of the opossum kidney PTH/PTHrP receptor (SEQ ID NO NO.:2) and porcine kidney calcitonin receptor (GenBank accession no. M74420). A stretch of 17 out of 18 amino acids in the putative
35 transmembrane domain VII are identical. Also, two out of

four N-linked glycosylation sites and the position of seven out of eight. potentially extracellular cysteines are conserved. Major differences between the two receptors appear to lie in their NH*-
5 terminal and COOH-terminal domains. Comparison of amino acid sequences of the rat secretin receptor (GenBank accession no. X59132) and the human PTH/PTHrP receptor indicates that there is a 43% identity between these two receptors, with a stretch of 21 out of 25 amino acids of the putative transmembrane domain VII being identical. The
10 similarity between the PTH/PTHrP, calcitonin and secretin receptors suggests that they represent a new family of seven transmembrane-spanning G protein-coupled receptors that activate adenylate cyclase. Given the amino acid sequences of these receptors, those skilled in the art would be able to compare these sequences for regions of
15 identity which would be useful in the design of nucleic acid probes which could then be used for the identification and isolation of other receptors which would belong to this family.

Deposit of Clones

The cDNA expression plasmids R15B, OK-0, and OK-H; the phage HPG1; and
20 a plasmid (termed 8A6) containing part of the human clone have been deposited with the American Type Culture Collection (ATCC), where they bear the respective accession numbers ATCC No. 68571, 68572, 68573, 40998 and 68570. Applicants' assignee, The General Hospital Corporation, represents that the ATCC is a depository affording
25 permanence of the deposits and ready accessibility thereto by the public if a patent is granted. All restrictions on the availability to the

public of the material so deposited will be irrevocably removed upon the granting of a patent. The material will be available during the pendency of the patent application. The deposited material will be
5 maintained with all the care necessary to keep it viable and uncontaminated for a period of at least five years after the most recent request for the furnishing of a sample of the deposited plasmid, and in any case, for a period of at least thirty (30) years after the date of deposit or for the enforceable life of the patent,
10 whichever period is longer. Applicants' assignee acknowledges its responsibility to replace the deposits should the depository be unable to furnish a sample when requested due to the condition of the deposit.

POLYPEPTIDES

15 Polypeptides according to the invention include the opossum and rat and human parathyroid hormone receptors as shown in Figs. 1-3 and 6, respectively, and any other naturally-occurring receptor which can be produced by methods analogous to those used to clone and express these receptors, or by methods utilizing as a probe all or part of one
20 of the sequences described herein. In addition, any analog or fragment of a PTH receptor capable of binding to a parathyroid hormone or a parathyroid hormone-related protein is within the invention.

Specific receptor analogs of interest include full-length or partial receptor proteins having an amino acid sequence which differs
25 only by conservative amino acid substitutions: for example, substitution of one amino acid for another of the same class (e.g., valine for glycine; arginine for lysine, etc.), or by one or more non-conservative amino-acid substitutions,

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deletions, or insertions located at positions which do not destroy the receptor's ability to bind to parathyroid hormone or parathyroid hormone-related protein.

Specific receptor fragments of particular interest include, but are not limited to, portions of the receptor deduced to be extracellular from the primary amino acid sequence, using a hydrophobicity/hydrophilicity calculation such as the Chou-Fasman method (see, e.g., Chou and Fasman, Ann. Rev. Biochem. 47:251, 1978).

10 Hydrophilic domains, particularly ones surrounded by hydrophobic stretches (e.g., transmembrane domains) of at least 10 amino acids, present themselves as strong candidates for extracellular domains. Fig. 21 illustrates a predicted arrangement of extracellular, intracellular, and transmembrane domains of one PTH receptor.

15

Examples of specific PTH receptor fragments include those with the following amino acid sequences (shown as standard single-letter symbols), derived from the deduced amino acid sequence of the R15B clone:

20

Extracellular domains:

- RP-1: TNETREREVFDRLGMIYTVG (SEQ ID NO.: 5)
RP-2: VLYSGFTLDEAERLTEEEL (SEQ ID NO.: 6)
RP-3: VTFFLYFLATNYYWILVEG (SEQ ID NO.: 7)
25 RP-4: Y-RATLANTGCWDLSSGHKKWIIQVP (SEQ ID NO.: 8)
RP-5: PYTEVSGTLWQIQMHYEM (SEQ ID NO.: 9)
RP-6: DDVFTKEEQIFLLHRAQA (SEQ ID NO.: 10)

Intracellular domains:

- RPI-7: FRRLHCTRNY (SEQ ID NO.: 11)
30 RPI-8: EKKYLWGFTL (SEQ ID NO.: 12)
RPI-9: VLATKLRETNAGRCDTRQQYRKLLK (SEQ ID NO.: 13)

These fragments were synthesized and purified by HPLC according to the method of Keutmann et al., (Endocrinology 117: 1230, 1984).

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EXPRESSION OF POLYPEPTIDES

Polypeptides according to the invention may be produced by expression from a recombinant nucleic acid having a sequence encoding part or all of a cell receptor of the invention, using any appropriate expression system: e.g., transformation of a suitable host cell (either prokaryotic or eukaryotic) with the recombinant nucleic acid in a suitable expression vehicle (e.g., pcDNAI). The precise host cell used is not critical to the invention; however, in the case wherein the polypeptides of the invention include all or part of the PTH/PTHrP receptor, the following host cells are preferred: COS cells, LLC-PK1 cells, OK cells, AtT20 cells, and CHO cells. The method of transfection and the choice of expression vehicle will depend on the host system selected. Mammalian cell transfection methods are described, e.g., in Ausubel et al. (Current Protocols in Molecular Biology, John Wiley & Sons, New York, 1989); expression vehicles may be chosen from those discussed, e.g., in Cloning Vectors: A Laboratory Manual (P.H. Pouwels et al., 1985, Supp. 1987). Stably transfected cells are produced via integration of receptor DNA into the host cell chromosomes. Suitable DNAs are inserted into pcDNA, pcDNAI-Neo, or another suitable plasmid, and then cells are transfected with this plasmid with or without cotransfection with psV-2-Neo, or psV-2-DHFR by standard electroporation, calcium phosphate, and/or DEAE/Dextran techniques. Selection of transfected cells is performed using progressively increasing levels of G418 (Geneticin, GIBCO), and if necessary, methotrexate.

DNA sequences encoding the polypeptides of the invention can also be expressed in a prokaryotic host cell. DNA encoding a cell receptor or receptor fragment is carried on a vector operably linked to control signals capable of effecting expression in the prokaryotic host.

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If desired, the coding sequence may contain, at its 5' end, a sequence encoding any of the known signal sequences capable of effecting secretion of the expressed protein into the periplasmic space of the host cell, thereby facilitating recovery of the protein and subsequent purification. Prokaryotes most frequently used are various strains of E. coli; however, other microbial strains may also be used. Plasmid vectors are used which contain replication origins, selectable markers, and control sequences derived from a species compatible with the microbial host. For example, E. coli may be transformed using derivatives of pBR322, a plasmid constructed by Bolivar et al. (Gene 2: 95, 1977) using fragments derived from three naturally-occurring plasmids, two isolated from species of Salmonella, and one isolated from E. coli. pBR322 contains genes from ampicillin and tetracycline resistance, and thus provides multiple selectable markers which can be either retained or destroyed in constructing the desired expression vector. Commonly used prokaryotic control sequences (also referred to as "regulatory elements") are defined herein to include promoters for transcription initiation, optionally with an operator, along with ribosome binding site sequences. Promoters commonly used to direct protein expression include the beta-lactamase (penicillinase), the lactose (lac) (Chang et al., Nature 198: 1056, 1977) and the tryptophan (Trp) promoter systems (Goeddel et al., Nucl. Acids Res. 8: 4057, 1980) as well as the lambda-derived P_L promoter and N-gene ribosome binding site (Simatake et al., Nature 292:128, 1981).

The nature of the cell receptor proteins of the invention is such that, upon expression within a cell, it is moved to the cellular membrane and partially through the membrane, so that part of it remains embedded in the

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membrane, part extends outside the cell, and part remains within the cell. Transformed cells bearing such embedded cell receptors may themselves be employed in the methods of the invention, or the receptor protein may be
5 extracted from the membranes and purified.

Expression of peptide fragments lacking the hydrophobic portions of the protein responsible for anchoring the intact protein in the cellular membrane would not be expected to become embedded in the membrane;
10 whether they remain within the cell or are secreted into the extracellular medium depends upon whether or not a mechanism promoting secretion (e.g., a signal peptide) is included. If secreted, the polypeptide of the invention can be harvested from the medium; if not, the cells must
15 be broken open and the desired polypeptide isolated from the entire contents of the cells. Specific examples of polypeptides which might be expressed include, without limitation:

1) Amino-terminal portion comprising amino acids
20 1-192, including the putative leader sequence, of the rat bone PTH/PTHrP receptor as shown in Fig. 3.

2) Amino-terminal portion comprising amino acids 27-192, excluding the putative leader sequence, of the rat bone PTH/PTHrP receptor as shown in Fig. 3.

25 3) The full-length PTH/PTHrP receptor from rat bone, as shown in Fig 3.

4) RP-1 (as described above).

5) RP-2 (as described above).

The polypeptide of the invention can be readily
30 purified using affinity chromatography. Antibodies to these polypeptides, or the receptor specific ligands, (e.g., the hormones PTH and PTHrP for the PTH/PTHrP receptor) may be covalently coupled to a solid phase support such as Sepharose 4 CNBr-activated sepharose
35 (Pharmacia), and used to separate the polypeptide of the

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invention from any contaminating substances. Typically 1 mg of ligand or antibody will be incubated with CNBr-activated sepharose at 4°C for 17-20 h (with shaking). The sepharose is rinsed with 1 M Tris HCL (pH8) to block excess active sites. The sepharose-PTH, sepharose-PTHrP, or sepharose-antibody is then incubated with the crude polypeptide in phosphate-buffered saline (pH 7.4) at 4°C for 2 h (with shaking). The sepharose is then typically packed in a column, thoroughly washed with PBS (typically 10 times the column volume), and eluted with dilute HCl in H₂O (pH 1.85). The eluate may then be concentrated by lyophylization and its purity checked, for example, by reverse phase HPLC.

ANTI-CELL RECEPTOR ANTIBODIES

Cell receptor or receptor fragments of the invention may be used to generate antibodies by any conventional method well known to those skilled in the art, including those which generate polyclonal antibodies and those which generate monoclonal antibodies. For example, the deduced amino acid sequence of the PTH receptor reveals a protein structure that appears to have several transmembrane (i.e., hydrophobic) domains interspersed with presumably extracellular and intracellular regions (see Fig. 21) analogous to those found in other G protein-linked receptors. This information can be used to guide the selection of regions of the receptor protein which would be likely to be exposed on the cell surface, and thus would be presented to antibodies in vivo. A short peptide representing one or more of such regions may be synthesized (e.g., chemically or by recombinant DNA techniques) and used to immunize an animal (e.g., a rabbit or a mouse) to generate polyclonal or monoclonal antibodies. For example, certain of the peptides of the PTH/PTHrP receptor listed above (RP-1, RP-5 and RP-6) have been

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chemically synthesized using standard techniques and used to generate polyclonal antibodies in rabbits by the following procedure:

A preparation of a given peptide emulsified with complete Freund's Adjuvant is injected intradermally into rabbits. Booster injections are emulsified in or complete adjuvant and injected at monthly intervals.

Antibody titer is assessed using either of two methods. First, serial dilutions of the antiserum in 1% normal rabbit serum are incubated with ^{125}I -labelled PTH/PTHrP receptor fragment by standard methods (e.g., see Segre et al., supra) for 24 h at 4° C. The bound ^{125}I -PTH/PTHrP receptor fragments are separated from unbound by addition of 100 μl of second antibody (anti-rabbit IgG, Sigma) diluted 1:20 and 1 ml of 5% polyethylene glycol, followed by centrifugation at 2000 rpm for 30 min. at 4° C. The supernatant is removed and the pellet analyzed for radioactivity in a γ -counter. In the second method, cell lines expressing either native (e.g., ROS 17/2.8, OK, SaOS-02 cells) or recombinant (COS cells or CHO cells transfected with R15B, OK-O or OK-H) PTH/PTHrP receptors are incubated with serially diluted antibody at 4°C, 20°C or 37°C for 1- 4 h. The cells are rinsed with PBS (x3) and incubated for 2 h at 4°C with ^{125}I -labelled (NEN, Dupont) or FITC-labelled (Sigma) second antibodies. After rinsing (x3 with PBS), the cells were either lysed with 0.1 M NaOH and counted in γ -counter (if ^{125}I -labelled second antibody was used) or fixed with 1% paraformaldehyde and examined by fluorescent microscopy (if FITC-labelled second antibody was used).

Another method for producing antibodies utilizes as antigen the intact cell receptor protein of the invention expressed on the surface of cells (e.g., mammalian cells, such as COS cells, transfected with DNA

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encoding the receptor). Such cells are prepared by standard techniques, e.g., by the DEAE-dextran transfection method, using a vector encoding and capable of directing high-level expression of the cell receptor.

5 Such cells may be used to generate polyclonal or monoclonal antibodies. For example, monoclonal antibodies specific for the PTH/PTHrP receptor may be produced by the following procedure:

Intact COS cells expressing high levels of rat
10 recombinant PTH receptors on the cell surface are injected intraperitoneally (IP) into Balb-c mice (Charles River Laboratories, Willmington, MA). The mice are boosted every 4 weeks by IP injection, and are hyperimmunized by an intravenous (IV) booster 3 days
15 before fusion. Spleen cells from the mice are isolated and are fused by standard methods to myeloma cells. Hybridomas are selected in standard hypoxanthine/aminopterin/thymine (HAT) medium, according to standard methods. Hybridomas secreting antibodies
20 which recognize the PTH receptor are initially identified by screening with cell lines which naturally express abundant copies of the PTH-receptor per cell (such as ROS17/2.8 or OK cells), using standard immunological techniques. Those hybridomas which produce antibodies
25 capable of binding to the PTH receptor are cultured and subcloned. Secondary screening with radioreceptor and cAMP stimulation assays can then be performed to further characterize the monoclonal antibodies (see below).

SCREENING FOR PTH RECEPTOR ANTAGONISTS AND AGONISTS

30 The polypeptides and antibodies of the invention and other compounds may be screened for PTH-competition and for antagonistic or agonistic properties using the assays described herein.

In one example, those antibodies that recognize
35 the PTH receptor on the intact cells are screened for

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their ability to compete with PTH or PTHrP for binding to a PTH/PTHrP receptor. Cells expressing PTH receptor on the cell surface are incubated with the ^{125}I -PTH analog, ^{125}I -NlePTH or ^{125}I -PTHrP in the presence or absence of the polyclonal or monoclonal antibody to be tested, for 4 h at 15°C. The antibody used may be from crude antiserum, cell medium, or ascites, or in purified form. After incubation, the cells are rinsed with binding buffer (e.g., physiological saline), lysed, and quantitatively analyzed for radioactivity using a gamma-counter. Antibodies that reduce binding of the PTH analog to the PTH receptor are classified as competitive; those which do not are noncompetitive.

Compounds, including antibodies and polypeptides, may be screened for their agonistic or antagonistic properties using the cAMP accumulation, intracellular calcium, and/or inositol phosphate assays described above. Cells expressing PTH receptor on the cell surface are incubated with PTH, PTH-receptor antibody, or a combination of both, for 5 - 60 minutes at 37°C, in the presence of 2 mM IBMX (3-isobutyl-1-methyl-xanthine, Sigma, St. Louis, MO). Cyclic AMP accumulation is measured by specific radio-immunoassay, as described above. A compound that competes with PTH for binding to the PTH receptor, and that inhibits the effect of PTH on cAMP accumulation, is considered a competitive PTH antagonist. Conversely, a compound that does not compete for PTH binding to the PTH receptor, but which still prevents PTH activation of cAMP accumulation (presumably by blocking the receptor activation site) is considered a non-competitive antagonist. A compound that competes with PTH for binding to the PTH receptor, and which stimulates cAMP accumulation in the presence or absence of PTH, is a competitive agonist. A compound that does not compete with PTH for binding to the PTH receptor but

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which is still capable of stimulating cAMP accumulation in the presence or absence of PTH, or which stimulates a higher accumulation than that observed by PTH alone, would be considered a non-competitive agonist.

5 USE

The polypeptides, antibodies, and other compounds of the invention are useful for the diagnosis, classification, prognosis, and/or treatment of disorders which may be characterized as related to the interaction
10 between a cell receptor of the invention and its specific ligand. For example, some forms of hypercalcemia and hypocalcemia are related to the interaction between PTH and PTHrP and the PTH/PTHrP receptor(s). Hypercalcemia is an condition in which there is an abnormal elevation
15 in serum calcium level; it is often associated with other diseases, including hyperparathyroidism, osteoporosis, carcinomas of the breast, lung and prostate, epidermoid cancers of the head and neck of the esophagus, multiple myeloma, and hypernephroma. Hypocalcemia, a condition in
20 which the serum calcium level is abnormally low, may result from a deficiency of effective PTH, e.g., following thyroid surgery.

In a first example, the compounds of the invention are used to manufacture diagnostic agents which are used
25 as diagnostic tools to diagnose hypercalcemia and to distinguish between hypercalcemic conditions, i.e., to differentiate hypercalcemia mediated by PTH or PTHrP (e.g., hyperparathyroidism and humoral hypercalcemia of malignancy), from hypercalcemia associated with diseases
30 which do not involve these factors (e.g., local osteolytic hypercalcemia mediated by the presence of metastatic tumor cells in direct contact with bone, and certain rare types of malignancy-related hypercalcemias mediated by an increase of humoral factors, such as
35 osteoclast activating factor (interleukin), lymphotoxin,

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calcitriol, type E prostaglandins, and vitamin D-like sterols).

In one method of diagnosis, serum total and/or ionized calcium levels are measured by standard techniques before and after the administration of the PTH or PTHrP antagonists of the invention. PTH or PTHrP related hypercalcemias would be detectable as a decrease in serum calcium levels following administration of the antagonist of the invention. In contrast, for hypercalcemic conditions mediated by factors other than PTH or PTHrP, the serum calcium levels would remain unchanged even after administration of the antagonist.

Another diagnostic application of the invention permits measurement of the level of PTH or PTHrP in a biological sample in order to diagnose PTH or PTHrP related tumors, e.g., tumors which are associated with humoral hypercalcemia of malignancy, and for monitoring the levels of PTH or PTHrP during cancer therapy. This method involves assaying binding of the recombinant parathyroid hormone receptor of the invention to PTH or PTHrP present in a tissue sample, using the binding assay described herein. The level of binding may be determined directly (e.g., by using radioactively labelled PTH receptor, and assaying the radioactivity bound to endogenous PTH). Alternatively, binding of PTH receptor to the sample (e.g., a tissue section) may be followed by staining of the tissue sections with an antibody specific for the PTH receptor, using standard immunological techniques (Chin et al., Hybridoma 5:339, 1986).

In a third diagnostic approach, one could stably transfect cell lines (by the methods described in Ausubel et al., Current Protocols in Molecular Biology, Wiley Publishers, New York, 1987) with a PTH receptor gene linked to an appropriate promoter (e.g., the metallothionine promoter). Alternatively, the PTH/PTHrP

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receptor could be expressed from a eukaryotic vector, i.e., pcDNAI, and cotransfected with a mutant DHFR gene that will allow further gene amplification via methotrexate selection (Simonsen et al., Proc. Natl. Acad. Sci., 80:2495-2499, 1983). Such high-level expression of the gene produces an immortal cell line which is oversensitive to PTH or PTHrP. Such cells provide a particularly useful tool for detecting serum blood levels of PTH or PTHrP. Such a cell line may be used for diagnosis of conditions involving elevated PTH or PTHrP levels (e.g., those described above) or for conditions involving unusually low levels of PTH or PTHrP (e.g., those described above). Such a cell line is also useful for monitoring the regression or increase of PTH or PTHrP levels during therapy for hypercalcemia or hypocalcemia, respectively.

A patient who is suspected of being hypercalcemic may be treated using the compounds of the invention. Rapid intervention is important because symptoms may appear abruptly and, unless reversed, can be fatal. In one application, serum calcium levels are stabilized by an immediate course of treatment which includes antagonists of PTH or PTHrP. Such antagonists include the compounds of the invention which have been determined (by the assays described herein) to interfere with PTH receptor-mediated cell activation. To administer the antagonist, the appropriate antibody or peptide (is used in the manufacture of a medicament, generally by being formulated in an appropriate carrier such as physiological saline, and administered intravenously, at a dosage that provides adequate competition for PTH or PTHrP binding to the PTH receptor (e.g., a dosage sufficient to lower the serum calcium level to below 10 mg/dl). Typical dosage would be 1 ng to 10 mg of the antibody or peptide per kg body weight per day.

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Treatment may be repeated as necessary for long term maintenance of acceptable calcium levels (i.e., levels < 10.1 mg/dl). This may be necessary for acute treatment of an underlying disease condition triggering
5 hypercalcemia; or it may be used, e.g., for chronic treatment of conditions such as osteoporosis.

In another application, the compounds of the invention which have been characterized, according to the methods of the invention, to be agonists are used
10 therapeutically to treat hypocalcemia: e.g., that resulting from the partial or complete surgical removal of the parathyroid glands. Agonists may be formulated in a suitable carrier (e.g., physiological saline) and are preferably administered intravenously in a dosage that
15 causes a rise in serum calcium to an acceptable level (i.e., approximately 8 mg/dl). A useful dosage range would be 1 ng to 10 mg of the agonist per kg body weight per day. Treatment may be repeated as necessary to maintain suitable serum calcium levels; long term
20 treatment may be necessary for patients who have undergone parathyroid gland removal.

The nucleic acids of the invention may also be used therapeutically. Oligonucleotides which are antisense to PTH receptor mRNA (or nucleic acid
25 constructs which express RNA that is antisense to PTH receptor mRNA) may be utilized as an anticancer therapy. This approach is useful, e.g., for hypercalcemias resulting from a genomic rearrangement or amplification which increases the amount or activity of PTH receptor,
30 PTH or PTHrP. The method would involve introduction of the antisense oligonucleotide into the tumor cells in vivo. The antisense strand hybridizes with endogenous PTH receptor mRNA, interfering with translation of the protein, thereby reducing production of PTH receptor in
35 such cells, and reducing PTH/PTHrP-associated neoplastic

growth. Methods for antisense design and introduction into host cells are described, for example, in Weinberg et al., U.S. Patent No. 4,740,463. The biochemical characterization of the OK-H, OK-0 and R15B PTH/PTHrP receptors of the invention demonstrate that the two transduction pathways now known to be triggered by the interaction of PTH with its receptor are distinct and may be separated. The predicted amino acid sequences of these receptors indicate that OK-H, which does not appear to activate inositol phosphate metabolism to any detectable degree, is 70 amino acids shorter at the carboxy-terminus than OK-0 or R15B. By using the sequences of the invention and the information disclosed herein, one could clone and then alter (e.g. by site-directed mutagenesis) PTH/PTHrP receptor genes from any species to generate PTH/PTHrP receptors which do not activate phospholipase C. This could potentially allow the separation of different PTH-mediated actions, including bone resorption and bone formation, and could of great importance for the treatment of various bone disorders such as osteoporosis.

Nucleic acids of the invention which encode a PTH receptor may also be linked to a selected tissue-specific promoter and/or enhancer and the resultant hybrid gene introduced, by standard methods (e.g., as described by Leder et al., U.S. Patent No. 4,736,866), into an animal embryo at an early developmental stage (e.g., the fertilized oocyte stage), to produce a transgenic animal which expresses elevated levels of PTH receptor in selected tissues (e.g., the osteocalcin promoter for bone). Such promoters are used to direct tissue-specific expression of the PTH receptor, in the transgenic animal. The form of PTH receptor utilized can be one which encodes a PTE receptor similar to that of the animal species used, or

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it can encode the PTH receptor homolog of a different species. In one particular example, transgenic chickens are engineered to express the PTH receptor from a promoter which directs high-level expression in chicken oviducts. Such an animal is expected to produce eggs with higher calcium content, and thus harder shells.

Other Embodiments

Other embodiments are within the following claims. For example, the nucleic acid of the invention includes genes or cDNAs or RNAs originally isolated from any vertebrate species, including birds or mammals such as marsupials, rodents, or humans. The high degree of homology demonstrated for the PTH receptors from such diverse species as opossum, rat, and human indicates that the methods of isolating PTH receptors disclosed herein will be broadly applicable to the isolation of related cell receptors from a wide variety of species.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Massachusetts General Hospital
 Segre, Gino V.
 Kronenberg, Henry M.
 Abou-Samra, Abdul-Badi
 Juppner, Harald
 Potts, Jr., John T.
 Schipani, Ernestina
- (ii) TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR
 AND DNA ENCODING SAME
- (iii) NUMBER OF SEQUENCES: 21
- (v) COMPUTER READABLE FORM:
 (A) MEDIUM TYPE: Diskette
 (B) COMPUTER: IBM™ Compatible
 (C) OPERATING SYSTEM: Windows™ 95
 (D) SOFTWARE: FastSEQ for Windows™ Version 2.0b
- (vi) CURRENT APPLICATION DATA:
 (A) CANADIAN PATENT APPLICATION NUMBER: 2,107,569
 (B) FILING DATE: APRIL 6, 1992
- (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: US07/681,702
 (B) FILING DATE: 1991-04-05
- (viii) 47984/4

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1862 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (ix) FEATURE:
 (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 98...1642
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGGGCACAGC CACCCTGTTG GTAGTCCAGG GGCCAGCCCA CTGAGCTGGC ATATCAGCTG	60
GTGGCCCCGT TGGACTCGGC CCTAGGGAAC GGCGGCG ATG GGA GCG CCC CGG ATC	115
Met Gly Ala Pro Arg Ile	
1 5	
TCG CAC AGC CTT GCC TTG CTC CTC TGC TGC TCC GTG CTC AGC TCC GTC	163
Ser His Ser Leu Ala Leu Leu Leu Cys Cys Ser Val Leu Ser Ser Val	

10					15					20						
TAC	GCA	CTG	GTG	GAT	GCC	GAT	GAT	GTC	ATA	ACG	AAG	GAG	GAG	CAG	ATC	211
Tyr	Ala	Leu	Val	Asp	Ala	Asp	Asp	Val	Ile	Thr	Lys	Glu	Glu	Gln	Ile	
		25					30					35				
ATT	CTT	CTG	CGC	AAT	GCC	CAG	GCC	CAG	TGT	GAG	CAG	CGC	CTG	AAA	GAG	259
Ile	Leu	Leu	Arg	Asn	Ala	Gln	Ala	Gln	Cys	Glu	Gln	Arg	Leu	Lys	Glu	
	40					45					50					
GTC	CTC	AGG	GTC	CCT	GAA	CTT	GCT	GAA	TCT	GCC	AAA	GAC	TGG	ATG	TCA	307
Val	Leu	Arg	Val	Pro	Glu	Leu	Ala	Glu	Ser	Ala	Lys	Asp	Trp	Met	Ser	
55					60					65					70	
AGG	TCT	GCA	AAG	ACA	AAG	AAG	GAG	AAA	CCT	GCA	GAA	AAG	CTT	TAT	CCC	355
Arg	Ser	Ala	Lys	Thr	Lys	Lys	Glu	Lys	Pro	Ala	Glu	Lys	Leu	Tyr	Pro	
				75					80					85		
CAG	GCA	GAG	GAG	TCC	AGG	GAA	GTT	TCT	GAC	AGG	AGC	CGG	CTG	CAG	GAT	403
Gln	Ala	Glu	Glu	Ser	Arg	Glu	Val	Ser	Asp	Arg	Ser	Arg	Leu	Gln	Asp	
			90					95					100			
GGC	TTC	TGC	CTA	CCT	GAG	TGG	GAC	AAC	ATT	GTG	TGC	TGG	CCT	GCT	GGA	451
Gly	Phe	Cys	Leu	Pro	Glu	Trp	Asp	Asn	Ile	Val	Cys	Trp	Pro	Ala	Gly	
	105						110					115				
GTG	CCC	GGC	AAG	GTG	GTG	GCC	GTG	CCC	TGC	CCC	GAC	TAC	TTC	TAC	GAC	499
Val	Pro	Gly	Lys	Val	Val	Ala	Val	Pro	Cys	Pro	Asp	Tyr	Phe	Tyr	Asp	
	120					125					130					
TTC	AAC	CAC	AAA	GGC	CGA	GCC	TAT	CGG	CGC	TGT	GAC	AGC	AAT	GGC	AGC	547
Phe	Asn	His	Lys	Gly	Arg	Ala	Tyr	Arg	Arg	Cys	Asp	Ser	Asn	Gly	Ser	
135					140					145					150	
TGG	GAG	CTG	GTG	CCT	GGG	AAC	AAC	CGG	ACA	TGG	GCG	AAT	TAC	AGC	GAA	595
Trp	Glu	Leu	Val	Pro	Gly	Asn	Asn	Arg	Thr	Trp	Ala	Asn	Tyr	Ser	Glu	
				155					160					165		
TGT	GTC	AAG	TTT	CTG	ACC	AAC	GAG	ACC	CGG	GAA	CGG	GAA	GTC	TTT	GAT	643
Cys	Val	Lys	Phe	Leu	Thr	Asn	Glu	Thr	Arg	Glu	Arg	Glu	Val	Phe	Asp	
			170					175					180			
CGC	CTC	GGA	ATG	ATC	TAC	ACT	GTG	GGC	TAC	TCC	ATC	TCT	CTG	GGC	TCC	691
Arg	Leu	Gly	Met	Ile	Tyr	Thr	Val	Gly	Tyr	Ser	Ile	Ser	Leu	Gly	Ser	
		185					190					195				
CTC	ACT	GTG	GCT	GTG	CTG	ATT	CTG	GGT	TAC	TTT	AGG	AGG	TTA	CAT	TGC	739
Leu	Thr	Val	Ala	Val	Leu	Ile	Leu	Gly	Tyr	Phe	Arg	Arg	Leu	His	Cys	
	200					205					210					
ACC	CGA	AAC	TAC	ATT	CAC	ATG	CAT	CTC	TTC	GTG	TCC	TTT	ATG	CTC	CGG	787
Thr	Arg	Asn	Tyr	Ile	His	Met	His	Leu	Phe	Val	Ser	Phe	Met	Leu	Arg	
215					220					225					230	
GCT	GTA	AGC	ATC	TTC	ATC	AAG	GAT	GCT	GTG	CTC	TAC	TCG	GGG	GTT	TCC	835
Ala	Val	Ser	Ile	Phe	Ile	Lys	Asp	Ala	Val	Leu	Tyr	Ser	Gly	Val	Ser	
			235						240					245		

ACA	GAT	GAA	ATC	GAG	CGC	ATC	ACC	GAG	GAG	GAG	CTG	AGG	GCC	TTC	ACA	883
Thr	Asp	Glu	Ile	Glu	Arg	Ile	Thr	Glu	Glu	Glu	Leu	Arg	Ala	Phe	Thr	
			250					255					260			
GAG	CCT	CCC	CCT	GCT	GAC	AAG	GCG	GGT	TTT	GTG	GGC	TGC	AGA	GTG	GCG	931
Glu	Pro	Pro	Pro	Ala	Asp	Lys	Ala	Gly	Phe	Val	Gly	Cys	Arg	Val	Ala	
		265					270					275				
GTA	ACC	GTC	TTC	CTT	TAC	TTC	CTG	ACC	ACC	AAC	TAC	TAC	TGG	ATC	CTG	979
Val	Thr	Val	Phe	Leu	Tyr	Phe	Leu	Thr	Thr	Asn	Tyr	Tyr	Trp	Ile	Leu	
	280					285					290					
GTG	GAA	GGC	CTC	TAC	CTT	CAC	AGC	CTC	ATC	TTC	ATG	GCT	TTT	TTC	TCT	1027
Val	Glu	Gly	Leu	Tyr	Leu	His	Ser	Leu	Ile	Phe	Met	Ala	Phe	Phe	Ser	
295					300					305					310	
GAG	AAA	AAG	TAT	CTC	TGG	GGT	TTC	ACA	TTA	TTT	GGC	TGG	GGC	CTC	CCT	1075
Glu	Lys	Lys	Tyr	Leu	Trp	Gly	Phe	Thr	Leu	Phe	Gly	Trp	Gly	Leu	Pro	
			315					320						325		
GCC	GTG	TTT	GTC	GCT	GTG	TGG	GTG	ACC	GTG	AGG	GCT	ACA	CTG	GCC	AAC	1123
Ala	Val	Phe	Val	Ala	Val	Trp	Val	Thr	Val	Arg	Ala	Thr	Leu	Ala	Asn	
			330					335					340			
ACT	GAG	TGC	TGG	GAC	CTG	AGT	TCG	GGG	AAT	AAG	AAA	TGG	ATC	ATA	CAG	1171
Thr	Glu	Cys	Trp	Asp	Leu	Ser	Ser	Gly	Asn	Lys	Lys	Trp	Ile	Ile	Gln	
		345					350					355				
GTG	CCC	ATC	CTG	GCA	GCT	ATT	GTG	GTG	AAC	TTT	ATT	CTT	TTT	ATC	AAT	1219
Val	Pro	Ile	Leu	Ala	Ala	Ile	Val	Val	Asn	Phe	Ile	Leu	Phe	Ile	Asn	
	360					365					370					
ATA	ATC	AGA	GTC	CTG	GCT	ACT	AAA	CTC	CGG	GAG	ACC	AAT	GCA	GGG	AGA	1267
Ile	Ile	Arg	Val	Leu	Ala	Thr	Lys	Leu	Arg	Glu	Thr	Asn	Ala	Gly	Arg	
375					380					385					390	
TGT	GAC	ACG	AGG	CAA	CAG	TAT	AGA	AAG	CTG	CTG	AAG	TCC	ACG	CTA	GTC	1315
Cys	Asp	Thr	Arg	Gln	Gln	Tyr	Arg	Lys	Leu	Leu	Lys	Ser	Thr	Leu	Val	
				395					400					405		
CTC	ATG	CCG	CTA	TTT	GGG	GTG	CAC	TAC	ATC	GTC	TTC	ATG	GCC	ACG	CCG	1363
Leu	Met	Pro	Leu	Phe	Gly	Val	His	Tyr	Ile	Val	Phe	Met	Ala	Thr	Pro	
			410					415					420			
TAC	ACA	GAA	GTA	TCA	GGG	ATT	CTT	TGG	CAA	GTC	CAA	ATG	CAC	TAT	GAA	1411
Tyr	Thr	Glu	Val	Ser	Gly	Ile	Leu	Trp	Gln	Val	Gln	Met	His	Tyr	Glu	
		425					430					435				
ATG	CTC	TTC	AAT	TCA	TTC	CAG	GGA	TTT	TTC	GTT	GCC	ATT	ATA	TAC	TGT	1459
Met	Leu	Phe	Asn	Ser	Phe	Gln	Gly	Phe	Phe	Val	Ala	Ile	Ile	Tyr	Cys	
	440					445					450					
TTC	TGC	AAT	GGA	GAG	GTA	CAA	GCA	GAG	ATC	AAG	AAG	TCA	TGG	AGC	CGA	1507
Phe	Cys	Asn	Gly	Glu	Val	Gln	Ala	Glu	Ile	Lys	Lys	Ser	Trp	Ser	Arg	
455					460					465					470	

TGG ACC CTG GCC TTG GAC TTC AAG CGG AAG GCC CGG AGT GGC AGC AGT	1555
Trp Thr Leu Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser	
475 480 485	
ACC TAC AGC TAT GGC CCC ATG GTG TCA CAT ACA AGT GTC ACC AAT GTG	1603
Thr Tyr Ser Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val	
490 495 500	
GGA CCT CGA GGG GGC TGG CCT TGT CCC TCA GCC CTC GAC TAGCTCCTGG	1652
Gly Pro Arg Gly Gly Trp Pro Cys Pro Ser Ala Leu Asp	
505 510 515	
GGCTGGAGCC AGTGCCAATG GCCATCACCA GTTGCCTGGC TATGTGAAGC ATGGTTCCAT	1712
TTCTGAGAAC TCATTGCCTT CATCTGGCCC AGAGCCTGGC ACCAAAGATG ACGGGTATCT	1772
CAATGGCTCT GGACTTTATG AGCCAATGGT TGGGGAACAG CCCCCTCCAC TCCTGGAGGA	1832
GGAGAGAGAG ACAGTCATGT GACCCATATC	1862

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1863 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 98...1852

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

TGGGCACAGC CACCCTGTTG GTAGTCCAGG GGCCAGCCCA CTGAGCTGGC ATATCAGCTG	60
GTGGCCCCGT TGGACTCGGC CCTAGGGAAC GGCGGCG ATG GGA GCG CCC CGG ATC	115
Met Gly Ala Pro Arg Ile	
1 5	
TCG CAC AGC CTT GCC TTG CTC CTC TGC TGC TCC GTG CTC AGC TCC GTC	163
Ser His Ser Leu Ala Leu Leu Leu Cys Cys Ser Val Leu Ser Ser Val	
10 15 20	
TAC GCA CTG GTG GAT GCC GAT GAT GTC ATA ACG AAG GAG GAG CAG ATC	211
Tyr Ala Leu Val Asp Ala Asp Asp Val Ile Thr Lys Glu Glu Gln Ile	
25 30 35	
ATT CTT CTG CGC AAT GCC CAG GCC CAG TGT GAG CAG CGC CTG AAA GAG	259
Ile Leu Leu Arg Asn Ala Gln Ala Gln Cys Glu Gln Arg Leu Lys Glu	
40 45 50	
GTC CTC AGG GTC CCT GAA CTT GCT GAA TCT GCC AAA GAC TGG ATG TCA	307
Val Leu Arg Val Pro Glu Leu Ala Glu Ser Ala Lys Asp Trp Met Ser	
55 60 65 70	
AGG TCT GCA AAG ACA AAG AAG GAG AAA CCT GCA GAA AAG CTT TAT CCC	355

Arg	Ser	Ala	Lys	Thr	Lys	Lys	Glu	Lys	Pro	Ala	Glu	Lys	Leu	Tyr	Pro	
				75					80					85		
CAG	GCA	GAG	GAG	TCC	AGG	GAA	GTT	TCT	GAC	AGG	AGC	CGG	CTG	CAG	GAT	403
Gln	Ala	Glu	Glu	Ser	Arg	Glu	Val	Ser	Asp	Arg	Ser	Arg	Leu	Gln	Asp	
			90					95					100			
GGC	TTC	TGC	CTA	CCT	GAG	TGG	GAC	AAC	ATT	GTG	TGC	TGG	CCT	GCT	GGA	451
Gly	Phe	Cys	Leu	Pro	Glu	Trp	Asp	Asn	Ile	Val	Cys	Trp	Pro	Ala	Gly	
		105					110					115				
GTG	CCC	GGC	AAG	GTG	GTG	GCC	GTG	CCC	TGC	CCC	GAC	TAC	TTC	TAC	GAC	499
Val	Pro	Gly	Lys	Val	Val	Ala	Val	Pro	Cys	Pro	Asp	Tyr	Phe	Tyr	Asp	
	120					125					130					
TTC	AAC	CAC	AAA	GGC	CGA	GCC	TAT	CGG	CGC	TGT	GAC	AGC	AAT	GGC	AGC	547
Phe	Asn	His	Lys	Gly	Arg	Ala	Tyr	Arg	Arg	Cys	Asp	Ser	Asn	Gly	Ser	
135					140					145					150	
TGG	GAG	CTG	GTG	CCT	GGG	AAC	AAC	CGG	ACA	TGG	GCG	AAT	TAC	AGC	GAA	595
Trp	Glu	Leu	Val	Pro	Gly	Asn	Asn	Arg	Thr	Trp	Ala	Asn	Tyr	Ser	Glu	
				155				160						165		
TGT	GTC	AAG	TTT	CTG	ACC	AAC	GAG	ACC	CGG	GAA	CGG	GAA	GTC	TTT	GAT	643
Cys	Val	Lys	Phe	Leu	Thr	Asn	Glu	Thr	Arg	Glu	Arg	Glu	Val	Phe	Asp	
			170					175					180			
CGC	CTC	GGA	ATG	ATC	TAC	ACT	GTG	GGC	TAC	TCC	ATC	TCT	CTG	GGC	TCC	691
Arg	Leu	Gly	Met	Ile	Tyr	Thr	Val	Gly	Tyr	Ser	Ile	Ser	Leu	Gly	Ser	
		185					190					195				
CTC	ACT	GTG	GCT	GTG	CTG	ATT	CTG	GGT	TAC	TTT	AGG	AGG	TTA	CAT	TGC	739
Leu	Thr	Val	Ala	Val	Leu	Ile	Leu	Gly	Tyr	Phe	Arg	Arg	Leu	His	Cys	
	200					205					210					
ACC	CGA	AAC	TAC	ATT	CAC	ATG	CAT	CTC	TTC	GTG	TCC	TTT	ATG	CTC	CGG	787
Thr	Arg	Asn	Tyr	Ile	His	Met	His	Leu	Phe	Val	Ser	Phe	Met	Leu	Arg	
215					220					225					230	
GCT	GTA	AGC	ATC	TTC	ATC	AAG	GAT	GCT	GTG	CTC	TAC	TCG	GGG	GTT	TCC	835
Ala	Val	Ser	Ile	Phe	Ile	Lys	Asp	Ala	Val	Leu	Tyr	Ser	Gly	Val	Ser	
				235				240					245			
ACA	GAT	GAA	ATC	GAG	CGC	ATC	ACC	GAG	GAG	GAG	CTG	AGG	GCC	TTC	ACA	883
Thr	Asp	Glu	Ile	Glu	Arg	Ile	Thr	Glu	Glu	Glu	Leu	Arg	Ala	Phe	Thr	
			250				255						260			
GAG	CCT	CCC	CCT	GCT	GAC	AAG	GCG	GGT	TTT	GTG	GGC	TGC	AGA	GTG	GCG	931
Glu	Pro	Pro	Pro	Ala	Asp	Lys	Ala	Gly	Phe	Val	Gly	Cys	Arg	Val	Ala	
		265					270					275				
GTA	ACC	GTC	TTC	CTT	TAC	TTC	CTG	ACC	ACC	AAC	TAC	TAC	TGG	ATC	CTG	979
Val	Thr	Val	Phe	Leu	Tyr	Phe	Leu	Thr	Thr	Asn	Tyr	Tyr	Trp	Ile	Leu	
	280					285					290					
GTG	GAA	GGC	CTC	TAC	CTT	CAC	AGC	CTC	ATC	TTC	ATG	GCT	TTT	TTC	TCT	1027
Val	Glu	Gly	Leu	Tyr	Leu	His	Ser	Leu	Ile	Phe	Met	Ala	Phe	Phe	Ser	

295					300					305					310	
GAG	AAA	AAG	TAT	CTC	TGG	GGT	TTC	ACA	TTA	TTT	GGC	TGG	GGC	CTC	CCT	1075
Glu	Lys	Lys	Tyr	Leu	Trp	Gly	Phe	Thr	Leu	Phe	Gly	Trp	Gly	Leu	Pro	
				315					320					325		
GCC	GTG	TTT	GTC	GCT	GTG	TGG	GTG	ACC	GTG	AGG	GCT	ACA	CTG	GCC	AAC	1123
Ala	Val	Phe	Val	Ala	Val	Trp	Val	Thr	Val	Arg	Ala	Thr	Leu	Ala	Asn	
			330					335					340			
ACT	GAG	TGC	TGG	GAC	CTG	AGT	TCG	GGG	AAT	AAG	AAA	TGG	ATC	ATA	CAG	1171
Thr	Glu	Cys	Trp	Asp	Leu	Ser	Ser	Gly	Asn	Lys	Lys	Trp	Ile	Ile	Gln	
		345					350					355				
GTG	CCC	ATC	CTG	GCA	GCT	ATT	GTG	GTG	AAC	TTT	ATT	CTT	TTT	ATC	AAT	1219
Val	Pro	Ile	Leu	Ala	Ala	Ile	Val	Val	Asn	Phe	Ile	Leu	Phe	Ile	Asn	
	360					365					370					
ATA	ATC	AGA	GTC	CTG	GCT	ACT	AAA	CTC	CGG	GAG	ACC	AAT	GCA	GGG	AGA	1267
Ile	Ile	Arg	Val	Leu	Ala	Thr	Lys	Leu	Arg	Glu	Thr	Asn	Ala	Gly	Arg	
375				380					385					390		
TGT	GAC	ACG	AGG	CAA	CAG	TAT	AGA	AAG	CTG	CTG	AAG	TCC	ACG	CTA	GTC	1315
Cys	Asp	Thr	Arg	Gln	Gln	Tyr	Arg	Lys	Leu	Leu	Lys	Ser	Thr	Leu	Val	
				395					400					405		
CTC	ATG	CCG	CTA	TTT	GGG	GTG	CAC	TAC	ATC	GTC	TTC	ATG	GCC	ACG	CCG	1363
Leu	Met	Pro	Leu	Phe	Gly	Val	His	Tyr	Ile	Val	Phe	Met	Ala	Thr	Pro	
			410					415					420			
TAC	ACA	GAA	GTA	TCA	GGG	ATT	CTT	TGG	CAA	GTC	CAA	ATG	CAC	TAT	GAA	1411
Tyr	Thr	Glu	Val	Ser	Gly	Ile	Leu	Trp	Gln	Val	Gln	Met	His	Tyr	Glu	
		425					430					435				
ATG	CTC	TTC	AAT	TCA	TTC	CAG	GGA	TTT	TTC	GTT	GCC	ATT	ATA	TAC	TGT	1459
Met	Leu	Phe	Asn	Ser	Phe	Gln	Gly	Phe	Phe	Val	Ala	Ile	Ile	Tyr	Cys	
	440					445					450					
TTC	TGC	AAT	GGA	GAG	GTA	CAA	GCA	GAG	ATC	AAG	AAG	TCA	TGG	AGC	CGA	1507
Phe	Cys	Asn	Gly	Glu	Val	Gln	Ala	Glu	Ile	Lys	Lys	Ser	Trp	Ser	Arg	
455				460					465					470		
TGG	ACC	CTG	GCC	TTG	GAC	TTC	AAG	CGG	AAG	GCC	CGG	AGT	GGC	AGC	AGT	1555
Trp	Thr	Leu	Ala	Leu	Asp	Phe	Lys	Arg	Lys	Ala	Arg	Ser	Gly	Ser	Ser	
				475				480					485			
ACC	TAC	AGC	TAT	GGC	CCC	ATG	GTG	TCA	CAT	ACA	AGT	GTC	ACC	AAT	GTG	1603
Thr	Tyr	Ser	Tyr	Gly	Pro	Met	Val	Ser	His	Thr	Ser	Val	Thr	Asn	Val	
			490					495					500			
GGA	CCT	CGA	GGG	GGG	CTG	GCC	TTG	TCC	CTC	AGC	CCT	CGA	CTA	GCT	CCT	1651
Gly	Pro	Arg	Gly	Gly	Leu	Ala	Leu	Ser	Leu	Ser	Pro	Arg	Leu	Ala	Pro	
		505					510					515				
GGG	GCT	GGA	GCC	AGT	GCC	AAT	GGC	CAT	CAC	CAG	TTG	CCT	GGC	TAT	GTG	1699
Gly	Ala	Gly	Ala	Ser	Ala	Asn	Gly	His	His	Gln	Leu	Pro	Gly	Tyr	Val	
	520					525					530					

AAC	AAG	GAC	GTG	CCC	ACC	GGC	AGC	AGG	CGC	AGA	GGG	CGT	CCC	TGT	CTG	399
Asn	Lys	Asp	Val	Pro	Thr	Gly	Ser	Arg	Arg	Arg	Gly	Arg	Pro	Cys	Leu	
	95					100					105					
CCC	GAG	TGG	GAC	AAC	ATC	GTT	TGC	TGG	CCA	TTA	GGG	GCA	CCA	GGT	GAA	447
Pro	Glu	Trp	Asp	Asn	Ile	Val	Cys	Trp	Pro	Leu	Gly	Ala	Pro	Gly	Glu	
110					115					120					125	
GTG	GTG	GCA	GTA	CCT	TGT	CCC	GAT	TAC	ATT	TAT	GAC	TTC	AAT	CAC	AAA	495
Val	Val	Ala	Val	Pro	Cys	Pro	Asp	Tyr	Ile	Tyr	Asp	Phe	Asn	His	Lys	
				130					135					140		
GGC	CAT	GCC	TAC	AGA	CGC	TGT	GAC	CGC	AAT	GGC	AGC	TGG	GAG	GTG	GTT	543
Gly	His	Ala	Tyr	Arg	Arg	Cys	Asp	Arg	Asn	Gly	Ser	Trp	Glu	Val	Val	
			145					150					155			
CCA	GGG	CAC	AAC	CGG	ACG	TGG	GCC	AAC	TAC	AGC	GAG	TGC	CTC	AAG	TTC	591
Pro	Gly	His	Asn	Arg	Thr	Trp	Ala	Asn	Tyr	Ser	Glu	Cys	Leu	Lys	Phe	
		160					165					170				
ATG	ACC	AAT	GAG	ACG	CGG	GAA	CGG	GAG	GTA	TTT	GAC	CGC	CTA	GGC	ATG	639
Met	Thr	Asn	Glu	Thr	Arg	Glu	Arg	Glu	Val	Phe	Asp	Arg	Leu	Gly	Met	
	175					180					185					
ATC	TAC	ACC	GTG	GGA	TAC	TCC	ATG	TCT	CTC	GCC	TCC	CTC	ACG	GTG	GCT	687
Ile	Tyr	Thr	Val	Gly	Tyr	Ser	Met	Ser	Leu	Ala	Ser	Leu	Thr	Val	Ala	
190					195					200					205	
GTG	CTC	ATC	CTG	GCC	TAT	TTT	AGG	CGG	CTG	CAC	TGC	ACG	CGC	AAC	TAC	735
Val	Leu	Ile	Leu	Ala	Tyr	Phe	Arg	Arg	Leu	His	Cys	Thr	Arg	Asn	Tyr	
				210					215					220		
ATC	CAC	ATG	CAC	ATG	TTC	CTG	TCG	TTT	ATG	CTG	CGC	GCC	GCG	AGC	ATC	783
Ile	His	Met	His	Met	Phe	Leu	Ser	Phe	Met	Leu	Arg	Ala	Ala	Ser	Ile	
			225					230					235			
TTC	GTG	AAG	GAC	GCT	GTG	CTC	TAC	TCT	GGC	TTC	ACG	CTG	GAT	GAG	GCC	831
Phe	Val	Lys	Asp	Ala	Val	Leu	Tyr	Ser	Gly	Phe	Thr	Leu	Asp	Glu	Ala	
		240					245					250				
GAG	CGC	CTC	ACA	GAG	GAA	GAG	TTG	CAC	ATC	ATC	GCG	CAG	GTG	CCA	CCT	879
Glu	Arg	Leu	Thr	Glu	Glu	Glu	Leu	His	Ile	Ile	Ala	Gln	Val	Pro	Pro	
	255					260					265					
CCG	CCG	GCC	GCT	GCC	GCC	GTA	GGC	TAC	GCT	GGC	TGC	CGC	GTG	GCG	GTG	927
Pro	Pro	Ala	Ala	Ala	Ala	Val	Gly	Tyr	Ala	Gly	Cys	Arg	Val	Ala	Val	
270					275					280					285	
ACC	TTC	TTC	CTC	TAC	TTC	CTG	GCT	ACC	AAC	TAC	TAC	TGG	ATT	CTG	GTG	975
Thr	Phe	Phe	Leu	Tyr	Phe	Leu	Ala	Thr	Asn	Tyr	Tyr	Trp	Ile	Leu	Val	
				290					295					300		
GAG	GGG	CTG	TAC	TTG	CAC	AGC	CTC	ATC	TTC	ATG	GCC	TTT	TTC	TCA	GAG	1023
Glu	Gly	Leu	Tyr	Leu	His	Ser	Leu	Ile	Phe	Met	Ala	Phe	Phe	Ser	Glu	
			305					310					315			

AAG	AAG	TAC	CTG	TGG	GGC	TTC	ACC	ATC	TTT	GGC	TGG	GGT	CTA	CCG	GCT	1071
Lys	Lys	Tyr	Leu	Trp	Gly	Phe	Thr	Ile	Phe	Gly	Trp	Gly	Leu	Pro	Ala	
		320					325					330				
GTC	TTC	GTG	GCT	GTG	TGG	GTC	GGT	GTC	AGA	GCA	ACC	TTG	GCC	AAC	ACT	1119
Val	Phe	Val	Ala	Val	Trp	Val	Gly	Val	Arg	Ala	Thr	Leu	Ala	Asn	Thr	
	335					340					345					
GGG	TGC	TGG	GAT	CTG	AGC	TCC	GGG	CAC	AAG	AAG	TGG	ATC	ATC	CAG	GTG	1167
Gly	Cys	Trp	Asp	Leu	Ser	Ser	Gly	His	Lys	Lys	Trp	Ile	Ile	Gln	Val	
350					355					360					365	
CCC	ATC	CTG	GCA	TCT	GTT	GTG	CTC	AAC	TTC	ATC	CTT	TTT	ATC	AAC	ATC	1215
Pro	Ile	Leu	Ala	Ser	Val	Val	Leu	Asn	Phe	Ile	Leu	Phe	Ile	Asn	Ile	
				370					375					380		
ATC	CGG	GTG	CTT	GCC	ACT	AAG	CTT	CGG	GAG	ACC	AAT	GCG	GGC	CGG	TGT	1263
Ile	Arg	Val	Leu	Ala	Thr	Lys	Leu	Arg	Glu	Thr	Asn	Ala	Gly	Arg	Cys	
			385					390					395			
GAC	ACC	AGG	CAG	CAG	TAC	CGG	AAG	CTG	CTC	AGG	TCC	ACG	TTG	GTG	CTC	1311
Asp	Thr	Arg	Gln	Gln	Tyr	Arg	Lys	Leu	Leu	Arg	Ser	Thr	Leu	Val	Leu	
		400					405					410				
GTG	CCG	CTC	TTT	GGT	GTC	CAC	TAC	ACC	GTC	TTC	ATG	GCC	TTG	CCG	TAC	1359
Val	Pro	Leu	Phe	Gly	Val	His	Tyr	Thr	Val	Phe	Met	Ala	Leu	Pro	Tyr	
	415					420					425					
ACC	GAG	GTC	TCA	GGG	ACA	TTG	TGG	CAG	ATC	CAG	ATG	CAT	TAT	GAG	ATG	1407
Thr	Glu	Val	Ser	Gly	Thr	Leu	Trp	Gln	Ile	Gln	Met	His	Tyr	Glu	Met	
430					435					440					445	
CTC	TTC	AAC	TCC	TTC	CAG	GGA	TTT	TTT	GTT	GCC	ATC	ATA	TAC	TGT	TTC	1455
Leu	Phe	Asn	Ser	Phe	Gln	Gly	Phe	Phe	Val	Ala	Ile	Ile	Tyr	Cys	Phe	
				450					455					460		
TGC	AAT	GGT	GAG	GTG	CAG	GCA	GAG	ATT	AGG	AAG	TCA	TGG	AGC	CGC	TGG	1503
Cys	Asn	Gly	Glu	Val	Gln	Ala	Glu	Ile	Arg	Lys	Ser	Trp	Ser	Arg	Trp	
			465					470					475			
ACA	CTG	GCG	TTG	GAC	TTC	AAG	CGC	AAA	GCA	CGA	AGT	GGG	AGT	AGC	AGC	1551
Thr	Leu	Ala	Leu	Asp	Phe	Lys	Arg	Lys	Ala	Arg	Ser	Gly	Ser	Ser	Ser	
		480					485					490				
TAC	AGC	TAT	GGC	CCA	ATG	GTG	TCT	CAC	ACG	AGT	GTG	ACC	AAT	GTG	GGC	1599
Tyr	Ser	Tyr	Gly	Pro	Met	Val	Ser	His	Thr	Ser	Val	Thr	Asn	Val	Gly	
	495					500					505					
CCC	CGT	GCA	GGA	CTC	AGC	CTC	CCC	CTC	AGC	CCC	CGC	CTG	CCT	CCT	GCC	1647
Pro	Arg	Ala	Gly	Leu	Ser	Leu	Pro	Leu	Ser	Pro	Arg	Leu	Pro	Pro	Ala	
510					515					520					525	
ACT	ACC	AAT	GGC	CAC	TCC	CAG	CTG	CCT	GGC	CAT	GCC	AAG	CCA	GGG	GCT	1695
Thr	Thr	Asn	Gly	His	Ser	Gln	Leu	Pro	Gly	His	Ala	Lys	Pro	Gly	Ala	
			530						535				540			
CCA	GCC	ACT	GAG	ACT	GAA	ACC	CTA	CCA	GTC	ACT	ATG	GCG	GTT	CCC	AAG	1743

Pro	Ala	Thr	Glu	Thr	Glu	Thr	Leu	Pro	Val	Thr	Met	Ala	Val	Pro	Lys	
			545					550					555			
GAC	GAT	GGA	TTC	CTT	AAC	GGC	TCC	TGC	TCA	GGC	CTG	GAT	GAG	GAG	GCC	1791
Asp	Asp	Gly	Phe	Leu	Asn	Gly	Ser	Cys	Ser	Gly	Leu	Asp	Glu	Glu	Ala	
		560					565					570				
TCC	GGG	TCT	GCG	CGG	CCG	CCT	CCA	TTG	TTG	CAG	GAA	GGA	TGG	GAA	ACA	1839
Ser	Gly	Ser	Ala	Arg	Pro	Pro	Pro	Leu	Leu	Gln	Glu	Gly	Trp	Glu	Thr	
		575				580				585						
GTC	ATG	TGACTGGGCA	CTAGGGGGCT	AGACTGCTGG	CCTGGGCACA	TGGACAGATG										1895
Val	Met															
590																
GACCAAGAAG	CCAGTGTTTG	GCTGGTTGTC	TATTCGGGAT	CTGGACCAGG	AAGATAACAA											1955
AAGGAAAATG	GAAGTGGACG	AAGCAGAGAA	GAAGGAAGAG	GTTTTGCAGG	AATTAAATAT											2015
GTTTCCTCAG	TTGGATGATG	AGGACACAAG	GAAGGC													2051

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 28...1806

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

GGGATCCCGC	GGCCCTAGGC	GGTGGCG	ATG	GGG	ACC	GCC	CGG	ATC	GCA	CCC	GGC					54
			Met	Gly	Thr	Ala	Arg	Ile	Ala	Pro	Gly					
			1				5									
CTG	GCG	CTC	CTG	CTC	TGC	TGC	CCC	GTG	CTC	AGC	TCC	GCG	TAC	GCG	CTG	102
Leu	Ala	Leu	Leu	Leu	Cys	Cys	Pro	Val	Leu	Ser	Ser	Ala	Tyr	Ala	Leu	
10					15				20						25	
GTG	GAT	GCA	GAT	GAC	GTC	ATG	ACT	AAA	GAG	GAA	CAG	ATC	TTC	CTG	CTG	150
Val	Asp	Ala	Asp	Asp	Val	Met	Thr	Lys	Glu	Glu	Gln	Ile	Phe	Leu	Leu	
				30					35					40		
CAC	CGT	GCT	CAG	GCC	CAG	TGC	GAA	AAA	CGG	CTC	AAG	GAG	GTC	CTG	CAG	198
His	Arg	Ala	Gln	Ala	Gln	Cys	Glu	Lys	Arg	Leu	Lys	Glu	Val	Leu	Gln	
			45					50					55			
AGG	CCA	GCC	AGC	ATA	ATG	GAA	TCA	GAC	AAG	GGA	TGG	ACA	TCT	GCG	TCC	246
Arg	Pro	Ala	Ser	Ile	Met	Glu	Ser	Asp	Lys	Gly	Trp	Thr	Ser	Ala	Ser	
		60					65					70				
ACA	TCA	GGG	AAG	CCC	AGG	AAA	GAT	AAG	GCA	TCT	GGG	AAG	CTC	TAC	CCT	294

Thr	Ser	Gly	Lys	Pro	Arg	Lys	Asp	Lys	Ala	Ser	Gly	Lys	Leu	Tyr	Pro	
	75					80					85					
GAG	TCT	GAG	GAG	GAC	AAG	GAG	GCA	CCC	ACT	GGC	AGC	AGG	TAC	CGA	GGG	342
Glu	Ser	Glu	Glu	Asp	Lys	Glu	Ala	Pro	Thr	Gly	Ser	Arg	Tyr	Arg	Gly	
90					95					100					105	
CGC	CCC	TGT	CTG	CCG	GAA	TGG	GAC	CAC	ATC	CTG	TGC	TGG	CCG	CTG	GGG	390
Arg	Pro	Cys	Leu	Pro	Glu	Trp	Asp	His	Ile	Leu	Cys	Trp	Pro	Leu	Gly	
				110					115					120		
GCA	CCA	GGT	GAG	GTG	GTG	GCT	GTG	CCC	TGT	CCG	GAC	TAC	ATT	TAT	GAC	438
Ala	Pro	Gly	Glu	Val	Val	Ala	Val	Pro	Cys	Pro	Asp	Tyr	Ile	Tyr	Asp	
			125					130					135			
TTC	AAT	CAC	AAA	GGC	CAT	GCC	TAC	CGA	CGC	TGT	GAC	CGC	AAT	GGC	AGC	486
Phe	Asn	His	Lys	Gly	His	Ala	Tyr	Arg	Arg	Cys	Asp	Arg	Asn	Gly	Ser	
		140					145					150				
TGG	GAG	CTG	GTG	CCT	GGG	CAC	AAC	AGG	ACG	TGG	GCC	AAC	TAC	AGC	GAG	534
Trp	Glu	Leu	Val	Pro	Gly	His	Asn	Arg	Thr	Trp	Ala	Asn	Tyr	Ser	Glu	
	155					160					165					
TGT	GTC	AAA	TTT	CTC	ACC	AAT	GAG	ACT	CGT	GAA	CGG	GAG	GTG	TTT	GAC	582
Cys	Val	Lys	Phe	Leu	Thr	Asn	Glu	Thr	Arg	Glu	Arg	Glu	Val	Phe	Asp	
170					175					180					185	
CGC	CTG	GGC	ATG	ATT	TAC	ACC	GTG	GGC	TAC	TCC	GTG	TCC	CTG	GCG	TCC	630
Arg	Leu	Gly	Met	Ile	Tyr	Thr	Val	Gly	Tyr	Ser	Val	Ser	Leu	Ala	Ser	
				190					195					200		
CTC	ACC	GTA	GCT	GTG	CTC	ATC	CTG	GCC	TAC	TTT	AGG	CGG	CTG	CAC	TGC	678
Leu	Thr	Val	Ala	Val	Leu	Ile	Leu	Ala	Tyr	Phe	Arg	Arg	Leu	His	Cys	
			205					210					215			
ACG	CGC	AAC	TAC	ATC	CAC	ATG	CAC	CTG	TTC	CTG	TCC	TTC	ATG	CTG	CGC	726
Thr	Arg	Asn	Tyr	Ile	His	Met	His	Leu	Phe	Leu	Ser	Phe	Met	Leu	Arg	
		220					225					230				
GCC	GTG	AGC	ATC	TTC	GTC	AAG	GAC	GCT	GTG	CTC	TAC	TCT	GGC	GCC	ACG	774
Ala	Val	Ser	Ile	Phe	Val	Lys	Asp	Ala	Val	Leu	Tyr	Ser	Gly	Ala	Thr	
	235					240					245					
CTT	GAT	GAG	GCT	GAG	CGC	CTC	ACC	GAG	GAG	GAG	CTG	CGC	GCC	ATC	GCC	822
Leu	Asp	Glu	Ala	Glu	Arg	Leu	Thr	Glu	Glu	Glu	Leu	Arg	Ala	Ile	Ala	
250					255					260					265	
CAG	GCG	CCC	CCG	CCG	CCT	GCC	ACC	GCC	GCT	GCC	GGC	TAC	GCG	GGC	TGC	870
Gln	Ala	Pro	Pro	Pro	Pro	Ala	Thr	Ala	Ala	Ala	Gly	Tyr	Ala	Gly	Cys	
				270					275					280		
AGG	GTG	GCT	GTG	ACC	TTC	TTC	CTT	TAC	TTC	CTG	GCC	ACC	AAC	TAC	TAC	918
Arg	Val	Ala	Val	Thr	Phe	Phe	Leu	Tyr	Phe	Leu	Ala	Thr	Asn	Tyr	Tyr	
			285					290					295			
TGG	ATT	CTG	GTG	GAG	GGG	CTG	TAC	CTG	CAC	AGC	CTC	ATC	TTC	ATG	GCC	966
Trp	Ile	Leu	Val	Glu	Gly	Leu	Tyr	Leu	His	Ser	Leu	Ile	Phe	Met	Ala	

300						305						310						
TTC	TTC	TCA	GAG	AAG	AAG	TAC	CTG	TGG	GGC	TTC	ACA	GTC	TTC	GGC	TGG			1014
Phe	Phe	Ser	Glu	Lys	Lys	Tyr	Leu	Trp	Gly	Phe	Thr	Val	Phe	Gly	Trp			
	315						320				325							
GGT	CTG	CCC	GCT	GTC	TTC	GTG	GCT	GTG	TGG	GTC	AGT	GTC	AGA	GCT	ACC			1062
Gly	Leu	Pro	Ala	Val	Phe	Val	Ala	Val	Trp	Val	Ser	Val	Arg	Ala	Thr			
	330				335					340					345			
CTG	GCC	AAC	ACC	GGG	TGC	TGG	GAC	TTG	AGC	TCC	GGG	AAC	AAA	AAG	TGG			1110
Leu	Ala	Asn	Thr	Gly	Cys	Trp	Asp	Leu	Ser	Ser	Gly	Asn	Lys	Lys	Trp			
				350					355					360				
ATC	ATC	CAG	GTG	CCC	ATC	CTG	GCC	TCC	ATT	GTG	CTC	AAC	TTC	ATC	CTC			1158
Ile	Ile	Gln	Val	Pro	Ile	Leu	Ala	Ser	Ile	Val	Leu	Asn	Phe	Ile	Leu			
			365					370					375					
TTC	ATC	AAT	ATC	GTC	CGG	GTG	CTC	GCC	ACC	AAG	CAG	CGG	GAG	ACC	AAC			1206
Phe	Ile	Asn	Ile	Val	Arg	Val	Leu	Ala	Thr	Lys	Gln	Arg	Glu	Thr	Asn			
		380					385					390						
GCC	GGC	CGG	TGT	GAC	ACA	CGG	CAG	CAG	TAC	CGG	AAG	CTG	CTC	AAA	TCC			1254
Ala	Gly	Arg	Cys	Asp	Thr	Arg	Gln	Gln	Tyr	Arg	Lys	Leu	Leu	Lys	Ser			
	395					400					405							
ACG	CTG	GTG	CTC	ATG	CCC	CTC	TTT	GGC	GTC	CAC	TAC	ATT	GTC	TTC	ATG			1302
Thr	Leu	Val	Leu	Met	Pro	Leu	Phe	Gly	Val	His	Tyr	Ile	Val	Phe	Met			
	410				415					420					425			
GCC	ACA	CCA	TAC	ACC	GAG	GTC	TCA	GGG	ACG	CTC	TGG	CAA	GTC	CAG	ATG			1350
Ala	Thr	Pro	Tyr	Thr	Glu	Val	Ser	Gly	Thr	Leu	Trp	Gln	Val	Gln	Met			
				430					435					440				
CAC	TAT	GAG	ATG	CTC	TTC	AAC	TCC	TTC	CAG	GGA	TTT	TTT	GTC	GCA	ATC			1398
His	Tyr	Glu	Met	Leu	Phe	Asn	Ser	Phe	Gln	Gly	Phe	Phe	Val	Ala	Ile			
			445					450					455					
ATA	TAC	TGT	TTC	TGC	AAT	GGC	GAG	GTA	CAA	GCT	GAG	ATC	AAG	AAA	TCT			1446
Ile	Tyr	Cys	Phe	Cys	Asn	Gly	Glu	Val	Gln	Ala	Glu	Ile	Lys	Lys	Ser			
		460				465						470						
TGG	AGC	CGC	TGG	ACA	CTG	GCA	CTG	GAC	TTC	AAG	CGA	AAG	GCA	CGC	AGC			1494
Trp	Ser	Arg	Trp	Thr	Leu	Ala	Leu	Asp	Phe	Lys	Arg	Lys	Ala	Arg	Ser			
	475					480					485							
GGG	AGC	AGC	AGC	TAT	AGC	TAC	GGC	CCC	ATG	GTG	TCC	CAC	ACA	AGT	GTG			1542
Gly	Ser	Ser	Ser	Tyr	Ser	Tyr	Gly	Pro	Met	Val	Ser	His	Thr	Ser	Val			
	490				495					500					505			
ACC	AAT	GTC	GGC	CCC	CGT	GTG	GGA	CTC	GGC	CTG	CCC	CTC	AGC	CCC	CGC			1590
Thr	Asn	Val	Gly	Pro	Arg	Val	Gly	Leu	Gly	Leu	Pro	Leu	Ser	Pro	Arg			
				510				515					520					
CTA	CTG	CCC	ACT	GCC	ACC	ACC	AAC	GGC	CAC	CCT	CAG	CTG	CCT	GGC	CAT			1638
Leu	Leu	Pro	Thr	Ala	Thr	Thr	Asn	Gly	His	Pro	Gln	Leu	Pro	Gly	His			
			525					530					535					

GCC AAG CCA GGG ACC CCA GCC CTG GAG ACC CTC GAG ACC ACA CCA CCT	1686
Ala Lys Pro Gly Thr Pro Ala Leu Glu Thr Leu Glu Thr Thr Pro Pro	
540 545 550	
GCC ATG GCT GCT CCC AAG GAC GAT GGG TTC CTC AAC GGC TCC TGC TCA	1734
Ala Met Ala Ala Pro Lys Asp Asp Gly Phe Leu Asn Gly Ser Cys Ser	
555 560 565	
GGC CTG GAC GAG GAG GCC TCT GGG CCT GAG CGG CCA CCT GCC CTG CTA	1782
Gly Leu Asp Glu Glu Ala Ser Gly Pro Glu Arg Pro Pro Ala Leu Leu	
570 575 580 585	
CAG GAA GAG TGG GAG ACA GTC ATG TGACCAGGCG CTGGGGGCTG GACCTGCTGA	1836
Gln Glu Glu Trp Glu Thr Val Met	
590	
CATAGTGGAT GGACAGATGG ACCAAAAGAT GGGTGGTTGA ATGATTTCCC ACTCAGGGCC	1896
TGGGGCCAAG AGGAAAAAAC AGGGGAAAAA AGAAAAAAA AAGAAAAAAG GAAAAAAA	1956
AAAAAAA AAAA	2010

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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

Thr	Asn	Glu	Thr	Arg	Glu	Arg	Glu	Val	Phe	Asp	Arg	Leu	Gly	Met	Ile
1				5					10					15	
Tyr	Thr	Val	Gly												
			20												

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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

Tyr	Leu	Tyr	Ser	Gly	Phe	Thr	Leu	Asp	Glu	Ala	Glu	Arg	Leu	Thr	Glu
1				5					10					15	
Glu	Glu	Leu													

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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

Val	Thr	Phe	Phe	Leu	Tyr	Phe	Leu	Ala	Thr	Asn	Tyr	Tyr	Trp	Ile	Leu
1				5					10					15	
Val	Glu	Gly													

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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

Tyr	Xaa	Arg	Ala	Thr	Leu	Ala	Asn	Thr	Gly	Cys	Trp	Asp	Leu	Ser	Ser
1				5					10					15	
Gly	His	Lys	Lys	Trp	Ile	Ile	Gln	Val	Pro						
			20				25								

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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

Pro	Tyr	Thr	Glu	Tyr	Ser	Gly	Thr	Leu	Trp	Gln	Ile	Gln	Met	His	Tyr
1				5					10					15	
Glu	Met														

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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

Asp	Asp	Val	Phe	Thr	Lys	Glu	Glu	Gln	Ile	Phe	Leu	Leu	His	Arg	Ala
1				5					10					15	

Gln Ala

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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

Phe	Phe	Arg	Leu	His	Cys	Thr	Arg	Asn	Tyr
1				5					10

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Glu	Lys	Lys	Tyr	Leu	Trp	Gly	Phe	Thr	Leu
1				5					10

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Val	Leu	Ala	Thr	Lys	Leu	Arg	Glu	Thr	Asn	Ala	Gly	Arg	Cys	Asp	Thr
1				5					10					15	
Arg	Gln	Gln	Tyr	Arg	Lys	Leu	Leu	Lys							
			20					25							

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGATGAGGCT GTGCAGGT

18

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

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

GGAATTCCAT GGGAGCGGCC CGGAT

25

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGGGATCCCG CGGCCCTAGG CGGT

24

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGTATAGCGT CCTTGACGA

19

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein


```

Val Phe Met Ala Thr Pro Tyr Thr Glu Val Ser Gly Ile Leu Trp Gln
      420                      425                      430
Val Gln Met His Tyr Glu Met Leu Phe Asn Ser Phe Gln Gly Phe Phe
      435                      440                      445
Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu Val Gln Ala Glu Ile
      450                      455                      460
Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala Leu Asp Phe Lys Arg Lys
465                      470                      475                      480
Ala Arg Ser Gly Ser Ser Thr Tyr Ser Tyr Gly Pro Met Val Ser His
      485                      490                      495
Thr Ser Val Thr Asn Val Gly Pro Arg Gly Gly Trp Pro Cys Pro Ser
      500                      505                      510
Ala Leu Asp
      515

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(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

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

```

225					230					235					240
Leu	Tyr	Ser	Gly	Val	Ser	Thr	Asp	Glu	Ile	Glu	Arg	Ile	Thr	Glu	Glu
				245					250					255	
Glu	Leu	Arg	Ala	Phe	Thr	Glu	Pro	Pro	Pro	Ala	Asp	Lys	Ala	Gly	Phe
			260					265					270		
Val	Gly	Cys	Arg	Val	Ala	Val	Thr	Val	Phe	Leu	Tyr	Phe	Leu	Thr	Thr
		275					280					285			
Asn	Tyr	Tyr	Trp	Ile	Leu	Val	Glu	Gly	Leu	Tyr	Leu	His	Ser	Leu	Ile
	290					295				300					
Phe	Met	Ala	Phe	Phe	Ser	Glu	Lys	Lys	Tyr	Leu	Trp	Gly	Phe	Thr	Leu
305					310					315					320
Phe	Gly	Trp	Gly	Leu	Pro	Ala	Val	Phe	Val	Ala	Val	Trp	Val	Thr	Val
			325						330					335	
Arg	Ala	Thr	Leu	Ala	Asn	Thr	Glu	Cys	Trp	Asp	Leu	Ser	Ser	Gly	Asn
			340					345					350		
Lys	Lys	Trp	Ile	Ile	Gln	Val	Pro	Ile	Leu	Ala	Ala	Ile	Val	Val	Asn
		355					360					365			
Phe	Ile	Leu	Phe	Ile	Asn	Ile	Ile	Arg	Val	Leu	Ala	Thr	Lys	Leu	Arg
	370					375					380				
Glu	Thr	Asn	Ala	Gly	Arg	Cys	Asp	Thr	Arg	Gln	Gln	Tyr	Arg	Lys	Leu
385					390					395					400
Leu	Lys	Ser	Thr	Leu	Val	Leu	Met	Pro	Leu	Phe	Gly	Val	His	Tyr	Ile
			405						410					415	
Val	Phe	Met	Ala	Thr	Pro	Tyr	Thr	Glu	Val	Ser	Gly	Ile	Leu	Trp	Gln
			420					425					430		
Val	Gln	Met	His	Tyr	Glu	Met	Leu	Phe	Asn	Ser	Phe	Gln	Gly	Phe	Phe
		435					440					445			
Val	Ala	Ile	Ile	Tyr	Cys	Phe	Cys	Asn	Gly	Glu	Val	Gln	Ala	Glu	Ile
	450					455				460					
Lys	Lys	Ser	Trp	Ser	Arg	Trp	Thr	Leu	Ala	Leu	Asp	Phe	Lys	Arg	Lys
465					470					475					480
Ala	Arg	Ser	Gly	Ser	Ser	Thr	Tyr	Ser	Tyr	Gly	Pro	Met	Val	Ser	His
			485						490					495	
Thr	Ser	Val	Thr	Asn	Val	Gly	Pro	Arg	Gly	Gly	Leu	Ala	Leu	Ser	Leu
			500					505					510		
Ser	Pro	Arg	Leu	Ala	Pro	Gly	Ala	Gly	Ala	Ser	Ala	Asn	Gly	His	His
		515					520					525			
Gln	Leu	Pro	Gly	Tyr	Val	Lys	His	Gly	Ser	Ile	Ser	Glu	Asn	Ser	Leu
	530					535					540				
Pro	Ser	Ser	Gly	Pro	Glu	Pro	Gly	Thr	Lys	Asp	Asp	Gly	Tyr	Leu	Asn
545					550					555					560
Gly	Ser	Gly	Leu	Tyr	Glu	Pro	Met	Val	Gly	Glu	Gln	Pro	Pro	Pro	Leu
			565						570					575	
Leu	Glu	Glu	Glu	Arg	Glu	Thr	Val	Met							
			580					585							

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

20/22

Phe	Gly	Val	His	Tyr	Thr	Val	Phe	Met	Ala	Leu	Pro	Tyr	Thr	Glu	Val
			420					425					430		
Ser	Gly	Thr	Leu	Trp	Gln	Ile	Gln	Met	His	Tyr	Glu	Met	Leu	Phe	Asn
		435					440					445			
Ser	Phe	Gln	Gly	Phe	Phe	Val	Ala	Ile	Ile	Tyr	Cys	Phe	Cys	Asn	Gly
	450					455					460				
Glu	Val	Gln	Ala	Glu	Ile	Arg	Lys	Ser	Trp	Ser	Arg	Trp	Thr	Leu	Ala
465					470					475					480
Leu	Asp	Phe	Lys	Arg	Lys	Ala	Arg	Ser	Gly	Ser	Ser	Ser	Tyr	Ser	Tyr
			485						490					495	
Gly	Pro	Met	Val	Ser	His	Thr	Ser	Val	Thr	Asn	Val	Gly	Pro	Arg	Ala
			500					505					510		
Gly	Leu	Ser	Leu	Pro	Leu	Ser	Pro	Arg	Leu	Pro	Pro	Ala	Thr	Thr	Asn
		515					520					525			
Gly	His	Ser	Gln	Leu	Pro	Gly	His	Ala	Lys	Pro	Gly	Ala	Pro	Ala	Thr
	530					535					540				
Glu	Thr	Glu	Thr	Leu	Pro	Val	Thr	Met	Ala	Val	Pro	Lys	Asp	Asp	Gly
545					550					555					560
Phe	Leu	Asn	Gly	Ser	Cys	Ser	Gly	Leu	Asp	Glu	Glu	Ala	Ser	Gly	Ser
			565						570					575	
Ala	Arg	Pro	Pro	Pro	Leu	Leu	Gln	Glu	Gly	Trp	Glu	Thr	Val	Met	
			580					585					590		

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 593 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

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

				165					170					175			
Glu	Thr	Arg	Glu	Arg	Glu	Val	Phe	Asp	Arg	Leu	Gly	Met	Ile	Tyr	Thr		
			180					185					190				
Val	Gly	Tyr	Ser	Val	Ser	Leu	Ala	Ser	Leu	Thr	Val	Ala	Val	Leu	Ile		
		195					200					205					
Leu	Ala	Tyr	Phe	Arg	Arg	Leu	His	Cys	Thr	Arg	Asn	Tyr	Ile	His	Met		
	210					215					220						
His	Leu	Phe	Leu	Ser	Phe	Met	Leu	Arg	Ala	Val	Ser	Ile	Phe	Val	Lys		
225					230					235					240		
Asp	Ala	Val	Leu	Tyr	Ser	Gly	Ala	Thr	Leu	Asp	Glu	Ala	Glu	Arg	Leu		
			245						250					255			
Thr	Glu	Glu	Glu	Leu	Arg	Ala	Ile	Ala	Gln	Ala	Pro	Pro	Pro	Pro	Ala		
			260					265						270			
Thr	Ala	Ala	Ala	Gly	Tyr	Ala	Gly	Cys	Arg	Val	Ala	Val	Thr	Phe	Phe		
		275					280					285					
Leu	Tyr	Phe	Leu	Ala	Thr	Asn	Tyr	Tyr	Trp	Ile	Leu	Val	Glu	Gly	Leu		
	290					295					300						
Tyr	Leu	His	Ser	Leu	Ile	Phe	Met	Ala	Phe	Phe	Ser	Glu	Lys	Lys	Tyr		
305					310					315					320		
Leu	Trp	Gly	Phe	Thr	Val	Phe	Gly	Trp	Gly	Leu	Pro	Ala	Val	Phe	Val		
			325						330					335			
Ala	Val	Trp	Val	Ser	Val	Arg	Ala	Thr	Leu	Ala	Asn	Thr	Gly	Cys	Trp		
			340					345					350				
Asp	Leu	Ser	Ser	Gly	Asn	Lys	Lys	Trp	Ile	Ile	Gln	Val	Pro	Ile	Leu		
		355					360					365					
Ala	Ser	Ile	Val	Leu	Asn	Phe	Ile	Leu	Phe	Ile	Asn	Ile	Val	Arg	Val		
	370					375					380						
Leu	Ala	Thr	Lys	Gln	Arg	Glu	Thr	Asn	Ala	Gly	Arg	Cys	Asp	Thr	Arg		
385					390					395					400		
Gln	Gln	Tyr	Arg	Lys	Leu	Leu	Lys	Ser	Thr	Leu	Val	Leu	Met	Pro	Leu		
			405						410					415			
Phe	Gly	Val	His	Tyr	Ile	Val	Phe	Met	Ala	Thr	Pro	Tyr	Thr	Glu	Val		
			420					425					430				
Ser	Gly	Thr	Leu	Trp	Gln	Val	Gln	Met	His	Tyr	Glu	Met	Leu	Phe	Asn		
	435						440					445					
Ser	Phe	Gln	Gly	Phe	Phe	Val	Ala	Ile	Ile	Tyr	Cys	Phe	Cys	Asn	Gly		
	450					455					460						
Glu	Val	Gln	Ala	Glu	Ile	Lys	Lys	Ser	Trp	Ser	Arg	Trp	Thr	Leu	Ala		
465					470					475					480		
Leu	Asp	Phe	Lys	Arg	Lys	Ala	Arg	Ser	Gly	Ser	Ser	Ser	Tyr	Ser	Tyr		
			485						490					495			
Gly	Pro	Met	Val	Ser	His	Thr	Ser	Val	Thr	Asn	Val	Gly	Pro	Arg	Val		
			500					505					510				
Gly	Leu	Gly	Leu	Pro	Leu	Ser	Pro	Arg	Leu	Leu	Pro	Thr	Ala	Thr	Thr		
	515					520						525					
Asn	Gly	His	Pro	Gln	Leu	Pro	Gly	His	Ala	Lys	Pro	Gly	Thr	Pro	Ala		
	530					535					540						
Leu	Glu	Thr	Leu	Glu	Thr	Thr	Pro	Pro	Ala	Met	Ala	Ala	Pro	Lys	Asp		
545					550					555					560		
Asp	Gly	Phe	Leu	Asn	Gly	Ser	Cys	Ser	Gly	Leu	Asp	Glu	Glu	Ala	Ser		
			565						570					575			
Gly	Pro	Glu	Arg	Pro	Pro	Ala	Leu	Leu	Gln	Glu	Glu	Trp	Glu	Thr	Val		
			580					585					590				
Met																	

THE EMBODIMENTS OF THE INVENTION IN WHICH AN EXCLUSIVE PROPERTY OR PRIVILEGE IS CLAIMED ARE DEFINED AS FOLLOWS:

1. Isolated DNA comprising a DNA sequence encoding a cell receptor of a vertebrate animal, said receptor having an amino acid sequence with at least 30% identity to the amino acid sequence of SEQ ID NO:20 and wherein said receptor binds parathyroid hormone or parathyroid hormone-related protein under physiological conditions.
2. Isolated DNA comprising a DNA sequence encoding a cell receptor of a vertebrate animal, wherein said receptor has an amino acid sequence with at least 50% identity to the amino acid sequence of SEQ ID NO:20 and wherein said receptor binds parathyroid hormone or parathyroid hormone-related protein under physiological conditions.
3. Isolated DNA comprising a DNA sequence encoding a cell receptor of a vertebrate animal, wherein said receptor has an amino acid sequence with at least 60% identity to the amino acid sequence of SEQ ID NO:20 and wherein said receptor binds parathyroid hormone or parathyroid hormone-related protein under physiological conditions.
4. Isolated DNA comprising a DNA sequence encoding a cell receptor of a vertebrate animal, wherein said receptor has an amino acid sequence with at least 75% identity to the amino acid sequence of SEQ ID NO:20 and wherein said receptor binds parathyroid hormone or parathyroid hormone-related protein under physiological conditions.
5. The isolated DNA of claim 1, wherein said DNA sequence encodes the amino acid sequence of SEQ ID NO. 18.
6. The isolated DNA of claim 1, wherein said DNA sequence encodes the amino acid sequence of SEQ ID NO. 20.
7. The isolated DNA of claim 1, wherein said DNA sequence encodes the amino acid sequence of SEQ ID NO. 21.
8. The isolated DNA of claim 1, wherein said DNA sequence hybridizes under stringent conditions to the complement of the DNA sequence of SEQ ID NO. 1.

9. The isolated DNA of claim 1, wherein said DNA sequence hybridizes under stringent conditions to the complement of the DNA sequence of SEQ ID NO. 3.
10. The isolated DNA of claim 1, wherein said DNA sequence hybridizes under stringent conditions to the complement of the DNA sequence of SEQ ID NO. 4.
11. The isolated DNA of any one of claims 1 to 10, wherein said DNA encodes a parathyroid hormone receptor.
12. A purified preparation of a vector, said vector comprising a DNA sequence as defined in any one of claims 1 to 11.
13. A transformed cell containing the isolated DNA encoding a cell receptor of any one of claims 1 to 11.
14. The cell of claim 13, wherein said cell is capable of expressing said cell receptor from said isolated DNA.
15. An essentially homogenous population of cells, each of which comprises the isolated DNA of any one of claims 1 to 11.
16. A method for producing a polypeptide, said method comprising:
 - providing a cell comprising isolated DNA as defined by any one of claims 1 to 11; and
 - culturing said cell under conditions permitting expression of a polypeptide from said DNA.
17. A single-stranded DNA comprising a portion of a parathyroid hormone receptor cDNA having a DNA sequence as defined by claim 11 and being at least 18 nucleotides long, wherein the parathyroid hormone receptor encoded by the single-stranded DNA binds parathyroid hormone or parathyroid hormone related protein under physiological conditions.

18. The single-stranded DNA of claim 17, wherein the DNA is at least 30 nucleotides long, and wherein the parathyroid hormone receptor encoded by the single-stranded DNA binds parathyroid hormone or parathyroid hormone related protein.
19. The single-stranded DNA of claim 17 or 18, wherein said DNA is antisense.
20. The single-stranded DNA of any one of claims 17 to 19, wherein said single-stranded DNA contains less than all of said cDNA.
21. The single-stranded DNA of any one of claims 17 to 20, wherein said DNA is detectably labeled.
22. Parathyroid hormone receptor produced by expression of an isolated DNA molecule as defined by claim 11.
23. An essentially purified preparation of the parathyroid hormone receptor of claim 22.
24. An essentially purified preparation of the parathyroid hormone receptor produced by the expression of the DNA of claim 7.
25. A polypeptide capable of binding parathyroid hormone or parathyroid hormone-related protein, and comprising at least six amino acids and less than the complete amino acid sequence of a parathyroid hormone receptor, said polypeptide comprising a sequence selected from the group of sequences:
- (a) TNETREREVFDRLGMIYTVG,
 - (b) YLYSGFTLDEAERLTEEEL,
 - (c) VTFFLYFLATNYYWILVEG,
 - (d) Y-RATLANTGCWDLSSGHKKWIIQVP,
 - (e) PYTEYSGTLWQIQMHYEM,
 - (f) DDVFTKEEQIFLLHRAQA,
 - (g) FFRLHCTRNY,
 - (h) EKKYLWGFTL,
 - (i) VLATKLRETNAGRCDTRQQYRKLLK, and
 - (j) a fragment of (a) to (i).

26. The polypeptide of claim 25, comprising a sequence selected from the group (a) to (i).
27. An essentially purified polypeptide capable of binding parathyroid hormone or parathyroid hormone-related protein, and comprising at least six amino acids of a sequence selected from the group of sequences:
- (a) TNETREREVFDRLGMIYTVG,
 - (b) YLYSGFTLDEAERLTEEEL,
 - (c) VTFFLYFLATNYYWILVEG,
 - (d) Y-RATLANTGCWDLSSGHKKWIIQVP,
 - (e) PYTEYSGTLWQIQMHYEM,
 - (f) DDVFTKEEQIFLLHRAQA,
 - (g) FFRLHCTRNY,
 - (h) EKKYLWGFTL,
 - (i) VLATKLRETNAGRCDTRQQYRKLLK,
 - (j) a fragment of (a) to (i), and
 - (k) a conservatively substituted variant of any one of (a) to (j).
28. The polypeptide of claim 27, comprising a sequence selected from the group of sequences: (a) to (i), and a conservatively substituted variant of any one of (a) to (i).
29. The polypeptide of claim 25, wherein said parathyroid hormone receptor is a human parathyroid receptor.
30. An isolated DNA molecule encoding a polypeptide of any one of claims 25 to 29.
31. A method for producing a polypeptide, said method comprising:
- providing a cell comprising the isolated DNA of claim 30; and
 - culturing said cell under conditions permitting expression of a polypeptide from said DNA.
32. A therapeutic composition comprising, in a pharmaceutically-acceptable carrier, a polypeptide of any one of claims 25 to 29.

33. A method for identifying a compound capable of competing with a parathyroid hormone for binding to a parathyroid hormone receptor, said method comprising:

(a) contacting the polypeptide of any one of claims 25 to 29 with a parathyroid hormone, (i) in the presence or (ii) in the absence of a candidate compound; and

(b) comparing (i) the level of binding of said polypeptide to said parathyroid hormone in the presence of said candidate compound, with (ii) the level of binding of said polypeptide to said parathyroid hormone in the absence of said candidate compound; a lower level of binding in the presence of said candidate compound than in its absence indicating that said candidate compound is capable of competing with said parathyroid hormone for binding to said receptor.

34. A method for identifying a compound capable of competing with a parathyroid hormone-related protein for binding to a parathyroid hormone receptor, said method comprising:

(a) contacting the polypeptide of any one of claims 25 to 29 with a parathyroid hormone-related protein, (i) in the presence or (ii) in the absence of a candidate compound; and

(b) comparing (i) the level of binding of said polypeptide to said parathyroid hormone-related protein in the presence of said candidate compound, with (ii) the level of binding of said polypeptide to said parathyroid hormone-related protein in the absence of said candidate compound; a lower level of binding in the presence of said candidate compound than in its absence indicating that said candidate compound is capable of competing with said parathyroid hormone-related protein for binding to said receptor.

35. A method for identifying a compound capable of competing with a parathyroid hormone for binding to a parathyroid hormone receptor, said method comprising:

(a) combining a parathyroid hormone with the cell of claim 14, (i) in the presence or (ii) in the absence of a candidate compound; and

(b) comparing (i) the level of binding of said receptor to said parathyroid hormone in the presence of said candidate compound, with (ii) the level of binding of said receptor to said parathyroid hormone in the absence of said candidate compound; a lower level of binding in the presence of said candidate compound than in its absence indicating that said candidate compound is capable of competing with said parathyroid hormone for binding to said receptor.

36. A method for identifying a DNA sequence homologous to a parathyroid hormone receptor-encoding DNA sequence, said method comprising:

- providing a genomic or cDNA library;

- contacting said library with the single-stranded DNA of claim 17 or 18, under conditions permitting hybridization between said single-stranded DNA and a homologous DNA sequence in said library; and
- identifying a clone from said library which hybridizes to said single-stranded DNA, said hybridization being indicative of the presence in said clone of a DNA sequence homologous to a parathyroid hormone receptor-encoding DNA sequence.

37. The parathyroid hormone receptor of claim 22 for use in therapy or diagnosis.
38. The polypeptide of any one of claims 25 to 29 for use in therapy or diagnosis.
39. The therapeutic composition of claim 32 for use in therapy for the inhibition of activation by parathyroid hormone or parathyroid hormone-related protein of a parathyroid hormone receptor of a mammal or for the reduction of the level of calcium in the blood of a mammal.
40. The parathyroid hormone receptor of claim 22 for use in the manufacture of a medicament for use in therapy for the inhibition of activation by parathyroid hormone or parathyroid hormone-related protein of a parathyroid hormone receptor of a mammal or for the reduction of the level of calcium in the blood of a mammal.
41. The polypeptide of any one of claims 25 to 29 for use in the manufacture of a medicament for use in therapy for the inhibition of activation by parathyroid hormone or parathyroid hormone-related protein of a parathyroid hormone receptor of a mammal or for the reduction of the level of calcium in the blood of a mammal.
42. A method for identifying a hypercalcemic condition in a patient which is mediated by parathyroid hormone or parathyroid hormone-related protein, the method comprising:
 - (a) determining the calcium level of a first blood sample from the patient,
 - (b) determining the calcium level of a second blood sample from the patient taken at a time subsequent after administration of the therapeutic composition of claim 32, and
 - (c) comparing the calcium levels of the two blood samples, a lower calcium level in the second blood sample being indicative of a condition related to parathyroid hormone or parathyroid hormone-related protein in the patient.

43. A method for production of a transgenic non-human vertebrate animal which expresses elevated levels of a parathyroid hormone receptor or analog of a parathyroid hormone receptor, the method comprising introducing a transgene encoding a polypeptide of any one of claims 25 to 29 into an animal embryo at an early developmental stage.
44. A method for production of a transformed cell from a cell of a non-human vertebrate animal, wherein said transformed cell expresses elevated levels of a parathyroid hormone receptor or analog of a parathyroid hormone receptor, the method comprising introducing a transgene encoding a polypeptide of any one of claims 25 to 29 into said non-human vertebrate animal.
45. A transformed cell produced by the method of claim 44, wherein said transformed cell expresses elevated levels of a parathyroid hormone receptor or analog of a parathyroid hormone receptor.
46. Isolated DNA comprising a DNA sequence selected from SEQ ID NO:1, SEQ ID NO:3, or SEQ ID NO:4.
47. The isolated DNA of claim 46, wherein the isolated DNA comprises the DNA sequence of SEQ ID NO: 1.
48. The isolated DNA of claim 46, wherein the isolated DNA comprises the DNA sequence of SEQ ID NO:3.
49. The isolated DNA of claim 46, wherein the isolated DNA comprises the DNA sequence of SEQ ID NO:4.
50. An isolated polypeptide comprising the amino acid sequence of SEQ ID NO: 18.
51. An isolated polypeptide comprising the amino acid sequence of SEQ ID NO: 20.
52. An isolated polypeptide comprising the amino acid sequence of SEQ ID NO: 21.
53. An isolated polypeptide consisting of the amino acid sequence of SEQ ID NO: 18.

54. An isolated polypeptide consisting of the amino acid sequence of SEQ ID NO: 20.
55. An isolated polypeptide consisting of the amino acid sequence of SEQ ID NO:21.
56. An antibody capable of forming an immune complex with a polypeptide of any one of claims 53 to 55.
57. A composition comprising the antibody of claim 56 and a pharmaceutically acceptable carrier.
58. The antibody of claim 56 for use in therapy or diagnosis.
59. The composition of claim 57 for use in therapy for the inhibition of activation by parathyroid hormone or parathyroid hormone-related protein of a parathyroid hormone receptor of a mammal or for the reduction of the level of calcium in the blood of a mammal.
60. The antibody of claim 56 for use in the manufacture of a medicament for use in therapy for the inhibition of activation by parathyroid hormone or parathyroid hormone-related protein of a parathyroid hormone receptor of a mammal or for the reduction of the level of calcium in the blood of a mammal.
61. A method for identifying a hypercalcemic condition in a patient which is mediated by parathyroid hormone or parathyroid hormone-related protein, the method comprising:
- (a) determining the calcium level of a first blood sample from the patient,
 - (b) determining the calcium level of a second blood sample from the patient taken at a subsequent time after administration of the composition of claim 57, and
 - (c) comparing the calcium levels of the two blood samples, a lower calcium level in the second blood sample being indicative of a condition related to parathyroid hormone of parathyroid hormone-related protein in the patient.
62. Isolated double- or single-stranded DNA comprising:
- (1) a DNA sequence encoding a naturally occurring parathyroid hormone receptor of a mammal, or

(2) the complement of said DNA sequence, said receptor having an amino acid sequence with at least 50% identity to the amino acid sequence encoded by SEQ ID NO: 3,
- wherein a single-stranded form of said isolated DNA hybridizes under stringent conditions to a hybridization probe consisting of an 18-nucleotide portion of a sequence selected from SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, or a sequence complementary to one of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, or SEQ ID NO: 4.

63. The isolated DNA of claim 62, wherein said DNA sequence is SEQ ID NO: 1.

64. The isolated DNA of claim 62, wherein said DNA sequence is SEQ ID NO: 3.

65. The isolated DNA of claim 62, wherein said DNA sequence is SEQ ID NO: 4.

66. The isolated DNA of claim 62, wherein said receptor has an amino acid sequence with at least 75% identity to the amino acid sequence encoded by SEQ ID NO: 3.

67. A cell in culture containing the isolated DNA of claim 62.

68. An essentially homogenous population of cells in culture, each of which comprises the isolated DNA of claim 62.

69. The isolated DNA according to claim 62, wherein said DNA is single-stranded.

70. The isolated single-stranded DNA according to claim 69, wherein said DNA is detectably labeled.

71. A purified preparation of a vector, said vector comprising a DNA sequence encoding a naturally occurring mammalian parathyroid hormone receptor, wherein a single-stranded form of said DNA sequence hybridizes under stringent conditions to a hybridization probe consisting of an 18-nucleotide portion of a sequence selected from SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, or a sequence complementary to one of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, or SEQ ID NO: 4.

72. A method for producing a polypeptide, said method comprising:

- providing a cell comprising isolated DNA encoding a naturally occurring mammalian parathyroid hormone receptor;
- culturing said cell under conditions permitting expression of said polypeptide from said DNA; and
- obtaining said polypeptide;
- provided that said DNA comprises a strand which hybridizes under stringent conditions to a hybridization probe consisting of an 18-nucleotide portion of a sequence selected from SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, or a sequence complementary to one of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, or SEQ ID NO: 4.

73. Isolated double- or single-stranded DNA comprising

(1) a DNA sequence encoding a naturally occurring parathyroid hormone receptor of a vertebrate animal, or

(2) the complement of said DNA sequence, said receptor having an amino acid sequence with at least 50% identity to the amino acid sequence encoded by SEQ ID NO: 3,

- wherein a single-stranded form of said isolated DNA hybridizes under stringent conditions to DNA having a sequence selected from SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, or a sequence complementary to one of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, or SEQ ID NO: 4.

74. A cell in culture containing the isolated DNA of claim 73.

75. The cell of claim 74, wherein said cell is capable of expressing said receptor from said DNA.

76. An essentially homogeneous population of cells in culture, each of which comprises the isolated DNA of claim 73.

77. A purified preparation of a vector, said vector comprising a DNA sequence encoding a naturally occurring parathyroid hormone receptor of a vertebrate animal, wherein a single-stranded form of said DNA sequence hybridizes under stringent conditions to DNA having a sequence selected from SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, or a sequence complementary to one of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, or SEQ ID NO: 4.

78. Isolated DNA encoding a peptide selected from RP1 (SEQ ID NO: 5), RP2 (SEQ ID NO: 6), RP3 (SEQ ID NO: 7), RP4 (SEQ ID NO: 8), RP5 (SEQ ID NO: 9), or RP6 (SEQ ID NO: 10).
79. A purified preparation of a vector, said vector comprising DNA according to claim 78.
80. A cell in culture containing DNA according to claim 78.
81. An essentially homogeneous population of cells in culture, each of which comprises DNA according to claim 78.
82. A method for producing a peptide selected from RP1 (SEQ ID NO: 5), RP2 (SEQ ID NO: 6), RP3 (SEQ ID NO: 7), RP4 (SEQ ID NO: 8), RP5 (SEQ ID NO: 9), or RP6 (SEQ ID NO: 10), said method comprising:
- providing a cell comprising isolated DNA according to claim 78;
 - culturing said cell under conditions permitting expression of said peptide from said DNA; and
 - obtaining said peptide.
83. An essentially purified preparation of a polypeptide comprising the amino acid sequence of a naturally-occurring mammalian parathyroid hormone receptor, said receptor having an amino acid sequence with at least 75% identity to the amino acid sequence of SEQ ID NO: 20.
84. A polypeptide consisting of at least six amino acids, and less than the complete amino acid sequence, of the human parathyroid hormone receptor represented by SEQ ID NO: 21, wherein said polypeptide binds parathyroid hormone or parathyroid hormone-related protein and comprises an amino acid sequence selected from:
- (a) SEQ ID NO:5,
 - (b) SEQ ID NO:6,
 - (c) SEQ ID NO:7,
 - (d) SEQ ID NO:8,
 - (e) SEQ ID NO:9,
 - (f) SEQ ID NO:10,
 - (g) SEQ ID NO:11,

- (h) SEQ ID NO:12,
- (i) SEQ ID NO:13, or
- (j) a fragment of any one of (a)-(i).

85. The polypeptide of claim 84, wherein said polypeptide comprises an amino acid sequence selected from:

- (a) SEQ ID NO:5,
- (b) SEQ ID NO:6,
- (c) SEQ ID NO:7,
- (d) SEQ ID NO:8,
- (e) SEQ ID NO:9,
- (f) SEQ ID NO:10,
- (g) SEQ ID NO:11,
- (h) SEQ ID NO:12, or
- (i) SEQ ID NO:13.

86. The preparation of claim 83, wherein the receptor is a human parathyroid hormone receptor encoded by SEQ ID NO:4.

87. The preparation of claim 83, wherein the receptor is an opossum or rat parathyroid hormone receptor encoded by SEQ ID NO:1, SEQ ID NO:2, or SEQ ID NO:3.

88. A composition comprising (a) a polypeptide having an amino acid sequence with at least 75% identity to the amino acid sequence of SEQ ID NO:20, and (b) a pharmaceutically-acceptable carrier, wherein said composition is substantially free from proteins and lipids with which said receptor is naturally associated.

89. The composition of claim 88, wherein the receptor is a human parathyroid hormone receptor.

90. A composition comprising (a) the polypeptide of claim 83, and (b) a pharmaceutically-acceptable carrier.

91. A composition comprising (a) the polypeptide of claim 85, and (b) a pharmaceutically-acceptable carrier.
92. The preparation of claim 83, wherein the polypeptide was produced upon expression of a recombinant DNA molecule encoding the receptor.
93. The preparation of claim 92, wherein the antisense strand of the recombinant DNA molecule hybridizes under conditions of high stringency to a hybridization probe consisting of an 18-nucleotide portion of a sequence selected from SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, or SEQ ID NO:4.
94. The preparation of claim 92, wherein the antisense strand of the recombinant DNA molecule hybridizes under conditions of high stringency to a hybridization probe consisting of a 30-nucleotide portion of a sequence selected from SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, or SEQ ID NO:4.
95. An antibody that is specifically immunoreactive with a naturally occurring, mammalian parathyroid hormone receptor with at least 75% identity to the amino acid sequence of SEQ ID NO:20.
96. A therapeutic composition comprising the antibody of claim 95 and a pharmaceutically-acceptable carrier.
97. The antibody of claim 95, wherein the receptor is a human parathyroid hormone receptor.
98. The antibody of claim 95, wherein the receptor is a rat parathyroid hormone receptor.
99. The antibody of claim 95, wherein the receptor is an opossum parathyroid hormone receptor.
100. The antibody of claim 95, wherein the receptor comprises an amino acid sequence of SEQ ID NO:18, SEQ ID NO:19, or SEQ ID NO:20.

101. The antibody of claim 97, wherein the receptor comprises an amino acid sequence of SEQ ID NO:21.
102. The antibody of claim 95, wherein the antibody binds to a peptide having an amino acid sequence selected from SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, or SEQ ID NO:10.
103. The antibody of claim 95 or 102, wherein the antibody is a monoclonal antibody.
104. The antibody of claim 95 or 102, wherein the antibody is a polyclonal antibody.
105. The antibody of claim 95 or 102, wherein the antibody competes with parathyroid hormone for binding to the receptor.
106. The composition of claim 96, wherein the receptor is a human parathyroid hormone receptor.
107. The composition of claim 96, wherein the receptor has the amino acid sequence encoded by SEQ ID NO:4.
108. The composition of claim 106, wherein the antibody competes with human parathyroid hormone for binding to the receptor.
109. The composition of claim 106, wherein the antibody is a monoclonal antibody and wherein the antibody binds to a peptide having an amino acid sequence selected from SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, or SEQ ID NO:10.
110. A method for identifying a compound that inhibits binding of a parathyroid hormone to a parathyroid hormone receptor by competitively binding to the parathyroid hormone receptor, the method comprising:
- (a) providing a recombinant polypeptide that: (i) comprises an amino acid sequence that is at least 30% identical to SEQ ID NO:20, and (ii) binds to parathyroid hormone;
 - (b) contacting the polypeptide with a parathyroid hormone, or a parathyroid hormone receptor-binding fragment thereof, in the presence of a candidate compound; and

(c) comparing the level of binding of the polypeptide to the parathyroid hormone or fragment thereof in the presence of the candidate compound with the level of binding of the polypeptide to the parathyroid hormone or fragment thereof in the absence of the candidate compound, wherein a lower level of binding in the presence of the candidate compound than in its absence indicates that the candidate compound competes with parathyroid hormone for binding to the receptor.

111. The method of claim 110, wherein the amino acid sequence is identical to the sequence of a fragment of a parathyroid hormone receptor.

112. The method of claim 110, wherein the amino acid sequence is identical to the sequence of a fragment of a human parathyroid hormone receptor.

113. The method of claim 110, wherein the amino acid sequence is identical to SEQ ID NO:21.

114. A method for identifying a compound that inhibits the binding of parathyroid hormone to a parathyroid hormone receptor, the method comprising:

(a) providing a recombinant polypeptide that: (i) consists of an amino acid sequence that is at least 30% identical to SEQ ID NO:20 and (ii) binds parathyroid hormone or a fragment thereof;

(b) contacting the polypeptide with parathyroid hormone, or a parathyroid hormone receptor-binding fragment thereof, and a test compound; and

(c) determining whether binding of the parathyroid hormone or fragment thereof to the polypeptide is decreased in the presence of the test compound, wherein a decrease in binding indicates that the test compound inhibits the binding of parathyroid hormone to the parathyroid hormone receptor.

115. The method of claim 114, wherein the amino acid sequence is identical to SEQ ID NO:21.

116. A method for identifying a compound that inhibits the binding of parathyroid hormone to a parathyroid hormone receptor, the method comprising:

(a) providing a recombinant parathyroid hormone receptor or a parathyroid hormone-binding fragment thereof, wherein the amino acid sequence of the parathyroid hormone receptor is at least 30% identical to SEQ ID NO: 20;

(b) contacting the parathyroid hormone receptor or fragment thereof with parathyroid hormone or a parathyroid receptor-binding fragment thereof, and a test compound; and

(c) determining whether binding of the parathyroid hormone or fragment thereof to the parathyroid hormone receptor or fragment thereof is decreased in the presence of the test compound, wherein a decrease in binding indicates that the test compound inhibits the binding of parathyroid hormone to the parathyroid hormone receptor.

117. The method of claim 110, wherein the amino acid sequence is identical to SEQ ID NO:21 with at least one conservative amino acid substitution.

118. A method for identifying a compound that inhibits binding of a parathyroid hormone to a parathyroid hormone receptor by competitively binding to the parathyroid hormone receptor, the method comprising:

(a) providing a recombinant polypeptide that: (i) comprises a fragment of a parathyroid hormone receptor having an amino acid sequence that is at least 30% identical to SEQ ID NO: 20, and (ii) binds to parathyroid hormone;

(b) contacting the polypeptide with a parathyroid hormone, or a parathyroid hormone receptor-binding fragment thereof, in the presence of a candidate compound; and

(c) comparing the level of binding of the polypeptide to the parathyroid hormone or fragment thereof in the presence of the candidate compound with the level of binding of the polypeptide to the parathyroid hormone or fragment thereof in the absence of the candidate compound, wherein a lower level of binding in the presence of the candidate compound than in its absence indicates that the candidate compound competes with parathyroid hormone for binding to the receptor.

119. The method of claim 110, wherein the amino acid sequence comprises one or more of SEQ ID NO:5 to SEQ ID NO:13.

120. The method of claim 110, wherein the amino acid sequence is identical to a fragment of an opossum parathyroid hormone receptor.

121. The method of claim 110, wherein the amino acid sequence is identical to a fragment of a rat parathyroid hormone receptor.
122. The method of claim 110, wherein the amino acid sequence is identical to SEQ ID NO:18.
123. The method of claim 110, wherein the amino acid sequence is identical to SEQ ID NO:19.
124. The method of claim 110, wherein the amino acid sequence is identical to SEQ ID NO:20.
125. The method of claim 110, wherein the amino acid sequence is at least 50% identical to SEQ ID NO:20.
126. The method of claim 110, wherein the amino acid sequence is at least 60% identical to SEQ ID NO:20.
127. The method of claim 110, wherein the amino acid sequence is at least 75% identical to SEQ ID NO:20.
128. The method of claim 114, wherein the amino acid sequence is identical to the sequence of a fragment of a parathyroid hormone receptor.
129. The method of claim 114, wherein the amino acid sequence is identical to the sequence of a fragment of a human parathyroid hormone receptor.
130. The method of claim 114, wherein the amino acid sequence is identical to SEQ ID NO:21 with at least one conservative amino acid substitution.
131. The method of claim 114, wherein the amino acid sequence comprises one or more of SEQ ID NO:5 to SEQ ID NO:13.

132. The method of claim 114, wherein the amino acid sequence is identical to a fragment of an opossum parathyroid hormone receptor.
133. The method of claim 114, wherein the amino acid sequence is identical to a fragment of a rat parathyroid hormone receptor.
134. The method of claim 114, wherein the amino acid sequence is identical to SEQ ID NO:18.
135. The method of claim 114, wherein the amino acid sequence is identical to SEQ ID NO:19.
136. The method of claim 114, wherein the amino acid sequence is identical to SEQ ID NO:20.
137. The method of claim 114, wherein the amino acid sequence is at least 50% identical to SEQ ID NO:20.
138. The method of claim 114, wherein the amino acid sequence is at least 60% identical to SEQ ID NO:20.
139. The method of claim 114, wherein the amino acid sequence is at least 75% identical to SEQ ID NO:20.
140. The method of claim 116, wherein the amino acid sequence is identical to SEQ ID NO:21.
141. The method of claim 116, wherein the amino acid sequence is identical to the sequence of a fragment of a human parathyroid hormone receptor.
142. The method of claim 116, wherein the amino acid sequence is identical to SEQ ID NO:21 with at least one conservative amino acid substitution.

143. The method of claim 116, wherein the amino acid sequence comprises part or all of any one of SEQ ID NO:5 to SEQ ID NO:13.

144. The method of claim 116, wherein the amino acid sequence is identical to a fragment of an opossum parathyroid hormone receptor.

145. The method of claim 116, wherein the amino acid sequence is identical to a fragment of a rat parathyroid hormone receptor.

146. The method of claim 116, wherein the amino acid sequence is identical to SEQ ID NO:18.

147. The method of claim 116, wherein the amino acid sequence is identical to SEQ ID NO:19.

148. The method of claim 116, wherein the amino acid sequence is identical to SEQ ID NO:20.

149. The method of claim 116, wherein the amino acid sequence is at least 50% identical to SEQ ID NO:20.

150. The method of claim 116, wherein the amino acid sequence is at least 60% identical to SEQ ID NO:20.

151. The method of claim 116, wherein the amino acid sequence is at least 75% identical to SEQ ID NO:20.

152. The method of claim 118, wherein the amino acid sequence is identical to SEQ ID NO:21.

153. The method of claim 118, wherein the amino acid sequence is identical to the sequence of a fragment of a human parathyroid hormone receptor.

154. The method of claim 118, wherein the amino acid sequence is identical to SEQ ID NO:21 with at least one conservative amino acid substitution.
155. The method of claim 118, wherein the amino acid sequence comprises one or more of SEQ ID NO:5 to SEQ ID NO:13.
156. The method of claim 118, wherein the amino acid sequence is identical to a fragment of an opossum parathyroid hormone receptor.
157. The method of claim 118, wherein the amino acid sequence is identical to a fragment of a rat parathyroid hormone receptor.
158. The method of claim 118, wherein the amino acid sequence is identical to SEQ ID NO:18.
159. The method of claim 118, wherein the amino acid sequence is identical to SEQ ID NO:19.
160. The method of claim 118, wherein the amino acid sequence is identical to SEQ ID NO:20.
161. The method of claim 118, wherein the amino acid sequence is at least 50% identical to SEQ ID NO:20.
162. The method of claim 118, wherein the amino acid sequence is at least 60% identical to SEQ ID NO:20.
163. The method of claim 118, wherein the amino acid sequence is at least 75% identical to SEQ ID NO:20.
164. An isolated DNA sequence encoding a cell receptor of a vertebrate animal, which receptor binds parathyroid hormone or parathyroid hormone-related protein under physiological conditions, said receptor having an amino acid sequence with at least 30% identity to the amino acid sequence encoded by SEQ ID NO: 3.

165. The isolated DNA of claim 164, wherein said DNA sequence is selected from SEQ ID NO: 1, SEQ ID NO:3, or SEQ ID NO:4.

166. The isolated DNA of claim 164, wherein said DNA sequence hybridizes under conditions of high stringency to a sequence complementary to the DNA sequence shown in SEQ ID NO: 1, SEQ ID NO: 3 or SEQ ID NO: 4.

167. A purified preparation of a vector, said vector comprising a DNA sequence according to any one of claims 164 to 166.

168. An isolated cell containing the isolated DNA of claim 164, wherein the cell is not a human germ cell, a human fertilized egg or a human embryonic stem cell.

169. The cell of claim 168, wherein said cell is capable of expressing said cell receptor from said isolated DNA.

170. A method for producing a polypeptide, said method comprising:
- providing a cell comprising isolated DNA according to any one of claims 164 to 166 or a fragment of said receptor; and
- culturing said cell under conditions permitting expression of a polypeptide from said DNA.

171. A single-stranded DNA having a portion of a parathyroid hormone receptor gene or receptor gene or a parathyroid hormone receptor cDNA according to any one of claims 164 to 166, said portion being at least 18 nucleotides long and wherein the parathyroid hormone receptor encoded by the single-stranded DNA binds parathyroid hormone or parathyroid hormone related protein.

172. The single-stranded DNA of claim 171, wherein said portion is less than all of said parathyroid hormone receptor gene.

173. The single-stranded DNA of claim 171 or 172, wherein said DNA is detectably labeled.

174. The single-stranded DNA of any one of claims 171 to 173, wherein said DNA is antisense.
175. An essentially purified preparation of the parathyroid hormone receptor produced by the expression of the DNA of claim 165.
176. A polypeptide comprising at least six amino acids and less than the complete amino acid sequence of parathyroid hormone receptor encoded by the isolated DNA according to any one of claims 164 to 166, said polypeptide being capable of binding parathyroid hormone or parathyroid hormone-related protein.
177. The polypeptide of claim 176, comprising
- (a) TNETREREVFDRLGMIYTVG,
 - (b) YLYSGFTLDEAERLTEEEL,
 - (c) VTFFLYFLATNYYWILVEG,
 - (d) Y-RATLANTGCWDLSSGHKKWIIQVP,
 - (e) PYTEYSGTLWQIQMHYEM,
 - (f) DDVFTKEEQIFLLHRAQA,
 - (g) FFRLHCTRNY,
 - (h) EKKYLWGFTL,
 - (i) VLATKLRETNAGRCDTRQQYRKLLK, or
 - (j) a fragment of (a) - (i) which is capable of binding parathyroid hormone or parathyroid hormone-related protein.
178. A polypeptide according to claim 176 or 177, wherein said parathyroid hormone receptor is a human parathyroid receptor.
179. The polypeptide of any one of claims 176 to 178 for use in therapy or diagnosis.
180. Use of a polypeptide according to any one of claims 176 to 178 for the manufacture of a medicament for use in therapy for the inhibition of activation by parathyroid hormone or parathyroid hormone-related protein of a parathyroid hormone receptor of a mammal or for the reduction of the level of calcium in the blood of a mammal.

181. An essentially purified preparation of the polypeptide of any one of claims 176 to 178.

182. A composition comprising, in a pharmaceutically-acceptable carrier, (a) a parathyroid hormone receptor encoded by the isolated DNA sequence of any one of claims 164 to 166 or (b) a polypeptide comprising a fragment of said receptor, wherein the receptor or the fragment binds parathyroid hormone or parathyroid-related protein under physiological conditions.

183. A purified antibody specifically forming an immune complex with a parathyroid hormone receptor encoded by the isolated DNA sequence of any one of claims 164 to 166.

184. A method for identifying a compound capable of competing with a parathyroid hormone or parathyroid hormone-related protein for binding to a parathyroid hormone receptor, said method comprising:

(a) contacting the polypeptide of any one of claims 176 to 178 with a parathyroid hormone or parathyroid hormone-related protein, (i) in the presence or (ii) in the absence of a candidate compound; and

(b) comparing (i) the level of binding of said polypeptide to said parathyroid hormone or parathyroid hormone-related protein in the presence of said candidate compound, with (ii) the level of binding of said polypeptide to said parathyroid hormone or parathyroid hormone-related protein in the absence of said candidate compound; a lower level of binding in the presence of said candidate compound than in its absence indicating that said candidate compound is capable of competing with said parathyroid hormone or parathyroid hormone-related protein for binding to said receptor.

185. A method for identifying a compound capable of competing with a parathyroid hormone for binding to a parathyroid hormone receptor, said method comprising:

(a) combining a parathyroid hormone with the cell of claim 169, (i) in the presence or (ii) in the absence of a candidate compound; and

(b) comparing (i) the level of binding of said receptor to said parathyroid hormone in the presence of said candidate compound, with (ii) the level of binding of said receptor to said parathyroid hormone in the absence of said candidate compound; a lower level of binding in the presence of said candidate compound than in its absence indicating that said candidate compound is capable of competing with said parathyroid hormone for binding to said receptor.

186. A method for identifying a hypercalcemic condition in a patient which is mediated by parathyroid hormone or parathyroid hormone-related protein, the method comprising
- (a) determining the calcium level of a first blood sample from the patient,
 - (b) determining the calcium level of a second blood sample from the patient taken at a time subsequent after administration of the composition of claim 182, and
 - (c) comparing the calcium levels of the two blood samples, a lower calcium level in the second blood sample being indicative of a condition related to parathyroid hormone or parathyroid hormone-related protein in the patient.
187. A method for identifying a hypercalcemic condition in a patient which is mediated by parathyroid hormone or parathyroid hormone-related protein, the method comprising
- (a) determining the calcium level of a first blood sample from the patient,
 - (b) determining the calcium level of a second blood sample from the patient taken at a subsequent time after administration of a composition comprising the antibody of claim 183, and
 - (c) comparing the calcium levels of the two blood samples, a lower calcium level in the second blood sample being indicative of a condition related to parathyroid hormone of parathyroid hormone-related protein in the patient.
188. A method for identifying a compound according to claim 184 or 185, further comprising the step of determining whether the compound is an agonist or antagonist of a parathyroid hormone receptor.
189. A therapeutic composition comprising the antibody of claim 183 and a pharmaceutically-acceptable carrier.
190. The antibody of claim 183 for use in therapy or diagnosis.
191. The therapeutic composition of claim 189 or the antibody of claim 183 for use in therapy for the inhibition of activation by parathyroid hormone or parathyroid hormone-related protein of a parathyroid hormone receptor of a mammal or for the reduction of the level of calcium in the blood of a mammal.

192. An oligonucleotide for use as an anti-cancer therapy, wherein the oligonucleotide is antisense to the parathyroid hormone receptor mRNA encoded by the DNA of any one of claims 164 to 166 or encodes RNA which is antisense to said mRNA.
193. The use of the oligonucleotide of claim 192 for the manufacture of a medicament for the treatment of hypocalcaemia.
194. Use of the oligonucleotide of claim 192 for the manufacture of a medicament for use in anti-cancer therapy.
195. A method of generating parathyroid hormone or parathyroid hormone- related protein receptors which do not activate phospholipase C comprising the steps of:
- providing an isolated DNA sequence according to claim 164; and
 - altering the sequence encoding the 70 amino acid carboxy terminus of the receptor such that the receptor does not activate phospholipase C.
196. An isolated DNA comprising a nucleic acid sequence that encodes a polypeptide comprising an amino acid sequence at least 75% identical to SEQ ID NO:20, wherein the polypeptide binds parathyroid hormone or parathyroid hormone-related protein.
197. The isolated DNA of claim 196, wherein the nucleic acid sequence encodes substantially all of SEQ ID NO:18.
198. The isolated DNA of claim 196, wherein the nucleic acid sequence encodes substantially all of SEQ ID NO: 19.
199. The isolated DNA of claim 196, wherein the nucleic acid sequence encodes substantially all of SEQ ID NO: 20.
200. The isolated DNA of claim 196, wherein the nucleic acid sequence encodes substantially all of SEQ ID NO: 21.
201. A cell in culture containing the isolated DNA of claim 196.

202. An essentially homogenous population of cells in culture, each of which comprises the isolated DNA of claim 196.
203. The isolated DNA of claim 196, wherein the DNA is single-stranded.
204. The single-stranded isolated DNA of claim 203, wherein the DNA is detectably labeled.
205. A vector comprising the isolated DNA of claim 196.
206. A method of producing a polypeptide, the method comprising the steps of:
(a) providing a cell comprising the isolated DNA of claim 196; and
(b) culturing the cell under conditions that permit expression of a polypeptide from the isolated DNA, to thereby produce the polypeptide.
207. A cell in culture containing the isolated DNA of claim 200.
208. An essentially homogenous population of cells in culture, each of which comprises the isolated DNA of claim 200.
209. The isolated DNA of claim 200, wherein the DNA is single-stranded.
210. The single-stranded isolated DNA of claim 209, wherein the DNA is detectably labeled.
211. A vector comprising the isolated DNA of claim 200.
212. A method of producing a polypeptide, the method comprising the steps of:
(a) providing a cell comprising the isolated DNA of claim 200; and
(b) culturing the cell under conditions that permit expression of a polypeptide from the isolated DNA, to thereby produce the polypeptide.
213. An isolated DNA comprising a sequence that hybridizes under conditions of high stringency to a probe the sequence of which consists of the coding sequence of SEQ ID NO: 1, SEQ ID NO: 2, or SEQ ID NO: 3, or a sequence complementary to the coding sequence of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, wherein the DNA encodes a polypeptide that binds to

parathyroid hormone or parathyroid hormone-related protein, and wherein conditions of high stringency include hybridizing at 42°C for 18-24h in a solution comprising 50% formamide, 4x saline sodium citrate (SSC), 2x Denhardt's solution, 10% Dextran sulphate and 100 µg/ml salmon sperm DNA and washing with 2x SSC/0.1% SDS for 30 minutes at 45°C.

214. A cell in culture containing the isolated DNA of claim 213.

215. An essentially homogenous population of cells in culture, each of which comprises the isolated DNA of claim 213.

216. The isolated DNA of claim 213, wherein the DNA is single-stranded.

217. The single-stranded isolated DNA of claim 216, wherein the DNA is detectably labeled.

218. A vector comprising the isolated DNA of claim 213.

219. A method of producing a polypeptide, the method comprising the steps of:
(a) providing a cell comprising the isolated DNA of claim 213; and
(b) culturing the cell under conditions that permit expression of a polypeptide from the isolated DNA, to thereby produce the polypeptide.

220. An isolated DNA comprising a sequence that hybridizes under conditions of high stringency to a probe the sequence of which consists of the coding sequence of SEQ ID NO: 4, or a sequence complementary to the coding sequence of SEQ ID NO: 4, wherein the DNA encodes a polypeptide that binds to parathyroid hormone or parathyroid hormone-related protein, and wherein conditions of high stringency include hybridizing at 42°C for 18-24h in a solution comprising 50% formamide, 4x saline sodium citrate (SSC), 2x Denhardt's solution, 10% Dextran sulphate and 100 µg/ml salmon sperm DNA and washing with 2x SSC/0.1% SDS for 30 minutes at room temperature and then with 1x SSC/0.1% SDS for 30 minutes at 45°C.

221. A cell in culture containing the isolated DNA of claim 220.

222. An essentially homogenous population of cells in culture, each of which comprises the isolated DNA of claim 220.

223. The isolated DNA of claim 220, wherein the DNA is single-stranded.
224. The single-stranded isolated DNA of claim 223, wherein the DNA is detectably labeled.
225. A vector comprising the isolated DNA of claim 220.
226. A method of producing a polypeptide, the method comprising the steps of:
(a) providing a cell comprising the isolated DNA of claim 220; and
(b) culturing the cell under conditions that permit expression of a polypeptide from the isolated DNA, to thereby produce the polypeptide.
227. An isolated DNA comprising a nucleotide sequence encoding a polypeptide comprising SEQ ID NO:18, SEQ ID NO:19 or SEQ ID NO:20.
228. The isolated DNA of claim 227, wherein the nucleotide sequence comprises the coding sequence of SEQ ID NO:1.
229. The isolated DNA of claim 227, wherein the nucleotide sequence comprises the coding sequence of SEQ ID NO:2.
230. The isolated DNA of claim 227, wherein the nucleotide sequence comprises the coding sequence of SEQ ID NO: 3.
231. A cell in culture containing the isolated DNA of claim 227.
232. An essentially homogenous population of cells in culture, each of which comprises the isolated DNA of claim 227.
233. The isolated DNA of claim 227, wherein the DNA is single-stranded.
234. The single-stranded isolated DNA of claim 233, wherein the DNA is detectably labeled.
235. A vector comprising the isolated DNA of claim 227.

236. A method of producing a polypeptide, the method comprising the steps of:
(a) providing a cell comprising the isolated DNA of claim 227; and
(b) culturing the cell under conditions that permit expression of a polypeptide from the isolated DNA, to thereby produce the polypeptide.
237. An isolated DNA comprising a nucleotide sequence encoding a polypeptide comprising SEQ ID NO: 21.
238. The isolated DNA of claim 237, wherein the nucleotide sequence comprises the coding sequence of SEQ ID NO:4.
239. A cell in culture containing the isolated DNA of claim 237.
240. An essentially homogenous population of cells in culture, each of which comprises the isolated DNA of claim 237.
241. The isolated DNA of claim 237, wherein the DNA is single-stranded.
242. The single-stranded isolated DNA of claim 241, wherein the DNA is detectably labeled.
243. A vector comprising the isolated DNA of claim 237.
244. A method of producing a polypeptide, the method comprising the steps of:
(a) providing a cell comprising the isolated DNA of claim 237; and
(b) culturing the cell under conditions that permit expression of a polypeptide from the isolated DNA, to thereby produce the polypeptide.
245. An isolated DNA comprising a nucleotide sequence encoding a polypeptide consisting of SEQ ID NO:18, SEQ ID NO:19 or SEQ ID NO:20.
246. An essentially homogenous population of cells in culture, each of which comprises the isolated DNA of claim 245.

247. The isolated DNA of claim 245, wherein the DNA is single-stranded.
248. The single-stranded isolated DNA of claim 247, wherein the DNA is detectably labeled.
249. A vector comprising the isolated DNA of claim 245.
250. A method of producing a polypeptide, the method comprising the steps of:
(a) providing a cell comprising the isolated DNA of claim 245; and
(b) culturing the cell under conditions that permit expression of a polypeptide from the isolated DNA, to thereby produce the polypeptide.
251. An isolated DNA comprising a nucleotide sequence encoding a polypeptide consisting of SEQ ID NO:21.
252. A cell in culture containing the isolated DNA of claim 251.
253. An essentially homogenous population of cells in culture, each of which comprises the isolated DNA of claim 251.
254. The isolated DNA of claim 251, wherein the DNA is single-stranded.
255. The single-stranded isolated DNA of claim 254, wherein the DNA is detectably labeled.
256. A vector comprising the isolated DNA of claim 251.
257. A method of producing a polypeptide, the method comprising the steps of:
(a) providing a cell comprising the isolated DNA of claim 251; and
(b) culturing the cell under conditions that permit expression of a polypeptide from the isolated DNA, to thereby produce the polypeptide.
258. An isolated DNA comprising a nucleotide sequence encoding a polypeptide comprising an extracellular domain of SEQ ID NO:18, SEQ ID NO:19 or SEQ ID NO:20 wherein the extracellular domain is capable of binding to parathyroid hormone or parathyroid related protein under physiological conditions.

259. A cell in culture containing the isolated DNA of claim 258.
260. An essentially homogenous population of cells in culture, each of which comprises the isolated DNA of claim 258.
261. The isolated DNA of claim 258, wherein the DNA is single-stranded.
262. The single-stranded isolated DNA of claim 261, wherein the DNA is detectably labeled.
263. A vector comprising the isolated DNA of claim 258.
264. A method of producing a polypeptide, the method comprising the steps of:
(a) providing a cell comprising the isolated DNA of claim 258; and
(b) culturing the cell under conditions that permit expression of a polypeptide from the isolated DNA, to thereby produce the polypeptide.
265. An isolated DNA comprising a nucleotide sequence encoding a polypeptide comprising an extracellular domain of SEQ ID NO:21.
266. A cell in culture containing the isolated DNA of claim 265.
267. An essentially homogenous population of cells in culture, each of which comprises the isolated DNA of claim 265.
268. The isolated DNA of claim 265, wherein the DNA is single-stranded.
269. The single-stranded isolated DNA of claim 268, wherein the DNA is detectably labeled.
270. A vector comprising the isolated DNA of claim 265.
271. A method of producing a polypeptide, the method comprising the steps of:
(a) providing a cell comprising the isolated DNA of claim 265; and

(b) culturing the cell under conditions that permit expression of a polypeptide from the isolated DNA, to thereby produce the polypeptide.

272. An isolated DNA comprising a nucleotide sequence encoding a polypeptide comprising SEQ ID NO:18, SEQ ID NO:19 or SEQ ID NO:20 with at least one conservative amino acid substitution, wherein the polypeptide binds parathyroid hormone or parathyroid hormone-related protein.

273. A cell in culture containing the isolated DNA of claim 272.

274. An essentially homogenous population of cells in culture, each of which comprises the isolated DNA of claim 272.

275. The isolated DNA of claim 272, wherein the DNA is single-stranded.

276. The single-stranded isolated DNA of claim 275, wherein the DNA is detectably labeled.

277. A vector comprising the isolated DNA of claim 272.

278. A method of producing a polypeptide, the method comprising the steps of:
(a) providing a cell comprising the isolated DNA of claim 272; and
(b) culturing the cell under conditions that permit expression of a polypeptide from the isolated DNA, to thereby produce the polypeptide.

279. An isolated DNA comprising a nucleotide sequence encoding a polypeptide comprising SEQ ID NO:21 with at least one conservative amino acid substitution, wherein the polypeptide binds parathyroid hormone or parathyroid hormone-related protein.

280. A cell in culture containing the isolated DNA of claim 279.

281. An essentially homogenous population of cells in culture, each of which comprises the isolated DNA of claim 279.

282. The isolated DNA of claim 279, wherein the DNA is single-stranded.

283. The single-stranded isolated DNA of claim 282, wherein the DNA is detectably labeled.
284. A vector comprising the isolated DNA of claim 279.
285. A method of producing a polypeptide, the method comprising the steps of:
- (a) providing a cell comprising the isolated DNA of claim 279; and
 - (b) culturing the cell under conditions that permit expression of a polypeptide from the isolated DNA, to thereby produce the polypeptide.

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FIG. 1

TGGGCACAGC CACCCTGTTG GTAGTCCAGG GGCCAGCCCA CTGAGCTGGC ATATCAGCTG 50

GTGGCCCCCGT TGGACTCGGC CCTAGGGAAC GGCGGCG ATG GGA GCG CCC CGG ATC 115
Met Gly Ala Pro Arg Ile
1 5

TCG CAC AGC CTT GCC TTG CTC CTC TGC TGC TCC GTG CTC AGC TCC GTC 157
Ser His Ser Leu Ala Leu Leu Leu Cys Cys Ser Val Leu Ser Ser Val
10 15 20

TAC GCA CTG GTG GAT GCC GAT GAT GTC ATA ACG AAG GAG GAG CAG ATC 211
Tyr Ala Leu Val Asp Ala Asp Asp Val Ile Thr Lys Glu Glu Gln Ile
25 30 35

ATT CTT CTG CGC AAT GCC CAG GCC CAG TGT GAG CAG CGC CTG AAA GAG 259
Ile Leu Leu Arg Asn Ala Gln Ala Gln Cys Glu Gln Arg Leu Lys Glu
40 45 50

GTC CTC AGG GTC CCT GAA CTT GCT GAA TCT GCC AAA GAC TGG ATG TCA 307
Val Leu Arg Val Pro Glu Leu Ala Glu Ser Ala Lys Asp Trp Met Ser
55 60 65 70

AGG TCT GCA AAG ACA AAG AAG GAG AAA CCT GCA GAA AAG CTT TAT CCC 355
Arg Ser Ala Lys Thr Lys Lys Glu Lys Pro Ala Glu Lys Leu Tyr Pro
75 80 85

CAG GCA GAG GAG TCC AGG GAA GTT TCT GAC AGG AGC CGG CTG CAG GAT 403
Gln Ala Glu Glu Ser Arg Glu Val Ser Asp Arg Ser Arg Leu Gln Asp
90 95 100

TGC TTC TGC CTA CCT GAG TGG AAC AAC ATT GTG TGC TGC CCT GCT GGA 411
Gly Phe Cys Leu Pro Glu Trp Asp Asn Ile Val Cys Trp Pro Ala Gly
105 110 115

GTG CCC GGC AAG GTG GTG GCC GTG CCC TGC CCC GAC TAC TTC TAC GAC 499
Val Pro Gly Lys Val Val Ala Val Pro Cys Pro Asp Tyr Phe Tyr Asp
120 125 130

TTC AAC CAC AAA GGC CGA GCC TAT CGG CGC TGT GAC AGC AAT GGC AGC 547
Phe Asn His Lys Gly Arg Ala Tyr Arg Arg Cys Asp Ser Asn Gly Ser
135 140 145 150

TGG GAG CTG GTG CCT GGG AAC AAC CGG ACA TGG GCG AAT TAC AGC GAA 595
Trp Glu Leu Val Pro Gly Asn Asn Arg Thr Trp Ala Asn Tyr Ser Glu
155 160 165

TGT GTC AAG TTT CTG ACC AAC GAG ACC CGG GAA CGG GAA GTC TTT GAT 643
Cys Val Lys Phe Leu Thr Asn Glu Thr Arg Glu Arg Glu Val Phe Asp
170 175 180

FIG. 1

CGC	CTC	GGA	ATG	ATC	TAC	ACT	GTG	GGC	TAC	TCC	ATC	TCT	CTG	GGC	TCC	691
Arg	Leu	Gly	Met	Ile	Tyr	Thr	Val	Gly	Tyr	Ser	Ile	Ser	Leu	Gly	Ser	
		185					190					195				
CTC	ACT	GTG	GCT	GTG	CTG	ATT	CTG	GGT	TAC	TTT	AGG	AGG	TTA	CAT	TGC	739
Leu	Thr	Val	Ala	Val	Leu	Ile	Leu	Gly	Tyr	Phe	Arg	Arg	Leu	His	Cys	
	200					205					210					
ACC	CGA	AAC	TAC	ATT	CAC	ATG	CAT	CTC	TTC	GTG	TCC	TTT	ATG	CTC	CGG	787
Thr	Arg	Asn	Tyr	Ile	His	Met	His	Leu	Phe	Val	Ser	Phe	Met	Leu	Arg	
215					220					225					230	
GCT	GTA	AGC	ATC	TTC	ATC	AAG	GAT	GCT	GTG	CTC	TAC	TCG	GGG	GTT	TCC	835
Ala	Val	Ser	Ile	Phe	Ile	Lys	Asp	Ala	Val	Leu	Tyr	Ser	Gly	Val	Ser	
				235					240					245		
ACA	GAT	GAA	ATC	GAG	CGC	ATC	ACC	GAG	GAG	GAG	CTG	AGG	GCC	TTC	ACA	883
Thr	Asp	Glu	Ile	Glu	Arg	Ile	Thr	Glu	Glu	Glu	Leu	Arg	Ala	Phe	Thr	
			250					255					260			
GAG	CCT	CCC	CCT	GCT	GAC	AAG	GCG	GGT	TTT	GTG	GGC	TGC	AGA	GTG	GCG	931
Glu	Pro	Pro	Pro	Ala	Asp	Lys	Ala	Gly	Phe	Val	Gly	Cys	Arg	Val	Ala	
		265					270					275				
GTA	ACC	GTC	TTC	CTT	TAC	TTC	CTG	ACC	ACC	AAC	TAC	TAC	TGG	ATC	CTG	979
Val	Thr	Val	Phe	Leu	Tyr	Phe	Leu	Thr	Thr	Asn	Tyr	Tyr	Trp	Ile	Leu	
	280					285					290					
GTG	GAA	GGC	CTC	TAC	CTT	CAC	AGC	CTC	ATC	TTC	ATG	GCT	TTT	TTC	TCT	1027
Val	Glu	Gly	Leu	Tyr	Leu	His	Ser	Leu	Ile	Phe	Met	Ala	Phe	Phe	Ser	
295					300					305					310	
GAG	AAA	AAG	TAT	CTC	TGG	GGT	TTC	ACA	TTA	TTT	GGC	TGG	GGC	CTC	CCT	1075
Glu	Lys	Lys	Tyr	Leu	Trp	Gly	Phe	Thr	Leu	Phe	Gly	Trp	Gly	Leu	Pro	
				315					320					325		
CCC	CTG	TTT	CTC	GCT	GTG	TGG	ATC	CC	CTG	AGG	GCT	ACA	CTG	GCC	AAC	1123
Ala	Val	Phe	Val	Ala	Val	Trp	Val	Thr	Val	Arg	Ala	Thr	Leu	Ala	Asn	
			330					335					340			
ACT	GAG	TGC	TGG	GAC	CTG	AGT	TCC	GGG	AAT	AAG	AAA	TGG	ATC	ATA	CAG	1171
Thr	Glu	Cys	Trp	Asp	Leu	Ser	Ser	Gly	Asn	Lys	Lys	Trp	Ile	Ile	Gln	
		345					350					355				
GTG	CCC	ATC	CTG	GCA	GCT	ATT	GTG	CTG	AAC	TTT	ATT	CTT	TTT	ATC	AAT	1219
Val	Pro	Ile	Leu	Ala	Ala	Ile	Val	Val	Asn	Phe	Ile	Leu	Phe	Ile	Asn	
	360					365					370					
ATA	ATC	AGA	GTC	CTG	GCT	ACT	AAA	CTC	CGG	GAG	ACC	AAT	GCA	GGG	AGA	1267
Ile	Ile	Arg	Val	Leu	Ala	Thr	Lys	Leu	Arg	Glu	Thr	Asn	Ala	Gly	Arg	
375					380					385					390	

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35.

TGT Cys	GAC Asp	ACG Thr	AGG Arg	CAA Gln	CAG Gln	TAT Tyr	AGA Arg	AAG Lys	CTG Leu	CTG Leu	AAG Lys	TCC Ser	ACG Thr	CTA Leu	GTC Val	1315
395 400 405																
CTC Leu	ATG Met	CCG Pro	CTA Leu	TTT Phe	GGG Gly	GTG Val	CAC His	TAC Tyr	ATC Ile	GTC Val	TTC Phe	ATG Met	GCC Ala	ACG Thr	CCG Pro	1353
410 415 420																
TAC Tyr	ACA Thr	GAA Glu	GTA Val	TCA Ser	GGG Gly	ATT Ile	CTT Leu	TGG Trp	CAA Gln	GTC Val	CAA Gln	ATG Met	CAC His	TAT Tyr	GAA Glu	1411
425 430 435																
ATG Met	CTC Leu	TTC Phe	AAT Asn	TCA Ser	TTC Phe	CAG Gln	GGA Gly	TTT Phe	TTC Phe	GTT Val	GCC Ala	ATT Ile	ATA Ile	TAC Tyr	TGT Cys	1459
440 445 450																
TTC Phe	TGC Cys	AAT Asn	GGA Gly	GAG Glu	GTA Val	CAA Gln	GCA Ala	GAG Glu	ATC Ile	AAG Lys	AAG Lys	TCA Ser	TGG Trp	AGC Ser	CGA Arg	1507
455 460 465 470																
TGG Trp	ACC Thr	CTG Leu	GCC Ala	TTG Leu	GAC Asp	TTC Phe	AAG Lys	CGG Arg	AAG Lys	GCC Ala	CGG Arg	AGT Ser	GGC Gly	AGC Ser	AGT Ser	1555
475 480 485																
ACC Thr	TAC Tyr	AGC Ser	TAT Tyr	GGC Gly	CCC Pro	ATG Met	GTG Val	TCA Ser	CAT His	ACA Thr	AGT Ser	GTC Val	ACC Thr	AAT Asn	GTG Val	1603
490 495 500																
GGA Gly	CCT Pro	CGA Arg	GGG Gly	GGC Gly	TGG Trp	CCT Pro	TGT Cys	CCC Pro	TCA Ser	GCC Ala	CTC Leu	GAC Asp	TAGCTCCTGG			1652
505 510 515																
GGCTGGAGCC AGTSCCAATG GCCATCACCA GTTGCCTGGC TATGTGAAGC ATGGTTCCAT 1712																
TTCTGAGAAC TCATTGCCTT CATCTGGCCC AGAGCCTGGC ACCAAAGATG ACGGGTATCT 1772																
CAATGGCTCT GGACTTTATG AGCCAATGGT TSGGGAACAG CCCCCTCCAC TCCTGGAGGA 1832																
GGAGAGAGAG ACAGTCATGT GACCCATATC 1862																

FIG. 2

TGGGCACAGC CACCCTGTTG GTAGTCCAGG GGCCAGCCCA CTGAGCTGGC ATATCAGCTG																60
GTGGCCCCGT TGGACTCGGC CCTAGGGAAC GGCGGGCG ATG GGA GCG CCC CGG ATC																115
Met Gly Ala Pro Arg Ile																
1 5																
TGG	CAC	AGC	CTT	GCC	TTG	CTC	CTC	TGC	TGC	TCC	GTG	CTC	AGC	TCC	GTC	163
Ser	His	Ser	Leu	Ala	Leu	Leu	Leu	Cys	Cys	Ser	Val	Leu	Ser	Ser	Val	
10 15 20																
TAC	GCA	CTG	GTG	GAT	GCC	GAT	GAT	GTC	ATA	ACG	AAG	GAG	GAG	CAG	ATC	211
Tyr	Ala	Leu	Val	Asp	Ala	Asp	Asp	Val	Ile	Thr	Lys	Glu	Glu	Gln	Ile	
25 30 35																
ATT	CTT	CTG	CGC	AAT	GCC	CAG	GCC	CAG	TGT	GAG	CAG	CGC	CTG	AAA	GAG	259
Ile	Leu	Leu	Arg	Asn	Ala	Gln	Ala	Gln	Cys	Glu	Gln	Arg	Leu	Lys	Glu	
40 45 50																
GTC	CTC	AGG	GTC	CCT	GAA	CTT	GCT	GAA	TCT	GCC	AAA	GAC	TGG	ATG	TCA	307
Val	Leu	Arg	Val	Pro	Glu	Leu	Ala	Glu	Ser	Ala	Lys	Asp	Trp	Met	Ser	
55 60 65 70																
AGG	TCT	GCA	AAG	ACA	AAG	AAG	GAG	AAA	CCT	GCA	GAA	AAG	CTT	TAT	CCC	355
Arg	Ser	Ala	Lys	Thr	Lys	Lys	Glu	Lys	Pro	Ala	Glu	Lys	Leu	Tyr	Pro	
75 80 85																
CAG	GCA	GAG	GAG	TCC	AGG	GAA	GTT	TCT	GAC	AGG	AGC	CGG	CTG	CAG	GAT	403
Gln	Ala	Glu	Glu	Ser	Arg	Glu	Val	Ser	Asp	Arg	Ser	Arg	Leu	Gln	Asp	
90 95 100																
GGC	TTC	TGC	CTA	CCT	GAG	TGG	GAC	AAC	ATT	GTG	TGC	TGG	CCT	GCT	GGA	451
Gly	Phe	Cys	Leu	Pro	Glu	Trp	Ser	Ser	Ile	Val	Cys	Trp	Pro	Ala	Gly	
105 110 115																
GTG	CCC	GGC	AAG	GTG	GTG	GCC	GTC	CCC	TGC	CCC	GAC	TAC	TTC	TAC	GAC	499
Val	Pro	Gly	Lys	Val	Val	Ala	Val	Trp	Cys	Pro	Asp	Tyr	Phe	Tyr	Asp	
120 125 130																
TTC	AAC	CAC	AAA	GGC	CGA	GCC	TAT	CGG	CGC	TGT	GAC	AGC	AAT	GGC	AGC	547
Phe	Asn	His	Lys	Gly	Arg	Ala	Tyr	Arg	Arg	Cys	Asp	Ser	Asn	Gly	Ser	
135 140 145 150																
TGG	GAG	CTG	GTG	CCT	GGG	AAC	AAC	CGG	ACA	TGG	GCG	AAT	TAC	AGC	GAA	595
Trp	Glu	Leu	Val	Pro	Gly	Asn	Asn	Arg	Thr	Trp	Ala	Asn	Tyr	Ser	Glu	
155 160 165																
TGT	GTC	AAG	TTT	CTG	ACC	AAC	GAG	ACC	CGG	GAA	CGG	GAA	GTC	TTT	GAT	643
Cys	Val	Lys	Phe	Leu	Thr	Asn	Glu	Thr	Arg	Glu	Arg	Glu	Val	Phe	Asp	
170 175 180																

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FIG. 2

CGC	CTC	GGA	ATG	ATC	TAC	ACT	GTG	GGC	TAC	TCC	ATC	TCT	CTG	GGC	TCC	691
Arg	Leu	Gly	Met	Ile	Tyr	Thr	Val	Gly	Tyr	Ser	Ile	Ser	Leu	Gly	Ser	
		185					190				195					
CTC	ACT	GTG	GCT	GTG	CTG	ATT	CTG	GGT	TAC	TTT	AGG	AGG	TTA	CAT	TGC	773
Leu	Thr	Val	Ala	Val	Leu	Ile	Leu	Gly	Tyr	Phe	Arg	Arg	Leu	His	Cys	
	200					205					210					
ACC	CGA	AAC	TAC	ATT	CAC	ATG	CAT	CTC	TTC	GTG	TCC	TTT	ATG	CTC	CGG	787
Thr	Arg	Asn	Tyr	Ile	His	Met	His	Leu	Phe	Val	Ser	Phe	Met	Leu	Arg	
	215				220					225					230	
GCT	GTA	AGC	ATC	TTC	ATC	AAG	GAT	GCT	GTG	CTC	TAC	TCG	GGG	GTT	TCC	805
Ala	Val	Ser	Ile	Phe	Ile	Lys	Asp	Ala	Val	Leu	Tyr	Ser	Gly	Val	Ser	
				235					240					245		
ACA	GAT	GAA	ATC	GAG	CGC	ATC	ACC	GAG	GAG	GAG	CTG	AGG	GCC	TTC	ACA	883
Thr	Asp	Glu	Ile	Glu	Arg	Ile	Thr	Glu	Glu	Glu	Leu	Arg	Ala	Phe	Thr	
			250					255					260			
GAG	CCT	CCC	CCT	GCT	GAC	AAG	GCG	GGT	TTT	GTG	GGC	TGC	AGA	GTG	GCG	931
Glu	Pro	Pro	Pro	Ala	Asp	Lys	Ala	Gly	Phe	Val	Gly	Cys	Arg	Val	Ala	
		265					270					275				
GTA	ACC	GTC	TTC	CTT	TAC	TTC	CTG	ACC	ACC	AAC	TAC	TAC	TGG	ATC	CTG	979
Val	Thr	Val	Phe	Leu	Tyr	Phe	Leu	Thr	Thr	Asn	Tyr	Tyr	Trp	Ile	Leu	
	280					285					290					
GTG	GAA	GGC	CTC	TAC	CTT	CAC	AGC	CTC	ATC	TTC	ATG	GCT	TTT	TTC	TCT	1027
Val	Glu	Gly	Leu	Tyr	Leu	His	Ser	Leu	Ile	Phe	Met	Ala	Phe	Phe	Ser	
	295				300					305					310	
GAG	AAA	AAG	TAT	CTC	TGG	GGT	TTC	ACA	TTA	TTT	GGC	TGG	GGC	CTC	CCT	1073
Glu	Lys	Lys	Tyr	Leu	Trp	Gly	Phe	Thr	Leu	Phe	Gly	Trp	Gly	Leu	Pro	
				315					320					325		
GCC	GTG	TTT	GTC	GCT	GTG	TGG	GTG	ACC	GTG	AGG	GCT	ACA	CTG	GCC	AAC	1123
Ala	Val	Phe	Val	Ala	Val	Trp	Val	Thr	Val	Arg	Ala	Thr	Leu	Ala	Asn	
			330				335						340			
ACT	GAG	TGC	TGG	GAC	CTG	AGT	TCG	GGG	AAT	AAG	AAA	TGG	ATC	ATA	CAG	1171
Thr	Glu	Cys	Trp	Asp	Leu	Ser	Ser	Gly	Asn	Lys	Lys	Trp	Ile	Ile	Gln	
		345					350					355				
GTG	CCC	ATC	CTG	GCA	GCT	ATT	GTG	GTG	AAC	TTT	ATT	CTT	TTT	ATC	AAT	1219
Val	Pro	Ile	Leu	Ala	Ala	Ile	Val	Val	Asn	Phe	Ile	Leu	Phe	Ile	Asn	
	360					365					370					
ATA	ATC	AGA	GTC	CTG	GCT	ACT	AAA	CTC	CGG	GAG	ACC	AAT	GCA	GGG	AGA	1267
Ile	Ile	Arg	Val	Leu	Ala	Thr	Lys	Leu	Arg	Glu	Thr	Asn	Ala	Gly	Arg	
	375				380					385					390	

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[illegible]

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FIG. 3

GGCGGGGGCC	GCGGCGGCGA	GCTCGGAGGC	CGGCGGCGGC	TGCCCCGAGG	GACGCGGCCC	60										
TAGGCGGTGG	CG	ATG	GGG	GCC	GCC	CGG	ATC	GCA	CCC	AGC	CTG	GCG	CTC	108		
		Met	Gly	Ala	Ala	Arg	Ile	Ala	Pro	Ser	Leu	Ala	Leu			
		1				5					10					
CTA	CTC	TGC	TGC	CCA	GTG	CTC	AGC	TCC	GCA	TAT	GCG	CTG	GTG	GAT	GCG	120
Leu	Leu	Cys	Cys	Pro	Val	Leu	Ser	Ser	Ala	Tyr	Ala	Leu	Val	Asp	Ala	
		15					20					25				
GAC	GAT	GTC	TTT	ACC	AAA	GAG	GAA	CAG	ATT	TTC	CTG	CTG	CAC	CGT	GCC	204
Asp	Asp	Val	Phe	Thr	Lys	Glu	Glu	Gln	Ile	Phe	Leu	Leu	His	Arg	Ala	
	30					35					40					
CAG	GCG	CAA	TGT	GAC	AAG	CTG	CTC	AAG	GAA	GTT	CTG	CAC	ACA	GCA	GCC	228
Gln	Ala	Gln	Cys	Asp	Lys	Leu	Leu	Lys	Glu	Val	Leu	His	Thr	Ala	Ala	
45					50					55					60	
AAC	ATA	ATG	GAG	TCA	GAC	AAG	GGC	TGG	ACA	CCA	GCA	TCT	ACG	TCA	GGG	252
Asn	Ile	Met	Glu	Ser	Asp	Lys	Gly	Trp	Thr	Pro	Ala	Ser	Thr	Ser	Gly	
				65				70						75		
AAG	CCC	AGG	AAA	GAG	AAG	GCA	TCG	GGA	AAG	TTC	TAC	CCT	GAG	TCT	AAA	276
Lys	Pro	Arg	Lys	Glu	Lys	Ala	Ser	Gly	Lys	Phe	Tyr	Pro	Glu	Ser	Lys	
			80					85					90			
GAG	AAC	AAG	GAC	GTG	CCC	ACC	GGC	AGC	AGG	CGC	AGA	GGG	CGT	CCC	TGT	300
Glu	Asn	Lys	Asp	Val	Pro	Thr	Gly	Ser	Arg	Arg	Arg	Gly	Arg	Pro	Cys	
		95					100					105				
CTG	CCC	GAG	TGG	GAC	AAC	ATC	GTT	TGC	TGG	CCA	TTA	GGG	GCA	CCA	GGT	324
Leu	Pro	Glu	Trp	Asp	Asn	Ile	Val	Cys	Trp	Pro	Leu	Gly	Ala	Pro	Gly	
	110					115					120					
GAA	GTG	GTG	GCA	GTA	CCT	TGT	CCC	GAT	TAC	ATT	TAT	GAC	TTC	AAT	CAC	348
Glu	Val	Val	Ala	Val	Pro	Cys	Pro	Asp	Tyr	Ile	Tyr	Asp	Phe	Asn	His	
125					130					135					140	
AAA	GGC	CAT	GCC	TAC	AGA	CGC	TGT	GAC	CGC	AAT	GGC	AGC	TGG	GAG	GTG	372
Lys	Gly	His	Ala	Tyr	Arg	Arg	Cys	Asp	Arg	Asn	Gly	Ser	Trp	Glu	Val	
				145				150					155			
GTT	CCA	GGG	CAC	AAC	CGG	ACG	TGG	GCC	AAC	TAC	AGC	GAG	TGC	CTC	AAG	396
Val	Pro	Gly	His	Asn	Arg	Thr	Trp	Ala	Asn	Tyr	Ser	Glu	Cys	Leu	Lys	
			160					165					170			
TTC	ATG	ACC	AAT	GAG	ACG	CGG	GAA	CGG	GAG	GTA	TTT	GAC	CGC	CTA	GGC	420
Phe	Met	Thr	Asn	Glu	Thr	Arg	Glu	Arg	Glu	Val	Phe	Asp	Arg	Leu	Gly	
		175					180					185				
ATG	ATC	TAC	ACC	GTG	GGA	TAC	TCC	ATG	TCT	CTC	GCC	TCC	CTC	ACG	GTG	444
Met	Ile	Tyr	Thr	Val	Gly	Tyr	Ser	Met	Ser	Leu	Ala	Ser	Leu	Thr	Val	
	190					195					200					

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FIG. 3

GCT Ala 205	GTG Val	CTC Leu	ATC Ile	CTG Leu	GCC Ala 210	TAT Tyr	TTT Phe	AGG Arg	CGG Arg	CTG Leu 215	CAC His	TGC Cys	ACG Thr	CGC Arg	AAC Asn 220	732
TAC Tyr	ATC Ile	CAC His	ATG Met	CAC His 225	ATG Met	TTC Phe	CTG Leu	TCG Ser	TTT Phe 230	ATG Met	CTG Leu	CGC Arg	GCC Ala	GCG Ala 235	AGC Ser	780
ATC Ile	TTC Phe	GTG Val	AAG Lys 240	GAC Asp	GCT Ala	GTG Val	CTC Leu	TAC Tyr 245	TCT Ser	GGC Gly	TTC Phe	ACG Thr	CTG Leu 250	GAT Asp	GAG Glu	828
GCC Ala	GAG Glu	CGC Arg 255	CTC Leu	ACA Thr	GAG Glu	GAA Glu	GAG Glu 260	TTG Leu	CAC His	ATC Ile	ATC Ile	GCG Ala 265	CAG Gln	GTG Val	CCA Pro	876
CCT Pro 270	CCG Pro	CCG Pro	GCC Ala	GCT Ala	GCC Ala	GCC Ala 275	GTA Val	GGC Gly	TAC Tyr	GCT Ala	GGC Gly 280	TGC Cys	CGC Arg	GTG Val	GCG Ala	924
GTG Val 285	ACC Thr	TTC Phe	TTC Phe	CTC Leu 290	TAC Tyr	TTC Phe	CTG Leu	GCT Ala 295	ACC Thr	AAC Asn	TAC Tyr	TAC Tyr	TGG Trp	ATT Ile 300	CTG Leu	972
GTG Val	GAG Glu	GGG Gly	CTG Leu 305	TAC Tyr	TTG Leu	CAC His	AGC Ser	CTC Leu 310	ATC Ile	TTC Phe	ATG Met	GCC Ala	TTT Phe 315	TTC Phe	TCA Ser	1020
GAG Glu	AAG Lys	AAG Lys 320	TAC Tyr	CTG Leu	TGG Trp	GGC Gly	TTC Phe 325	ACC Thr	ATC Ile	TTT Phe	GGC Gly	TGG Trp 330	GGT Gly	CTA Leu	CCG Pro	1068
GCT Ala	GTC Val 335	TTC Phe	GTG Val	GCT Ala	GTG Val	TGG Trp 340	GTC Val	GGT Gly	GTC Val	AGA Arg	GCA Ala 345	ACC Thr	TTG Leu	GCC Ala	AAC Asn	1116
ACT Thr 350	GGG Gly	TGC Cys	TGG Trp	GAT Asp	CTG Leu 355	AGC Ser	TCC Ser	AGG Ser	CAC His	AAG Lys 360	AAG Lys	TGG Trp	ATC Ile	ATC Ile	CAG Gln 365	1164
GTG Val	CCC Pro	ATC Ile	CTG Leu	GCA Ala 370	TCT Ser	GTT Val	GTG Val	CTC Leu 375	AAC Asn	TTC Phe	ATC Ile	CTT Leu	TTT Phe	ATC Ile 380	AAC Asn	1212
ATC Ile	ATC Ile	CGG Arg	GTG Val 385	CTT Leu	GCC Ala	ACT Thr	AAG Lys	CTT Leu 390	CGG Arg	GAG Glu	ACC Thr	AAT Asn	GCG Ala 395	GGC Gly	CGG Arg	1260
TGT Cys	GAC Asp	ACC Thr 400	AGG Arg	CAG Gln	CAG Gln	TAC Tyr	CGG Arg 405	AAG Lys	CTG Leu	CTC Leu	AGG Arg	TCC Ser 410	ACG Thr	TTG Leu	GTG Val	1308

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FIG. 3

CTC	GTG	CCG	CTC	TTT	GGT	GTC	CAC	TAC	ACC	GTC	TTC	ATG	GCC	TTG	CCG	1356
Leu	Val	Pro	Leu	Phe	Gly	Val	His	Tyr	Thr	Val	Phe	Met	Ala	Leu	Pro	
415						420					425					
TAC	ACC	GAG	GTC	TCA	GGG	ACA	TTG	TGG	CAG	ATC	CAG	ATG	CAT	TAT	GAG	1404
Tyr	Thr	Glu	Val	Ser	Gly	Thr	Leu	Trp	Gln	Ile	Gln	Met	His	Tyr	Glu	
430					435					440					445	
ATG	CTC	TTC	AAC	TCC	TTC	CAG	GGA	TTT	TTT	GTT	GCC	ATC	ATA	TAC	TGT	1452
Met	Leu	Phe	Asn	Ser	Phe	Gln	Gly	Phe	Phe	Val	Ala	Ile	Ile	Tyr	Cys	
				450				455						460		
TTC	TGC	AAT	GGT	GAG	GTG	CAG	GCA	GAG	ATT	AGG	AAG	TCA	TGG	AGC	CGC	1500
Phe	Cys	Asn	Gly	Glu	Val	Gln	Ala	Glu	Ile	Arg	Lys	Ser	Trp	Ser	Arg	
			465					470					475			
TGG	ACA	CTG	GCG	TTG	GAC	TTC	AAG	CGC	AAA	GCA	CGA	AGT	GGG	AGT	AGC	1548
Trp	Thr	Leu	Ala	Leu	Asp	Phe	Lys	Arg	Lys	Ala	Arg	Ser	Gly	Ser	Ser	
		480					485					490				
AGC	TAC	AGC	TAT	GGC	CCA	ATG	GTG	TCT	CAC	ACG	AGT	GTG	ACC	AAT	GTG	1596
Ser	Tyr	Ser	Tyr	Gly	Pro	Met	Val	Ser	His	Thr	Ser	Val	Thr	Asn	Val	
	495					500					505					
GGC	CCC	CGT	GCA	GGA	CTC	AGC	CTC	CCC	CTC	AGC	CCC	CGC	CTG	CCT	CCT	1644
Gly	Pro	Arg	Ala	Gly	Leu	Ser	Leu	Pro	Leu	Ser	Pro	Arg	Leu	Pro	Pro	
510					515					520					525	
GCC	ACT	ACC	AAT	GGC	CAC	TCC	CAG	CTG	CCT	GGC	CAT	GCC	AAG	CCA	GGG	1692
Ala	Thr	Thr	Asn	Gly	His	Ser	Gln	Leu	Pro	Gly	His	Ala	Lys	Pro	Gly	
				530				535					540			
GCT	CCA	GCC	ACT	GAG	ACT	GAA	ACC	CTA	CCA	GTC	ACT	ATG	GCG	GTT	CCC	1740
Ala	Pro	Ala	Thr	Glu	Thr	Glu	Thr	Leu	Pro	Val	Thr	Met	Ala	Val	Pro	
			545					550					555			
AAG	GAC	GAT	GGA	ATC	CTT	AAC	GGC	TCC	TGC	TCA	GGC	CTG	GAT	GAG	GAG	1788
Lys	Asp	Asp	Gly	Phe	Leu	Asn	Gly	Ser	Cys	Ser	Gly	Leu	Asp	Glu	Glu	
		560					565					570				
GCC	TCC	GGG	TCT	GCG	CGG	CCG	CCT	CCA	TTG	TTG	CAG	GAA	GGA	TGG	GAA	1836
Ala	Ser	Gly	Ser	Ala	Arg	Pro	Pro	Pro	Leu	Leu	Gln	Glu	Gly	Trp	Glu	
	575					580					585					
ACA	GTC	ATG	TGACTGGGCA	CTAGGGGGCT	AGACTGCTGG	CCTGGGCACA	1885									
Thr	Val	Met														
590																
TGGACAGATG	GACCAAGAAG	CCAGTGTTTG	GCTGGTTGTC	TATTCGGGAT	CTGGACCAGG	1945										
AAGATAACAA	AAGGAAAATG	GAAGTGGACG	AAGCAGAGAA	GAAGGAAGAG	GTTTTGCAGG	2005										
AATTAAATAT	GTTTCCTCAG	TTGGATGATG	AGGACACAAG	GAAGGC		2051										

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Fig. 4

1 MGAARIAPSLALLCCPVLSSAYALVDADDVFTKEEQIFLLHRAQAQCDK 50
| | | : | | . | | | | | | | | | | | | | | | : | | | | | | : | | | | | : .
1 MGAPRISHSLALLCCSVLSSVYALVDADDVITKEEQIILLRNAQAQCEQ 50
51 LLKEVLHTAANIMESDKGWTTPASTSGKPRKEKASGKFYPESKENKDVPTG 100
| | | | : . : : | | . | : | | : | | : | | : . : | : | : . : | : .
51 RLKEVLR.VPELAESAEDW..MRSAXTKKEXPAEKLYPQAEESREVSER 97
101 SRRRGRPCLP2EWONIVCWPLGAPGEVVAVPCPDYIYDFNHHKGHAYRRCDR 150
| | . : | | | | | | | | | | | | | | | | | | : | | | | | : | | | | | .
98 SRLQDGFCLPEWONIVCWPAAGVPGKVVAVPCPDYFYDFNHHKGRAYRRCDR 147
151 NGSHEVVPCHNRTWANYSECLKFMETNETREREVFDRLGMIYTVGYSHSLA 200
| | | | : | | : | : | | :
148 NGSWELVPGNRTWANYSECVRPLTNETREREVFDRLGMIYTVGYSHSLG 197
201 SLTVAVLILAYFRRLHCTRNYIHMHLFVSVFHLRAVSIFIKDAVLYSGFTL 250
| | | | | | | | : | : | | | | | .
198 SLTVAVLILAYFRRLHCTRNYIHMHLFVSVFHLRAVSIFIKDAVLYSGVST 247
251 DEAEERLTEEELHIIAQVPPPPAAAAGVYAGCRVAVTFFLYFLATNYHWIL 300
| | | | : | | | : . : | | : | . | : . | | | | | . | | | | | | | | |
248 DEIERITEEELRAFT...PPPADKAGFVGCRVAVTVFLYFLTTNYHWIL 294
301 VEGLYLHSLIFMAFFSEKKYLVGFTIFGNGLP2AVFVAVWVGVRATLANTG 350
| | | | | | | | | | | | | | | | | | : | | | | | | | | | | | | | | | :
295 VEGLYLHSLIFMAFFSEKKYLVGFTLFGNGLP2AVFVAVWVTVRATLANTE 344
351 CNDLSSCHKKWIIQVPILASVVLNFIILFINIIRVLATKLRETNAGRCDDR 400
| | | | | : |
345 CNDLSSGNKKWIIQVPILAAIVVNFIILFINIIRVLATKLRETNAGRCDDR 394
401 QOYRKLLRSTLVLPVPLFGVHYTVFMALPYTEVSGTLWQIQMHYENLHNSF 450
| | | | | : | | | | | : | | | | | . | | | | | | | | | | | | | | | | | |
395 QOYRKLLKSTLVLPVPLFGVHYIVFMATPYTEVSGILWQVQMHYENLHNSF 444
451 QGFFVAIIYCFNGEVOAEIRKSWSRWTLALDFKRRKARSGSSSYSGPHV 500
| | | | | | | | | | | | | | | | | | : | | | | | | | | | | | | | | | |
445 QGFFVAIIYCFNGEVOAEIRKSWSRWTLALDFKRRKARSGSSTYSYSGPHV 494
501 SHTSVTVGFRAGLSLPLSPRLPP...ATTNCHSOLPGHAKPGAPATETE 547
| | | | | | | | : | | . | | | | : | | | | | | | | | | | | | | | | | |
495 SHTSVTVGFRAGLSLPLSPRLAPGAGASANGHQLPGYVKHGSISENSL 544
548 TL2VTVMAVPRDDGFLNGSCSGLDEEASGSEARPPPLLQEGWETVM. 591
| | | | . : . | | | | | | | | | | | | | | | | | | : | | : | | | |
545 PSSGFEPTXDDGYLNG..SGLYEPHVG.ECP2PLLZEERETVM* 586

Gap Weight:	3.000	Average Match:	0.540
Length Weight:	0.100	Average Mismatch:	-0.396
Quality:	712.2	Length:	595
Ratio:	1.215	Gaps:	6
Percent Similarity:	87.113	Percent Identity:	77.835

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Fig. 5

R15 MGAARIAPSL ALLLCCPVLS SAYALVDADD VPTKEEQIFL LHRAQAQCDK 50
OkO MGAPRISHSL ALLLCCSVLS SVYALVDADD VITKEEQIIL LRNAQAQCEQ 50
Okh MGAPRISHSL ALLLCCSVLS SVYALVDADD VITKEEQIIL LRNAQAQCEQ 50

----- A -----

R15 LLKEVLHTAA NIMESDKGWT PASTSGKPRK EKASGKPYPE SKENKDVPTG 100
OkO RLKEVLR.VP ELAESAKDW. .MSRSAKTKK EKPAEKLYPQ AZESREVS DR 97
Okh RLKEVLR.VP ELAESAKDW. .MSRSAKTKK EKPAEKLYPQ AZESREVS DR 97

R15 SRRRGPRCLP EWDNIVCWPL GAPGEVVAVP CPDYIYDFNH KGHAYRRC DR 150
OkO SRLQDGFCLP EWDNIVCWPA GVP GKVVAVP CPDYFYDFNH KGRAYRRC DS 147
Okh SRLQDGFCLP EWDNIVCWPA GVP GKVVAVP CPDYFYDFNH KGRAYRRC DS 147

----- B -----

R15 NGSWEVVP GH NRTWANYSEC LKFM TNETRE REVFDRLGMI YTVGYSHSLA 200
OkO NGSWELVPGN NRTWANYSEC VKFLTNETRE REVFDRLGMI YTVGY SISLG 197
Okh NGSWELVPGN NRTWANYSEC VKFLTNETRE REVFDRLGMI YTVGY SISLG 197

R15 SLTVAVLILA YFRRLHCTRN YIHM HFLSF MLRAASIFVK DAVLYSGFTL 250
OkO SLTVAVLILG YFRRLHCTRN YIHM HLFVSF MLRAVSIFIK DAVLYSGVST 247
Okh SLTVAVLILG YFRRLHCTRN YIHM HLFVSF MLRAVSIFIK DAVLYSGVST 247

-- C -----

----- D -----

R15 DEAE RLTEEE LHIIAQVPPP PAAA VGYAG CRVAVTFPLY FLATNYYWIL 300
OkO DEIERITEEE LRAFTE...P PPADKAGFVG CRVAVTVPLY FLTTNYYWIL 294
Okh DEIERITEEE LRAFTE...P PPADKAGFVG CRVAVTVPLY FLTTNYYWIL 294

----- E -----

R15 VEGLYLHSLI FMAFFSEKKY LWGFTIFGWG LPAVFVAVWV GVRATLAN TG 350
OkO VEGLYLHSLI FMAFFSEKKY LWGFTLFGWG LPAVFVAVWV TVRATLAN TE 344
Okh VEGLYLHSLI FMAFFSEKKY LWGFTLFGWG LPAVFVAVWV TVRATLAN TE 344

----- F -----

----- G -----

R15 CWDLSSGNKK WIIQVPILAS VVLN FILFIN IIRVLATKLR ETNAGRC DTR 400
OkO CWDLSSGNKK WIIQVPILAA IVVN FILFIN IIRVLATKLR ETNAGRC DTR 394
Okh CWDLSSGNKK WIIQVPILAA IVVN FILFIN IIRVLATKLR ETNAGRC DTR 394

----- H -----

R15 QQYRKLLRST LVLVPLFGVH YTVFMALPYT EVSGTLWQIQ MHYEMLFNSF 450
OkO QQYRKLLKST LVLNPLFGVH YIVFMATPYT EVSGILWQVQ MHYEMLFNSF 444
Okh QQYRKLLKST LVLNPLFGVH YIVFMATPYT EVSGILWQVQ MHYEMLFNSF 444

----- I -----

R15 QGFFVAIIYC FCNGEVQAEI RKSWSRWTLA LDFKRKARSG SSSYSYGPMV 500
OkO QGFFVAIIYC FCNGEVQAEI KKSWSRWTLA LDFKRKARSG SSTYSYGPMV 494
Okh QGFFVAIIYC FCNGEVQAEI KKSWSRWTLA LDFKRKARSG SSTYSYGPMV 494

-- J -----

R15 SHTSVTNVGP RAGLSLPLSP RLPP...ATT NGHSQLPGHA KPGAPATETE 547
OkO SHTSVTNVGP RGGLALSLSF RLAPGAGASA NGHHQLPGYV KHGSISENSL 544
Okh SHTSVTNVGP RGG..... .WPCPSA LD 515

R15 TLPVTMAVPR DDGFLNGSCS GLDEEASGSA RPPPLLQEGW ETVH 591
OkO PSSGPEPGTK DDGYLNG..S GLYEPHVG.E QPPPLLEER ETVH 585

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FIG. 6

With 1 enzymes: SACT

February 27, 1992 18:30 ..

GGGATCCCGCGGGCCCTAGGCGGTGGCGatgggGAccGCCcggatcgcacccggcctggcg
2 -----+----- 61
CCCTAGGGCGCCGGGATCCGCCACCGCtaccCTggCGggcctagcgtgggcccggaccgc

b M G T A R T A P G L A -

ctcctgctctgctgccccgtgctcagctccgggtacgcgctgggtggatgcagatgacgtc
62 -----+----- 121
gaggacgagacgacggggcacgagtcgaggcgcatgcgcgaccacctacgtctactgcag

b L L L C C P V L S S A Y A L V D A D D V -

atgactaaagaggaacagatcttcctgctgccccgtgctcaggccccagtgcgaaaaacgg
122 -----+----- 181
tactgattttctcttctgcttagaaggacgacgtggcaccgagtcggggtcacgctttctgce

b M T K E E Q I F L L H R A Q A Q C E K R -

ctcaaggagggtccctgcagaggccagccagcatatcggaatcagacaagggtatggacatct
132 -----+----- 241
gagttcctccaggacgtctccggtcgggtcgtattaccttagtctgttccctacctgtaga

b L K E V L Q R P A S I M E S D K G W T S -

gggtccacatcagggaagcccaggaaagataagggcatctgggaagctctacctgagttct
242 -----+----- 301
ggcagggtgtagtcccttcgggtccctttctattccgtagacccttcgagatgggactcaga

b A S T S G K P R K D K A S G K L Y P E S -

gaggaggaacaaggaggcaccactggcagcaggtaccgaggcgccccgtctgcccggaa
302 -----+----- 361
ctccctccctgttccctccgtgggtgacccgtcgtccatggctcccgggggacagacggcctt

b E E D Y E A P T E S I R G R P C L P E -

tgggaccacatccctgtgctggccgctggggggcaccacggcgaggtgggtggctgtgccctgt
362 -----+----- 421
accctgggtgtaggacacgacccggcgacccccgtgggtccactccaccaccgacacgggaca

b W D H I L C W P L G A P E E V V A V P C -

ccggactacatttatgacttcaatcacaaaggccatgcctaccgaegctgtgaccgcaat
422 -----+----- 481
ggcctgatgtaaatactgaagttagtggttccggtaaggatgggtgcgacactggcggtta

b P D Y I Y D F N H K G A A Y R R C D R N -

ggcagctgggagctcgtgacctgggcacacacaggaacctggggccaactacagcgagtggtgc
482 -----+----- 541
ccgtccaccctcgaccacggacccctgttctccctccaccgggttgatgtcgtccacacag

14/30

1032 tgggacttgagctccgggaacaaaaagtggaatcccccaggtgccccatccctggccctccatt
----- 1141
acccctgaactcgagggcccttggtttttccacctagtaggtccacgggtaggaccggaggttaa
W D L S S S N K K W I I Q V P I L A S I -
1142 gtgctcaacttccatccctcttccatcaatatccctccgggtgctcggccaccaagcagcgggag
----- 1201
cacgagttgaagtaggagaagttagttatagcagggccacgagcgggtgggttcgtcgccctc
V L N F I L F I N I V R V L A T K Q R E -
1202 accaacgcccggccgggtgtgacacacggcagcagataccggaagctgctcaaateccacgctg
----- 1261
tgggttggggccggccacactgtgtgcccgtatgtccatggcccttcgacgagtttaggtgcgac
T N A G R C D T R Q I V R K L L K S T L -
1262 gtgctcatgccccctctttggcggtccactacattgtcttccatggccacaccatacacccgag
----- 1321
cacgagtacgggggagaaaccgcaggtgattgtacagaagtaccgggtgtgggtatgtggctc
V L M P L F G V H Y I V F M A T P Y T E -
1322 gtctcagggacgctctggcaagtccagatgcactatgagatgctcttccactccttccag
----- 1381
cagagtcctctgggagaccgttcaggtctacgtccataccttacgagaagttgaggaaggtc
V S G T L W Q V Q M H Y E M L F N S F Q -
1382 ggattttttgtcggcaatcatactctctctctccatggcgaggtacaagctgagatcaag
----- 1441
cctaaaaaacagcgttagtatatgacaaagacgttaccgctccatgttcgactctagttc
G F F V A I I Y C F I H S E V Q A E I K -
1442 aaatccttggagccgctggacactggcactggactccagcgaaggcacgcagcgggagc
----- 1501
tttagaacctcggggacctgtgacctgaccttaacttcgcttccgtgggtcgccctcg
K S W S R W T L A I I T H R K A R S G S -
1502 agcagctataagctacggcccccctgggtgtcccccacagctgtgaccaatgtcggcccccg
----- 1561
tcgtcgatatcgatgccgggggtaccacaggtgtgttccactgggttacagccgggggca
S S Y S Y G P M V S H T E V T N V G P R -
1562 gtgggactcgggctgccccctcagccccccgcttactgcccactgcccaccaccaacgggccac
----- 1621
caccctgagccgggacggggagtcggggggcggtatccgggtgacgggtgggttgcgggtg
V G L G L P L S P R L I E T A T T N G H -
1622 cctcagctgcttggccatgccaaagccaggacccccacccctggagaccctcgagaccaca
----- 1681
ggagtcgacgggacctgacgggtccgggtccctgggttcgggaacctctgggagctctgggtg
P Q L P G H A K P G T F A L E T L E T T -

[illegible]

gggaccgtaccgacgagggttccttgctaccctaaaggagtggccgaggacgagtccggac

gacgaqgaqgcccctctgggccttgagcggccacccggccctgctacaggaagagctgggagaca

ctgctcctccggagacccggactcggcggcggacggacgatgtccttcctcaccctctgt

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caattacactcgtccgcgacccccgacctggacgactgtatcacctacctgtctacctcggc

aaagatcggcggctgaatgatttccactcaaggcccgggccaaagaggaaaaaacaggg

ttttaccacccaacttactaaagggtgagtcacggaccacgggtctctcttttttctgtcc

Q aaaaaaaQaaaaaaaaaaaQaaaaaaQqaaaaaaasasasasasasasasasasasasasas

[illegible][illegible]

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

Saci

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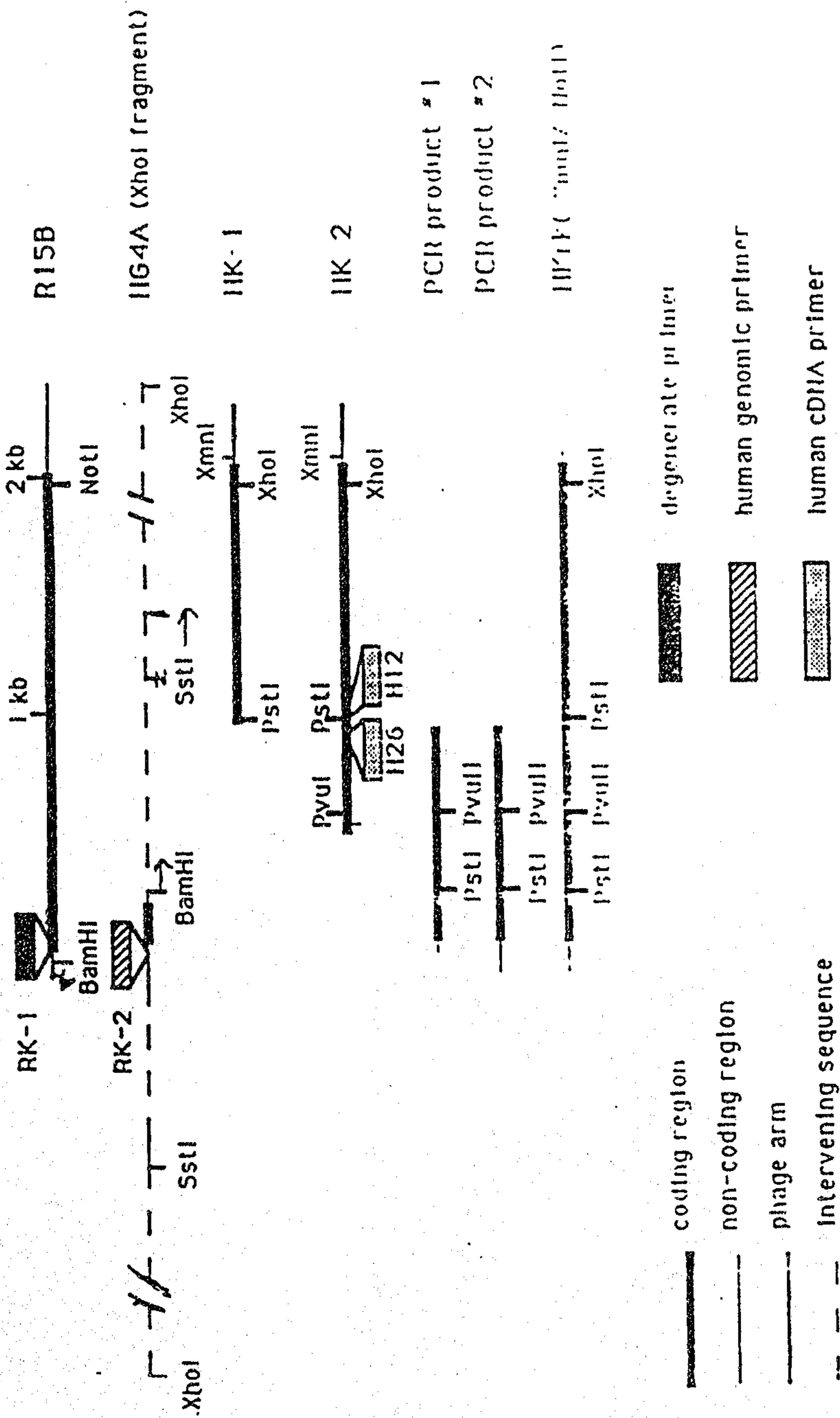


Fig. 7

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117-411.
117-111.

Fig.3

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TRANSLATE of: 1k.seq check: 9/54 from: 29 to: 1810

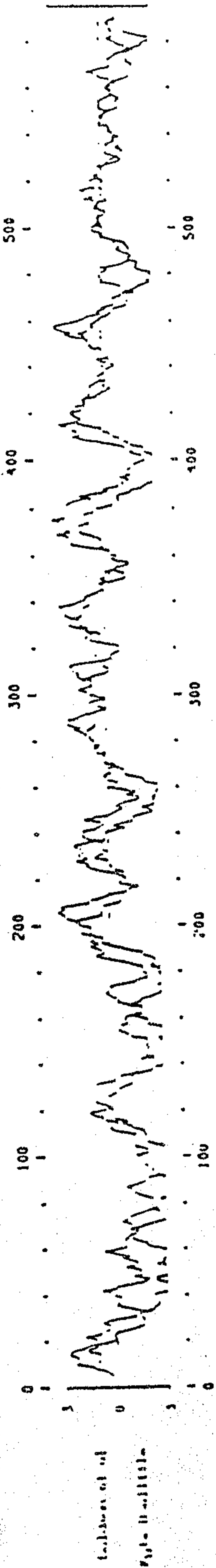
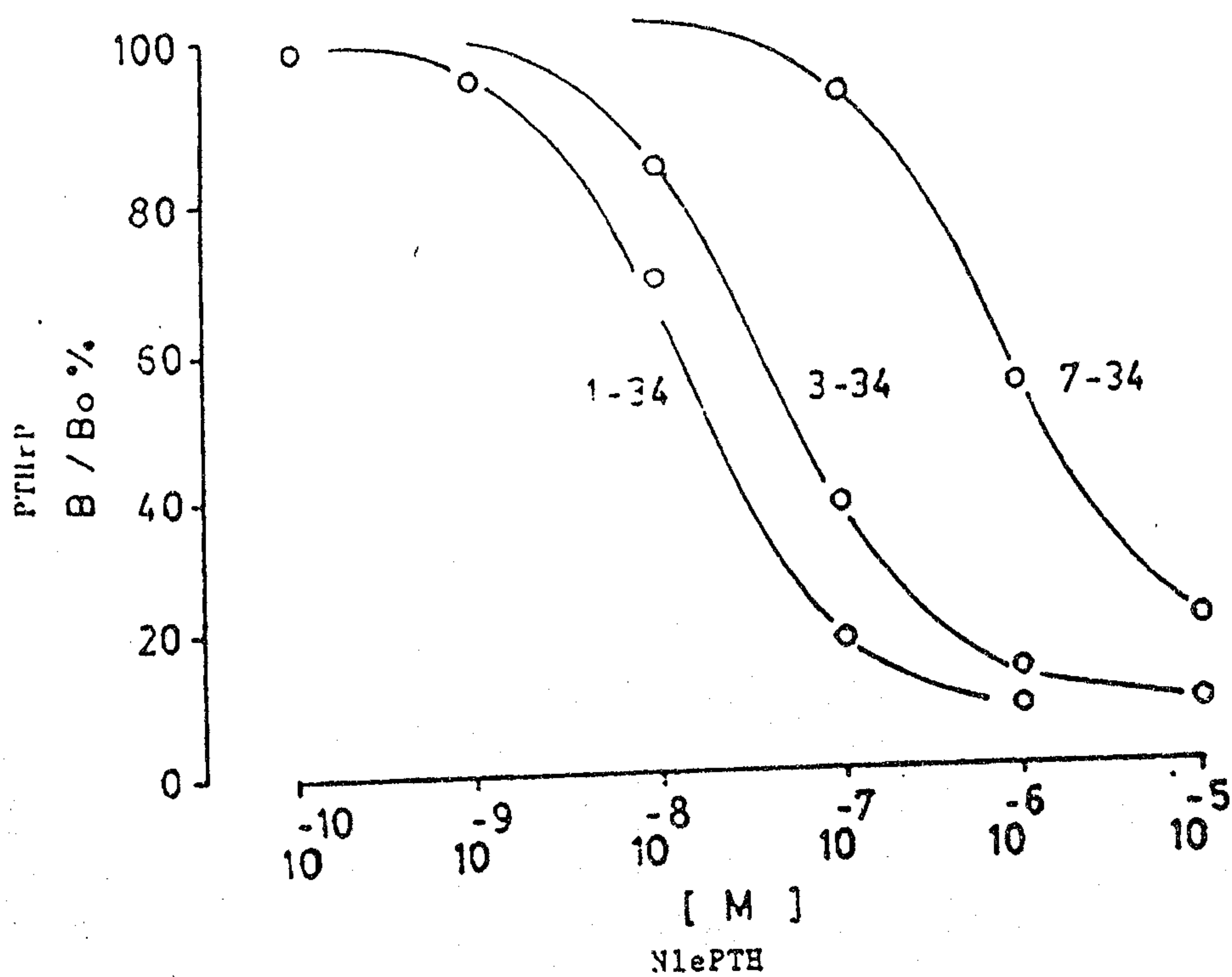
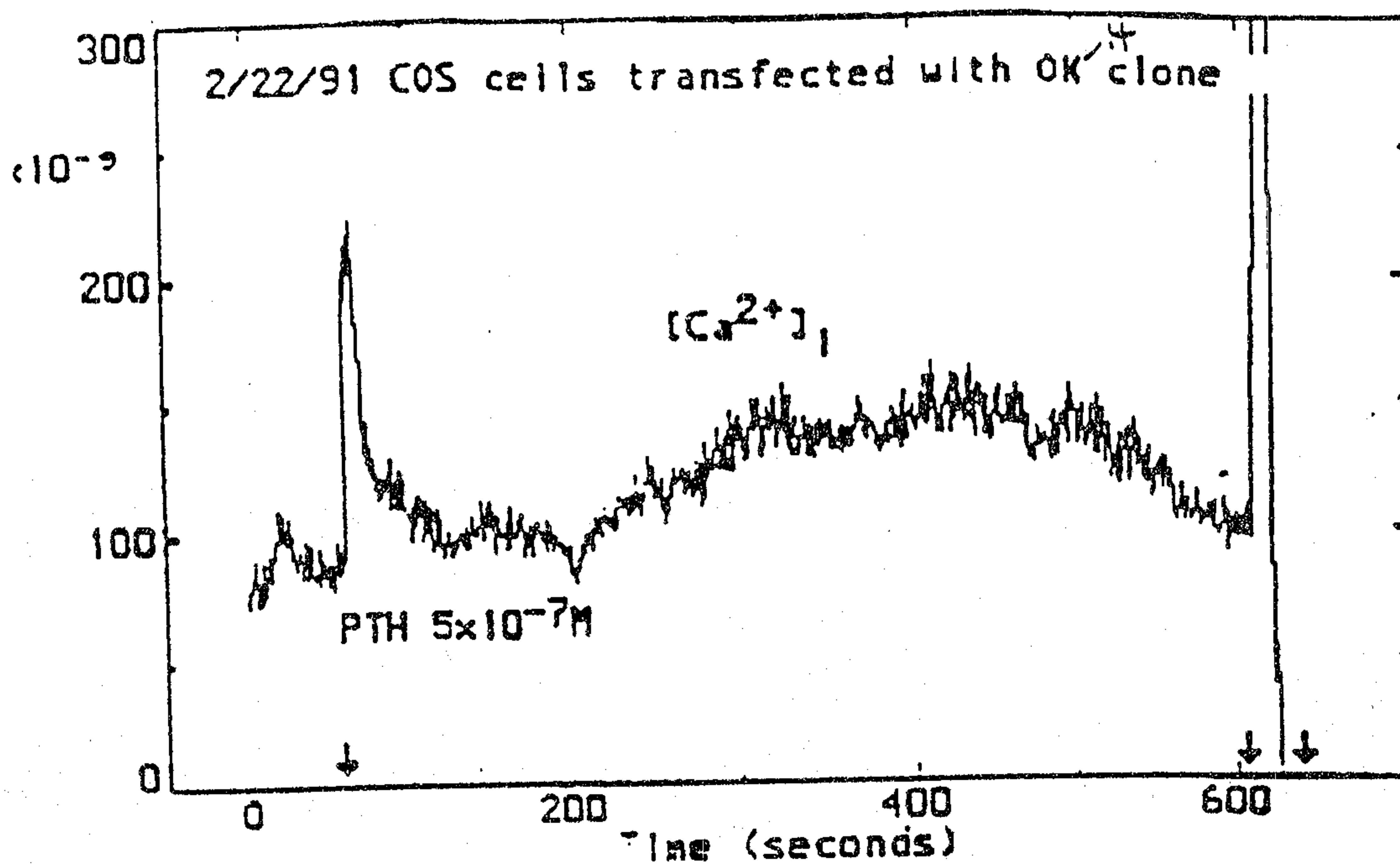


FIG. 9



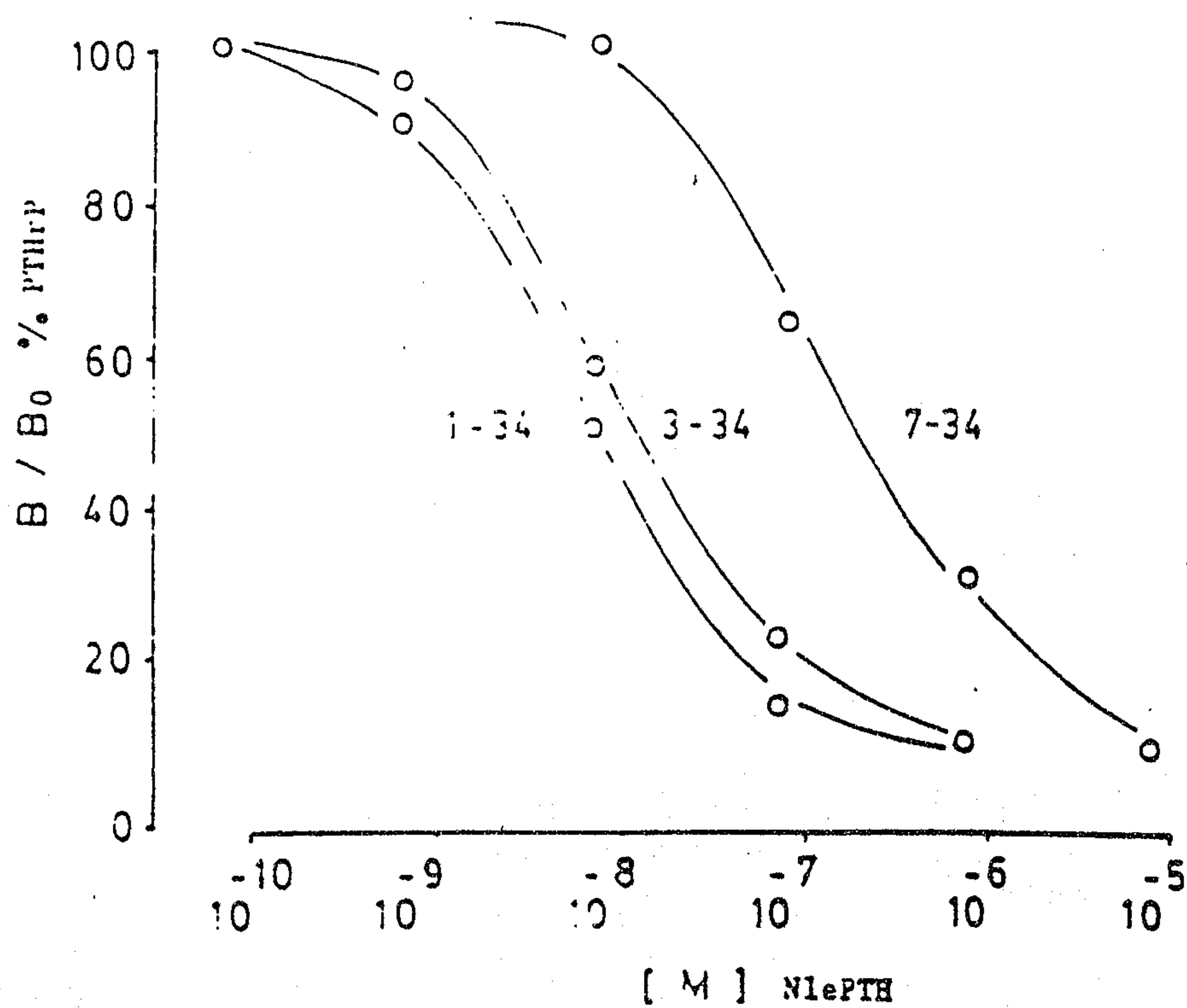
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FIG. 10



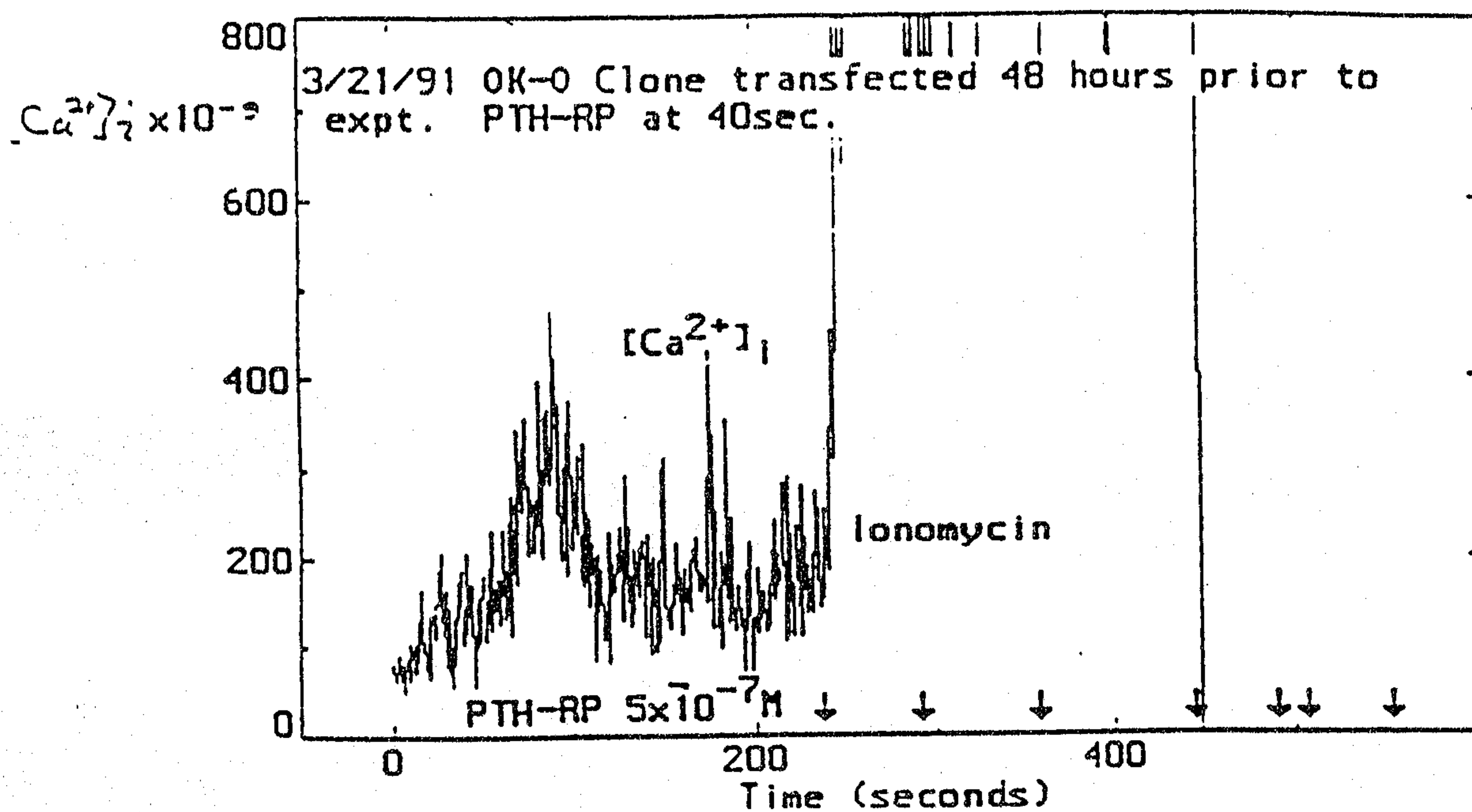
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Fig. 11



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FIG.12



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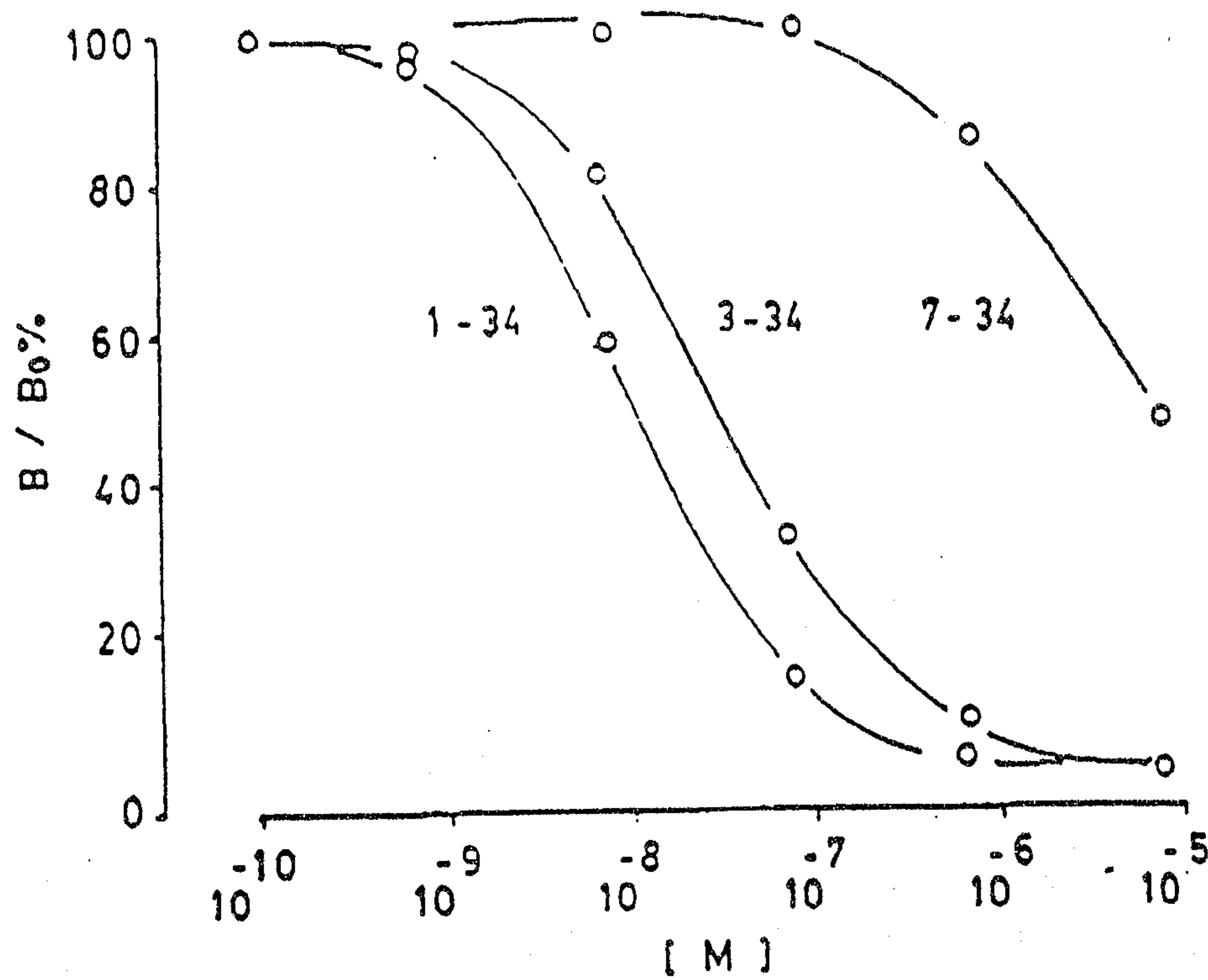
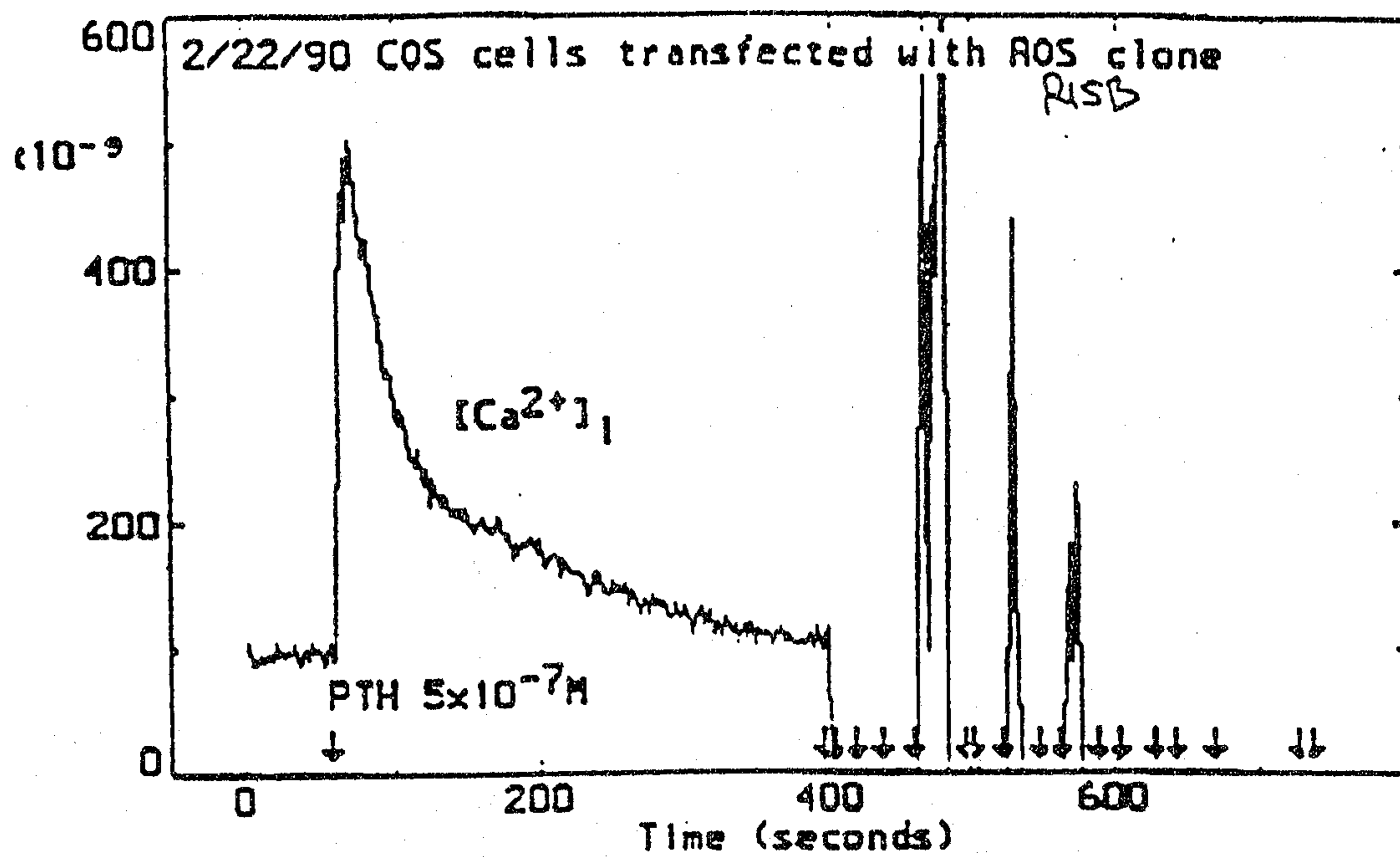


FIG. 13

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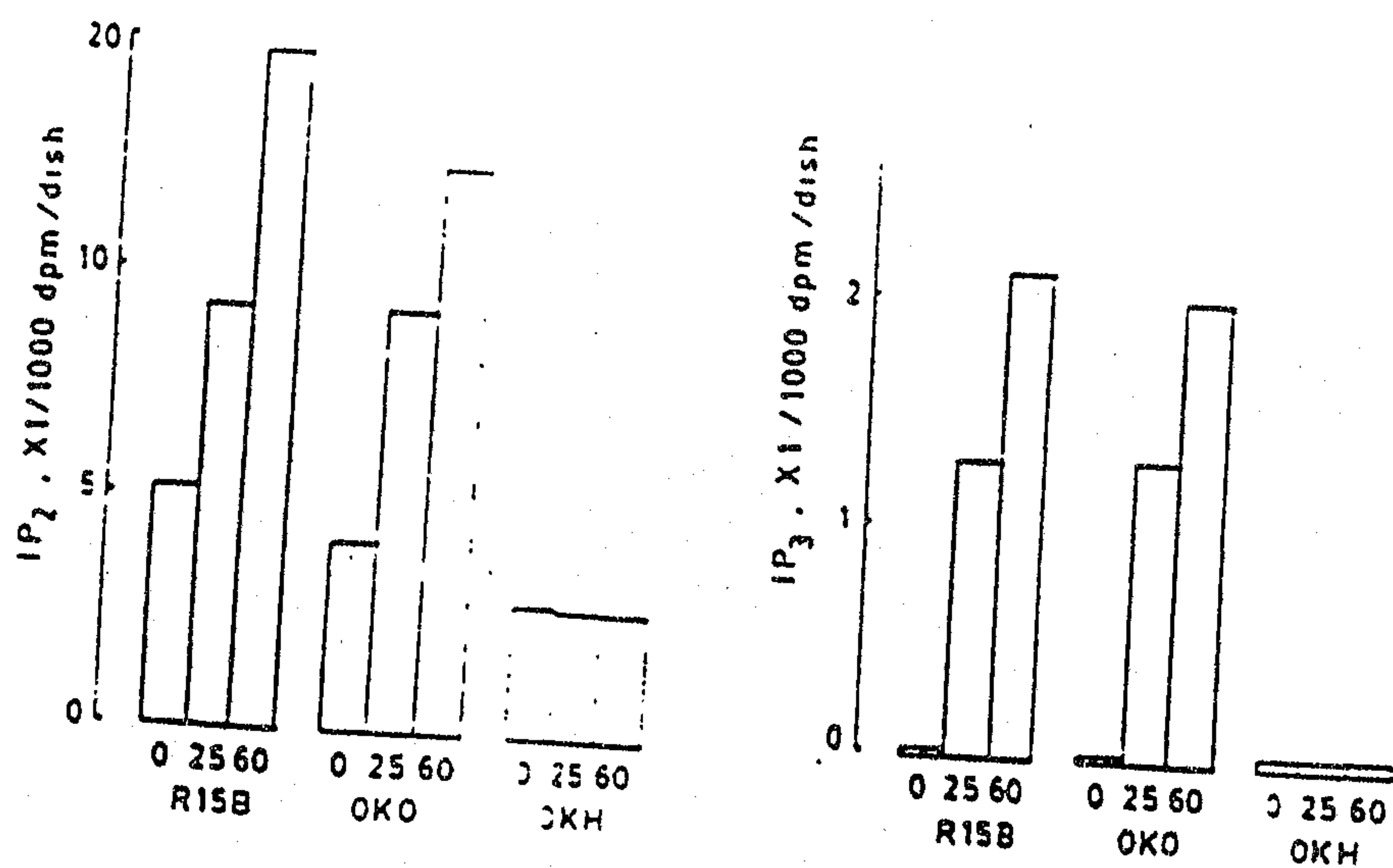
FIG. 14



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FIG. 15



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FIG. 16

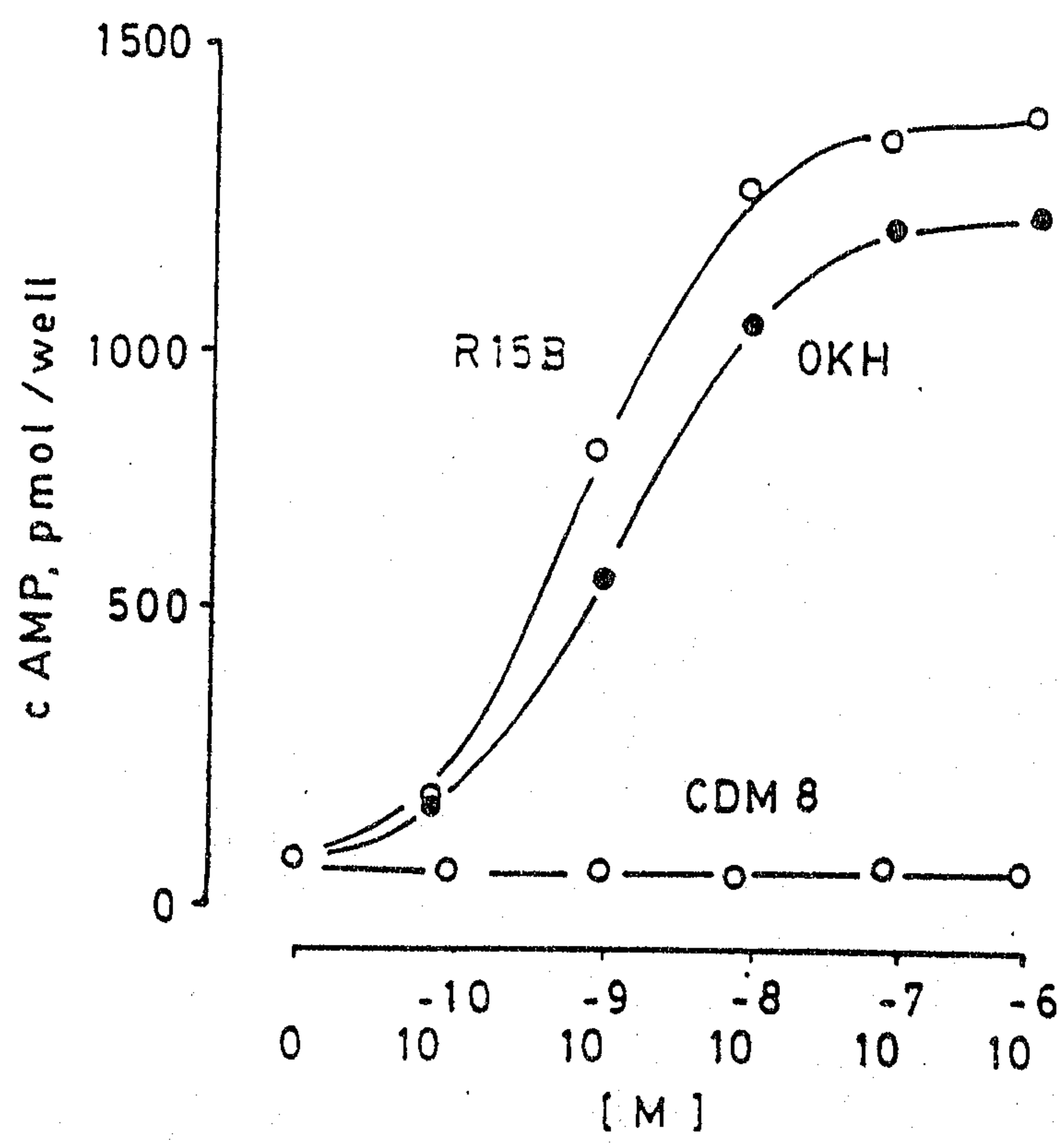


Fig. 17

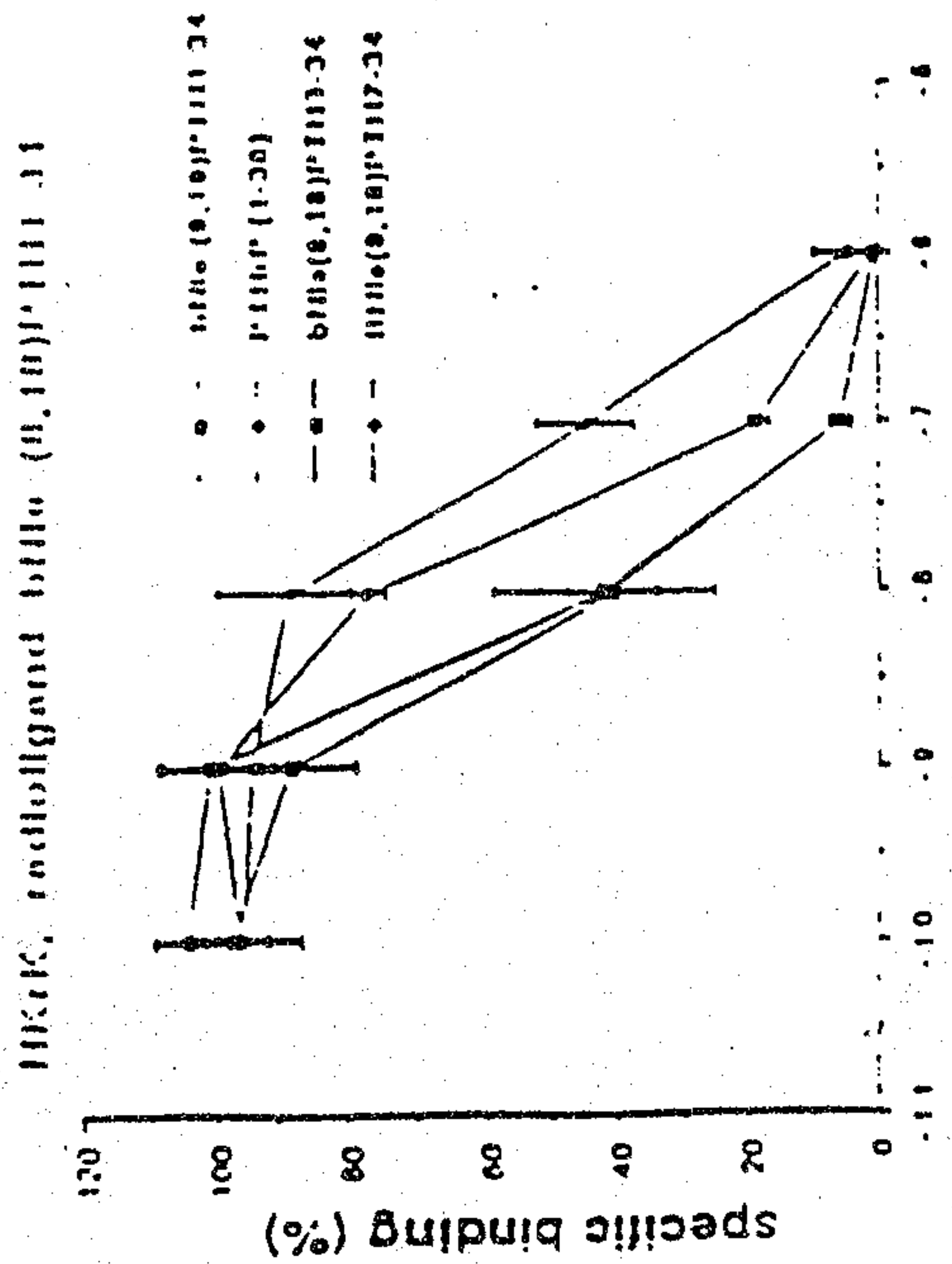
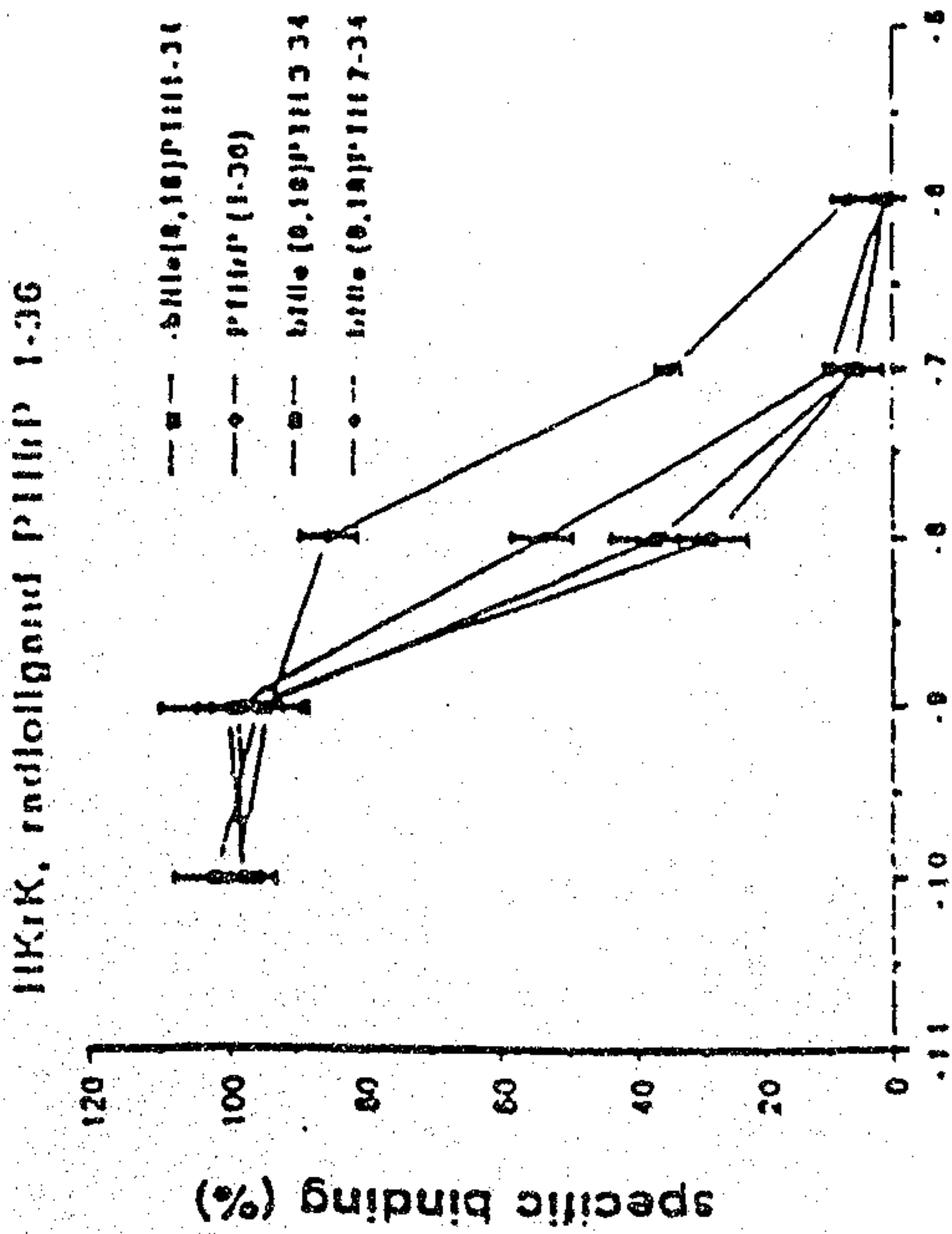
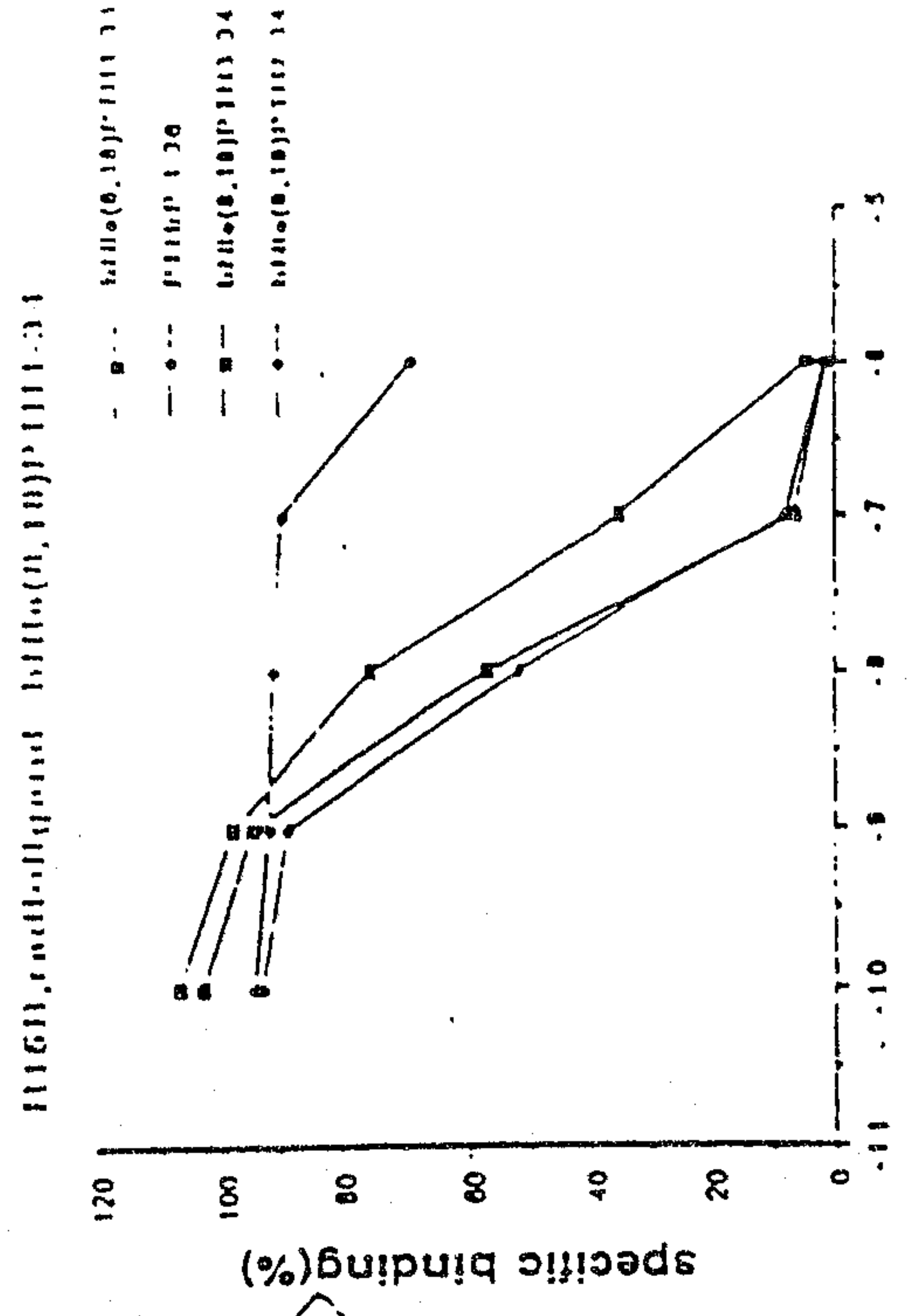
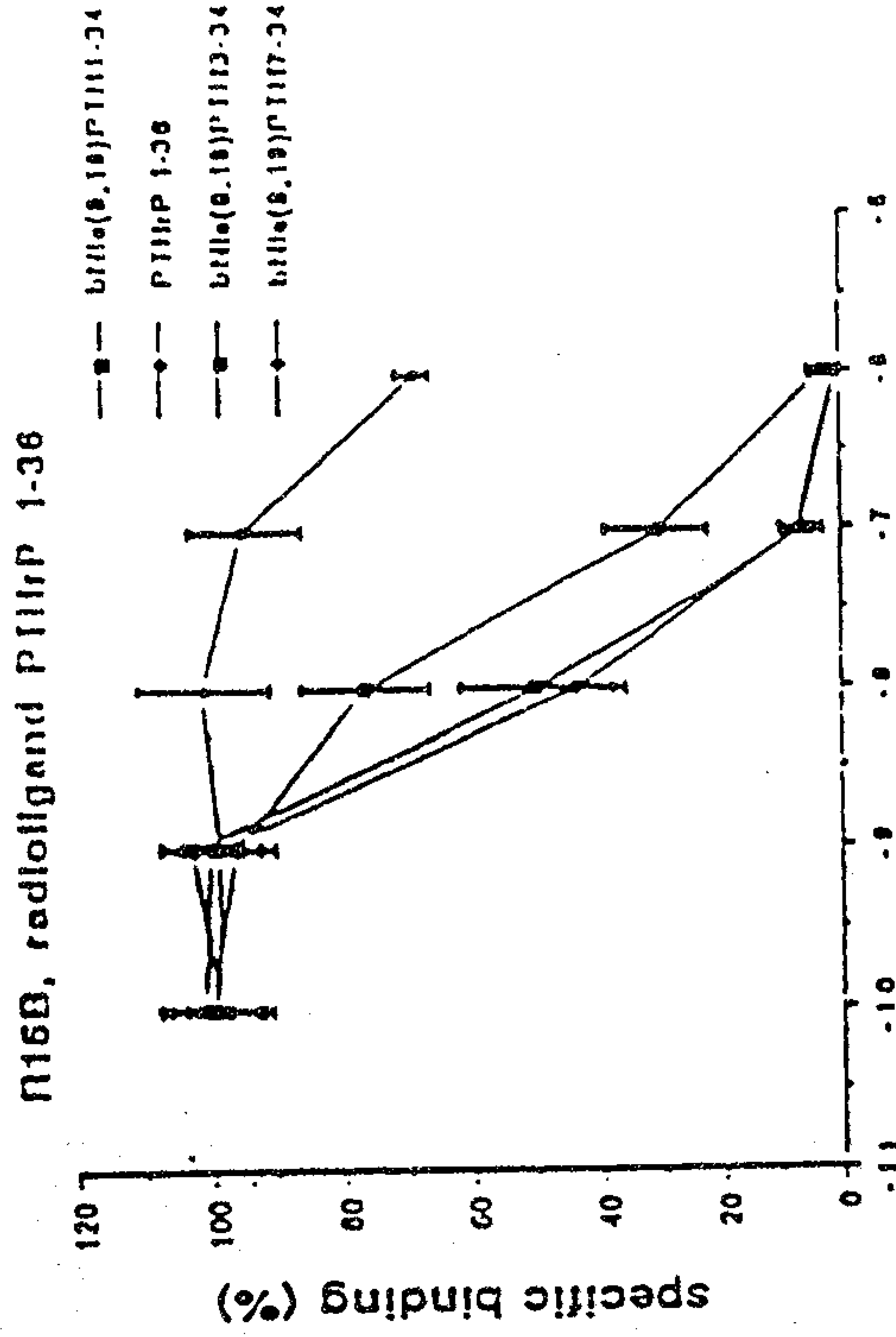


FIG. 18

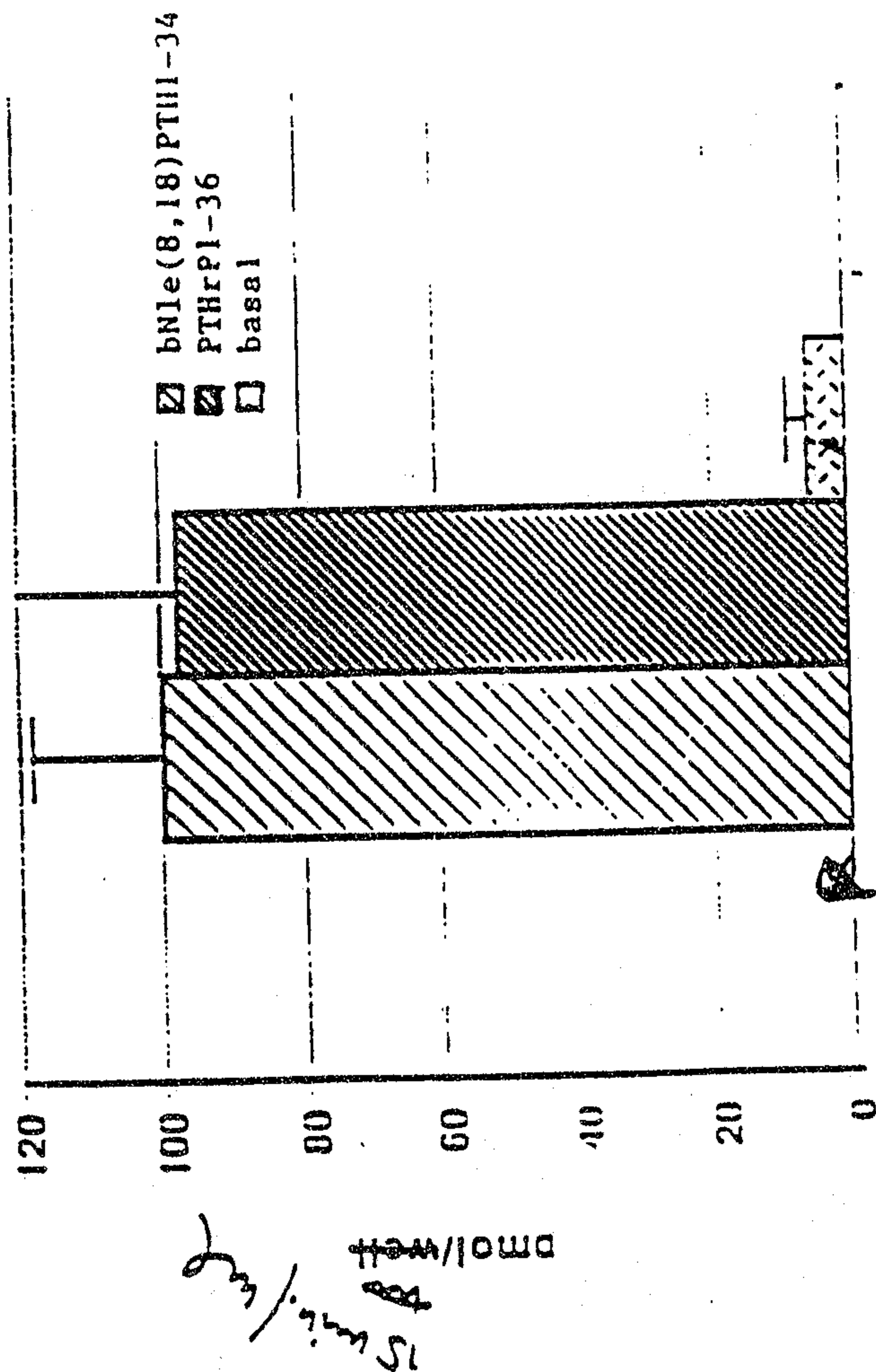


Fig. 19

A B

285 →

185 →

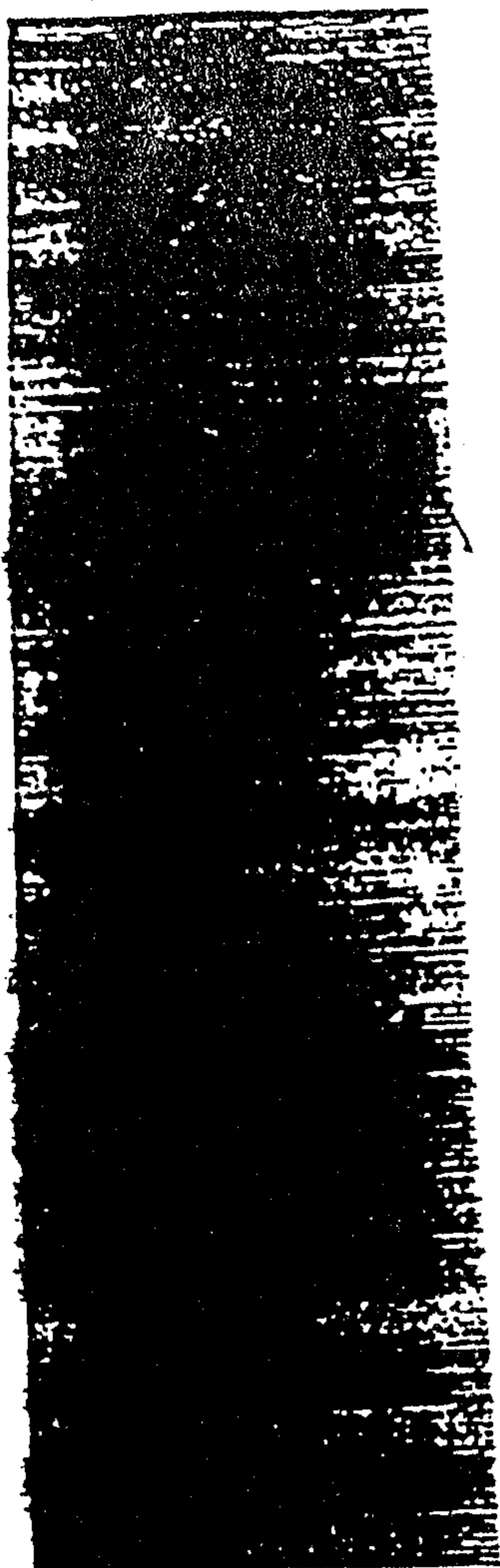
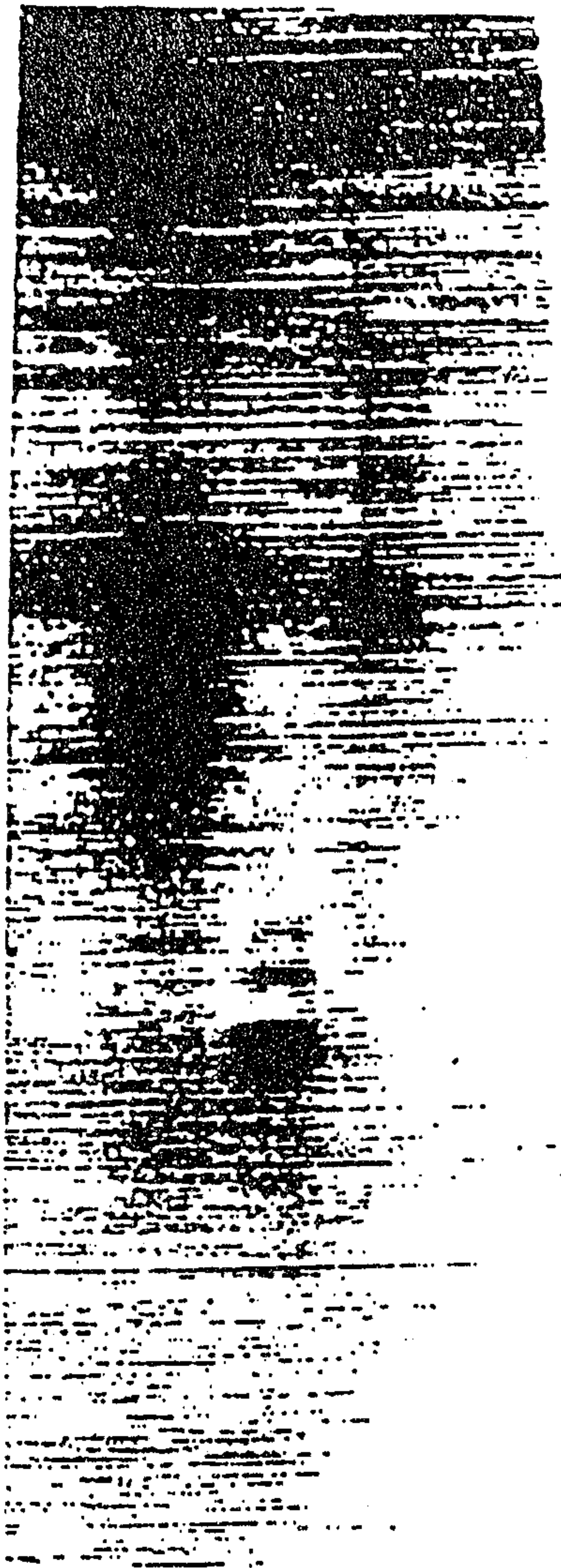


Fig. 20



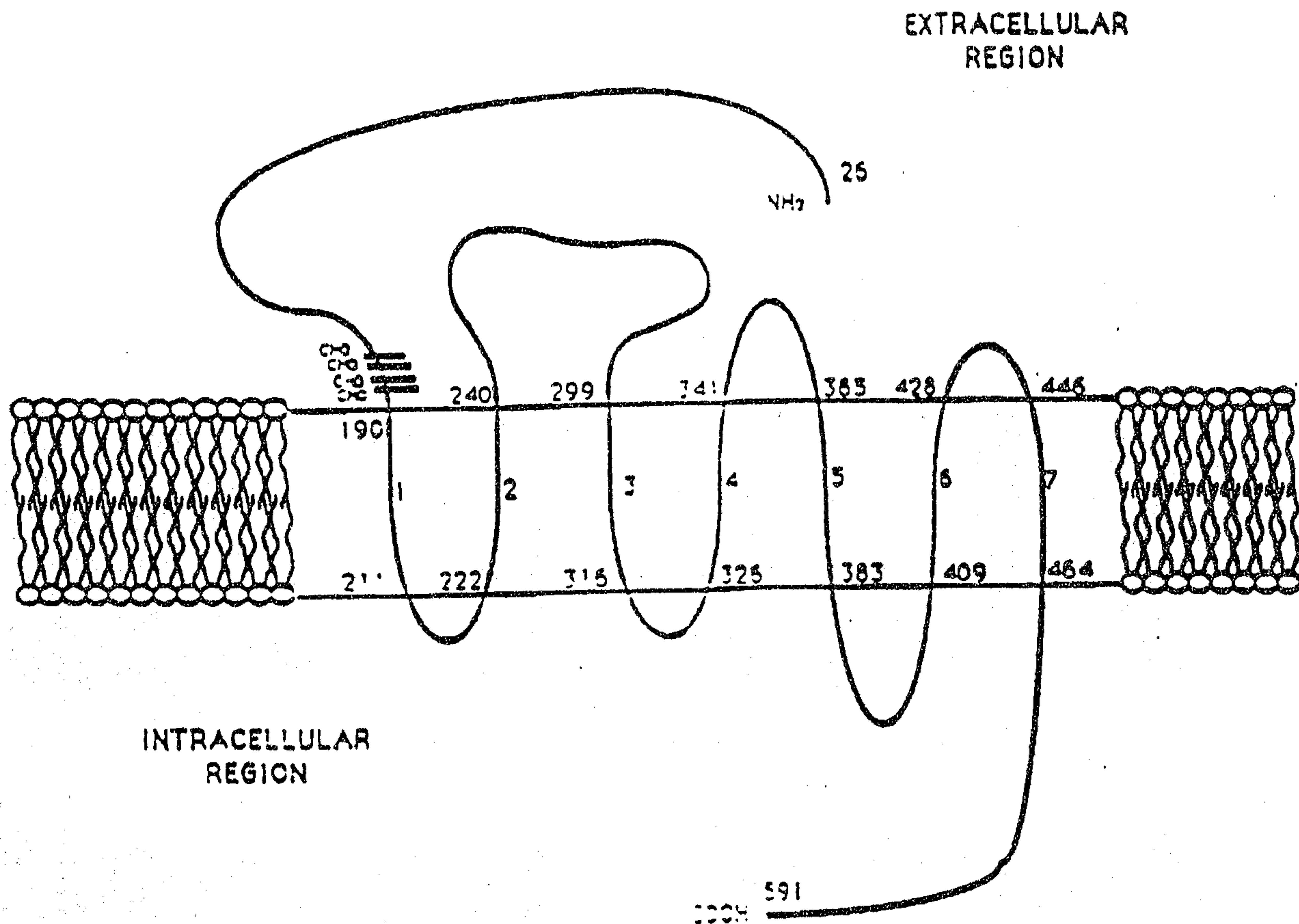
3

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Fig. 21

RAT BONE PTH/PTHrP RECEPTOR



AMINO ACID SEQUENCE OF 7 PUTATIVE TRANS-MEMBRANE REGIONS

