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(54) Titre : MORPHOGENESE INDUITE PAR DES PROTEINES

(54) Title: PROTEIN-INDUCED MORPHOGENESIS

(57) **Abrégé/Abstract:**

This invention relates to amino acid sequence data, structural features, homologies and various other data characterizing morphogenic proteins. There is also disclosed methods of producing these proteins from natural and recombinant sources and from synthetic constructs. The invention also relates to morphogenic devices comprising these proteins and a suitably modified tissue-specific matrix. Methods of inducing non-chondrogenic tissue growth in mammals are also disclosed. The proteins are useful in inducing the developmental cascade of tissue morphogenesis for a variety of tissues in mammals different from bone or cartilage. The proteins of the morphogenic devices comprise a pair of folded polypeptides, the amino acid sequence of each comprises a sequence sharing at least 70% homology with the C-terminal seven-cysteine domain of human OP-1, mouse OP-1, human OP-2 or mouse OP-2, residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8; or an essentially 102 amino acid sequence having cysteine residues at relative positions 1, 30, 34, 66, 67, 99 and 101 therein, wherein at least 70% of amino acid residues within said sequence are selected independently from residues occupying the corresponding positions within residues 38-139 of Seq. ID Nos., 5, 6, 7 or 8, or conservative substitutions of said corresponding residues.



Abstract of Disclosure

This invention relates to amino acid sequence data, structural features, homologies and various other data characterizing morphogenic proteins. There is also disclosed methods of producing these proteins from natural and recombinant sources and from synthetic constructs. The invention also relates to morphogenic devices comprising these proteins and a suitably modified tissue-specific matrix. Methods of inducing non-chondrogenic tissue growth in mammals are also disclosed. The proteins are useful in inducing the developmental cascade of tissue morphogenesis for a variety of tissues in mammals different from bone or cartilage. The proteins of the morphogenic devices comprise a pair of folded polypeptides, the amino acid sequence of each comprises a sequence sharing at least 70% homology with the C-terminal seven-cysteine domain of human OP-1, mouse OP-1, human OP-2 or mouse OP-2, residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8; or an essentially 102 amino acid sequence having cysteine residues at relative positions 1, 30, 34, 66, 67, 99 and 101 therein, wherein at least 70% of amino acid residues within said sequence are selected independently from residues occupying the corresponding positions within residues 38-139 of Seq. ID Nos., 5, 6, 7 or 8, or conservative substitutions of said corresponding residues.

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PROTEIN-INDUCED MORPHOGENESISBackground of the Invention

This invention relates to morphogenic proteins which can induce tissue morphogenesis in mammals; to methods of identifying these proteins and obtaining them from natural sources or producing synthetic forms of these proteins by expressing recombinant DNA encoding the proteins; to the fabrication of tissue-specific acellular matrices; and to methods for promoting tissue stasis, repair and regeneration, and methods for increasing progenitor cell populations using these proteins.

Cell differentiation is the central characteristic of morphogenesis which initiates in the embryo, and continues to various degrees throughout the life of an organism in adult tissue repair and regeneration mechanisms. The degree of morphogenesis in adult tissue varies among different tissues and is related, among other things, to the degree of cell turnover in a given tissue. On this basis, tissues can be divided into three broad categories: (1) tissues with static cell populations such as nerve and skeletal muscle where there is no cell division and most of the

cells formed during early development persist throughout adult life; (2) tissues containing conditionally renewing populations such as liver where there is generally little cell division but, in response to an appropriate stimulus, cells can divide to produce daughters of the same differentially defined type; and (3) tissues with permanently renewing populations including blood, testes and stratified squamous epithelia which are characterized by rapid and continuous cell turnover in the adult. Here, the terminally differentiated cells have a relatively short life span and are replaced through proliferation of a distinct subpopulation of cells, known as stem or progenitor cells.

15

The cellular and molecular events which govern the stimulus for differentiation of these cells is an area of intensive research. In the medical field, it is anticipated that the discovery of factor(s) which control cell differentiation and tissue morphogenesis will significantly advance medicine's ability to repair and regenerate diseased or damaged mammalian tissues and organs. Particularly useful areas include reconstructive surgery and in the treatment of tissue degenerative diseases including arthritis, emphysema, osteoporosis, cardiomyopathy, cirrhosis, and degenerative nerve diseases.

A number of different factors have been isolated in recent years which appear to play a role in cell differentiation. Some of these factors are gene transcription activators such as the NOTCH gene, identified in *Drosophila* and the related XOTCH gene identified in *Xenopus*, as well as a number of transcription activators identified in *Caenorhabditis elegans*.

The hemopoietic system, because of its continually renewing cell population, is an area of concentrated study. Factors identified in this system which may be involved in cell renewal include

5 interleukin 3 (IL-3), erythropoietin, the CSFs (GM-CSF, G-CSF, M-CSF et al.) and various stem cell growth factors.

Other proteins thought to play a role in cell

10 differentiation include proteins that are members of the family of insulin-like growth factors (IGF), members of the family of heparin-binding growth factors, (e.g., FGF - acidic and basic fibroblast growth factors, and ECDGF - embryonal carcinoma-derived

15 growth factor) as well as several transforming oncogenes (hst and int-2, see for example, Heath et al., (1988), J. Cell Sci. Suppl. 10:256-256.) DIF (Differentiation Inducing Factor), identified in Dictyostelium discoideum, is another bioregulatory

20 protein, directing prestock cell differentiation in that organism.

The structurally related proteins of the TGF- β superfamily of proteins also have been identified as

25 involved in a variety of developmental events. For example, TGF- β and the polypeptides of the inhibin/activin group appear to play a role in the regulation of cell growth and differentiation. MIS (Mullerian Inhibiting Substance) causes regression of

30 the Mullerian duct in development of the mammalian male embryo, and DPP, the gene product of the Drosophila decapentaplegic complex is required for appropriate dorsal-ventral specification. Similarly, Vg-1 is involved in mesoderm induction in Xenopus, and Vgr-1

35 has been identified in a variety of developing murine tissues.

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Another source that has revealed a wealth of information is in the area of bone morphogenesis. The development and study of a bone model system has

5 identified the developmental cascade of bone differentiation as consisting of chemotaxis of mesenchymal cells, proliferation of these progenitor cells, differentiation of these cells into chondroblasts, cartilage calcification, vascular

10 invasion, bone formation, remodeling, and finally, marrow differentiation (Reddi (1981) Collagen Rel. Res. 1:209-206). Proteins capable of inducing endochondral bone formation in a mammal when implanted in association with a matrix now have been identified in a

15 number of different mammalian species, as have the genes encoding these proteins, (see, for example, U.S. Patent No. 4,968,590 and U.S. Patent No. 5,011,691, Ozkaynak, et al., (1990) EMBO J 9:2085-2093, and Ozkaynak et al., (1991) Biochem. Biophys. Res. Commn.

20 179:116-123 and United States patent number 5,266,683 issued on November 30, 1993. These proteins, which share significant amino acid sequence homology with one another as well as structural similarities with various members of

25 the TGF-B super family of proteins, have been shown to induce endochondral bone formation and/or cartilage formation when implanted in a mammal in association with a suitably modified matrix.

30 Proteins capable of inducing a similar developmental cascade of tissue morphogenesis of other tissues have not been identified.

It is an object of this invention to provide

35 morphogenic proteins ("morphogens"), and methods for identifying these proteins, which are capable of inducing the developmental cascade of tissue

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morphogenesis for a variety of tissues in mammals different from bone or cartilage. This morphogenic activity includes the ability to induce proliferation and differentiation of progenitor cells, and the

5 ability to support and maintain the differentiated phenotype through the progression of events that results in the formation of adult tissue. Another object is to provide genes encoding these proteins as well as methods for the expression and isolation of

10 these proteins, from either natural sources or biosynthetic sources, using recombinant DNA techniques. Still another object is to provide tissue-specific acellular matrices that may be used in combination with these proteins, and methods for their production.

15 Other objects include providing methods for increasing a progenitor cell population in a mammal, methods for stimulating progenitor cells to differentiate in vivo or in vitro and maintain their differentiated phenotype, methods for inducing tissue-specific growth

20 in vivo and methods for the replacement of diseased or damaged tissue in vivo. These and other objects and features of the invention will be apparent from the description, drawings, and claims which follow.

Summary of the Invention

This invention provides morphogenic proteins ("morphogens") capable of inducing the developmental cascade of tissue morphogenesis in a mammal. In particular, these proteins are capable of inducing the proliferation of uncommitted progenitor cells, and inducing the differentiation of these stimulated progenitor cells in a tissue-specific manner under appropriate environmental conditions. In addition, the morphogens are capable of supporting the growth and maintenance of these differentiated cells. These morphogenic activities allow the proteins of this invention to initiate and maintain the developmental cascade of tissue morphogenesis in an appropriate, morphogenically permissive environment, stimulating stem cells to proliferate and differentiate in a tissue-specific manner, and inducing the progression of events that culminate in new tissue formation. These morphogenic activities also allow the proteins to stimulate the "redifferentiation" of cells previously induced to stray from their differentiation path. Under appropriate environmental conditions it is anticipated that these morphogens also may stimulate the "dedifferentiation" of committed cells (see infra.)

In one aspect of the invention, the proteins and compositions of this invention are useful in the replacement of diseased or damaged tissue in a mammal, particularly when the damaged tissue interferes with normal tissue or organ function. Accordingly, it is anticipated that the proteins of this invention will be useful in the repair of damaged tissue such as, for example, damaged lung tissue resulting from emphysema, cirrhotic kidney or liver tissue, damaged heart or

blood vessel tissue, as may result from
cardiomyopathies and/or atherothrombotic or
cardioembolic strokes, damaged stomach tissue resulting
from ulceric perforations or their repair, damaged
5 neural tissue as may result from physical injury,
degenerative diseases such as Alzheimer's disease or
multiple sclerosis or strokes, damaged dentin tissue as
may result from disease or mechanical injury. When the
proteins of this invention are provided to, or their
10 expression stimulated at, a tissue-specific locus, the
developmental cascade of tissue morphogenesis is
induced (see *infra*). Cells stimulated ex vivo by
contact with the proteins or agents capable of
stimulating morphogen expression in these cells also
15 may be provided to the tissue locus. In these cases
the existing tissue provides the necessary matrix
requirements, providing a suitable substratum for the
proliferating and differentiating cells in a
morphogenically permissive environment, as well as
20 providing the necessary signals for directing the
tissue-specificity of the developing tissue.
Alternatively, the proteins or stimulated cells may be
combined with a formulated matrix and implanted as a
device at a locus in vivo. The formulated matrix
25 should be a biocompatible, preferably biodegradable,
appropriately modified tissue-specific acellular matrix
having the characteristics described below.

In many instances, the loss of tissue function
30 results from scar tissue, formed in response to an
initial or repeated injury to the tissue. The degree
of scar tissue formation generally depends on the
regenerative properties of the injured tissue, and on
the degree and type of injury. Thus, in another

aspect, the invention includes morphogens that may be used to prevent or substantially inhibit the formation of scar tissue by providing the morphogens, or morphogen-stimulated cells, to a newly injured tissue
5 loci (see infra).

The morphogens of this invention also may be used to increase or regenerate a progenitor or stem cell population in a mammal. For example, progenitor
10 cells may be isolated from an individual's bone marrow, stimulated ex vivo for a time and at a morphogen concentration sufficient to induce the cells to proliferate, and returned to the bone marrow. Other sources of progenitor cells that may be suitable
15 include biocompatible cells obtained from a cultured cell line, stimulated in culture, and subsequently provided to the body. Alternatively, the morphogen may be provided systemically, or implanted, injected or otherwise provided to a progenitor cell population in
20 an individual to induce its mitogenic activity in vivo. For example, an agent capable of stimulating morphogen expression in the progenitor cell population of interest may be provided to the cells in vivo, for example systemically, to induce mitogenic activity.
25 Similarly, a particular population of hemopoietic stem cells may be increased by the morphogens of this invention, for example by perfusing an individual's blood to extract the cells of interest, stimulating these cells ex vivo, and returning the stimulated cells
30 to the blood. It is anticipated that the ability to augment an individual's progenitor cell population will significantly enhance existing methods for treating disorders resulting from a loss or reduction of a renewable cell population. Two particularly
35 significant applications include the treatment of blood

disorders and impaired or lost immune function. Other cell populations whose proliferation may be exploited include the stem cells of the epidermis, which may be used in skin tissue regeneration, and the stem cells of the gastrointestinal lining, for example, in the healing of ulcers.

In still another aspect of the invention, the morphogens also may be used to support the growth and maintenance of differentiated cells, inducing existing differentiated cells to continue expressing their phenotype. It is anticipated that this activity will be particularly useful in the treatment of tissue disorders where loss of function is caused by cells becoming senescent or quiescent, such as may occur in osteoporosis. Application of the protein directly to the cells to be treated, or providing it by systemic injection, can be used to stimulate these cells to continue expressing their phenotype, thereby significantly reversing the effects of the dysfunction (see *infra*). Alternatively, administration of an agent capable of stimulating morphogen expression in vivo also may be used. In addition, the morphogens of this invention also may be used in gene therapy protocols to stimulate the growth of quiescent cells, thereby potentially enhancing the ability of these cells to incorporate exogenous DNA.

In yet another aspect of the invention, the morphogens of this invention also may be used to induce "redifferentiation" of cells that have strayed from their differentiation pathway, such as can occur during tumorigenesis. It is anticipated that this activity of the proteins will be particularly useful in treatments to reduce or substantially inhibit the growth of

neoplasms. The method also is anticipated to induce the de-and re-differentiation of these cells. As described supra, the proteins may be provided to the cells directly or systemically, or an agent capable of stimulating morphogen expression in vivo may be provided.

Finally, modulations of endogenous morphogen levels may be monitored as part of a method for detecting tissue dysfunction. Specifically, modulations in endogenous morphogen levels are anticipated to reflect changes in tissue or organ stasis. Tissue stasis may be monitored by detecting changes in the levels of the morphogen itself. For example, tissue samples may be obtained at intervals and the concentration of the morphogen present in the tissue detected by standard protein detection means known to those skilled in the art. As an example, a binding protein capable of interacting specifically with the morphogen of interest, such as an anti-morphogen antibody, may be used to detect the morphogen in a standard immunoassay. The morphogen levels detected then may be compared, the changes in the detected levels being indicative of the status of the tissue. Modulations in endogenous morphogen levels also may be monitored by detecting fluctuations in the body's natural antibody titer to morphogens (see infra.)

The morphogenic proteins and compositions of this invention can be isolated from a variety of naturally-occurring sources, or they may be constructed biosynthetically using conventional recombinant DNA technology. Similarly, the matrices may be derived from organ-specific tissue, or they may be formulated synthetically, as described below.

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A key to these developments was the discovery and characterization of naturally-occurring osteogenic proteins followed by observation of their remarkable properties. These proteins, originally isolated from bone, are capable of inducing the full developmental cascade of bone formation, including vascularization, mineralization, and bone marrow differentiation, when implanted in a mammalian body in association with a suitably modified matrix. Native proteins capable of inducing this developmental cascade, as well as DNA sequences encoding these proteins now have been isolated and characterized for a number of different species (e.g., human and mouse OP-1, OP-2, and CBMP-2. See, for example, U.S. Patent Nos. 4,968,590 and 5,011,691; U.S. Patent No. 5,266,683 issued on November 30, 1993; Sampath et al. (1990) J. Bio. Chem 265:13198-13205; Ozkaynak, et al. (1990) EMBO J 9:2085-2 093 and Ozkaynak, et al. (1991) Biochem. Biophys. Res. Commn. 179:116-123.) The mature forms of these proteins share substantial amino acid sequence homology, especially in the C-terminal regions of the mature proteins. In particular, the proteins share a conserved six or seven cysteine skeleton in this region (e.g., the linear arrangement of these C-terminal cysteine residues is essentially conserved in the different proteins, in addition to other, apparently required amino acids (see Table II, *infra*)).

Polypeptide chains not normally associated with bone or bone formation, but sharing substantial amino acid sequence homology with the C-terminus of the osteogenic proteins, including the conserved six or seven cysteine skeleton, also have been identified as competent for inducing bone in mammals. Among these are amino acid sequences identified in *Drosophila* and

Xenopus, (e.g., DPP and Vgl; see, for example, U.S. Patent No. 5,011,691 and Table II, *infra*). In addition, non-native biosynthetic constructs designed based on extrapolation from these sequence homologies, including the conserved six or seven cysteine skeleton, have been shown to induce endochondral bone formation in mammals when implanted in association with an appropriate matrix (see U.S. Pat. No. 5,011,691 and Table III, *infra*).

10

It has now been discovered that this "family" of proteins sharing substantial amino acid sequence homology and the conserved six or seven cysteine skeleton are true morphogens, capable of inducing, in addition to bone and cartilage, tissue-specific morphogenesis for a variety of other organs and tissues. The proteins apparently bind to surface receptors or otherwise contact and interact with progenitor cells, predisposing or stimulating the cells to proliferate and differentiate in a morphogenically permissive environment. The morphogens are capable of inducing the developmental cascade of cellular and molecular events that culminate in the formation of new organ-specific tissue, including any vascularization, connective tissue formation, and nerve enervation as required by the naturally occurring tissue.

It also has been discovered that the way in which the cells differentiate, whether, for example, they differentiate into bone-producing osteoblasts, hemopoietic cells, or liver cells, depends on the nature of their local environment (see *infra*). Thus, in addition to requiring a suitable substratum on which to anchor, the proliferating and differentiating cells also require appropriate signals to direct their

tissue-specificity. These signals may take the form of cell surface markers.

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5 When the morphogens (or progenitor cells stimulated by these morphogens) are provided at a tissue-specific locus (e.g., by systemic injection or by implantation or injection at a tissue-specific locus, or by administration of an agent capable of
10 stimulating morphogen expression in vivo), the existing tissue at that locus, whether diseased or damaged, has the capacity of acting as a suitable matrix. Alternatively, a formulated matrix may be externally provided together with the stimulated progenitor cells
15 or morphogen, as may be necessary when the extent of injury sustained by the damaged tissue is large. The matrix should be a biocompatible, suitably modified acellular matrix having dimensions such that it allows the influx, differentiation, and proliferation of
20 migratory progenitor cells, and is capable of providing a morphogenically permissive environment (see *infra*). The matrix preferably is tissue-specific, and biodegradable.

25 Formulated matrices may be generated from dehydrated organ-specific tissue, prepared for example, by treating the tissue with solvents to substantially remove the non-structural components from the tissue. Alternatively, the matrix may be formulated
30 synthetically using a biocompatible, preferably in vivo

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biodegradable, structural polymer such as collagen in association with suitable tissue-specific cell attachment factors. Currently preferred structural polymers comprise tissue-specific collagens. Currently preferred cell attachment factors include glycosaminoglycans and proteoglycans. The matrix further may be treated with an agent or agents to increase the number of pores and micropits on its surfaces, so as to enhance the influx, proliferation and differentiation of migratory progenitor cells from the body of the mammal.

Among the proteins useful in this invention are proteins originally identified as osteogenic proteins, such as the OP-1, OP-2 and CBMP2 proteins, as well as amino acid sequence-related proteins such as DPP (from *Drosophila*), Vgl (from *Xenopus*), Vgr-1 (from mouse, see Table II and Seq. ID Nos. 5-14), and the recently identified GDF-1 protein (Seq. ID No. 14). The members of this family, which include members of the TGF- β super-family of proteins, share substantial amino acid sequence homology in their C-terminal regions. Table I, below, describes the various morphogens identified to date, including their nomenclature as used herein, and Seq. ID references.

TABLE I

30	"OP-1"	Refers generically to the group of morphogenically active proteins expressed from part or all of a DNA sequence encoding OP-1 protein, including allelic and species variants thereof, e.g., human
35		OP-1 ("hOP-1", Seq. ID No. 5, mature

protein amino acid sequence), or mouse
OP-1 ("mOP-1", Seq. ID No. 6, mature
protein amino acid sequence.) The
conserved seven cysteine skeleton is
5 defined by residues 38 to 139 of Seq. ID
Nos. 5 and 6. The cDNA sequences and the
amino acids encoding the full length
proteins are provided in Seq. Id Nos. 16
and 17 (hOP1) and Seq. ID Nos. 18 and 19
10 (mOP1.) The mature proteins are defined
by residues 293-431 (hOP1) and 292-430
(mOP1). The "pro"regions of the proteins,
cleaved to yield the mature,
morphogenically active proteins are
15 defined essentially by residues 30-292
(hOP1) and residues 30-291 (mOP1).

"OP-2"

20 refers generically to the group of active
proteins expressed from part or all of a
DNA sequence encoding OP-2 protein,
including allelic and species variants
thereof, e.g., human OP-2 ("hOP-2", Seq.
ID No. 7, mature protein amino acid
sequence) or mouse OP-2 ("mOP-2", Seq. ID
25 No. 8, mature protein amino acid
sequence). The conserved seven cysteine
skeleton is defined by residues 38 to 139
of Seq. ID Nos. 7 and 8. The cDNA
sequences and the amino acids encoding the
full length proteins are provided in Seq.
30 Id Nos. 20 and 21 (hOP2) and Seq. ID Nos.
22 and 23 (mOP2.) The mature proteins are
defined essentially by residues 264-402
(hOP2) and 261-399 (mOP2). The "pro"
35 regions of the proteins, cleaved to yield

the mature, morphogenically active proteins are defined essentially by residues 18-263 (hOP2) and residues 18-260 (mOP1).

- 5
"CBMP2" refers generically to the morphogenically active proteins expressed from a DNA sequence encoding the CBMP2 proteins, including allelic and species variants thereof, e.g., human CBMP2A ("CBMP2A(fx)", Seq ID No. 9) or human CBMP2B DNA ("CBMP2B(fx)", Seq. ID No. 10).
- 10
- 15
"DPP(fx)" refers to protein sequences encoded by the Drosophila DPP gene and defining the conserved seven cysteine skeleton (seq. ID No. 11).
- 20
"Vgl(fx)" refers to protein sequences encoded by the Xenopus Vgl gene and defining the conserved seven cysteine skeleton (Seq. ID No. 12).
- 25
"Vgr-1(fx)" refers to protein sequences encoded by the murine Vgr-1 gene and defining the conserved seven cysteine skeleton (Seq. ID No. 13).
- 30
"GDF-1(fx)" refers to protein sequences encoded by the human GDF-1 gene and defining the conserved seven cysteine skeleton (seq. ID No. 14).

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The OP-2 proteins have an additional cysteine residue in this region (e.g., see residue 41 of Seq. ID Nos. 7 and 8), in addition to the conserved cysteine skeleton in common with the other proteins in this family. The GDF-1 protein has a four amino acid insert within the conserved skeleton (residues 44-47 of Seq. ID No. 14) but this insert likely does not interfere with the relationship of the cysteines in the folded structure. In addition, the CBMP2 proteins are missing one amino acid residue within the cysteine skeleton.

The morphogens are inactive when reduced, but are active as oxidized homodimers and when oxidized in combination with other morphogens of this invention. Thus, as defined herein, a morphogen of this invention is a dimeric protein comprising a pair of polypeptide chains, wherein each polypeptide chain comprises at least the C-terminal six cysteine skeleton defined by residues 43-139 of Seq. ID No. 5, including functionally equivalent arrangements of these cysteines (e.g., amino acid insertions or deletions which alter the linear arrangement of the cysteines in the sequence but not their relationship in the folded structure), such that, when the polypeptide chains are folded, the dimeric protein species comprising the pair of polypeptide chains has the appropriate three-dimensional structure, including the appropriate intra- or inter-chain disulfide bonds such that the protein is capable of acting as a morphogen as defined herein. Specifically, the protein is capable of all of the following biological functions in a morphogenically permissive environment: stimulating proliferation of progenitor cells; stimulating the differentiation of progenitor cells; stimulating the proliferation of differentiated cells; and supporting the growth and maintenance of differentiated cells, including the

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"redifferentiation" of these cells. In addition, it is also anticipated that the morphogens of this invention will be capable of inducing dedifferentiation of committed cells under appropriate environmental
5 conditions.

In one preferred aspect, the morphogens of this invention comprise one of two species of generic amino acid sequences: Generic Sequence 1 (Seq. ID
10 No. 1) or Generic Sequence 2 (Seq. ID No. 2); where each Xaa indicates one of the 20 naturally-occurring L-isomer, α -amino acids or a derivative thereof. Generic Sequence 1 comprises the conserved six cysteine skeleton and Generic Sequence 2 comprises the conserved
15 six cysteine skeleton plus the additional cysteine identified in OP-2 (see residue 36, Seq. ID No. 2). In another preferred aspect, these sequences further comprise the following additional sequence at their N-terminus:

20

Cys Xaa Xaa Xaa Xaa (Seq. ID No. 15)
1 5

Preferred amino acid sequences within the
25 foregoing generic sequences include: Generic Sequence 3 (Seq. ID No. 3) and Generic Sequence 4 (Seq. ID No. 4), listed below, which accommodate the homologies shared among the various preferred members of this morphogen family identified to date (see Table II), as
30 well as the amino acid sequence variation among them. Generic Sequences 3 and 4 are composite amino acid sequences of the proteins presented in Table II and identified in Seq. ID Nos. 5-14. The generic sequences include both the amino acid identity shared by the
35 sequences in Table II, as well as alternative residues

for the variable positions within the sequence. Note that these generic sequences allow for an additional cysteine at position 41 or 46 in Generic Sequences 3 or 4, respectively, providing an appropriate cysteine skeleton where inter- or intramolecular disulfide bonds can form, and contain certain critical amino acids which influence the tertiary structure of the proteins.

Generic Sequence 3

	10	20	30	40	50	60	65
		Leu	Tyr	Val	Xaa	Phe	
		1			5		
		Xaa	Xaa	Xaa	Gly	Trp	Xaa
					10		
		Xaa	Ala	Pro	Xaa	Gly	Xaa
							Ala
15	15				20		
		Xaa	Tyr	Cys	Xaa	Gly	Xaa
							Cys
				25			30
		Xaa	Pro	Xaa	Xaa	Xaa	Xaa
					35		
20		Xaa	Xaa	Xaa	Asn	His	Ala
							Xaa
					40		45
		Xaa	Xaa	Leu	Xaa	Xaa	Xaa
							Xaa
					50		
		Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
							Cys
25	55						60
		Cys	Xaa	Pro	Xaa	Xaa	Xaa
							Xaa
					65		

Xaa Xaa Xaa Leu Xaa Xaa Xaa

70

75

Xaa Xaa Xaa Xaa Val Xaa Leu Xaa

80

5 Xaa Xaa Xaa Xaa Met Xaa Val Xaa

85

90

Xaa Cys Gly Cys Xaa

95

wherein each Xaa is independently selected from a group
10 of one or more specified amino acids defined as
follows: "Res." means "residue" and Xaa at res.4 =
(Ser, Asp or Glu); Xaa at res.6 = (Arg, Gln, Ser or
Lys); Xaa at res.7 = (Asp or Glu); Xaa at res.8 = (Leu
or Val); Xaa at res.11 = (Gln, Leu, Asp, His or Asn);
15 Xaa at res.12 = (Asp, Arg or Asn); Xaa at res.14 = (Ile
or Val); Xaa at res.15 = (Ile or Val); Xaa at res.18 =
(Glu, Gln, Leu, Lys, Pro or Arg); Xaa at res.20 = (Tyr
or Phe); Xaa at res.21 = (Ala, Ser, Asp, Met, His, Leu
or Gln); Xaa at res.23 = (Tyr, Asn or Phe); Xaa at
20 res.26 = (Glu, His, Tyr, Asp or Gln); Xaa at res.28 =
(Glu, Lys, Asp or Gln); Xaa at res.30 = (Ala, Ser, Pro
or Gln); Xaa at res.31 = (Phe, Leu or Tyr); Xaa at
res.33 = (Leu or Val); Xaa at res.34 = (Asn, Asp, Ala
or Thr); Xaa at res.35 = (Ser, Asp, Glu, Leu or Ala);
25 Xaa at res.36 = (Tyr, Cys, His, Ser or Ile); Xaa at
res.37 = (Met, Phe, Gly or Leu); Xaa at res.38 = (Asn
or Ser); Xaa at res.39 = (Ala, Ser or Gly); Xaa at
res.40 = (Thr, Leu or Ser); Xaa at res.44 = (Ile or
Val); Xaa at res.45 = (Val or Leu); Xaa at res.46 =
30 (Gln or Arg); Xaa at res.47 = (Thr, Ala or Ser); Xaa at
res.49 = (Val or Met); Xaa at res.50 = (His or Asn);
Xaa at res.51 = (Phe, Leu, Asn, Ser, Ala or Val); Xaa

at res.52 = (Ile, Met, Asn, Ala or Val); Xaa at res.53
 = (Asn, Lys, Ala or Glu); Xaa at res.54 = (Pro or Ser);
 Xaa at res.55 = (Glu, Asp, Asn, or Gly); Xaa at res.56
 = (Thr, Ala, Val, Lys, Asp, Tyr, Ser or Ala); Xaa at
 5 res.57 = (Val, Ala or Ile); Xaa at res.58 = (Pro or
 Asp); Xaa at res.59 = (Lys or Leu); Xaa at res.60 =
 (Pro or Ala); Xaa at res.63 = (Ala or Val); Xaa at
 res.65 = (Thr or Ala); Xaa at res.66 = (Gln, Lys, Arg
 or Glu); Xaa at res.67 = (Leu, Met or Val); Xaa at
 10 res.68 = (Asn, Ser or Asp); Xaa at res.69 = (Ala, Pro
 or Ser); Xaa at res.70 = (Ile, Thr or Val); Xaa at
 res.71 = (Ser or Ala); Xaa at res.72 = (Val or Met);
 Xaa at res.74 = (Tyr or Phe); Xaa at res.75 = (Phe, Tyr
 or Leu); Xaa at res.76 = (Asp or Asn); Xaa at res.77 =
 15 (Asp, Glu, Asn or Ser); Xaa at res.78 = (Ser, Gln, Asn
 or Tyr); Xaa at res.79 = (Ser, Asn, Asp or Glu); Xaa at
 res.80 = (Asn, Thr or Lys); Xaa at res.82 = (Ile or
 Val); Xaa at res.84 = (Lys or Arg); Xaa at res.85 =
 (Lys, Asn, Gln or His); Xaa at res.86 = (Tyr or His);
 20 Xaa at res.87 = (Arg, Gln or Glu); Xaa at res.88 =
 (Asn, Glu or Asp); Xaa at res.90 = (Val, Thr or Ala);
 Xaa at res.92 = (Arg, Lys, Val, Asp or Glu); Xaa at
 res.93 = (Ala, Gly or Glu); and Xaa at res.97 = (His or
 Arg); and Generic Seq. 4:

25

Generic Sequence 4

	Cys	Xaa	Xaa	Xaa	Xaa	Leu	Tyr	Val	Xaa	Phe
	1				5					10
30	Xaa	Xaa	Xaa	Gly	Trp	Xaa	Xaa	Trp	Xaa	
				15						
	Xaa	Ala	Pro	Xaa	Gly	Xaa	Xaa	Ala		
	20				25					
	Xaa	Tyr	Cys	Xaa	Gly	Xaa	Cys	Xaa		
35			30					35		

Xaa Pro Xaa Xaa Xaa Xaa Xaa
 40
 Xaa Xaa Xaa Asn His Ala Xaa Xaa
 45 50
 5 Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa
 55
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
 60 65
 Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa
 10 70
 Xaa Xaa Xaa Leu Xaa Xaa Xaa
 75 80
 Xaa Xaa Xaa Xaa Val Xaa Leu Xaa
 85
 15 Xaa Xaa Xaa Xaa Met Xaa Val Xaa
 90 95
 Xaa Cys Gly Cys Xaa
 100

wherein each Xaa is independently selected from a group
 20 of one or more specified amino acids as defined by the
 following: "Res." means "residue" and Xaa at res.2 =
 (Lys or Arg); Xaa at res.3 = (Lys or Arg); Xaa at res.4
 = (His or Arg); Xaa at res.5 = (Glu, Ser, His, Gly, Arg
 or Pro); Xaa at res.9 = (Ser, Asp or Glu); Xaa at
 25 res.11 = (Arg, Gln, Ser or Lys); Xaa at res.12 = (Asp
 or Glu); Xaa at res.13 = (Leu or Val); Xaa at res.16 =
 (Gln, Leu, Asp, His or Asn); Xaa at res.17 = (Asp, Arg,
 or Asn); Xaa at res.19 = (Ile or Val); Xaa at res.20 =
 (Ile or Val); Xaa at res.23 = (Glu, Gln, Leu, Lys, Pro
 30 or Arg); Xaa at res.25 = (Tyr or Phe); Xaa at res.26 =
 (Ala, Ser, Asp, Met, His, Leu, or Gln); Xaa at res.28 =
 (Tyr, Asn or Phe); Xaa at res.31 = (Glu, His, Tyr, Asp
 or Gln); Xaa at res.33 = Glu, Lys, Asp or Gln); Xaa at
 res.35 = (Ala, Ser or Pro); Xaa at res.36 = (Phe, Leu
 35 or Tyr); Xaa at res.38 = (Leu or Val); Xaa at res.39 =

(Asn, Asp, Ala or Thr); Xaa at res.40 = (Ser, Asp, Glu, Leu or Ala); Xaa at res.41 = (Tyr, Cys, His, Ser or Ile); Xaa at res.42 = (Met, Phe, Gly or Leu); Xaa at res.44 = (Ala, Ser or Gly); Xaa at res.45 = (Thr, Leu or Ser); Xaa at res.49 = (Ile or Val); Xaa at res.50 = (Val or Leu); Xaa at res.51 = (Gln or Arg); Xaa at res.52 = (Thr, Ala or Ser); Xaa at res.54 = (Val or Met); Xaa at res.55 = (His or Asn); Xaa at res.56 = (Phe, Leu, Asn, Ser, Ala or Val); Xaa at res.57 = (Ile, Met, Asn, Ala or Val); Xaa at res.58 = (Asn, Lys, Ala or Glu); Xaa at res.59 = (Pro or Ser); Xaa at res.60 = (Glu, Asp, or Gly); Xaa at res.61 = (Thr, Ala, Val, Lys, Asp, Tyr, Ser or Ala); Xaa at res.62 = (Val, Ala or Ile); Xaa at res.63 = (Pro or Asp); Xaa at res.64 = (Lys or Leu); Xaa at res.65 = (Pro or Ala); Xaa at res.68 = (Ala or Val); Xaa at res.70 = (Thr or Ala); Xaa at res.71 = (Gln, Lys, Arg or Glu); Xaa at res.72 = (Leu, Met or Val); Xaa at res.73 = (Asn, Ser or Asp); Xaa at res.74 = (Ala, Pro or Ser); Xaa at res.75 = (Ile, Thr or Val); Xaa at res.76 = (Ser or Ala); Xaa at res.77 = (Val or Met); Xaa at res.79 = (Tyr or Phe); Xaa at res.80 = (Phe, Tyr or Leu); Xaa at res.81 = (Asp or Asn); Xaa at res.82 = (Asp, Glu, Asn or Ser); Xaa at res.83 = (Ser, Gln, Asn or Tyr); Xaa at res.84 = (Ser, Asn, Asp or Glu); Xaa at res.85 = (Asn, Thr or Lys); Xaa at res.87 = (Ile or Val); Xaa at res.89 = (Lys or Arg); Xaa at res.90 = (Lys, Asn, Gln or His); Xaa at res.91 = (Tyr or His); Xaa at res.92 = (Arg, Gln or Glu); Xaa at res.93 = (Asn, Glu or Asp); Xaa at res.95 = (Val, Thr or Ala); Xaa at res.97 = (Arg, Lys, Val, Asp or Glu); Xaa at res.98 = (Ala, Gly or Glu); and Xaa at res.102 = (His or Arg).

Particularly useful sequences for use as morphogens in this invention include the C-terminal

domains, e.g., the C-terminal 96-102 amino acid residues of Vgl, Vgr-1, DPP, OP-1, OP-2, CBMP-2A, CBMP-2B and GDF-1 (see Table II, *infra*, and Seq. ID Nos. 5-14) which include at least the conserved six or
5 seven cysteine skeleton. In addition, biosynthetic constructs designed from the generic sequences, such as COP-1, 3-5, 7, 16 (see Table III, *infra*) also are useful. Other sequences include the C-terminal CBMP3 and the inhibins/activin proteins (see, for example,
10 U.S. Pat. Nos. 4,968,590 and 5,011,691). Accordingly, other useful sequences are those sharing at least 70% amino acid sequence homology, and preferably 80% homology with any of the sequences above. These are anticipated to include allelic and species variants and
15 mutants, and biosynthetic muteins, as well as novel members of this morphogenic family of proteins. Particularly envisioned in the family of related proteins are those proteins exhibiting morphogenic activity and wherein the amino acid changes from the
20 preferred sequences include conservative changes, e.g., those as defined by Dayoff et al., Atlas of Protein Sequence and Structure; vol. 5, Suppl. 3, pp. 345-362, (M.O. Dayoff, ed., Nat'l BioMed. Research Fdn., Washington, D.C. 1979).

25

The currently most preferred protein sequences useful as morphogens in this invention include those having greater than 60% identity, preferably greater than 65% identity, with the amino acid sequence
30 defining the conserved six cysteine skeleton of hOP1 (e.g., residues 43-139 of Seq. ID No. 5). These most preferred sequences include both allelic and species variants of the OP1 and OP2 proteins.

The invention thus provides proteins comprising any of the polypeptide chains described above, whether isolated from naturally-occurring sources, or produced by recombinant DNA techniques, and
5 includes allelic and species variants of these proteins, naturally-occurring or biosynthetic mutants thereof, as well as various truncated and fusion constructs. Deletion or addition mutants also are envisioned to be active (see infra), including those
10 which may alter the conserved C-terminal cysteine skeleton, provided that the alteration does not functionally disrupt the relationship of these cysteines in the folded structure. Accordingly, such active forms are considered the equivalent of the
15 specifically described constructs disclosed herein. The proteins may include forms having varying glycosylation patterns, varying N-termini, a family of related proteins having regions of amino acid sequence homology, and active truncated or mutated forms of
20 native or biosynthetic proteins, produced by expression of recombinant DNA in host cells.

The morphogenic proteins can be expressed from intact or truncated cDNA or from synthetic DNAs in
25 procaryotic or eucaryotic host cells, and purified, cleaved, refolded, and dimerized to form morphogenically active compositions. Currently preferred host cells include E. coli or mammalian cells, such as CHO, COS or BSC cells.

30 Thus, in view of this disclosure, skilled genetic engineers can isolate genes from cDNA or genomic libraries of various different species which encode appropriate amino acid sequences, or construct
35 DNAs from oligonucleotides, and then can express them

in various types of host cells, including both
procaryotes and eucaryotes, to produce large quantities
of active proteins capable of inducing tissue-specific
cell differentiation and tissue morphogenesis in a
5 variety of mammals including humans.

The invention thus further comprises these
methods of inducing tissue-specific morphogenesis using
the morphogenic proteins of this invention and
10 pharmaceutical and therapeutic agents comprising the
morphogens of this invention. The invention further
comprises the use of these morphogens in the
manufacture of pharmaceuticals for various medical
procedures, including procedures for inducing tissue
15 growth, procedures for inducing progenitor cell
proliferation, procedures to inhibit neoplasm growth
and procedures to promote phenotypic cell expression of
differentiated cells.

Brief Description of the Drawings

The foregoing and other objects and features of this invention, as well as the invention itself, may
5 be more fully understood from the following description, when read together with the accompanying drawings, in which:

FIGURE 1 is a photomicrograph of a Northern
10 Blot identifying Vgr-1 specific transcripts in various adult murine tissues;

FIGURE 2 is a photomicrograph of a Northern
Blot identifying mOP-1-specific mRNA expression in
15 various murine tissues prepared from 2 week old mice (panel A) and 5 week old mice (Panel B);

FIGURE 3 is a photomicrograph of Northern
Blots identifying mRNA expression of EF-Tu
20 (A, control), mOP-1 (B, D), and Vgr-1 (C) in (1) 17-day embryos and (2) 3-day post natal mice;

FIGURE 4A and 4B are photomicrographs showing
the presence of OP-1 (by immunofluorescence staining)
25 in the cerebral cortex (A) and spinal cord (B);

FIGURE 5A and 5B are photomicrographs
illustrating the ability of morphogen (OP-1) to induce
undifferentiated NG108 cells (5A) to undergo
30 differentiation of neural morphology (5B).

FIGURE 6A-6D are photomicrographs showing the
effect of morphogen (OP-1) on human embryo carcinoma
cell redifferentiation;
35

FIGURE 7 is a photomicrograph showing the effects of phosphate buffered saline (PBS, animal 1) or morphogen (OP-1, animal 2) on partially hepatectomized rats;

5

FIGURE 8A - 8C are photomicrographs showing the effect of no treatment (8A), carrier matrix treatment (8B) and morphogen treatment (OP-1,8C) on dentin regeneration.

10

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Detailed Description

Purification protocols first were developed which enabled isolation of the osteogenic (bone inductive) protein present in crude protein extracts from mammalian bone. (See PCT US 89/01453, and U.S. 4,968,590.) The development of the procedure, coupled with the availability of fresh calf bone, enabled isolation of substantially pure bovine osteogenic protein (BOP). BOP was characterized significantly; its ability to induce cartilage and ultimately endochondral bone growth in cat, rabbit, and rat were demonstrated and studied; it was shown to be able to induce the full developmental cascade of bone formation previously ascribed to unknown protein or proteins in heterogeneous bone extracts. This dose dependent and highly specific activity was present whether or not the protein was glycosylated (see U.S. Patent No. 4,968,958, filed 4/8/88 and Sampath et al., (1990) J. Biol. Chem. 265: pp. 13198-13205). Sequence data obtained from the bovine materials suggested probe designs which were used to isolate genes encoding osteogenic proteins from different species. Human and murine osteogenic protein counterparts have now been identified and characterized (see, for example, U.S. Pat. No. 5,011,691, Ozkaynak, et al., (1990) EMBO J 9:2085-2093, and Ozkaynak et al., (1991) Biochem. Biophys. Res. Commn. 179:116-123, and United States Patent 5,266,683 which issued on November 30, 1993.

Sequence data from the bovine materials also suggested substantial homology with a number of proteins known in the art which were not known to play a role in bone formation. Bone formation assays

performed with these proteins showed that, when these proteins were implanted in a mammal in association with a suitable matrix, cartilage and endochondral bone formation was induced (see, for example, U.S. Patent
5 No. 5,011,691.) One of these proteins is DPP, a *Drosophila* protein known to play a role in dorsal-ventral specification and required for the correct morphogenesis of the imaginal discs. Two other
10 proteins are related sequences identified in *Xenopus* and mouse (Vgl and Vgr-1, respectively), thought to play a role in the control of growth and differentiation during embryogenesis. While DPP and Vgr-1 (or Vgr-1-like) transcripts have been identified in a variety of tissues (embryonic, neonatal and adult,
15 Lyons et al., (1989) PNAS 86:4554-4 558, and see *infra*), Vgl transcripts, which are maternally inherited and spatially restricted to the vegetal endoderm, decline dramatically after gastrulation.

20 From these homologies a generic consensus sequence was derived which encompasses the active sequence required for inducing bone morphogenesis in a mammal when implanted in association with a matrix. The generic sequence has at least a conserved six
25 cysteine skeleton (Generic Sequence 1, Seq. ID No. 1) or, optionally, a 7-cysteine skeleton (Generic Sequence 2, Seq. ID No. 2), which includes the conserved six cysteine skeleton defined by Generic Sequence 1, and an additional cysteine at residue 36,
30 accomodating the additional cysteine residue identified in the OP2 proteins. Each "Xaa" in the generic sequences indicates that any one of the 20 naturally-occurring L-isomer, α -amino acids or a derivative

thereof may be used at that position. Longer generic sequences which also are useful further comprise the following sequence at their N-termini:

5

Cys Xaa Xaa Xaa Xaa (Seq. ID No. 15)
1 5

Biosynthetic constructs designed from this
10 generic consensus sequence also have been shown to induce cartilage and/or endochondral bone formation (e.g., COP-1, COP-3, COP-4, COP-5, COP-7 and COP-16, described in U.S. Patent No. 5,011,691 and presented below in Table III.) Table II, set forth below,
15 compares the amino acid sequences of the active regions of native proteins that have been identified as morphogens, including human OP-1 (hOP-1, Seq. ID Nos. 5 and 16-17), mouse OP-1 (mOP-1, Seq. ID Nos. 6 and 18-19), human and mouse OP-2 (Seq. ID Nos. 7, 8, and 20-22), CBMP2A (Seq. ID No. 9), CBMP2B (Seq. ID No. 10), DPP (from Drosophila, Seq. ID No. 11), Vgl, (from Xenopus, Seq. ID No. 12), Vgr-1 (from mouse, Seq. ID No. 13), and GDF-1 (Seq. ID No. 14.) In the table, three dots indicates that the amino acid in that
25 position is the same as the amino acid in hOP-1. Three dashes indicates that no amino acid is present in that position, and are included for purposes of illustrating homologies. For example, amino acid residue 60 of CBMP-2A and CBMP-2B is "missing". Of course, both
30 these amino acid sequences in this region comprise Asn-Ser (residues 58, 59), with CBMP-2A then comprising Lys and Ile, whereas CBMP-2B comprises Ser and Ile.

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TABLE II

	hOP-1	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val	
	mOP-1	...	...	...	...	...	...	...	...	
5	hOP-2	...	Arg	Arg	...	...	...	...	...	
	mOP-2	...	Arg	Arg	...	...	...	...	...	
	DPP	...	Arg	Arg	...	Ser	...	...	...	
	Vgl	...	...	Lys	Arg	His	...	...	...	
	Vgr-1	...	...	...	...	Gly	...	...	...	
10	CBMP-2A	...	...	Arg	...	Pro	...	...	...	
	CBMP-2B	...	Arg	Arg	...	Ser	...	...	...	
	GDF-1	...	Arg	Ala	Arg	Arg	...	...	...	
		1				5				
15	hOP-1	Ser	Phe	Arg	Asp	Leu	Gly	Trp	Gln	Asp
	mOP-1	...	...	...	...	...	...	...	...	...
	hOP-2	...	...	Gln	...	...	...	...	Leu	...
	mOP-2	Ser	...	...	...	...	...	...	Leu	...
20	DPP	Asp	...	Ser	...	Val	...	...	Asp	...
	Vgl	Glu	...	Lys	...	Val	...	...	...	Asn
	Vgr-1	...	...	Gln	...	Val	...	...	...	...
	CBMP-2A	Asp	...	Ser	...	Val	...	...	Asn	...
	CBMP-2B	Asp	...	Ser	...	Val	...	...	Asn	...
25	GDF-1	...	...	...	Glu	Val	...	...	His	Arg
			10					15		
	hOP-1	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala
	mOP-1	...	...	...	...	...	...	...	...	...
30	hOP-2	...	Val	...	...	...	Gln	...	...	Ser
	mOP-2	...	Val	...	...	...	Gln	...	...	Ser
	DPP	...	...	Val	...	...	Leu	...	...	Asp
	Vgl	...	Val	...	...	...	Gln	...	...	Met
	Vgr-1	...	...	...	...	...	Lys	...	...	...

	CBMP-2A	...	...	Val	...	...	Pro	...	...	His
	CBMP-2B	...	...	Val	...	...	Pro	...	...	Gln
	GDF-1	...	Val	...	...	...	Arg	...	Phe	Leu
				20					25	
5										
	hOP-1	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
	mOP-1	...	...	...	...	...	...	...	...	...
	hOP-2	...	...	...	...	...	...	...	...	Ser
10	mOP-2	...	...	...	...	...	...	...	...	...
	DPP	...	...	...	...	His	...	Lys	...	Pro
	Vgl	...	Asn	...	...	Tyr	...	...	...	Pro
	Vgr-1	...	Asn	...	...	Asp	...	...	...	Ser
	CBMP-2A	...	Phe	...	...	His	...	Glu	...	Pro
15	CBMP-2B	...	Phe	...	...	His	...	Asp	...	Pro
	GDF-1	...	Asn	...	...	Gln	...	Gln	...	...
					30					35
	hOP-1	Phe	Pro	Leu	Asn	Ser	Tyr	Met	Asn	Ala
20	mOP-1	...	...	...	...	...	...	...	...	...
	hOP-2	...	...	...	Asp	...	Cys	...	...	...
	mOP-2	...	...	...	Asp	...	Cys	...	...	...
	DPP	...	...	...	Ala	Asp	His	Phe	...	Ser
	Vgl	Tyr	...	...	Thr	Glu	Ile	Leu	...	Gly
25	Vgr-1	...	...	...	...	Ala	His	...	...	...
	CBMP-2A	...	...	...	Ala	Asp	His	Leu	...	Ser
	CBMP-2B	...	...	...	Ala	Asp	His	Leu	...	Ser
	GDF-1	Leu	...	Val	Ala	Leu	Ser	Gly	Ser**	...
						40				
30										
	hOP-1	Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu
	mOP-1	...	...	...	...	...	...	...	...	...
	hOP-2	...	...	...	...	...	Leu	...	Ser	...
	mOP-2	...	...	...	...	...	Leu	...	Ser	...
35	DPP	...	...	...	...	Val	...	...	...	...

[illegible]

5	hOP-2	...	Ser	...	Thr	...	...	...	...	Tyr
	mOP-2	...	Ser	...	Thr	...	...	...	...	Tyr
	Vgl	Met	Ser	Pro	...	...	Met	...	Phe	Tyr
	Vgr-1	Val	...	...	...	...	...	...	...	...
	DPP	...	Asp	Ser	Val	Ala	Met	...	...	Leu
	CBMP-2A	...	Ser	...	...	...	Met	...	...	Leu
	CBMP-2B	...	Ser	...	...	...	Met	...	...	Leu
	GDF-1	...	Ser	Pro	...	...	...	...	Phe	...
75										80
10	hOP-1	Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys
	mOP-1	...	...	...	...	...	...	...	...	...
	hOP-2	...	Ser	...	Asn	...	...	...	...	Arg
	mOP-2	...	Ser	...	Asn	...	...	...	...	Arg
	DPP	Asn	...	Gln	...	Thr	...	Val	...	...
	Vgl	...	Asn	Asn	Asp	...	...	Val	...	Arg
	Vgr-1	...	...	Asn	...	...	...	...	...	...
	CBMP-2A	...	Glu	Asn	Glu	Lys	...	Val	...	...
15	CBMP-2B	...	Glu	Tyr	Asp	Lys	...	Val	...	...
	GDF-1	...	Asn	...	Asp	...	...	Val	...	Arg
85										
20	hOP-1	Lys	Tyr	Arg	Asn	Met	Val	Val	Arg	
	mOP-1	...	...	...	...	...	...	...	...	
	hOP-2	...	His	...	...	...	...	...	Lys	
	mOP-2	...	His	...	...	...	...	...	Lys	
	DPP	Asn	...	Gln	Glu	...	Thr	...	Val	
	Vgl	His	...	Glu	...	...	Ala	...	Asp	
	Vgr-1	...	...	...	...	...	...	...	...	
	CBMP-2A	Asn	...	Gln	Asp	...	...	...	Glu	
30	CBMP-2B	Asn	...	Gln	Glu	...	...	...	Glu	
	GDF-1	Gln	...	Glu	Asp	...	...	...	Asp	
90										95

5	COP-1	Gly	Trp	Asp	Asp	Trp	Ile	Ile	Ala
	COP-3	...	...	...	...	...	...	Val	...
	COP-4	...	...	...	...	...	...	Val	...
	COP-5	...	...	...	...	...	...	Val	...
	COP-7	...	...	Asn	...	...	...	Val	...
	COP-16	...	...	Asn	...	...	...	Val	...
		10					15		
10	COP-1	Pro	Val	Asp	Phe	Asp	Ala	Tyr	Tyr
	COP-3	...	Pro	Gly	Tyr	Gln	...	Phe	...
	COP-4	...	Pro	Gly	Tyr	Gln	...	Phe	...
	COP-5	...	Pro	Gly	Tyr	Gln	...	Phe	...
	COP-7	...	Pro	Gly	Tyr	His	...	Phe	...
	COP-16	...	Pro	Gly	Tyr	Gln	...	Phe	...
15				20					25
20	COP-1	Cys	Ser	Gly	Ala	Cys	Gln	Phe	Pro
	COP-3	...	...	...	...	...	...	...	...
	COP-4	...	...	...	...	...	...	...	...
	COP-5	...	His	...	Glu	...	Pro	...	...
	COP-7	...	His	...	Glu	...	Pro	...	...
	COP-16	...	His	...	Glu	...	Pro	...	...
				30					
25									
30	COP-1	Ser	Ala	Asp	His	Phe	Asn	Ser	Thr
	COP-3	...	...	...	...	...	...	...	...
	COP-4	...	...	...	...	...	...	...	...
	COP-5	Leu	...	...	...	...	...	...	...
	COP-7	Leu	...	...	...	Leu	...	...	...
	COP-16	Leu	...	...	...	...	...	...	...
			35					40	

5	COP-1	Asn	His	Ala	Val	Val	Gln	Thr	Leu	Val
	COP-3	...	...	...	...	...	...	...	...	...
	COP-4	...	...	...	...	...	...	...	...	...
	COP-5	...	...	...	...	...	...	...	...	...
	COP-7	...	...	...	...	...	...	...	...	...
	COP-16	...	...	...	...	...	...	...	...	...
					45					

10	COP-1	Asn	Asn	Met	Asn	Pro	Gly	Lys	Val
	COP-3	...	...	...	...	...	...	...	...
	COP-4	...	...	...	...	...	...	...	...
	COP-5	...	Ser	Val	...	Ser	Lys	Ile	---
	COP-7	...	Ser	Val	...	Ser	Lys	Ile	---
15	COP-16	...	Ser	Val	...	Ser	Lys	Ile	---
55									

20	COP-1	Pro	Lys	Pro	Cys	Cys	Val	Pro	Thr
	COP-3	...	...	...	...	...	...	...	...
	COP-4	...	...	...	...	...	...	...	...
	COP-5	...	...	Ala	...	...	...	...	...
	COP-7	...	...	Ala	...	...	...	...	...
	COP-16	...	...	Ala	...	...	...	...	...
25			60			65			

30	COP-1	Glu	Leu	Ser	Ala	Ile	Ser	Met	Leu	
	COP-3	...	...	...	...	...	...	...	...	
	COP-4	...	...	...	...	...	...	...	...	
	COP-5	...	...	...	...	...	...	...	...	
	COP-7	...	...	...	...	...	...	...	...	
	COP-16	...	...	...	...	...	...	...	...	
					70					

35

5	COP-1	Tyr	Leu	Asp	Glue	Asn	Ser	Thr	Val
	COP-3	...	...	...	...	...	Glu	Lys	...
	COP-4	...	...	...	...	...	Glu	Lys	...
	COP-5	...	...	...	...	...	Glu	Lys	...
	COP-7	...	...	...	...	...	Glu	Lys	...
	COP-16	...	...	...	...	...	Glu	Lys	...
		75					80		
10	COP-1	Val	Leu	Lys	Asn	Tyr	Gln	Glu	Met
	COP-3	...	...	...	...	...	...	...	...
	COP-4	...	...	...	...	...	...	...	...
	COP-5	...	...	...	...	...	...	...	...
	COP-7	...	...	...	...	...	...	...	...
	COP-16	...	...	...	...	...	...	...	...
				85					90
20	COP-1	Thr	Val	Val	Gly	Cys	Gly	Cys	Arg
	COP-3	Val	...	Glu	...	...	...	...	...
	COP-4	Val	...	Glu	...	...	...	...	...
	COP-5	Val	...	Glu	...	...	...	...	...
	COP-7	Val	...	Glu	...	...	...	...	...
	COP-16	Val	...	Glu	...	...	...	...	...
25									
						95			

30 As is apparent from the foregoing amino acid
sequence comparisons, significant amino acid changes
can be made within the generic sequences while
retaining the morphogenic activity. For example, while
the GDF-1 protein sequence depicted in Table II shares
35 only about 50% amino acid identity with the hOP1

sequence described therein, the GDF-1 sequence shares greater than 70% amino acid sequence homology with the hOP1 sequence, where homology is defined by allowed conservative amino acid changes within the sequence as
5 defined by Dayoff, et al., Atlas of Protein Sequence and Structure vol.5, supp.3, pp.345-362, (M.O. Dayoff, ed., Nat'l BioMed. Res. Fd'n, Washington D.C. 1979.)

It now has been discovered that the family of
10 proteins described by these sequences also is capable of initiating and maintaining the tissue-specific developmental cascade in tissues other than bone and cartilage. When combined with naive progenitor cells as disclosed herein, these proteins, termed morphogens,
15 are capable of inducing the proliferation and differentiation of the progenitor cells. In the presence of appropriate tissue-specific signals to direct the differentiation of these cells, and a morphogenically permissive environment, these
20 morphogens are capable of reproducing the cascade of cellular and molecular events that occur during embryonic development to yield functional tissue.

A key to these developments was the creation
25 of a mammalian tissue model system, namely a model system for endochondral bone formation, and investigation of the cascade of events important for bone tissue morphogenesis. Work on this system has enabled discovery not only of bone inductive
30 morphogens, but also of tissue inductive morphogens and their activities. The methods used to develop the bone model system, now well known in the art, along with the proteins of this invention, can be used to create model systems for other tissues, such as liver (see infra).

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Using the model system for endochondral bone formation, it also has been discovered that the local environment in which the morphogenic material is placed is important for tissue morphogenesis. As used herein, "local environment" is understood to include the tissue structural matrix and the environment surrounding the tissue. For example, in addition to needing an appropriate anchoring substratum for their proliferation, the morphogen-stimulated cells need signals to direct the tissue-specificity of their differentiation. These signals vary for the different tissues and may include cell surface markers. In addition, vascularization of new tissue requires a local environment which supports vascularization. Using the bone model system as an example, it is known that, under standard assay conditions, implanting osteoinductive morphogens into loose mesenchyme in the absence of a tissue-specifying matrix generally does not result in endochondral bone formation unless very high concentrations of the protein are implanted. By contrast, implanting relatively low concentrations of the morphogen in association with a suitably modified bone-derived matrix results in the formation of fully functional endochondral bone (see, for example, Sampath et al. (1981) PNAS 78:7599-7 603 and U.S. Patent No. 4,975,526). In addition, a synthetic matrix comprised of a structural polymer such as tissue-specific collagen and tissue-specific cell attachment factors such as tissue-specific glycosylaminoglycans, will allow endochondral bone formation (see, for example, PCT publication US91/03603, published December 12, 1991 (WO 91/18558). Finally, if the morphogen and a suitable bone or cartilage-specific matrix (e.g., comprising Type I cartilage) are implanted together in loose mesenchyme, cartilage and endochondral bone formation will result, including the formation of bone marrow and

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a vascular system. However, if the same composition is provided to a nonvascular environment, such as to cultured cells in vitro or at an cartilage-specific locus, tissue development does not continue beyond
5 cartilage formation (see *infra*). Similarly, a morphogenic composition containing a cartilage-specific matrix composed of Type 2 collagen is expected to induce formation of non-cartilage tissue in vivo (e.g., hyaline). However, if the composition is provided to a
10 vascular-supporting environment, such as loose mesenchyme, the composition is capable of inducing the differentiation of proliferating progenitor cells into chondrocytes and osteoblasts, resulting in bone formation.

15

It also has been discovered that tissue morphogenesis requires a morphogenically permissive environment. Clearly, in fully-functioning healthy tissue that is not composed of a permanently renewing
20 cell population, there must exist signals to prevent continued tissue growth. Thus, it is postulated that there exists a control mechanism, such as a feedback control mechanism, which regulates the control of cell growth and differentiation. In fact, it is known that
25 both TGF- β , and MIS are capable of inhibiting cell growth when present at appropriate concentrations. In addition, using the bone model system it can be shown that osteogenic devices comprising a bone-derived carrier (matrix) that has been demineralized and
30 guanidine-extracted to substantially remove the noncollagenous proteins does allow endochondral bone formation when implanted in association with an

osteoinductive morphogen. If, however, the bone-derived carrier is not demineralized but rather is washed only in low salt, for example, induction of endochondral bone formation is inhibited, suggesting
5 the presence of one or more inhibiting factors within the carrier.

Another key to these developments was determination of the broad distribution of these
10 morphogens in developing and adult tissue. For example, DPP is expressed in both embryonic and developing *Drosophila* tissue. Vgl has been identified in *Xenopus* embryonic tissue. Vgr-1 transcripts have been identified in a variety of murine tissues,
15 including embryonic and developing brain, lung, liver, kidney and calvaria (dermal bone) tissue. Recently, Vgr-1 transcripts also have been identified in adult murine lung, kidney, heart, and brain tissue, with especially high abundance in the lung (see infra).

20 OP-1 and the CBMP2 proteins, both first identified as bone morphogens, have been identified in mouse and human placenta, hippocampus, calvaria and osteosarcoma tissue as determined by identification of
25 OP-1 and CMBP2-specific sequences in cDNA libraries constructed from these tissues (see Ozkaynak, et al., (1990) EMBO J 9:2085-2093, and Ozkaynak et al., (1991) Biochem. Biophys. Res. Commn. 179:116-123). Additionally, the OP-1 protein is present in a variety
30 of embryonic and developing tissues including kidney, liver, heart, adrenal tissue and brain as determined by Western blot analysis and immunolocalization (see infra). OP-1-specific transcripts also have been identified in both embryonic and developing tissues,
35 most abundantly in developing kidney, bladder and brain

(see infra). OP-1 also has been identified as a mesoderm inducing factor present during embryogenesis (see infra). Moreover, OP-1 has been shown to be associated with in satellite muscle cells and
5 associated with pluripotential stem cells in bone marrow following damage to adult murine endochondral bone, indicating its morphogenic role in tissue repair and regeneration. In addition, the recently identified protein GDF-1 (see Table II) has been identified in
10 neural tissue (Lee, (1991) PNAS 88 4250-4254).

Exemplification

IDENTIFICATION AND ISOLATION OF MORPHOGENS

15

Among the proteins useful in this invention are proteins originally identified as bone inductive proteins, such as the OP-1, OP-2 and the CBMP proteins, as well as amino acid sequence-related proteins such as
20 DPP (from Drosophila), Vgl (from Xenopus) and Vgr-1 (from mouse, see Table II and Sequence Listing). The members of this family, which include particular members of the TGF- β super family of structurally related proteins, share substantial amino acid sequence
25 homology in their C-terminal regions. The OP-2 proteins have an extra cysteine residue in this region (position 41 of Seq. ID Nos. 7 and 8), in addition to the conserved cysteine skeleton in common with the other proteins in this family. The proteins are
30 inactive when reduced, but are active as oxidized homodimeric species as well as when oxidized in combination with other morphogens.

Accordingly, the morphogens of this invention
35 can be described by either of the following two species

of generic amino acid sequences: Generic Sequence 1 or Generic Sequence 2, (Seq. ID Nos. 1 and 2), where each Xaa indicates one of the 20 naturally-occurring L-isomer, α -amino acids or a derivative thereof.

5 Particularly useful sequences that fall within this family of proteins include the 96-102 C-terminal residues of Vgl, Vgr-1, DPP, OP-1, OP-2, CBMP-2A, CBMP-2B, and GDF-1, as well as their intact mature amino acid sequences. In addition, biosynthetic

10 constructs designed from the generic sequences, such as COP-1, COP-3-5, COP-7, and COP-16 also are useful (see, for example, U.S. Pat. No. 5,011,691.)

Generic sequences showing preferred amino

15 acids compiled from sequences identified to date and useful as morphogens (e.g., Tables II and III) are described by Generic Sequence 3 (Seq. ID No. 3) and Generic Sequence 4 (Seq. ID No. 4). Note that these generic sequences have a 7 or 8-cysteine skeleton where

20 inter- or intramolecular disulfide bonds can form, and contain certain critical amino acids which influence the tertiary structure of the proteins. It is also contemplated that the differing N-termini of the naturally occurring proteins provide a tissue-specific

25 or other, important modulating activity of these proteins.

Given the foregoing amino acid and DNA sequence information, the level of skill in the art,

30 and the disclosures of U.S. Patent Nos. 4,968,590 and 5,011,691, PCT application US 89/01469, published October 19, 1989 (WO89/09788), and Ozkaynak, et al., (1990) EMBO J 9:2085-2093, and Ozkaynak et al., (1991) Biochem. Biophys. Res. Commn. 179:116-123 the

35 disclosures of which are incorporated herein by reference, various DNAs can be constructed which encode

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at least the active region of a morphogen of this invention, and various analogs thereof (including allelic variants and those containing genetically engineered mutations), as well as fusion proteins, truncated forms of the mature proteins, deletion and insertion mutants, and similar constructs. Moreover, DNA hybridization probes can be constructed from fragments of the genes encoding any of these proteins, including sequences encoding the active regions or the pro regions of the proteins (see *infra*), or designed de novo from the generic sequence. These probes then can be used to screen different genomic and cDNA libraries to identify additional morphogenic proteins from different tissues.

15

The DNAs can be produced by those skilled in the art using well known DNA manipulation techniques involving genomic and cDNA isolation, construction of synthetic DNA from synthesized oligonucleotides, and cassette mutagenesis techniques. 15-100mer oligonucleotides may be synthesized on a Biosearch DNA Model 8600 Synthesizer, and purified by polyacrylamide gel electrophoresis (PAGE) in Tris-Borate-EDTA buffer. The DNA then may be electroeluted from the gel. Overlapping oligomers may be phosphorylated by T4 polynucleotide kinase and ligated into larger blocks which also may be purified by PAGE.

The DNA from appropriately identified clones then can be isolated, subcloned (preferably into an expression vector), and sequenced. Plasmids containing sequences of interest then can be transfected into an appropriate host cell for expression of the morphogen and further characterization. The host may be a

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procaryotic or eucaryotic cell since the former's inability to glycosylate protein will not destroy the protein's morphogenic activity. Useful host cells include E. coli, Saccharomyces, the insect/baculovirus cell system, myeloma cells, and various other mammalian cells. The vectors additionally may encode various sequences to promote correct expression of the recombinant protein, including transcription promoter and termination sequences, enhancer sequences, preferred ribosome binding site sequences, preferred mRNA leader sequences, preferred signal sequences for protein secretion, and the like.

The DNA sequence encoding the gene of interest also may be manipulated to remove potentially inhibiting sequences or to minimize unwanted secondary and tertiary structure formation. The recombinant morphogen also may be expressed as a fusion protein. After being translated, the protein may be purified from the cells themselves or recovered from the culture medium. All biologically active protein forms comprise dimeric species joined by disulfide bonds or otherwise associated, produced by refolding and oxidizing one or more of the various recombinant polypeptide chains within an appropriate eucaryotic cell or in vitro after expression of individual subunits. A detailed description of morphogens expressed from recombinant DNA in E. coli and in numerous different mammalian cells is disclosed in PCT publication US90/05903, published May 2, 1991 (WO91/05802) and United States Patent 5,266,683 which issued on November 30, 1993.

Alternatively, morphogenic polypeptide chains can be synthesized chemically using conventional peptide synthesis techniques well known to those having

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ordinary skill in the art. For example, the proteins may be synthesized intact or in parts on a Biosearch solid phase peptide synthesizer, using standard operating procedures. Completed chains then are
5 deprotected and purified by HPLC (high pressure liquid chromatography). If the protein is synthesized in parts, the parts may be peptide bonded using standard methodologies to form the intact protein. In general, the manner in which the morphogens are made can be
10 conventional and does not form a part of this invention.

MORPHOGEN DISTRIBUTION

15 The generic function of the morphogens of this invention throughout the life of the organism can be evidenced by their expression in a variety of disparate mammalian tissues. Determination of the tissue distribution of morphogens also may be used to identify
20 different morphogens expressed in a given tissue, as well as to identify new, related morphogens. The proteins (or their mRNA transcripts) are readily identified in different tissues using standard methodologies and minor modifications thereof in
25 tissues where expression may be low. For example, protein distribution may be determined using standard Western blot analysis or immunofluorescent techniques, and antibodies specific to the morphogen or morphogens of interest. Similarly, the distribution of morphogen
30 transcripts may be determined using standard Northern hybridization protocols and transcript-specific probes.

Any probe capable of hybridizing specifically to a transcript, and distinguishing the transcript of
35 interest from other, related transcripts may be used.

Because the morphogens of this invention share such high sequence homology in their active, C-terminal domains, the tissue distribution of a specific morphogen transcript may best be determined using a probe specific for the pro region of the immature protein and/or the N-terminal region of the mature protein. Another useful sequence is the 3' non-coding region flanking and immediately following the stop codon. These portions of the sequence vary substantially among the morphogens of this invention, and accordingly, are specific for each protein. For example, a particularly useful Vgr-1-specific probe sequence is the PvuII-SacI fragment, a 265 bp fragment encoding both a portion of the untranslated pro region and the N-terminus of the mature sequence (see Lyons et al. (1989) PNAS 86:4554-4558 for a description of the cDNA sequence). Similarly, particularly useful mOP-1-specific probe sequences are the BstXI-BglI fragment, a 0.68 Kb sequence that covers approximately two-thirds of the mOP-1 pro region; a StuI-StuI fragment, a 0.2 Kb sequence immediately upstream of the 7-cysteine domain; and the Earl-PstI fragment, an 0.3 Kb fragment containing a portion of the 3'untranslated sequence (See Seq. ID No. 18, where the pro region is defined essentially by residues 30-291.) Similar approaches may be used, for example, with hOP1 (Seq. ID No. 16) or human or mouse OP2 (Seq. ID Nos. 20 and 22.)

Using these morphogen-specific probes, which may be synthetically engineered or obtained from cloned sequences, morphogen transcripts can be identified in mammalian tissue, using standard methodologies well known to those having ordinary skill in the art. Briefly, total RNA is prepared from various adult murine tissues (e.g., liver, kidney, testis, heart,

brain, thymus and stomach) by a standard methodology such as by the method of Chomczyaski et al. ((1987) Anal. Biochem 162:156-159) and described below. Poly (A)+ RNA is prepared by using oligo (dT)-cellulose chromatography (e.g., Type 7, from Pharmacia LKB Biotechnology, Inc.). Poly (A)+ RNA (generally 15 μ g) from each tissue is fractionated on a 1% agarose/formaldehyde gel and transferred onto a Nytran membrane (Schleicher & Schuell). Following the transfer, the membrane is baked at 80°C and the RNA is cross-linked under UV light (generally 30 seconds at 1 mW/cm²). Prior to hybridization, the appropriate probe (e.g., the PvuII-SacI Vgr-1 fragment) is denatured by heating. The hybridization is carried out in a lucite cylinder rotating in a roller bottle apparatus at approximately 1 rev/min for approximately 15 hours at 37°C using a hybridization mix of 40% formamide, 5 x Denhardts, 5 x SSPE, and 0.1% SDS. Following hybridization, the non-specific counts are washed off the filters in 0.1 x SSPE, 0.1% SDS at 50°C. Northern blots performed using Vgr-1 probes specific to the variable N terminus of the mature sequence indicate that the Vgr-1 message is approximately 3.5 Kb.

Figure 1 is a photomicrograph representing a Northern blot analysis probing a number of adult murine tissues with the Vgr-1 specific probes: liver, kidney, testis, heart, brain, thymus and stomach, represented in lanes 3-10, respectively. Lanes 1 and 12 are size standards and lanes 2 and 11 are blank. Among the tissues tested, Vgr-1 appears to be expressed most abundantly in adult lung, and to a lesser extent in adult kidney, heart and brain. These results confirm and expand on earlier studies identifying Vgr-1 and Vgr-1-like transcripts in several embryonic and adult

murine tissue (Lyons et al. (1989) PNAS 86:4554-4558),
as well as studies identifying OP-1 and CBMP2 in
various human cDNA libraries (e.g., placenta,
hippocampus, calvaria, and osteosarcoma, see Ozkaynak
5 et al., (1990) EMBO 9:2085-2093).

Using the same general probing methodology,
mOP-1 transcripts also have been identified in a
variety of murine tissues, including embryo and various
10 developing tissues, as can be seen in Figures 2 and 3.
Details of the probing methodology are disclosed in
Ozkaynak, et al., (1991) Biochem. Biophys. Res. Commn.
179:116-123, the disclosure of which is incorporated
herein. The Northern blots represented in Figure 2
15 probed RNA prepared from developing brain, spleen,
lung, kidney (and adrenal gland), heart, and liver in
13 day post natal mice (panel A) or 5 week old mice
(panel B). The OP-1 specific probe was a probe
containing the 3' untranslated sequences described
20 supra (0.34 Kb EarI-Pst I fragment). As a control for
RNA recovery, EF-Tu (translational elongation factor)
mRNA expression also was measured (EF-Tu expression is
assumed to be relatively uniform in most tissues).

25 The arrowheads indicate the OP1-specific messages
observed in the various tissues. As can be seen in
Fig. 2, OP-1 expression levels vary significantly in
the spleen, lung, kidney and adrenal tissues, while the
EF-Tu mRNA levels are constant. Uniformly lower levels
30 of EF-Tu mRNA levels were found in the heart, brain and
liver. As can be seen from the photomicrograph, the
highest levels of OP-1 mRNA appear to be in kidney and
adrenal tissue, followed by the brain. By contrast,
heart and liver did not give a detectable signal. Not

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shown are additional analyses performed on bladder tissue, which shows significant OP-1 mRNA expression, at levels close to those in kidney/adrenal tissue. The Northern blots also indicate that, like GDF-1, OP-1 mRNA expression may be bicistronic in different tissues. Four transcripts can be seen: 4 Kb, 2.4 Kb, 2.2 Kb, and 1.8 Kb transcripts can be identified in the different tissues, and cross probing with OP-1 specific probes from the proregion and N-terminal sequences of the gene indicate that these transcripts are OP-1 specific.

A side by side comparison of OP-1 and Vgr-1 in Figure 3 shows that the probes distinguish between the morphogens Vgr-1 and OP-1 transcripts in the different tissues, and also highlights the multiple transcription of OP-1 in different tissues. Specifically, Fig. 3 compares the expression of OP-1 (Panels B and D), Vgr-1 (Panel C) and EF-Tu (Panel A) (control) mRNA in 17 day embryos (lane 1) and 3 day post-natal mice (lane 2). The same filter was used for sequential hybridizations with labeled DNA probes specific for OP-1 (Panels B and D), Vgr-1 (Panel C), and EF-Tu (Panel A). Panel A: the EF-Tu specific probe (control) was the 0.4 Kb HindIII-SacI fragment (part of the protein coding region), the SacI site used belonged to the vector; Panel B: the OP-1 specific probe was the 0.68 Kb BstXI-BglI fragment containing pro region sequences; Panel D; the OP-1 specific probe was the 0.34 Kb EarI-PstI fragment containing the 3' untranslated sequence; Panel C: the Vgr-1 specific probe was the 0.26 Kb PvuII-SacI fragment used in the Vgr-1 blots described above.

The 1.8-2.5 Kb OP-1 mRNA appears approximately two times higher in three day post natal mice than in 17 day embryos, perhaps reflecting phases in bone and/or kidney development. In addition, of the four messages
5 found in brain, the 2.2 Kb transcript appears most abundant, whereas in lung and spleen the 1.8 Kb message predominates. Finally, careful separation of the renal and adrenal tissue in five week old mice reveals that the 2.2 Kb transcripts were derived from renal tissue
10 and the 4 Kb mRNA is more prominent in adrenal tissue (see Figure 2).

Similarly, using the same general probing methodology, BMP3 and CBMP2B transcripts recently have
15 been identified in abundance in lung tissue.

Morphogen distribution in embryonic tissue can be determined using five or six-day old mouse embryos and standard immunofluorescence techniques in concert
20 with morphogen-specific antisera. For example, rabbit anti-OP-1 antisera is readily obtained using any of a number of standard antibody protocols well known to those having ordinary skill in the art. The antibodies then are fluorescently labelled using standard
25 procedures. A five or six-day old mouse embryo then is thin-sectioned and the various developing tissues probed with the labelled antibody, again following standard protocols. Using this technique, OP-1 protein has been detected in developing brain and heart.

30

This method also may be used to identify morphogens in adult tissues undergoing repair. For example, a fracture site can be induced in a rat long bone such as the femur. The fracture then is allowed
35 to heal for 2 or 3 days. The animal then is sacrificed

and the fractured site sectioned and probed for the presence of the morphogen e.g., OP-1, with fluorescently labelled rabbit anti-OP-1 antisera using standard immunolocalization methodology. This
5 technique identifies OP-1 in muscle satellite cells, the progenitor cells for the development of muscle, cartilage and endochondral bone. In addition, OP-1 is detected with potential pluripotential stem cells in the bone marrow, indicating its morphogenic role in
10 tissue repair and regeneration.

OP-1 protein also has been identified in rat brain using standard immunofluorescence staining technique. Specifically, adult rat brain (2-3 months old) and
15 spinal cord is frozen and sectioned. Anti-OP-1, raised in rabbits and purified on an OP-1 affinity column prepared using standard methodologies, was added to the sections under standard conditions for specific binding. Goat anti-rabbit IgG, labelled with
20 fluorescence, then was used to visualize OP-1 antibody binding to tissue sections.

As can be seen in FIG 4A and 4B, immunofluorescence staining demonstrates the presence of OP-1 in adult rat
25 central nervous system (CNS.) Similar and extensive staining is seen in both the brain (4A) and spinal cord (4B). OP-1 appears to be predominantly localized to the extracellular matrix of the grey matter, present in all areas except the neuronal cell bodies. In white
30 matter, staining appears to be confined to astrocytes. A similar staining pattern also was seen in newborn rat (10 day old) brain sections.

CELL DIFFERENTIATION

The ability of morphogens of this invention to induce cell differentiation can be determined by culturing early mesenchymal cells in the presence of the morphogen and then studying the histology of the cultured cells by staining with toluidine blue. For example, it is known that rat mesenchymal cells destined to become mandibular bone, when separated from the overlying epithelial cells at stage 11 and cultured in vitro under standard tissue culture conditions, will not continue to differentiate. However, if these same cells are left in contact with the overlying endoderm for an additional day, at which time they become stage 12 cells, they will continue to differentiate on their own in vitro to form chondrocytes. Further differentiation into osteoblasts and, ultimately, mandibular bone, requires an appropriate local environment, e.g., a vascularized environment.

It has now been discovered that stage 11 mesenchymal cells, cultured in vitro in the presence of a morphogen, e.g., OP-1, continue to differentiate in vitro to form chondrocytes. These stage 11 cells also continue to differentiate in vitro if they are cultured with the cell products harvested from the overlying endodermal cells. Moreover, OP-1 can be identified in the medium conditioned by endodermal cells either by Western blot or immunofluorescence. This experiment may be performed with other morphogens and with different mesenchymal cells to assess the cell differentiation capability of different morphogens, as well as their distribution in different developing tissues.

As another example of morphogen-induced cell differentiation, the effect of OP-1 on the

differentiation of neuronal cells has been tested in culture. Specifically, the effect of OP-1 on the NG108-15 neuroblastoma x glioma hybrid clonal cell line has been assessed. The cell line shows a fibroblastic-
5 type morphology in culture. The cell line can be induced to differentiate chemically using 0.5 mM butyrate, 1% DMSO or 500 mM Forskolin, inducing the expression of virtually all important neuronal properties of cultured primary neurons. However,
10 chemical induction of these cells also induces cessation of cell division.

In the present experiment NG108-15 cells were subcultured on poly-L-lysine coated 6 well plates.
15 Each well contained 40-50,000 cells in 2.5 ml of chemically defined medium. On the third day 2.5 μ l of OP-1 in 60% ethanol containing 0.025% trifluoroacetic was added to each well. OP-1 concentrations of 0, 1, 10, 40 and 100 ng/ml were tested. The media was
20 changed daily with new aliquots of OP-1. After four days with 40 and 100 ng OP-1/ml concentrations, OP-1 induced differentiation of the NG108-15 cells. Figure 5 shows the morphological changes that occur. The OP-1 induces clumping and rounding of the cells and
25 the production of neurite outgrowths (processes). Compare FIG 5A (naive NG108-15 cells) with FIG 5B, showing the effects of OPI-treated cells. Thus the OP-1 can induce the cells to differentiate into a neuronal cell morphology. Some of the outgrowths
30 appear to join in a synaptic-type junction. This effect was not seen in cells incubated with TGF-B1 at concentrations of 1 to 100 ng/ml.

The neuroprotective effects of OP-1 were
35 demonstrated by comparison with chemical

differentiation agents on the NG108-15 cells. 50,000 cells were plated on 6 well plates and treated with butyrate, DMSO, Forskolin or OP-1 for four days. Cell counts demonstrated that in the cultures containing the
5 chemical agents the differentiation was accompanied by a cessation of cell division. In contrast, the cells induced to differentiate by OP-1 continued to divide, as determined by H^3 -thymidine uptake. The data suggest that OP-1 is capable of maintaining the stability of
10 the cells in culture after differentiation.

As yet another, related example, the ability of the morphogens of this invention to induce the "redifferentiation" of transformed cells also has been
15 assessed. Specifically, the effect of OP-1 on human EC cells (embryo carcinoma cells, NTERA-Z CL.D1) is disclosed herein. In the absence of an external stimulant these cells can be maintained as undifferentiated stem cells, and can be induced to grow
20 in serum free media (SFM). In the absence of morphogen treatment the cells proliferate rampantly and are anchorage-independent. The effect of morphogen treatment is seen in Figs. 6A-D. Figs 6A and 6B show 4 days of growth in SFM in the presence of OP-1
25 (25ng/ml, 6A) or the absence of morphogen (6B). Figs. 6C and 6D are 5 days growth in the presence of 10ng/ml OP-1 (6C) or no morphogen (6D). Figs. 6C and 6D are at 10x and 20x magnification compared to FIGs 6A and 5B. As can readily be seen, in the presence of
30 OP-1, EC cells grow as flattened cells, becoming anchorage dependent. In addition, growth rate is reduced approximately 10 fold. Finally, the cells are induced to differentiate.

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The morphogens of this invention also may be used to maintain a cell's differentiated phenotype. This morphogenic capability is particularly useful for
5 inducing the continued expression of phenotype in senescent or quiescent cells.

The phenotypic maintenance capability of morphogens is readily assessed. A number of
10 differentiated cells become senescent or quiescent after multiple passages under standard tissue culture conditions in vitro. However, if these cells are cultivated in vitro in association with a morphogen of this invention, the cells are induced to maintain
15 expression of their phenotype through multiple passages. For example, the alkaline phosphatase activity of cultured osteoblasts, like cultured osteosarcoma cells and calvaria cells, is significantly reduced after multiple passages in vitro.
20 However, if the cells are cultivated in the presence of a morphogen (e.g., OP-1), alkaline phosphatase activity is maintained over extended periods of time. Similarly, phenotypic expression of myocytes also is maintained in the presence of the morphogen. This
25 experiment may be performed with other morphogens and different cells to assess the phenotypic maintenance capability of different morphogens on cells of differing origins.

30 Phenotypic maintenance capability also may be assessed in vivo, using a rat model for osteoporosis, disclosed in co-pending Canadian patent application serial number 2,116,559. As disclosed therein, Long Evans rats are ovariectomized to produce
35 an osteoporotic condition resulting from decreased

estrogen production. Eight days after ovariectomy, rats are systemically provided with phosphate buffered saline (PBS) or OP-1 (21 μ g or 20 μ g) for 22 days. The rats then are sacrificed and serum alkaline phosphatase levels, serum calcium levels, and serum osteocalcin levels are determined, using standard methodologies. Three-fold higher levels of osteocalcin levels are found in rats provided with 1 or 20 μ g of OP-1. Increased alkaline phosphatase levels also were seen. Histomorphometric analysis on the tibial diaphysical bone shows OP-1 can reduce bone mass lost due to the drop in estrogen levels.

CELL STIMULATION

The ability of the morphogens of this invention to stimulate the proliferation of progenitor cells also can be assayed readily in vitro. Useful naive stem cells include pluripotential stem cells, which may be isolated from bone marrow or umbilical cord blood using conventional methodologies, (see, for example, Faradji et al., (1988) Vox Sang. 55 (3):133-138 or Broxmeyer et al., (1989) PNAS 86 (10):3828-3832), as well as naive stem cells obtained from blood. Alternatively, embryonic cells (e.g., from a cultured mesodermal cell line) may be useful.

Another method for obtaining progenitor cells and for determining the ability of morphogens to stimulate cell proliferation is to capture progenitor cells from an in vivo source. For example, a biocompatible matrix material able to allow the influx of migratory progenitor cells may be implanted at an in vivo site long enough to allow the influx of migratory progenitor cells. For example, a bone-derived,

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guanidine-extracted matrix, formulated as disclosed for example in Sampath et al. ((1983) PNAS 80:6591-6595), or U.S. Patent No. 4,975,526, may be implanted into a rat at a subcutaneous site, essentially following the method of Sampath et al. (ibid). After three days the implant is removed, and the progenitor cells associated with the matrix dispersed and cultured.

Progenitor cells, however obtained, then are incubated in vitro with a suspected morphogen under standard cell culture conditions well known to those having ordinary skill in the art. In the absence of external stimuli, the progenitor cells do not, or minimally proliferate on their own in culture. However, if the cells are cultured in the presence of a morphogen, such as OP-1, they are stimulated to proliferate. Cell growth can be determined visually or spectrophotometrically using standard methods well known in the art.

20

PROLIFERATION OF PROGENITOR CELL POPULATIONS

Progenitor cells may be stimulated to proliferate in vivo or ex vivo. The cells may be stimulated in vivo by injecting or otherwise providing a sterile preparation containing the morphogen into the individual. For example, the hemopoietic pluripotential stem cell population of an individual may be stimulated to proliferate by injecting or otherwise providing an appropriate concentration of the morphogen to the individual's bone marrow.

Progenitor cells may be stimulated ex vivo by contacting progenitor cells of the population to be enhanced with a morphogen under sterile conditions at a

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concentration and for a time sufficient to stimulate proliferation of the cells. In general, a period of from about 10 minutes to about 24 hours should be sufficient. The stimulated cells then are provided to
5 the individual as, for example, by injecting the cells to an appropriate in vivo locus. Suitable biocompatible progenitor cells may be obtained by any of the methods known in the art or described herein.

10 REGENERATION OF DAMAGED OR DISEASED TISSUE

The morphogens of this invention may be used to repair diseased or damaged mammalian tissue. The tissue to be repaired is preferably assessed, and
15 excess necrotic or interfering scar tissue removed as needed, by surgical, chemical, ablating or other methods known in the medical arts.

The morphogen then may be provided directly to
20 the tissue locus as part of a sterile, biocompatible composition, either by surgical implantation or injection. Alternatively, a sterile, biocompatible composition containing morphogen-stimulated progenitor cells may be provided to the tissue locus. The
25 existing tissue at the locus, whether diseased or damaged, provides the appropriate matrix to allow the proliferation and tissue-specific differentiation of progenitor cells. In addition, a damaged or diseased tissue locus, particularly one that has been further
30 assaulted by surgical means, provides a morphogenically permissive environment. For some tissues, it is envisioned that systemic provision of the morphogen will be sufficient.

In some circumstances, particularly where tissue damage is extensive, the tissue may not be capable of providing a sufficient matrix for cell influx and proliferation. In these instances, it may
5 be necessary to provide the morphogen or morphogen-stimulated progenitor cells to the tissue locus in association with a suitable, biocompatible formulated matrix, prepared by any of the means described below. The matrix preferably is tissue-specific, in vivo
10 biodegradable, and comprises particles having dimensions within the range of 70-850 μ m, most preferably 150-420 μ m.

The morphogens of this invention also may be used
15 to prevent or substantially inhibit scar tissue formation following an injury. If a morphogen is provided to a newly injured tissue locus, it can induce tissue morphogenesis at the locus, preventing the aggregation of migrating fibroblasts into non-
20 differentiated connective tissue. The morphogen preferably is provided as a sterile pharmaceutical preparation injected into the tissue locus within five hours of the injury. Several non-limiting examples follow, illustrating the morphogens regenerate
25 capabilities in different issues. The proteins of this invention previously have been shown to be capable of inducing cartilage and endochondral bone formation (See, for example U.S. Patent No. 5,011,691).

30 As an example, protein-induced morphogenesis of substantially injured liver tissue following a partial hepatectomy is disclosed. Variations on this general protocol may be used to test morphogen activity in other different tissues. The general method involves
35 excising an essentially nonregenerating portion of a

tissue and providing the morphogen, preferably as a soluble pharmaceutical preparation to the excised tissue locus, closing the wound and examining the site at a future date. Like bone, liver has a potential to
5 regenerate upon injury during post-fetal life.

Morphogen, (e.g., purified recombinant human OP-1, mature form), was solubilized (1 mg/ml) in 50% ethanol (or compatible solvent) containing 0.1% trifluoroacetic
10 acid (or compatible acid). The injectable OP-1 solution was prepared by diluting one volume of OP-1/solvent-acid stock solution with 9 volumes of 0.2% rat serum albumin in sterile PBS (phosphate-buffered saline).
15

Growing rats or aged rats were anesthetized by using ketamine. Two of the liver lobes (left and right) were cut out (approximately 1/3 of the lobe) and the OP-1 was injected locally at multiple sites along
20 the cut ends. The amount of OP-1 injected was 100 μ g in 100 of PBS/RSA (phosphate buffered saline/rat serum albumin) injection buffer. Placebo samples are injection buffer without OP-1. Five rats in each group were used. The wound was closed and the rats were
25 allowed to eat normal food and drink tap water.

After 12 days, the rats were sacrificed and liver regeneration was observed visually. The photomicrograph in Fig. 7 illustrates dramatically the
30 regenerative effects of OP-1 on liver regeneration. The OP-1-injected group showed complete liver tissue regeneration and no sign remained of any cut in the liver (animal 2). By contrast, in the control group into which only PBS was injected only minimal
35 regeneration was evidenced (animal 1). In addition, the incision remains in this sample.

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As another example, the ability of the morphogens of this invention to induce dentinogenesis also was assessed. To date, the unpredictable response of dental pulp tissue to injury is a basic clinical problem in dentistry. Cynomolgus monkeys were chosen as primate models as monkeys are presumed to be more indicative of human dental biology than models based on lower non-primate mammals.

10

Using standard dental surgical procedures, small areas (e.g., 2mm) of dental pulps were surgically exposed by removing the enamel and dentin immediately above the pulp (by drilling) of sample teeth, performing a partial amputation of the coronal pulp tissue, inducing hemostasis, application of the pulp treatment, and sealing and filling the cavity by standard procedures.

20

Pulp treatments used were: OP-1 dispersed in a carrier matrix; carrier matrix alone and no treatment. Twelve teeth per animal (four for each treatment) were prepared, and two animals were used. At four weeks, teeth were extracted and processed histologically for analysis of dentin formation, and/or ground to analyze dentin mineralization. FIG.8 illustrates dramatically the effect of morphogen on osteodentin reparation. FIG. 8A is a photomicrograph of the control treatment (PBS) and shows little or no reparation. FIG. 8B is a photomicrograph of treatment with carrier alone, showing minimal reparation. By contrast, treatment with morphogen (FIG. 8C) shows significant reparation. The results of FIG. 8 indicate that OP-1-CM (OP-1 plus

30

carrier matrix) reliably induced formation of reparative or osteodentin bridges on surgically exposed healthy dental pulps. By contrast, pulps treated with carrier matrix alone, or not treated failed to form
5 reparative dentin.

As another example, the morphogen-induced regenerative effects on central nervous system (CNS) repair may be assessed using a rat brain stab model. Briefly, male Long Evans rats are anesthetized and the head area prepared for surgery. The calvariae is exposed using standard surgical procedures and a hole drilled toward the center of each lobe using a 0.035K wire, just piercing the calvariae. 25 μ l solutions
10 containing either morphogen (OP-1, 25 μ g) or PBS then is provided to each of the holes by Hamilton syringe. Solutions are delivered to a depth approximately 3 mm below the surface, into the underlying cortex, corpus callosum and hippocampus. The skin then is sutured and
15 the animal allowed to recover.

Three days post surgery, rats are sacrificed by decapitation and their brains processed for sectioning. Scar tissue formation is evaluated by immunofluorescence staining for glial fibrillary acidic protein, a marker
25 protein for glial scarring, to qualitatively determine the degree of scar formation. Sections also are probed with anti-OP-1 antibodies to determine the presence of OP-1. Reduced levels of glial fibrillary acidic
30 protein are anticipated in the tissue sections of animals treated with morphogen, evidencing the ability of morphogen to inhibit glial scar formation, thereby stimulating nerve regeneration.

35

MORPHOGEN ACTIVITY MODULATION

Antibodies to morphogens of this invention have been identified in healthy human sera. In addition, implanting devices comprising morphogens (e.g., OP-1) have been discovered to induce an increase in anti-morphogen antibodies (e.g., anti-OP-1 antibodies). It is anticipated that these antibodies comprise part of the body's regulation of morphogen activity in vivo. The presence of the antibodies, and fluctuations in their levels, which are readily monitored, can provide a useful method for monitoring tissue stasis and tissue viability (e.g., identification of a pathological state). For example, standard radioimmunoassays or ELISA may be used to detect and quantify endogenous anti-morphogen antibodies in sera. Antibodies or other binding proteins capable of detecting anti-morphogen antibodies may be obtained using standard methodologies.

20 MATRIX PREPARATION

The morphogens of this invention may be implanted surgically, dispersed in a biocompatible, preferably in vivo biodegradable matrix appropriately modified to provide a structure in which the morphogen may be dispersed and which allows the influx, differentiation and proliferation of migrating progenitor cells. The matrix also should provide signals capable of directing the tissue specificity of the differentiating cells, as well as a morphogenically permissive environment, being essentially free of growth inhibiting signals.

In the absence of these features the matrix does not appear to be suitable as part of a morphogenic composition. Recent studies on osteogenic devices

(morphogens dispersed within a formulated matrix) using matrices formulated from polylactic acid and/or polyglycolic acid biopolymers, ceramics (a-tri-calcium-phosphate), or hydroxyapatite show that these materials, by themselves, are unable to provide the appropriate environment for inducing de novo endochondral bone formation in rats by themselves. In addition, matrices formulated from commercially available highly purified, reconstituted collagens or naturally-derived non-bone, species-specific collagen (e.g., from rat tail tendon) also are unsuccessful in inducing bone when implanted in association with an osteogenic protein. These matrices apparently lack specific structurally-related features which aid in directing the tissue specificity of the morphogen-stimulated, differentiating progenitor cells.

The formulated matrix may be shaped as desired in anticipation of surgery or may be shaped by the physician or technician during surgery. Thus, the material may be used in topical, subcutaneous, intraperitoneal, or intramuscular implants to repair tissue or to induce its growth de novo. The matrix preferably is biodegradable in vivo, being slowly absorbed by the body and replaced by new tissue growth, in the shape or very nearly in the shape of the implant.

Details of how to make and how to use the matrices useful in this invention are disclosed below.

TISSUE-DERIVED MATRICES

Suitable biocompatible, in vivo biodegradable acellular matrices may be prepared from naturally-

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occurring tissue. The tissue is treated with suitable agents to substantially extract the cellular, nonstructural components of the tissue. The agents also should be capable of extracting any growth
5 inhibiting components associated with the tissue. The resulting material is a porous, acellular matrix, substantially depleted in nonstructurally-associated components.

10 The matrix also may be further treated with agents that modify the matrix, increasing the number of pores and micropits on its surfaces. Those skilled in the art will know how to determine which agents are best suited to the extraction of nonstructural
15 components for different tissues. For example, soft tissues such as liver and lung may be thin-sectioned and exposed to a nonpolar solvent such as, for example, 100% ethanol, to destroy the cellular structure of the tissue and extract nonstructural components. The
20 material then is dried and pulverized to yield nonadherent porous particles. Structural tissues such as cartilage and dentin where collagen is the primary component may be demineralized and extracted with guanidine, essentially following the method of Sampath
25 et al. (1983) PNAS 80:6591-6595. For example, pulverized and demineralized dentin is extracted with five volumes of 4M guanidine-HCl, 50mM Tris-HCl, pH 7.0 for 16 hours at 4°C. The suspension then is filtered. The insoluble material that remains is collected and
30 used to fabricate the matrix. The material is mostly collagenous in manner. It is devoid of morphogenic activity. The matrix particles may further be treated with a collagen fibril-modifying agent that extracts potentially unwanted components from the matrix, and
35 alters the surface structure of the matrix material.

Useful agents include acids, organic solvents or heated aqueous media. A detailed description of these matrix treatments are disclosed in U.S. Patent No. 4,975,526 and PCT publication US90/00912, published September 7, 1990 (WO90/10018).

The currently most preferred agent is a heated aqueous fibril-modifying medium such as water, to increase the matrix particle surface area and porosity. The currently most preferred aqueous medium is an acidic aqueous medium having a pH of less than about 4.5, e.g., within the range of about pH 2 - pH 4 which may help to "swell" the collagen before heating. 0.1% acetic acid, which has a pH of about 3, currently is most preferred. 0.1 M acetic acid also may be used.

Various amounts of delipidated, demineralized guanidine-extracted bone collagen are heated in the aqueous medium (1g matrix/30ml aqueous medium) under constant stirring in a water jacketed glass flask, and maintained at a given temperature for a predetermined period of time. Preferred treatment times are about one hour, although exposure times of between about 0.5 to two hours appear acceptable. The temperature employed is held constant at a temperature within the range of about 37°C to 65°C. The currently preferred heat treatment temperature is within the range of about 45°C to 60°C.

After the heat treatment, the matrix is filtered, washed, lyophilized and used for implant. Where an acidic aqueous medium is used, the matrix also is preferably neutralized prior to washing and lyophilization. A currently preferred neutralization buffer is a 200mM sodium phosphate buffer, pH 7.0. To

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neutralize the matrix, the matrix preferably first is allowed to cool following thermal treatment, the acidic aqueous medium (e.g., 0.1% acetic acid) then is removed and replaced with the neutralization buffer and the
5 matrix agitated for about 30 minutes. The neutralization buffer then may be removed and the matrix washed and lyophilized.

Other useful fibril-modifying treatments include
10 acid treatments (e.g., trifluoroacetic acid and hydrogen fluoride) and solvent treatments such as dichloromethane, acetonitrile, isopropanol and chloroform, as well as particular acid/solvent combinations.

15

After contact with the fibril-modifying agent, the treated matrix may be washed to remove any extracted components, following a form of the procedure set forth below:

20

1. Suspend matrix preparation in TBS (Tris-buffered saline) 1g/200 ml and stir at 4°C for 2 hrs; or in 6 M urea, 50 mM Tris-HCl, 500 mM NaCl, pH 7.0 (UTBS) or water and stir at room temperature (RT) for
25 30 minutes (sufficient time to neutralize the pH);

2. Centrifuge and repeat wash step; and

3. Centrifuge; discard supernatant; water
30 wash residue; and then lyophilize.

SYNTHETIC TISSUE-SPECIFIC MATRICES

35 In addition to the naturally-derived tissue-

2 4 6 7 8

specific matrices described above, useful tissue-specific matrices may be formulated synthetically if appropriately modified. These porous biocompatible, in vivo biodegradable synthetic matrices are disclosed in

5 PCT publication US91/03603, published December 12, 1991 (WO91/18558). Briefly, the matrix comprises a porous crosslinked structural polymer of biocompatible, biodegradable collagen and appropriate, tissue-specific glycosaminoglycans as tissue-specific

10 cell attachment factors. Collagen derived from a number of sources may be suitable for use in these synthetic matrices, including insoluble collagen, acid-soluble collagen, collagen soluble in neutral or basic aqueous solutions, as well as those

15 collagens which are commercially available.

Glycosaminoglycans (GAGs) or mucopolysaccharides are hexosamine-containing

20 polysaccharides of animal origin that have a tissue specific distribution, and therefore may be used to help determine the tissue specificity of the morphogen-stimulated differentiating cells. Reaction with the GAGs also provides collagen with another valuable

25 property, i.e., inability to provoke an immune reaction (foreign body reaction) from an animal host.

Chemically, GAGs are made up of residues of hexoseamines glycosidically bound and alternating in a

30 more-or-less regular manner with either hexouronic acid or hexose moieties (see, e.g., Dodgson et al. in Carbohydrate Metabolism and its Disorders (Dickens et al., eds.) Vol. 1, Academic Press (1968)). Useful GAGs include hyaluronic acid, heparin, heparin sulfate,

35 chondroitin 6-sulfate, chondroitin 4-sulfate, dermatan

sulfate, and keratin sulfate. Other GAGs are suitable for forming the matrix described herein, and those skilled in the art will either know or be able to ascertain other suitable GAGs using no more than
5 routine experimentation. For a more detailed description of mucopolysaccharides, see Aspinall, Polysaccharides, Pergamon Press, Oxford (1970). For example, as disclosed in U.S. Application Serial No. 529,852, chondroitin-6-sulfate can be used where
10 endochondral bone formation is desired. Heparin sulfate, on the other hand, may be used to formulate synthetic matrices for use in lung tissue repair.

Collagen can be reacted with a GAG in aqueous
15 acidic solutions, preferably in diluted acetic acid solutions. By adding the GAG dropwise into the aqueous collagen dispersion, coprecipitates of tangled collagen fibrils coated with GAG results. This tangled mass of fibers then can be homogenized to form a homogeneous
20 dispersion of fine fibers and then filtered and dried.

Insolubility of the collagen-GAG products can be raised to the desired degree by covalently cross-linking these materials, which also serves to raise the
25 resistance to resorption of these materials. In general, any covalent cross-linking method suitable for cross-linking collagen also is suitable for cross-linking these composite materials, although crosslinking by a dehydrothermal process is preferred.
30

When dry, the crosslinked particles are essentially spherical, with diameters of about 500 μm . Scanning electron microscopy shows pores of about 20 μm on the surface and 40 μm on the interior. The
35 interior is made up of both fibrous and sheet-like

structures, providing surfaces for cell attachment. The voids interconnect, providing access to the cells throughout the interior of the particle. The material appears to be roughly 99.5% void volume, making the material very efficient in terms of the potential cell mass that can be grown per gram of microcarrier.

The morphogens described herein can be combined and dispersed in an appropriately modified tissue-specific matrix using any of the methods described below:

1. Ethanol Precipitation

Matrix is added to the morphogen dissolved in guanidine-HCl. Samples are vortexed and incubated at a low temperature. Samples are then further vortexed. Cold absolute ethanol is added to the mixture which is then stirred and incubated. After centrifugation (microfuge, high speed) the supernatant is discarded. The matrix is washed with cold concentrated ethanol in water and then lyophilized.

2. Acetonitrile Trifluoroacetic Acid Lyophilization

In this procedure, morphogen in an acetonitrile trifluoroacetic acid (ACN/TFA) solution is added to the carrier material. Samples are vigorously vortexed many times and then lyophilized.

3. Buffered Saline Lyophilization

Morphogen preparations in physiological saline may also be vortexed with the matrix and lyophilized to

produce morphogenically active material.

BIOASSAY

5

The following sets forth various procedures for evaluating the in vivo morphogenic utility of the morphogens and morphogenic compositions of this invention. The proteins and compositions may be
10 injected or surgically implanted in a mammal, following any of a number of procedures well known in the art. For example, surgical implant bioassays may be performed essentially following the procedure of Sampath et al. (1983) PNAS 80:6591-6595.

15

Histological Evaluation

Histological sectioning and staining is preferred to determine the extent of morphogenesis in vivo, particularly in tissue repair procedures.
20 Excised implants are fixed in Bouins Solution, embedded in paraffin, and cut into 6-8 μ m sections. Staining with toluidine blue or hemotoxylin/eosin demonstrates clearly the ultimate development of the new tissue.
25 Twelve day implants are usually sufficient to determine whether the implants contain newly induced tissue.

Successful implants exhibit a controlled progression through the stages of induced tissue
30 development allowing one to identify and follow the tissue-specific events that occur. For example, in endochondral bone formation the stages include:
(1) leukocytes on day one; (2) mesenchymal cell migration and proliferation on days two and three;
35 (3) chondrocyte appearance on days five and six;

- (4) cartilage matrix formation on day seven;
(5) cartilage calcification on day eight; (6) vascular invasion, appearance of osteoblasts, and formation of new bone on days nine and ten; (7) appearance of
5 osteoblastic and bone remodeling and dissolution of the implanted matrix on days twelve to eighteen; and
(8) hematopoietic bone marrow differentiation in the ossicle on day twenty-one.

10 Biological Markers

In addition to histological evaluation, biological markers may be used as a marker for tissue morphogenesis. Useful markers include tissue-specific
15 enzymes whose activities may be assayed (e.g., spectrophotometrically) after homogenization of the implant. These assays may be useful for quantitation and for obtaining an estimate of tissue formation quickly after the implants are removed from the animal.
20 For example, alkaline phosphatase activity may be used as a marker for osteogenesis.

Incorporation of systemically provided morphogens may be followed using tagged morphogens
25 (e.g., radioactively labelled) and determining their localization in new tissue, and/or by monitoring their disappearance from the circulatory system using a standard pulse-chase labeling protocol. The morphogen also may be provided with a tissue-specific molecular
30 tag, whose uptake may be monitored and correlated with the concentration of morphogen provided. As an example, ovary removal in female rats results in reduced bone alkaline phosphatase activity, rendering the rats predisposed to osteoporosis. If the female
35 rats now are provided with a morphogen, e.g., OP-1, a

reduction in the systemic concentration of calcium (CA^{2+}) is seen, which correlates with the presence of the provided morphogen and can be shown to correspond to increased alkaline phosphatase activity.

5

The invention may be embodied in other specific forms without departing from the spirit or essential characteristics thereof. The present embodiments are therefore to be considered in all
10 respects as illustrative and not restrictive, the scope of the invention being indicated by the appended claims rather than by the foregoing description, and all changes which come within the meaning and range of equivalency of the claims are therefore intended to be
15 embraced therein.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: COHEN, CHARLES M.
KUBERASAMPATH, THANGAVEL
PANG, ROY H.L.
OPPERMANN, HERMANN
RUEGER, DAVID C.
 - (ii) TITLE OF INVENTION: PROTEIN-INDUCED MORPHOGENESIS
 - (iii) NUMBER OF SEQUENCES: 23
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: TESTA, HURWITZ & THIBEAULT
 - (B) STREET: 53 STATE STREET
 - (C) CITY: BOSTON
 - (D) STATE: MASSACHUSETTS
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 02109
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 667,274
 - (B) FILING DATE: 11-MAR-1991
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 752,764
 - (B) FILING DATE: 30-AUG-1991
- (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: amino acids
 - (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: Generic Sequence 1

(D) OTHER INFORMATION: Each Xaa indicates one of the 20 naturally-occurring L-isomer, α -amino acids or a derivative thereof.

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

```

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1                               5
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
10                             15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa
20                             25
Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
30                             35
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
40                             45                             50
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
55                             60
Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65                             70
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
75                             80
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
85                             90
Xaa Cys Xaa
95

```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: Generic Sequence 2

(D) OTHER INFORMATION: Each Xaa indicates one of the 20 naturally-occurring L-isomer, α -amino acids or a derivative thereof.

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

```

                Xaa Xaa Xaa Xaa Xaa Xaa
                  1               5
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
              10               15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa
              20               25
Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa
              30               35
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
              40               45               50
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
              55               60
Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
              65               70
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
              75               80
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
              85               90
Xaa Cys Xaa
              95

```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: Generic Sequence 3

(D) OTHER INFORMATION: wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.

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

```
      Leu Tyr Val Xaa Phe
      1               5
Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa
      10
Xaa Ala Pro Gly Xaa Xaa Xaa Ala
      15               20
Xaa Tyr Cys Xaa Gly Xaa Cys Xaa
      25               30
Xaa Pro Xaa Xaa Xaa Xaa Xaa
      35
Xaa Xaa Xaa Asn His Ala Xaa Xaa
      40               45
Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa
      50
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
      55               60
Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa
      65
Xaa Xaa Xaa Leu Xaa Xaa Xaa
      70               75
Xaa Xaa Xaa Xaa Val Xaa Leu Xaa
      80
Xaa Xaa Xaa Xaa Met Xaa Val Xaa
      85               90
Xaa Cys Gly Cys Xaa
      95
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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: Generic Sequence 4

(D) OTHER INFORMATION: wherein each
Xaa is independently selected from
a group of one or more specified
amino acids as defined in the
specification.

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

Cys	Xaa	Xaa	Xaa	Xaa	Leu	Tyr	Val	Xaa	Phe
1				5					10
Xaa	Xaa	Xaa	Gly	Trp	Xaa	Xaa	Trp	Xaa	
				15					
Xaa	Ala	Pro	Xaa	Gly	Xaa	Xaa	Ala		
20					25				
Xaa	Tyr	Cys	Xaa	Gly	Xaa	Cys	Xaa		
		30					35		
Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa			
				40					
Asn	Xaa	Xaa	Asn	His	Ala	Xaa	Xaa		
		45					50		
Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Xaa		
				55					
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys		
		60					65		
Cys	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa		
				70					

Xaa Xaa Xaa Leu Xaa Xaa Xaa
 75 80
 Xaa Xaa Xaa Xaa Val Xaa Leu Xaa
 85
 Xaa Xaa Xaa Xaa Met Xaa Val Xaa
 90 95
 Xaa Cys Gly Cys Xaa
 100

- (2) INFORMATION FOR SEQ ID NO:5:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 139 amino acids
 - (B) TYPE: amino acids
 - (C) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE:
 - (A) NAME: hOP-1 (mature form)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ser	Thr	Gly	Ser	Lys	Gln	Arg	Ser	Gln
1				5				
Asn	Arg	Ser	Lys	Thr	Pro	Lys	Asn	Gln
10					15			
Glu	Ala	Leu	Arg	Met	Ala	Asn	Val	Ala
	20					25		
Glu	Asn	Ser	Ser	Ser	Asp	Gln	Arg	Gln
		30					35	
Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val
			40					45
Ser	Phe	Arg	Asp	Leu	Gly	Trp	Gln	Asp
				50				
Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala
55					60			
Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
	65					70		

Phe	Pro	Leu	Asn	Ser	Tyr	Met	Asn	Ala
		75					80	
Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu
			85					90
Val	His	Phe	Ile	Asn	Pro	Glu	Thr	Val
				95				
Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln
100					105			
Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr	Phe
	110					115		
Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys
		120					125	
Lys	Tyr	Arg	Asn	Met	Val	Val	Arg	Ala
			130					135
Cys	Gly	Cys	His					

(2)

INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: mOP-1 (mature form)

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

Ser	Thr	Gly	Gly	Lys	Gln	Arg	Ser	Gln
1				5				
Asn	Arg	Ser	Lys	Thr	Pro	Lys	Asn	Gln
10					15			
Glu	Ala	Leu	Arg	Met	Ala	Ser	Val	Ala
	20					25		

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Glu	Asn	Ser	Ser	Ser	Asp	Gln	Arg	Gln
		30					35	
Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val
			40					45
Ser	Phe	Arg	Asp	Leu	Gly	Trp	Gln	Asp
			50					
Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala
55					60			
Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
	65					70		
Phe	Pro	Leu	Asn	Ser	Tyr	Met	Asn	Ala
		75					80	
Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu
			85					90
Val	His	Phe	Ile	Asn	Pro	Asp	Thr	Val
				95				
Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln
100					105			
Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr	Phe
	110					115		
Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys
		120					125	
Lys	Tyr	Arg	Asn	Met	Val	Val	Arg	Ala
			130					135
Cys	Gly	Cys	His					

(2)

INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: hOP-2 (mature form)

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

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

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(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: mOP-2 (mature form)

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

Ala	Ala	Arg	Pro	Leu	Lys	Arg	Arg	Gln
1				5				
Pro	Lys	Lys	Thr	Asn	Glu	Leu	Pro	His
10					15			
Pro	Asn	Lys	Leu	Pro	Gly	Ile	Phe	Asp
	20					25		
Asp	Gly	His	Gly	Ser	Arg	Gly	Arg	Glu
		30					35	
Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
			40					45
Arg	Phe	Arg	Asp	Leu	Gly	Trp	Leu	Asp
				50				
Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
55					60			
Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
	65					70		
Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
		75					80	
Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
			85					90
Val	His	Leu	Met	Lys	Pro	Asp	Val	Val
				95				
Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
100					105			

Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
	110					115		
Asp	Ser	Ser	Asn	Asn	Val	Ile	Leu	Arg
		120					125	
Lys	His	Arg	Asn	Met	Val	Val	Lys	Ala
			130					135
Cys	Gly	Cys	His					

(2)

INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: CBMP-2A(fx)

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

Cys	Lys	Arg	His	Pro	Leu	Tyr	Val	Asp	Phe	Ser
1				5					10	
Asp	Val	Gly	Trp	Asn	Asp	Trp	Ile	Val	Ala	Pro
		15						20		
Pro	Gly	Tyr	His	Ala	Phe	Tyr	Cys	His	Gly	Glu
	25					30				
Cys	Pro	Phe	Pro	Leu	Ala	Asp	His	Leu	Asn	Ser
	35					40				
Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu	Val	Asn
	45				50				55	
Ser	Val	Asn	Ser	Lys	Ile	Pro	Lys	Ala	Cys	Cys
		60						65		
Val	Pro	Thr	Glu	Leu	Ser	Ala	Ile	Ser	Met	Leu
		70					75			
Tyr	Leu	Asp	Glu	Asn	Glu	Lys	Val	Val	Leu	Lys
	80						85			

```

Asn Tyr Gln Asp Met Val Val Glu Gly Cys Gly
      90                               95
Cys Arg
100

```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids
(B) TYPE: amino acids
(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) **FEATURE:**

(A) NAME: CBMP-2B(fx)

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

						Cys	Arg	Arg	His	Ser
						1				5
Leu	Tyr	Val	Asp	Phe	Ser	Asp	Val	Gly	Trp	Asn
				10					15	
Asp	Trp	Ile	Val	Ala	Pro	Pro	Gly	Tyr	Gln	Ala
			20					25		
Phe	Tyr	Cys	His	Gly	Asp	Cys	Pro	Phe	Pro	Leu
		30					35			
Ala	Asp	His	Leu	Asn	Ser	Thr	Asn	His	Ala	Ile
	40					45				
Val	Gln	Thr	Leu	Val	Asn	Ser	Val	Asn	Ser	Ser
50					55					60
Ile	Pro	Lys	Ala	Cys	Cys	Val	Pro	Thr	Glu	Leu
			65						70	
Ser	Ala	Ile	Ser	Met	Leu	Tyr	Leu	Asp	Glu	Tyr
			75					80		
Asp	Lys	Val	Val	Leu	Lys	Asn	Tyr	Gln	Glu	Met
		85						90		

Val Val Glu Gly Cys Gly Cys Arg
95 100

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) **FEATURE:**

(A) NAME: DPP(fx)

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

[illegible]

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: Vgr-1(fx)

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

```

Cys Lys Lys His Glu Leu Tyr Val Ser Phe Gln
 1             5             10
Asp Val Gly Trp Gln Asp Trp Ile Ile Ala Pro
          15             20
Xaa Gly Tyr Ala Ala Asn Tyr Cys Asp Gly Glu
          25             30
Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala
          35             40
Thr Asn His Ala Ile Val Gln Thr Leu Val His
          45             50             55
Val Met Asn Pro Glu Tyr Val Pro Lys Pro Cys
          60             65
Cys Ala Pro Thr Lys Val Asn Ala Ile Ser Val
          70             75
Leu Tyr Phe Asp Asp Asn Ser Asn Val Ile Leu
          80             85
Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys
          90             95
Gly Cys His
100

```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: protein

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(vi) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (F) TISSUE TYPE: BRAIN

(ix) FEATURE:
 (D) OTHER INFORMATION:
 /product= "GDF-1 (fx)"

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

Cys	Arg	Ala	Arg	Arg	Leu	Tyr	Val	Ser	Phe	Arg	Glu	Val	Gly	
1				5					10					
Trp	His	Arg	Trp	Val	Ile	Ala	Pro	Arg	Gly	Phe	Leu	Ala	Asn	Tyr
15				20					25					
Cys	Gln	Gly	Gln	Cys	Ala	Leu	Pro	Val	Ala	Leu	Ser	Gly	Ser	Gly
30				35					40					
Gly	Pro	Pro	Ala	Leu	Asn	His	Ala	Val	Leu	Arg	Ala	Leu	Met	His
45				50					55					
Ala	Ala	Ala	Pro	Gly	Ala	Ala	Asp	Leu	Pro	Cys	Cys	Val	Pro	Ala
60				65					70					
Arg	Leu	Ser	Pro	Ile	Ser	Val	Leu	Phe	Phe	Asp	Asn	Ser	Asp	Asn
75				80					85					
Val	Val	Leu	Arg	Gln	Tyr	Glu	Asp	Met	Val	Val	Asp	Glu	Cys	Gly
90				95					100					
Cys	Arg													
105														

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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

Cys	Xaa	Xaa	Xaa	Xaa
1				5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: HOMO SAPIENS
- (F) TISSUE TYPE: HIPPOCAMPUS

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 49..1341
- (D) OTHER INFORMATION: /standard_name= "hOP1"

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

```

GGTGCGGGCC CGGAGCCCGG AGCCCGGGTA GCGCGTAGAG CCGGCGCG ATG CAC GTG      57
                                   Met His Val
                                   1

CGC TCA CTG CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA      105
Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala
    5                      10                      15

CCC CTG TTC CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC      153
Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn
  20                      25                      30                      35

GAG GTG CAC TCG AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG      201
Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg
                      40                      45                      50

CGG GAG ATG CAG CGC GAG ATC CTC TCC ATT TTG GGC TTG CCC CAC CGC      249
Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg
                      55                      60                      65

CCG CGC CCG CAC CTC CAG GGC AAG CAC AAC TCG GCA CCC ATG TTC ATG      297
Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met
                      70                      75                      80

CTG GAC CTG TAC AAC GCC ATG GCG GTG GAG GAG GGC GGC GGG CCC GGC      345
Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly
    85                      90                      95

GGC CAG GGC TTC TCC TAC CCC TAC AAG GCC GTC TTC AGT ACC CAG GGC      393
Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly
100                      105                      110                      115

```

CCC	CCT	CTG	GCC	AGC	CTG	CAA	GAT	AGC	CAT	TTC	CTC	ACC	GAC	GCC	GAC	441
Pro	Pro	Leu	Ala	Ser	Leu	Gln	Asp	Ser	His	Phe	Leu	Thr	Asp	Ala	Asp	
				120					125					130		
ATG	GTC	ATG	AGC	TTC	GTC	AAC	CTC	GTG	GAA	CAT	GAC	AAG	GAA	TTC	TTC	489
Met	Val	Met	Ser	Phe	Val	Asn	Leu	Val	Glu	His	Asp	Lys	Glu	Phe	Phe	
			135					140					145			
CAC	CCA	CGC	TAC	CAC	CAT	CGA	GAG	TTC	CGG	TTT	GAT	CTT	TCC	AAG	ATC	537
His	Pro	Arg	Tyr	His	His	Arg	Glu	Phe	Arg	Phe	Asp	Leu	Ser	Lys	Ile	
		150					155					160				
CCA	GAA	GGG	GAA	GCT	GTC	ACG	GCA	GCC	GAA	TTC	CGG	ATC	TAC	AAG	GAC	585
Pro	Glu	Gly	Glu	Ala	Val	Thr	Ala	Ala	Glu	Phe	Arg	Ile	Tyr	Lys	Asp	
	165					170					175					
TAC	ATC	CGG	GAA	CGC	TTC	GAC	AAT	GAG	ACG	TTC	CGG	ATC	AGC	GTT	TAT	633
Tyr	Ile	Arg	Glu	Arg	Phe	Asp	Asn	Glu	Thr	Phe	Arg	Ile	Ser	Val	Tyr	
180					185					190					195	
CAG	GTG	CTC	CAG	GAG	CAC	TTG	GGC	AGG	GAA	TCG	GAT	CTC	TTC	CTG	CTC	681
Gln	Val	Leu	Gln	Glu	His	Leu	Gly	Arg	Glu	Ser	Asp	Leu	Phe	Leu	Leu	
				200					205					210		
GAC	AGC	CGT	ACC	CTC	TGG	GCC	TCG	GAG	GAG	GGC	TGG	CTG	GTG	TTT	GAC	729
Asp	Ser	Arg	Thr	Leu	Trp	Ala	Ser	Glu	Glu	Gly	Trp	Leu	Val	Phe	Asp	
			215					220					225			
ATC	ACA	GCC	ACC	AGC	AAC	CAC	TGG	GTG	GTC	AAT	CCG	CGG	CAC	AAC	CTG	777
Ile	Thr	Ala	Thr	Ser	Asn	His	Trp	Val	Val	Asn	Pro	Arg	His	Asn	Leu	
		230					235					240				
GGC	CTG	CAG	CTC	TCG	GTG	GAG	ACG	CTG	GAT	GGG	CAG	AGC	ATC	AAC	CCC	825
Gly	Leu	Gln	Leu	Ser	Val	Glu	Thr	Leu	Asp	Gly	Gln	Ser	Ile	Asn	Pro	
	245					250					255					
AAG	TTG	GCG	GGC	CTG	ATT	GGG	CGG	CAC	GGG	CCC	CAG	AAC	AAG	CAG	CCC	873
Lys	Leu	Ala	Gly	Leu	Ile	Gly	Arg	His	Gly	Pro	Gln	Asn	Lys	Gln	Pro	
260					265					270					275	
TTC	ATG	GTG	GCT	TTC	TTC	AAG	GCC	ACG	GAG	GTC	CAC	TTC	CGC	AGC	ATC	921
Phe	Met	Val	Ala	Phe	Phe	Lys	Ala	Thr	Glu	Val	His	Phe	Arg	Ser	Ile	
				280					285					290		
CGG	TCC	ACG	GGG	AGC	AAA	CAG	CGC	AGC	CAG	AAC	CGC	TCC	AAG	ACG	CCC	969
Arg	Ser	Thr	Gly	Ser	Lys	Gln	Arg	Ser	Gln	Asn	Arg	Ser	Lys	Thr	Pro	
			295					300					305			
AAG	AAC	CAG	GAA	GCC	CTG	CGG	ATG	GCC	AAC	GTG	GCA	GAG	AAC	AGC	AGC	1017
Lys	Asn	Gln	Glu	Ala	Leu	Arg	Met	Ala	Asn	Val	Ala	Glu	Asn	Ser	Ser	
		310					315					320				

AGC GAC CAG AGG CAG GCC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe 325 330 335	1065
CGA GAC CTG GGC TGG CAG GAC TGG ATC ATC GCG CCT GAA GGC TAC GCC Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala 340 345 350 355	1113
GCC TAC TAC TGT GAG GGG GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met 360 365 370	1161
AAC GCC ACC AAC CAC GCC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn 375 380 385	1209
CCG GAA ACG GTG CCC AAG CCC TGC TGT GCG CCC ACG CAG CTC AAT GCC Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Glu Leu Asn Ala 390 395 400	1257
ATC TCC GTC CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC CTG AAG AAA Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys 405 410 415	1305
TAC AGA AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCCTCC Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His 420 425 430	1351
GAGAATTCAG ACCCTTTGGG GCCAAGTTTT TCTGGATCCT CCATTGCTCG CCTTGGCCAG	1411
GAACCAGCAG ACCAACTGCC TTTTGTGAGA CCTTCCCCTC CCTATCCCCA ACTTTAAAGG	1471
TGTGAGAGTA TTAGGAAACA TGAGCAGCAT ATGGCTTTTG ATCAGTTTTT CAGTGGCAGC	1531
ATCCAATGAA CAAGATCCTA CAAGCTGTGC AGGCAAAACC TAGCAGGAAA AAAAAACAAC	1591
GCATAAAGAA AAATGGCCGG GCCAGGTCAT TGGCTGGGAA GTCTCAGCCA TGCACGGACT	1651
CGTTTCCAGA GGTAATTATG AGCGCCTACC AGCCAGGCCA CCCAGCCGTG GGAGGAAGGG	1711
GGCGTGGCAA GGGGTGGGCA CATTGGTGTC TGTGCGAAAG GAAAATTGAC CCGGAAGTTC	1771
CTGTAATAAA TGTCACAATA AAACGAATGA ATGAAAAAAAA AAAAAAAAAA A	1822

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 431 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(D) OTHER INFORMATION: /Product="OP1-PP"

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

Met	His	Val	Arg	Ser	Leu	Arg	Ala	Ala	Ala	Pro	His	Ser	Phe	Val	Ala	1	5	10	15
Leu	Trp	Ala	Pro	Leu	Phe	Leu	Leu	Arg	Ser	Ala	Leu	Ala	Asp	Phe	Ser	20	25	30	
Leu	Asp	Asn	Glu	Val	His	Ser	Ser	Phe	Ile	His	Arg	Arg	Leu	Arg	Ser	35	40	45	
Gln	Glu	Arg	Arg	Glu	Met	Gln	Arg	Glu	Ile	Leu	Ser	Ile	Leu	Gly	Leu	50	55	60	
Pro	His	Arg	Pro	Arg	Pro	His	Leu	Gln	Gly	Lys	His	Asn	Ser	Ala	Pro	65	70	75	80
Met	Phe	Met	Leu	Asp	Leu	Tyr	Asn	Ala	Met	Ala	Val	Glu	Glu	Gly	Gly	85	90	95	
Gly	Pro	Gly	Gly	Gln	Gly	Phe	Ser	Tyr	Pro	Tyr	Lys	Ala	Val	Phe	Ser	100	105	110	
Thr	Gln	Gly	Pro	Pro	Leu	Ala	Ser	Leu	Gln	Asp	Ser	His	Phe	Leu	Thr	115	120	125	
Asp	Ala	Asp	Met	Val	Met	Ser	Phe	Val	Asn	Leu	Val	Glu	His	Asp	Lys	130	135	140	
Glu	Phe	Phe	His	Pro	Arg	Tyr	His	His	Arg	Glu	Phe	Arg	Phe	Asp	Leu	145	150	155	160
Ser	Lys	Ile	Pro	Glu	Gly	Glu	Ala	Val	Thr	Ala	Ala	Glu	Phe	Arg	Ile	165	170	175	
Tyr	Lys	Asp	Tyr	Ile	Arg	Glu	Arg	Phe	Asp	Asn	Glu	Thr	Phe	Arg	Ile	180	185	190	
Ser	Val	Tyr	Gln	Val	Leu	Gln	Glu	His	Leu	Gly	Arg	Glu	Ser	Asp	Leu	195	200	205	
Phe	Leu	Leu	Asp	Ser	Arg	Thr	Leu	Trp	Ala	Ser	Glu	Glu	Gly	Trp	Leu	210	215	220	
Val	Phe	Asp	Ile	Thr	Ala	Thr	Ser	Asn	His	Trp	Val	Val	Asn	Pro	Arg	225	230	235	240
His	Asn	Leu	Gly	Leu	Gln	Leu	Ser	Val	Glu	Thr	Leu	Asp	Gly	Gln	Ser	245	250	255	

Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
 260 265 270
 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
 275 280 285
 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
 290 295 300
 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
 305 310 315 320
 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
 325 330 335
 Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
 340 345 350
 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
 355 360 365
 Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
 370 375 380
 Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
 385 390 395 400
 Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
 405 410 415
 Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
 420 425 430

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1873 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: MURIDAE
 - (F) TISSUE TYPE: EMBRYO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 104..1393
 - (D) OTHER INFORMATION: /note= "MOP1 (CDNA)"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTGCAGCAAG	TGACCTCGGG	TCGTGGACCG	CTGCCCTGCC	CCCTCCGCTG	CCACCTGGGG	60										
CGGCGCGGGC	CCGGTGCCCC	GGATCGCGCG	TAGAGCCGGC	GCG	ATG CAC GTG CGC	115										
					Met His Val Arg											
					1											
TCG	CTG	CGC	GCT	GCG	GCG	CCA	CAC	AGC	TTC	GTG	GCG	CTC	TGG	GCG	CCT	163
Ser	Leu	Arg	Ala	Ala	Ala	Pro	His	Ser	Phe	Val	Ala	Leu	Trp	Ala	Pro	
5					10					15					20	
CTG	TTC	TTG	CTG	CGC	TCC	GCC	CTG	GCC	GAT	TTC	AGC	CTG	GAC	AAC	GAG	211
Leu	Phe	Leu	Leu	Arg	Ser	Ala	Leu	Ala	Asp	Phe	Ser	Leu	Asp	Asn	Glu	
				25					30					35		
GTG	CAC	TCC	AGC	TTC	ATC	CAC	CGG	CGC	CTC	CGC	AGC	CAG	GAG	CGG	CGG	259
Val	His	Ser	Ser	Phe	Ile	His	Arg	Arg	Leu	Arg	Ser	Gln	Glu	Arg	Arg	
			40					45					50			
GAG	ATG	CAG	CGG	GAG	ATC	CTG	TCC	ATC	TTA	GGG	TTG	CCC	CAT	CGC	CCG	307
Glu	Met	Gln	Arg	Glu	Ile	Leu	Ser	Ile	Leu	Gly	Leu	Pro	His	Arg	Pro	
		55				60						65				
CGC	CCG	CAC	CTC	CAG	GGA	AAG	CAT	AAT	TCG	GCG	CCC	ATG	TTC	ATG	TTG	355
Arg	Pro	His	Leu	Gln	Gly	Lys	His	Asn	Ser	Ala	Pro	Met	Phe	Met	Leu	
	70					75					80					
GAC	CTG	TAC	AAC	GCC	ATG	GCG	GTG	GAG	GAG	AGC	GGG	CCG	GAC	GGA	CAG	403
Asp	Leu	Tyr	Asn	Ala	Met	Ala	Val	Glu	Glu	Ser	Gly	Pro	Asp	Gly	Gln	
85					90					95					100	
GGC	TTC	TCC	TAC	CCC	TAC	AAG	GCC	GTC	TTC	AGT	ACC	CAG	GGC	CCC	CCT	451
Gly	Phe	Ser	Tyr	Pro	Tyr	Lys	Ala	Val	Phe	Ser	Thr	Gln	Gly	Pro	Pro	
				105					110					115		
TTA	GCC	AGC	CTG	CAG	GAC	AGC	CAT	TTC	CTC	ACT	GAC	GCC	GAC	ATG	GTC	499
Leu	Ala	Ser	Leu	Gln	Asp	Ser	His	Phe	Leu	Thr	Asp	Ala	Asp	Met	Val	
			120					125					130			
ATG	AGC	TTC	GTC	AAC	CTA	GTG	GAA	CAT	GAC	AAA	GAA	TTC	TTC	CAC	CCT	547
Met	Ser	Phe	Val	Asn	Leu	Val	Glu	His	Asp	Lys	Glu	Phe	Phe	His	Pro	
		135				140						145				
CGA	TAC	CAC	CAT	CGG	GAG	TTC	CGG	TTT	GAT	CTT	TCC	AAG	ATC	CCC	GAG	595
Arg	Tyr	His	His	Arg	Glu	Phe	Arg	Phe	Asp	Leu	Ser	Lys	Ile	Pro	Glu	
	150					155					160					
GGC	GAA	GCG	GTG	ACC	GCA	GCC	GAA	TTC	AGG	ATC	TAT	AAG	GAC	TAC	ATC	643
Gly	Glu	Ala	Val	Thr	Ala	Ala	Glu	Phe	Arg	Ile	Tyr	Lys	Asp	Tyr	Ile	
165					170				175						180	

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

ACA GTA CCC AAG CCC TGC TGT GCG CCC ACC CAG CTC AAC GCC ATC TCT	1315
Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser	
390 395 400	
GTC CTC TAC TTC GAC GAC AGC TCT AAT GTC ATC CTG AAG AAG TAC AGA	1363
Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg	
405 410 415 420	
AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCTTCC TGAGACCCTG	1413
Asn Met Val Val Arg Ala Cys Gly Cys His	
425 430	
ACCTTTGCGG GGCCACACCT TTCCAAATCT TCGATGTCTC ACCATCTAAG TCTCTCACTG	1473
CCCACCTTGG CGAGGAGAAC AGACCAACCT CTCCTGAGCC TTCCCTCACC TCCCAACCGG	1533
AAGCATGTAA GGGTTCCAGA AACCTGAGCG TGCAGCAGCT GATGAGCGCC CTTTCCTTCT	1593
GGCACGTGAC GGACAAGATC CTACCAGCTA CCACAGCAAA CGCCTAAGAG CAGGAAAAAT	1653
GTCTGCCAGG AAAGTGTCCA GTGTCCACAT GGCCCCTGGC GCTCTGAGTC TTTGAGGAGT	1713
AATCGCAAGC CTCGTTCAGC TGCAGCAGAA GGAAGGGCTT AGCCAGGGTG GGCGCTGGCG	1773
TCTGTGTTGA AGGGAAACCA AGCAGAAGCC ACTGTAATGA TATGTCACAA TAAAACCCAT	1833
GAATGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAGAATTC	1873

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 430 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (D) OTHER INFORMATION: /product= "mOP1-PP"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala	
1 5 10 15	
Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser	
20 25 30	
Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser	
35 40 45	

Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
 50 55 60
 Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
 65 70 75 80
 Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Ser Gly
 85 90 95
 Pro Asp Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr
 100 105 110
 Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp
 115 120 125
 Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu
 130 135 140
 Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser
 145 150 155 160
 Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr
 165 170 175
 Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Gln Ile Thr
 180 185 190
 Val Tyr Gln Trp Leu Gln Glu His Ser Gly Arg Glu Ser Asp Leu Phe
 195 200 205
 Leu Leu Asp Ser Arg Thr Ile Trp Ala Ser Glu Glu Gly Trp Leu Val
 210 215 220
 Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His
 225 230 235 240
 Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile
 245 250 255
 Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys
 260 265 270
 Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Leu Arg
 275 280 285
 Ser Ile Arg Ser Thr Gly Gly Lys Gln Arg Ser Gln Asn Arg Ser Lys
 290 295 300
 Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Ser Val Ala Glu Asn
 305 310 315 320
 Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val
 325 330 335

GGCGCCGGCA	GAGCAGGAGT	GGCTGGAGGA	GCTGTGGTTG	GAGCAGGAGG	TGGCACGGCA	60
GGGCTGGAGG	GCTCCCTATG	AGTGGCGGAG	ACGGCCCAGG	AGGCGCTGGA	GCAACAGCTC	120
CCACACCGCA	CCAAGCGGTG	GCTGCAGGAG	CTCGCCCATC	GCCCCTGCGC	TGCTCGGACC	180
GCGGCCACAG	CCGGA CTGGC	GGGTACGGCG	GCGACAGAGG	CATTGGCCGA	GAGTCCCAGT	240
CCGCAGAGTA	GCCCCGGCCT	CGAGGCGGTG	GCGTCCCGGT	CCTCTCCGTC	CAGGAGCCAG	300
GACAGGTGTC	GCGCGGCGGG	GCTCCAGGGA	CCGCGCCTGA	GGCCGGCTGC	CCGCCCGTCC	360
CGCCCCGCCC	CGCCGCCCCG	CGCCGCCCCG	GCCCAGCCTC	CTTGCCGTG	GGGCGTCCCC	420

AGGCCCTGGG TCGGCCGCGG AGCCGATGCG CGCCCGCTGA GCGCCCCAGC TGAGCGCCCC	480
CGGCCTGCC ATG ACC GCG CTC CCC GGC CCG CTC TGG CTC CTG GGC CTG Met Thr Ala Leu Pro Gly Pro Leu Trp Leu Leu Gly Leu 1 5 10	528
GCG CTA TGC GCG CTG GGC GGG GGC GGC CCC GGC CTG CGA CCC CCG CCC Ala Leu Cys Ala Leu Gly Gly Gly Gly Pro Gly Leu Arg Pro Pro Pro 15 20 25	576
GGC TGT CCC CAG CGA CGT CTG GGC GCG CGC GAG CGC CGG GAC GTG CAG Gly Cys Pro Gln Arg Arg Leu Gly Ala Arg Glu Arg Arg Asp Val Gln 30 35 40 45	624
CGC GAG ATC CTG GCG GTG CTC GGG CTG CCT GGG CGG CCC CGG CCC CGC Arg Glu Ile Leu Ala Val Leu Gly Leu Pro Gly Arg Pro Arg Pro Arg 50 55 60	672
GCG CCA CCC GCC GCC TCC CGG CTG CCC GCG TCC GCG CCG CTC TTC ATG Ala Pro Pro Ala Ala Ser Arg Leu Pro Ala Ser Ala Pro Leu Phe Met 65 70 75	720
CTG GAC CTG TAC CAC GCC ATG GCC GGC GAC GAC GAC GAG GAC GGC GCG Leu Asp Leu Tyr His Ala Met Ala Gly Asp Asp Asp Glu Asp Gly Ala 80 85 90	768
CCC GCG GAG CGG CGC CTG GGC CGC GCC GAC CTG GTC ATG AGC TTC GTT Pro Ala Glu Arg Arg Leu Gly Arg Ala Asp Leu Val Met Ser Phe Val 95 100 105	816
AAC ATG GTG GAG CGA GAC CGT GCC CTG GGC CAC CAG GAG CCC CAT TGG Asn Met Val Glu Arg Asp Arg Ala Leu Gly His Gln Glu Pro His Trp 110 115 120 125	864
AAG GAG TTC CGC TTT GAC CTG ACC CAG ATC CCG GCT GGG GAG GCG GTC Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile Pro Ala Gly Glu Ala Val 130 135 140	912
ACA GCT GCG GAG TTC CGG ATT TAC AAG GTG CCC AGC ATC CAC CTG CTC Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val Pro Ser Ile His Leu Leu 145 150 155	960
AAC AGG ACC CTC CAC GTC AGC ATG TTC CAG GTG GTC CAG GAG CAG TCC Asn Arg Thr Leu His Val Ser Met Phe Gln Val Val Gln Glu Gln Ser 160 165 170	1008
AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT CTT CAG ACG CTC CGA GCT Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp Leu Gln Thr Leu Arg Ala 175 180 185	1056
GGA GAC GAG GGC TGG CTG GTG CTG GAT GTC ACA GCA GCC AGT GAC TGC Gly Asp Glu Gly Trp Leu Val Leu Asp Val Thr Ala Ala Ser Asp Cys 190 195 200 205	1104

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TGG Trp	TTG Leu	CTG Leu	AAG Lys	CGT Arg 210	CAC His	AAG Lys	GAC Asp	CTG Leu	GGA Gly 215	CTC Leu	CGC Arg	CTC Leu	TAT Tyr	GTG Val 220	GAG Glu	1152
ACT Thr	GAG Glu	GAC Asp	GGG Gly 225	CAC His	AGC Ser	GTG Val	GAT Asp	CCT Pro 230	GGC Gly	CTG Leu	GCC Ala	GGC Gly	CTG Leu 235	CTG Leu	GGT Gly	1200
CAA Gln	CGG Arg	GCC Ala 240	CCA Pro	CGC Arg	TCC Ser	CAA Gln	CAG Gln 245	CCT Pro	TTC Phe	GTG Val	GTC Val	ACT Thr 250	TTC Phe	TTC Phe	AGG Arg	1248
GCC Ala	AGT Ser 255	CCG Pro	AGT Ser	CCC Pro	ATC Ile	CGC Arg 260	ACC Thr	CCT Pro	CGG Arg	GCA Ala	GTG Val 265	AGG Arg	CCA Pro	CTG Leu	AGG Arg	1296
AGG Arg 270	AGG Arg	CAG Gln	CCG Pro	AAG Lys	AAA Lys 275	AGC Ser	AAC Asn	GAG Glu	CTG Leu	CCG Pro 280	CAG Gln	GCC Ala	AAC Asn	CGA Arg	CTC Leu 285	1344
CCA Pro	GGG Gly	ATC Ile	TTT Phe	GAT Asp 290	GAC Asp	GTC Val	CAC His	GGC Gly	TCC Ser 295	CAC His	GGC Gly	CGG Arg	CAG Gln	GTC Val 300	TGC Cys	1392
CGT Arg	CGG Arg	CAC His	GAG Glu 305	CTC Leu	TAC Tyr	GTC Val	AGC Ser	TTC Phe 310	CAG Gln	GAC Asp	CTC Leu	GGC Gly	TGG Trp 315	CTG Leu	GAC Asp	1440
TGG Trp	GTC Val	ATC Ile 320	GCT Ala	CCC Pro	CAA Gln	GGC Gly	TAC Tyr 325	TCG Ser	GCC Ala	TAT Tyr	TAC Tyr	TGT Cys 330	GAG Glu	GGG Gly	GAG Glu	1488
TGC Cys	TCC Ser 335	TTC Phe	CCA Pro	CTG Leu	GAC Asp	TCC Ser 340	TGC Cys	ATG Met	AAT Asn	GCC Ala	ACC Thr 345	AAC Asn	CAC His	GCC Ala	ATC Ile	1536
CTG Leu 350	CAG Gln	TCC Ser	CTG Leu	GTG Val	CAC His 355	CTG Leu	ATG Met	AAG Lys	CCA Pro	AAC Asn 360	GCA Ala	GTC Val	CCC Pro	AAG Lys	GCG Ala 365	1584
TGC Cys	TGT Cys	GCA Ala	CCC Pro	ACC Thr 370	AAG Lys	CTG Leu	AGC Ser	GCC Ala	ACC Thr 375	TCT Ser	GTG Val	CTC Leu	TAC Tyr	TAT Tyr 380	GAC Asp	1632
AGC Ser	AGC Ser	AAC Asn	AAC Asn 385	GTC Val	ATC Ile	CTG Leu	CGC Arg	AAA Lys 390	CAC His	CGC Arg	AAC Asn	ATG Met	GTG Val 395	GTC Val	AAG Lys	1680
GCC Ala	TGC Cys	GGC Gly 400	TGC Cys	CAC His	T	GAGTCAGCCC	GCCCAGCCCT	ACTGCAG								1723

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) OTHER INFORMATION: /product= "hOP2-PP"

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

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

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Lys Arg His Lys Asp Leu Gly Leu Arg Leu Tyr Val Glu Thr Glu Asp
 210 215 220
 Gly His Ser Val Asp Pro Gly Leu Ala Gly Leu Leu Gly Gln Arg Ala
 225 230 235 240
 Pro Arg Ser Gln Gln Pro Phe Val Val Thr Phe Phe Arg Ala Ser Pro
 245 250 255
 Ser Pro Ile Arg Thr Pro Arg Ala Val Arg Pro Leu Arg Arg Arg Gln
 260 265 270
 Pro Lys Lys Ser Asn Glu Leu Pro Gln Ala Asn Arg Leu Pro Gly Ile
 275 280 285
 Phe Asp Asp Val His Gly Ser His Gly Arg Gln Val Cys Arg Arg His
 290 295 300
 Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp Trp Val Ile
 305 310 315 320
 Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly Glu Cys Ser Phe
 325 330 335
 Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala Ile Leu Gln Ser
 340 345 350
 Leu Val His Leu Met Lys Pro Asn Ala Val Pro Lys Ala Cys Cys Ala
 355 360 365
 Pro Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn
 370 375 380
 Asn Val Ile Leu Arg Lys His Arg Asn Met Val Val Lys Ala Cys Gly
 385 390 395 400
 Cys His

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1926 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: MURIDAE
 - (F) TISSUE TYPE: EMBRYO

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 93..1289
 (D) OTHER INFORMATION: /note= "mOP2 cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCCAGGCACA GGTGCGCCGT CTGGTCCTCC CCGTCTGGCG TCAGCCGAGC	50
CCGACCAGCT ACCAGTGGAT GCGCGCCGGC TGAAAGTCCG AG ATG GCT ATG CGT	104
Met Ala Met Arg	
1	
CCC GGG CCA CTC TGG CTA TTG GGC CTT GCT CTG TGC GCG CTG GGA GGC	152
Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu Cys Ala Leu Gly Gly	
5 10 15 20	
GGC CAC GGT CCG CGT CCC CCG CAC ACC TGT CCC CAG CGT CGC CTG GGA	200
Gly His Gly Pro Arg Pro Pro His Thr Cys Pro Gln Arg Arg Leu Gly	
25 30 35	
GCG CGC GAG CGC CGC GAC ATG CAG CGT GAA ATC CTG GCG GTG CTC GGG	248
Ala Arg Glu Arg Arg Asp Met Gln Arg Glu Ile Leu Pro Val Leu Gly	
40 45 50	
CTA CCG GGA CGG CCC CGA CCC CGT GCA CAA CCC GCG GCT GCC CGG CAG	296
Leu Pro Gly Arg Pro Arg Pro Arg Ala Gln Pro Ala Ala Ala Arg Gln	
55 60 65	
CCA GCG TCC GCG CCC CTC TTC ATG TTG GAC CTA TAC CAC GCC ATG ACC	344
Pro Ala Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr His Ala Met Thr	
70 75 80	
GAT GAC GAC GAC GGC GGG CCA CCA CAG GCT CAC TTA GGC CGT GCC GAC	392
Asp Asp Asp Asp Gly Gly Pro Pro Gln Ala His Leu Gly Arg Ala Asp	
85 90 95 100	
CTG GTC ATG AGC TTC GTC AAC ATG GTG GAA CGC GAC CGT ACC CTG GGC	440
Leu Val Met Ser Phe Val Asn Met Val Glu Arg Asp Arg Thr Leu Gly	
105 110 115	
TAC CAG GAG CCA CAC TGG AAG GAA TTC CAC TTT GAC CTA ACC CAG ATC	488
Tyr Gln Glu Pro His Trp Lys Glu Phe His Phe Asp Leu Thr Gln Ile	
120 125 130	
CCT GCT GGG GAG GCT GTC ACA GCT GCT GAG TTC CGG ATC TAC AAA GAA	536
Pro Ala Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Glu	
135 140 145	
CCC AGC ACC CAC CCG CTC AAC ACA ACC CTC CAC ATC AGC ATG TTC GAA	584
Pro Ser Thr His Pro Leu Asn Thr Thr Leu His Ile Ser Met Phe Glu	
150 155 160	

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GTG Val 165	GTC Val	CAA Gln	GAG Glu	CAC His	TCC Ser 170	AAC Asn	AGG Arg	GAG Glu	TCT Ser	GAC Asp 175	TTG Leu	TTC Phe	TTT Phe	TTG Leu	GAT Asp 180	632
CTT Leu	CAG Gln	ACG Thr	CTC Leu	CGA Arg 185	TCT Ser	GGG Gly	GAC Asp	GAG Glu	GGC Gly 190	TGG Trp	CTG Leu	GTG Val	CTG Leu	GAC Asp 195	ATC Ile	680
ACA Thr	GCA Ala	GCC Ala	AGT Ser 200	GAC Asp	CGA Arg	TGG Trp	CTG Leu	CTG Leu 205	AAC Asn	CAT His	CAC His	AAG Lys	GAC Asp 210	CTG Leu	GGA Gly	728
CTC Leu	CGC Arg	CTC Leu 215	TAT Tyr	GTG Val	GAA Glu	ACC Thr	GCG Ala 220	GAT Asp	GGG Gly	CAC His	AGC Ser	ATG Met 225	GAT Asp	CCT Pro	GGC Gly	776
CTG Leu 230	GCT Ala	GGT Gly	CTG Leu	CTT Leu	GGA Gly	CGA Arg 235	CAA Gln	GCA Ala	CCA Pro	CGC Arg	TCC Ser 240	AGA Arg	CAG Gln	CCT Pro	TTC Phe	824
ATG Met 245	GTA Val	ACC Thr	TTC Phe	TTC Phe	AGG Arg 250	GCC Ala	AGC Ser	CAG Gln	AGT Ser	CCT Pro 255	GTG Val	CGG Arg	GCC Ala	CCT Pro	CGG Arg 260	872
GCA Ala	GCG Ala	AGA Arg	CCA Pro	CTG Leu 265	AAG Lys	AGG Arg	AGG Arg	CAG Gln	CCA Pro 270	AAG Lys	AAA Lys	ACG Thr	AAC Asn	GAG Glu 275	CTT Leu	920
CCG Pro	CAC His	CCC Pro	AAC Asn 280	AAA Lys	CTC Leu	CCA Pro	GGG Gly	ATC Ile 285	TTT Phe	GAT Asp	GAT Asp	GGC Gly	CAC His 290	GGT Gly	TCC Ser	968
CGC Arg	GGC Gly	AGA Arg 295	GAG Glu	GTT Val	TGC Cys	CGC Arg	AGG Arg 300	CAT His	GAG Glu	CTC Leu	TAC Tyr	GTC Val 305	AGC Ser	TTC Phe	CGT Arg	1016
GAC Asp 310	CTT Leu	GGC Gly	TGG Trp	CTG Leu	GAC Asp	TGG Trp 315	GTC Val	ATC Ile	GCC Ala	CCC Pro	CAG Gln 320	GGC Gly	TAC Tyr	TCT Ser	GCC Ala	1064
TAT Tyr 325	TAC Tyr	TGT Cys	GAG Glu	GGG Gly	GAG Glu 330	TGT Cys	GCT Ala	TTC Phe	CCA Pro	CTG Leu 335	GAC Asp	TCC Ser	TGT Cys	ATG Met	AAC Asn 340	1112
GCC Ala	ACC Thr	AAC Asn	CAT His	GCC Ala 345	ATC Ile	TTG Leu	CAG Gln	TCT Ser	CTG Leu 350	GTG Val	CAC His	CTG Leu	ATG Met	AAG Lys 355	CCA Pro	1160
GAT Asp	GTT Val	GTC Val	CCC Pro 360	AAG Lys	GCA Ala	TGC Cys	TGT Cys	GCA Ala 365	CCC Pro	ACC Thr	AAA Lys	CTG Leu	AGT Ser 370	GCC Ala	ACC Thr	1208

TCT GTG CTG TAC TAT GAC AGC AGC AAC AAT GTC ATC CTG CGT AAA CAC	1256
Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His	
375 380 385	
CGT AAC ATG GTG GTC AAG GCC TGT GGC TGC CAC TGAGGCCCG CCCAGCATCC	1309
Arg Asn Met Val Val Lys Ala Cys Gly Cys His	
390 395	
TGCTTCTACT ACCTTACCAT CTGGCCGGGC CCCTCTCCAG AGGCAGAAAC CCTTCTATGT	1369
TATCATAGCT CAGACAGGGG CAATGGGAGG CCCTTCACTT CCCCTGGCCA CTCCTGCTA	1429
AAATTCTGGT CTTTCCCAGT TCCTCTGTCC TTCATGGGGT TTCGGGGCTA TCACCCCGCC	1489
CTCTCCATCC TCCTACCCCA AGCATAGACT GAATGCACAC AGCATCCCAG AGCTATGCTA	1549
ACTGAGAGGT CTGGGGTCAG CACTGAAGGC CCACATGAGG AAGACTGATC CTTGGCCATC	1609
CTCAGCCCAC AATGGCAAAT TCTGGATGGT CTAAGAAGGC CGTGGAATTC TAAACTAGAT	1669
GATCTGGGCT CTCTGCACCA TTCATTGTGG CAGTTGGGAC ATTTTITAGGT ATAACAGACA	1729
CATACACTTA GATCAATGCA TCGCTGTACT CCTTGAAATC AGAGCTAGCT TGTTAGAAAA	1789
AGAATCAGAG CCAGGTATAG CGGTGCATGT CATTAAATCCC AGCGCTAAAG AGACAGAGAC	1849
AGGAGAATCT CTGTGAGTTC AAGGCCACAT AGAAAGAGCC TGTCTCGGGA GCAGGAAAAA	1909
AAAAAAAAAC GGAATTC	1926

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (D) OTHER INFORMATION: /product= "mOP2-PP"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met	Ala	Met	Arg	Pro	Gly	Pro	Leu	Trp	Leu	Leu	Gly	Leu	Ala	Leu	Cys	
1				5					10					15		
Ala	Leu	Gly	Gly	Gly	His	Gly	Pro	Arg	Pro	Pro	His	Thr	Cys	Pro	Gln	
		20						25					30			
Arg	Arg	Leu	Gly	Ala	Arg	Glu	Arg	Arg	Asp	Met	Gln	Arg	Glu	Ile	Leu	Ala
		35					40					45				

Val Leu Gly Leu Pro Gly Arg Pro Arg Pro Arg Ala Gln Pro Ala Ala
 50 55 60 65
 Ala Arg Gln Pro Ala Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr His Ala
 70 75 80
 Met Thr Asp Asp Asp Asp Gly Gly Pro Pro Gln Ala His Leu Gly Arg
 85 90 95
 Ala Asp Leu Val Met Ser Phe Val Asn Met Val Glu Arg Asp Arg Thr
 100 105 110
 Leu Gly Tyr Gln Glu Pro His Trp Lys Glu Phe His Phe Asp Leu Thr
 115 120 125 130
 Gln Ile Pro Ala Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr
 135 140 145
 Lys Glu Pro Ser Thr His Pro Leu Asn Thr Thr Leu His Ile Ser Met
 150 155 160
 Phe Glu Val Val Gln Glu His Ser Asn Arg Glu Ser Asp Leu Phe Phe
 165 170 175
 Leu Asp Leu Gln Thr Leu Arg Ser Gly Asp Glu Gly Trp Leu Val Leu
 180 185 190
 Asp Ile Thr Ala Ala Ser Asp Arg Trp Leu Leu Asn His His Lys Asp
 195 200 205 210
 Leu Gly Leu Arg Leu Tyr Val Glu Thr Ala Asp Gly His Ser Met Asp
 215 220 225
 Pro Gly Leu Ala Gly Leu Leu Gly Arg Gln Ala Pro Arg Ser Arg Gln
 230 235 240
 Pro Phe Met Val Thr Phe Phe Arg Ala Ser Gln Ser Pro Val Arg Ala
 245 250 255
 Pro Arg Ala Ala Arg Pro Leu Lys Arg Arg Gln Pro Lys Lys Thr Asn
 260 265 270
 Glu Leu Pro His Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp Gly His
 275 280 285 290
 Gly Ser Arg Gly Arg Glu Val Cys Arg Arg His Glu Leu Tyr Val Ser
 295 300 305
 Phe Arg Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr
 310 315 320

Ser Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asp Ser Cys
325 330 335

Met Asn Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met
340 345 350

Lys Pro Asp Val Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser
355 360 365 370

Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg
375 380 385

Lys His Arg Asn Met Val Val Lys Ala Cys Gly Cys His
390 395

We claim:

1. A composition comprising a morphogen and isolated mammalian progenitor cells, said morphogen comprising a dimeric protein that induces tissue-specific morphogenesis in a mammal and comprises a pair of folded polypeptides, the amino acid sequence of each of which comprises
 - (a) a sequence sharing at least 70% homology with the C-terminal seven-cysteine domain of human OP-1, mouse OP-1, human OP-2 or mouse OP-2, which correspond to residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8, respectively; or
 - (b) an essentially 102 amino acid sequence having cysteine residues at relative positions 1, 30, 34, 66, 67, 99 and 101 therein, wherein at least 70% of amino acid residues within said sequence are selected independently from residues occupying the corresponding positions within residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8, or conservative substitutions of said corresponding residues.
2. A composition comprising a morphogen and isolated mammalian progenitor cells, stimulated ex vivo by exposure to said morphogen at a concentration and for a time sufficient such that said progenitor cells, when disposed in vivo within a non-cartilaginous mammalian tissue locus, are capable of non-chondrogenic tissue-specific differentiation and proliferation within said locus, said morphogen comprising a dimeric protein that induces tissue-specific morphogenesis in a mammal and comprises a pair of folded polypeptides, the amino acid sequence of each of which comprises
 - (a) a sequence sharing at least 70% homology with the C-terminal seven-cysteine domain of human OP-1, mouse OP-1, human OP-2 or mouse OP-2, which correspond to residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8, respectively; or
 - (b) an essentially 102 amino acid sequence having cysteine residues at relative positions 1, 30, 34, 66, 67, 99 and 101 therein, wherein at least 70% of amino acid residues within said sequence are selected

independently from residues occupying the corresponding positions within residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8, or conservative substitutions of said corresponding residues.

3. The composition of claim 1 or 2 wherein said progenitor cells are hemopoietic pluripotential stem cells.
4. The composition of claim 1 or 2 wherein said progenitor cells are of mesenchymal origin.
5. A composition for inducing the formation of non-chondrogenic replacement tissue at a noncartilaginous tissue locus in a mammal comprising:
 - a biocompatible, acellular matrix having components specific for said tissue and capable of providing a morphogenically permissive, tissue-specific environment; and
 - a morphogen absorbed on said matrix at a concentration sufficient for inducing a developmental cascade of tissue-specific morphogenesis at said locus, said morphogen comprising a dimeric protein that induces tissue-specific morphogenesis in a mammal and comprises a pair of folded polypeptides, the amino acid sequence of each of which comprises
 - (a) a sequence sharing at least 70% homology with the C-terminal seven-cysteine domain of human OP-1, mouse OP-1, human OP-2 or mouse OP-2, which correspond to residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8, respectively; or
 - (b) an essentially 102 amino acid sequence having cysteine residues at relative positions 1, 30, 34, 66, 67, 99 and 101 therein, wherein at least 70% of amino acid residues within said sequence are selected independently from residues occupying the corresponding positions within

residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8, or conservative substitutions of said corresponding residues.

6. A composition for inducing the formation of non-chondrogenic replacement tissue at a noncartilaginous tissue locus in a mammal comprising:

a biocompatible, acellular matrix capable of providing a morphogenically permissive environment; and

a morphogen absorbed on said matrix at a concentration sufficient for inducing a developmental cascade of tissue-specific morphogenesis at said locus,

said morphogen comprising a dimeric protein that induces tissue-specific morphogenesis in a mammal and comprises a pair of folded polypeptides, the amino acid sequence of each of which comprises
 - (a) a sequence sharing at least 70% homology with the C-terminal seven-cysteine domain of human OP-1, mouse OP-1, human OP-2 or mouse OP-2, which correspond to residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8, respectively; or
 - (b) an essentially 102 amino acid sequence having cysteine residues at relative positions 1, 30, 34, 66, 67, 99 and 101 therein, wherein at least 70% of amino acid residues within said sequence are selected independently from residues occupying the corresponding positions within residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8, or conservative substitutions of said corresponding residues.
7. The composition of claim 5 or 6 wherein said matrix is biodegradable.
8. The composition of claim 5 or 6 wherein said matrix is derived from organ-specific tissue.

9. The composition of claim 5 or 6 wherein said matrix comprises collagen and cell attachment factors selected from the group consisting of glycosaminoglycans and proteoglycans.
10. The composition of claim 5 or 6 wherein said matrix defines pores of a dimension sufficient to permit the influx, differentiation and proliferation of migratory progenitor cells from the body of said mammal.
11. The composition of claim 1, 2, 5 or 6 wherein the sequences of said morphogen polypeptides comprise:
 - (a) an amino acid sequence sharing at least 80% homology with the sequence of one of said C-terminal seven cysteine domains; or
 - (b) an essentially 102 amino acid sequence having said cysteine residues and wherein at least 80% of amino acid residues are selected independently from said corresponding residues of said C-terminal seven cysteine domains or are conservative substitutions thereof.
12. The composition of claim 11 wherein the sequences of said morphogen polypeptides comprise an amino acid sequence having greater than 60% amino acid identity with the sequence of one of said C-terminal seven cysteine domains.
13. The composition of claim 12 wherein the sequences of said morphogen polypeptides comprise an amino acid sequence having greater than 65% identity with the sequence of one of said C-terminal seven cysteine domains.
14. The composition of claim 1, 2, 5 or 6 wherein the sequences of said morphogen polypeptides each comprise a sequence selected from residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8 or naturally occurring or biosynthetic variants thereof.

15. The composition of claim 1, 2, 5 or 6 wherein said essentially 102 amino acid sequence has at least 101 amino acids.
16. The composition of claim 1, 2, 5 or 6 wherein said essentially 102 amino acid sequence has at most 106 amino acids.
17. The composition of claim 1, 2, 5 or 6 wherein the sequences of said morphogen polypeptides each comprise an amino acid sequence selected from Seq. ID Nos. 9, 10, 11, 12, 13 or 14 (which correspond to CBMP2A(fx), CBMP2B(fx), DPP(fx), Vgl(fx), Vgr-1(fx) or GDF-1(f), respectively), or naturally occurring or biosynthetic variants thereof.
18. The composition of claim 14 wherein the sequences of said morphogen polypeptides each further comprise an amino acid sequence selected from residues 1-37 of Seq. ID Nos. 5, 6, 7 or 8, or naturally occurring or biosynthetic variants thereof, such that the sequences of said polypeptides each comprise a sequence selected from residues 1-139 of Seq. ID Nos. 5, 6, 7 or 8 or naturally occurring or biosynthetic variants thereof.
19. A method of increasing a population of mammalian progenitor cells ex vivo, comprising the step of:

contacting isolated mammalian progenitor cells with a morphogen at a concentration and for a time sufficient such that said progenitor cells are stimulated to proliferate, said morphogen comprising a dimeric protein that induces tissue-specific morphogenesis in a mammal and comprises a pair of folded polypeptides, the amino acid sequence of each of which comprises
 - (a) a sequence sharing at least 70% homology with the C-terminal seven-cysteine domain of human OP-1, mouse OP-1, human OP-2 or mouse OP-2, which correspond to residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8, respectively; or

(b) an essentially 102 amino acid sequence having cysteine residues at relative positions 1, 30, 34, 66, 67, 99 and 101 therein, wherein at least 70% of amino acid residues within said sequence are selected independently from residues occupying the corresponding positions within residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8, or conservative substitutions of said corresponding residues; and,

maintaining said stimulated progenitor cells under conditions sufficient for said cells to proliferate, such that the population thereof increases.

20. The method of claim 19 wherein said progenitor cells are of mesenchymal origin.

21. A method of inhibiting senescence-associated loss of phenotype or function of differentiated mammalian cells ex vivo, comprising the steps of:

contacting said differentiated cells with a morphogen at a concentration and for a time sufficient to inhibit or delay senescence or quiescence of said cells, said morphogen comprising a dimeric protein that induces tissue-specific morphogenesis in a mammal and comprises a pair of folded polypeptides, the amino acid sequence of each of which comprises

(a) a sequence sharing at least 70% homology with the C-terminal seven-cysteine domain of human OP-1, mouse OP-1, human OP-2 or mouse OP-2, which correspond to residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8, respectively; or

(b) an essentially 102 amino acid sequence having cysteine residues at relative positions 1, 30, 34, 66, 67, 99 and 101 therein, wherein at least 70% of amino acid residues within said sequence are selected independently from residues occupying the corresponding positions within residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8, or conservative substitutions of said corresponding residues; and

maintaining said cells under conditions wherein, in the absence of morphogen, said cells would become senescent or quiescent.

22. A method of restoring phenotype or tissue-specific function to differentiated, senescent or quiescent mammalian cells ex vivo, comprising the steps of contacting said cells with a morphogen at a concentration and for a time sufficient to stimulate said cells to reexpress tissue-specific phenotype or function, said morphogen comprising a dimeric protein that induces tissue-specific morphogenesis in a mammal and comprises a pair of folded polypeptides, the amino acid sequence of each of which comprises

- (a) a sequence sharing at least 70% homology with the C-terminal seven-cysteine domain of human OP-1, mouse OP-1, human OP-2 or mouse OP-2, which correspond to residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8, respectively; or
- (b) an essentially 102 amino acid sequence having cysteine residues at relative positions 1, 30, 34, 66, 67, 99 and 101 therein, wherein at least 70% of amino acid residues within said sequence are selected independently from residues occupying the corresponding positions within residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8, or conservative substitutions of said corresponding residues; and

maintaining said cells under conditions wherein, in the absence of morphogen, said cells would fail to express said phenotype or function.

23. A method for diagnosing tissue dysfunction in a human, the method comprising the steps of :
- (a) detecting the presence in said human of an endogenous antibody that binds to a morphogen. said morphogen comprising a dimeric protein that induces tissue-

specific morphogenesis in a mammal and comprises a pair of folded polypeptides, the amino acid sequence of each of which comprises

- (A) a sequence sharing at least 70% homology with the C-terminal seven-cysteine domain of human OP-1, mouse OP-1, human OP-2 or mouse OP-2, which correspond to residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8, respectively; or
- (B) an essentially 102 amino acid sequence having cysteine residues at relative positions 1, 30, 34, 66, 67, 99 and 101 therein, wherein at least 70% of amino acid residues within said sequence are selected independently from residues occupying the corresponding positions within residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8, or conservative substitutions of said corresponding residues;
- (b) repeating said detection step, after a time interval has elapsed; and
- (c) comparing said detected concentrations, wherein a change in the detected concentrations is indicative of said tissue dysfunction.

24. A method for evaluating injury or dysfunction of a mammalian tissue, the method comprising the step of:

- (a) detecting presence of a morphogen in said tissue, said morphogen comprising a dimeric protein that induces tissue-specific morphogenesis in a mammal and comprises a pair of folded polypeptides, the amino acid sequence of each of which comprises

- (A) a sequence sharing at least 70% homology with the C-terminal seven-cysteine domain of human OP-1, mouse OP-1, human OP-2 or mouse OP-2, which correspond to residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8, respectively; or

- (B) an essentially 102 amino acid sequence having cysteine residues at relative positions 1, 30, 34, 66, 67, 99 and 101 therein, wherein at least 70% of amino acid residues within said sequence are selected independently from residues occupying the corresponding positions within residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8, or conservative substitutions of said corresponding residues; and
- (b) assessing whether morphogen detected in said tissue differs from a level thereof detected in uninjured or normally functional tissue, a difference whereof is indicative of said injury or dysfunction.
25. The method of claim 24 comprising the additional steps of:
- (c) repeating said detection step, after a time interval has elapsed; and
- (d) comparing said detected concentrations, wherein a change in said detected concentrations is indicative of a change in the status of injury or dysfunction in said tissue.
26. The method of claim 19, 21, 22, 23, 24, or 25 wherein the sequences of said morphogen polypeptides comprise an amino acid sequence having greater than 60% amino acid identity with the sequence of one of said C-terminal seven cysteine domains.
27. The method of claim 19, 21, 22, 23, 24, or 25 wherein said essentially 102 amino acid sequence has at least 101 amino acids.
28. The method of claim 19, 21, 22, 23, 24, or 25 wherein said essentially 102 amino acid sequence has at most 106 amino acids.
29. The method of claim 19, 21, 22, 23, 24, or 25 wherein the sequences of said morphogen polypeptides each comprise a sequence selected from residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8 or naturally occurring or biosynthetic variants thereof.

30. The method of claim 19, 21, 22, 23, 24, or 25 wherein the sequences of said morphogen polypeptides each comprise an amino acid sequence selected from Seq. ID Nos. 9, 10, 11, 12, 13 or 14 (which correspond to CBMP2A(fx), CBMP2B(fx), DPP(fx), Vgl(fx), Vgr-1(fx) or GDF-1(f), respectively), or naturally occurring or biosynthetic variants thereof.
31. The method of claim 29 wherein the sequences of said morphogen polypeptides each further comprise an amino acid sequence selected from residues 1-37 of Seq. ID Nos. 5, 6, 7 or 8, or naturally occurring or biosynthetic variants thereof, such that the sequences of said polypeptides each comprise a sequence selected from residues 1-139 of Seq. ID Nos. 5, 6, 7 or 8 or naturally occurring or biosynthetic variants thereof.
32. Use of a morphogen for the manufacture of a pharmaceutical for inducing non-chondrogenic morphogenesis of mammalian tissue, said morphogen comprising a dimeric protein that induces tissue-specific morphogenesis in a mammal and comprises a pair of folded polypeptides, the amino acid sequence of each of which comprises
- (a) a sequence sharing at least 70% homology with the C-terminal seven-cysteine domain of human OP-1, mouse OP-1, human OP-2 or mouse OP-2, which correspond to residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8, respectively; or
 - (b) an essentially 102 amino acid sequence having cysteine residues at relative positions 1, 30, 34, 66, 67, 99 and 101 therein, wherein at least 70% of amino acid residues within said sequence are selected independently from residues occupying the corresponding positions within residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8, or conservative substitutions of said corresponding residues.
33. Use of a morphogen for the manufacture of a pharmaceutical for inducing proliferation ex vivo of mammalian progenitor cells, said morphogen comprising a dimeric protein that induces tissue-specific morphogenesis in a mammal and

comprises a pair of folded polypeptides, the amino acid sequence of each of which comprises

- (a) a sequence sharing at least 70% homology with the C-terminal seven-cysteine domain of human OP-1, mouse OP-1, human OP-2 or mouse OP-2, which correspond to residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8, respectively; or
- (b) an essentially 102 amino acid sequence having cysteine residues at relative positions 1, 30, 34, 66, 67, 99 and 101 therein, wherein at least 70% of amino acid residues within said sequence are selected independently from residues occupying the corresponding positions within residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8, or conservative substitutions of said corresponding residues.

- 34. Use of a morphogen for the manufacture of a pharmaceutical for inhibiting senescence-associated loss of phenotype or function of differentiated mammalian cells, said morphogen comprising a dimeric protein that induces tissue-specific morphogenesis in a mammal and comprises a pair of folded polypeptides, the amino acid sequence of each of which comprises
 - (a) a sequence sharing at least 70% homology with the C-terminal seven-cysteine domain of human OP-1, mouse OP-1, human OP-2 or mouse OP-2, which correspond to residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8, respectively; or
 - (b) an essentially 102 amino acid sequence having cysteine residues at relative positions 1, 30, 34, 66, 67, 99 and 101 therein, wherein at least 70% of amino acid residues within said sequence are selected independently from residues occupying the corresponding positions within residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8, or conservative substitutions of said corresponding residues.
- 35. Use of a morphogen for the manufacture of a pharmaceutical for restoring phenotype or tissue-specific function to differentiated, senescent or quiescent mammalian cells, said morphogen comprising a dimeric protein that induces

tissue-specific morphogenesis in a mammal and comprises a pair of folded polypeptides, the amino acid sequence of each of which comprises

- (a) a sequence sharing at least 70% homology with the C-terminal seven-cysteine domain of human OP-1, mouse OP-1, human OP-2 or mouse OP-2, which correspond to residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8, respectively; or
 - (b) an essentially 102 amino acid sequence having cysteine residues at relative positions 1, 30, 34, 66, 67, 99 and 101 therein, wherein at least 70% of amino acid residues within said sequence are selected independently from residues occupying the corresponding positions within residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8, or conservative substitutions of said corresponding residues.
36. Use according to claim 32, 33, 34 or 35 wherein the sequences of said morphogen polypeptides comprise an amino acid sequence having greater than 60% amino acid identity with the sequence of one of said C-terminal seven cysteine domains.
37. Use according to claim 32, 33, 34 or 35 wherein said essentially 102 amino acid sequence has at least 101 amino acids.
38. Use according to claim 32, 33, 34 or 35 wherein said essentially 102 amino acid sequence has at most 106 amino acids.
39. Use according to claim 32, 33, 34 or 35 wherein the sequences of said morphogen polypeptides each comprise a sequence selected from residues 38-139 of Seq. ID. No. 5, 6, 7 or 8, or naturally occurring or biosynthetic variants thereof.
40. Use according to claim 32, 33, 34 or 35 wherein the sequences of said morphogen polypeptides each comprise an amino acid sequence selected from Seq. ID Nos. 9.

10, 11, 12, 13 or 14 (CBMP2A(fx), CBMP2B(fx), DPP(fx), Vgl(fx), Vgr-1(fx) or GDF-1(f)), or naturally occurring or biosynthetic variants thereof.

41. Use according to claim 39 wherein the sequences of said morphogen polypeptides each further comprise an amino acid sequence selected from residues 1-37 of Seq. ID Nos. 5, 6, 7 or 8, or naturally occurring or biosynthetic variants thereof, such that the sequences of said polypeptides each comprise a sequence selected from residues 1-139 of Seq. ID No. 5, 6, 7 or 8, or naturally occurring or biosynthetic variants thereof.

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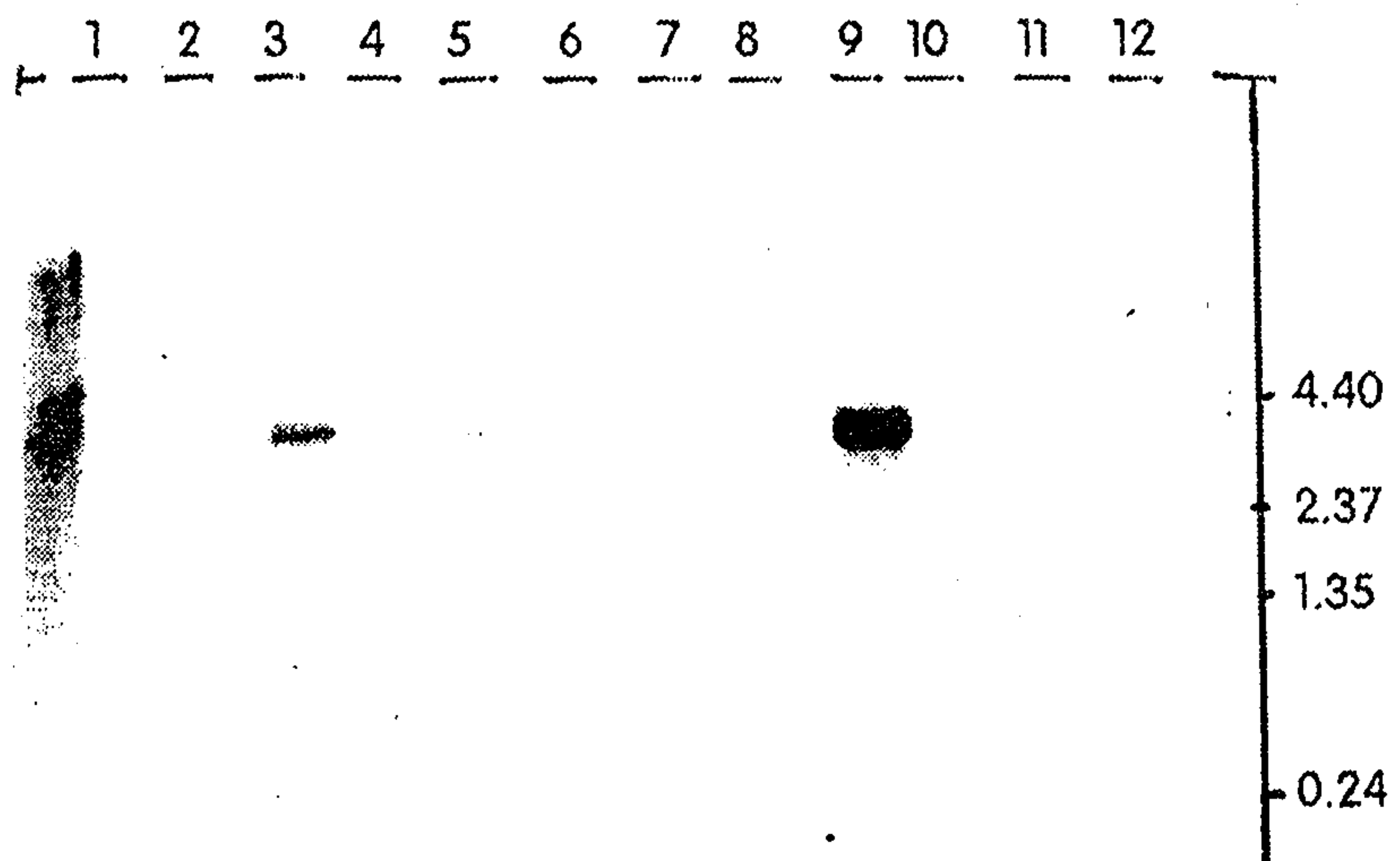


Fig. 1

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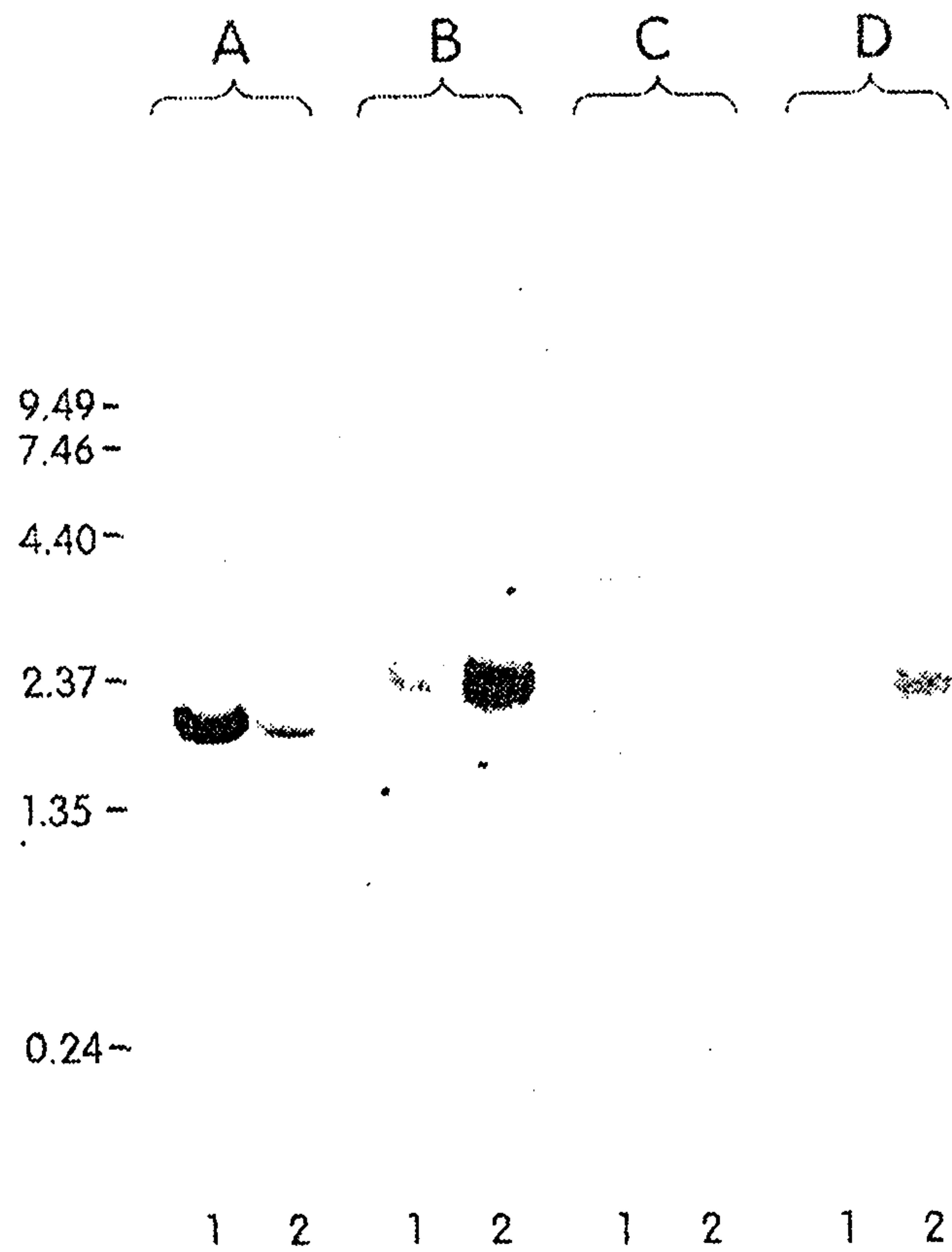


Fig. 2

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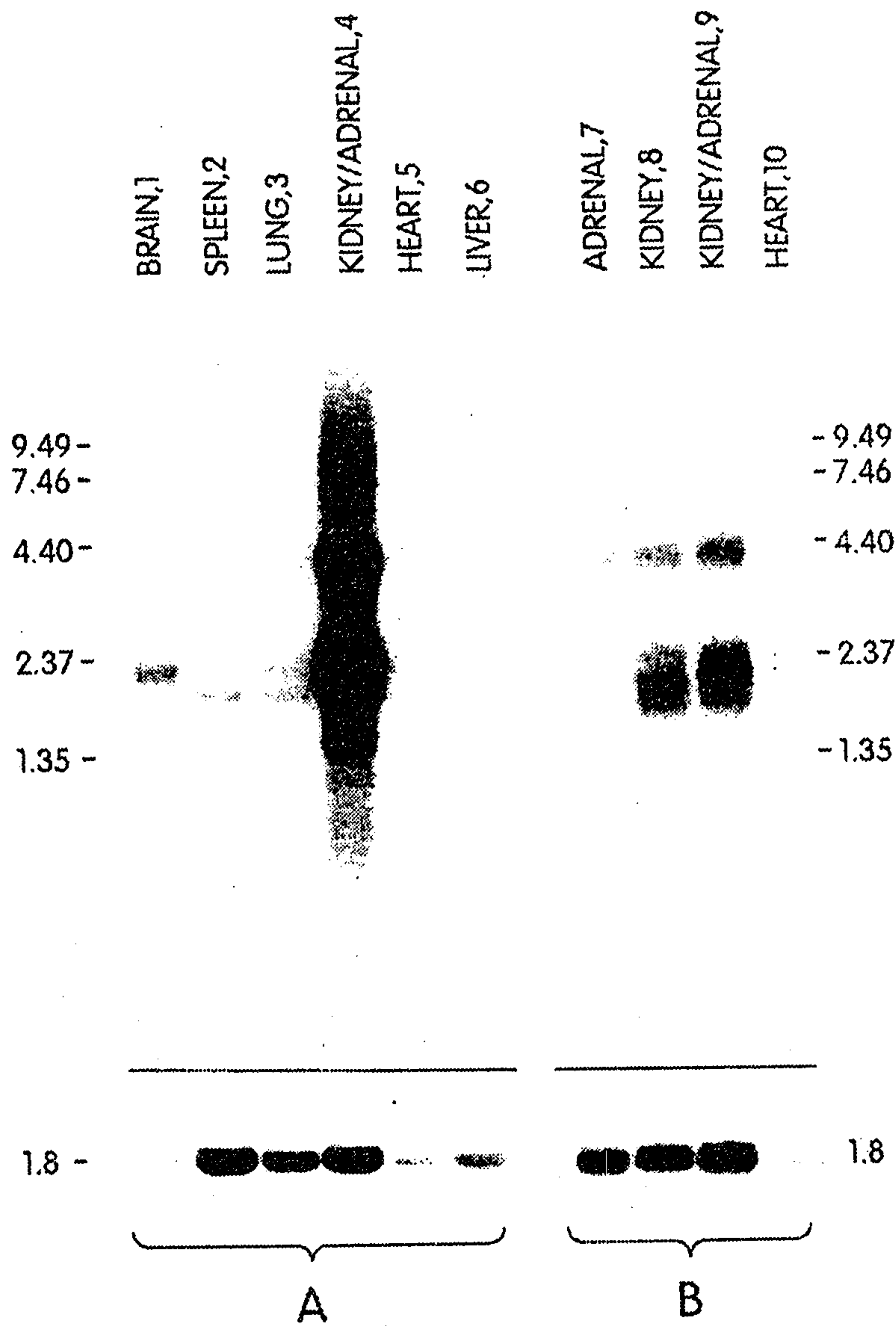


Fig. 3

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Fig. 4A

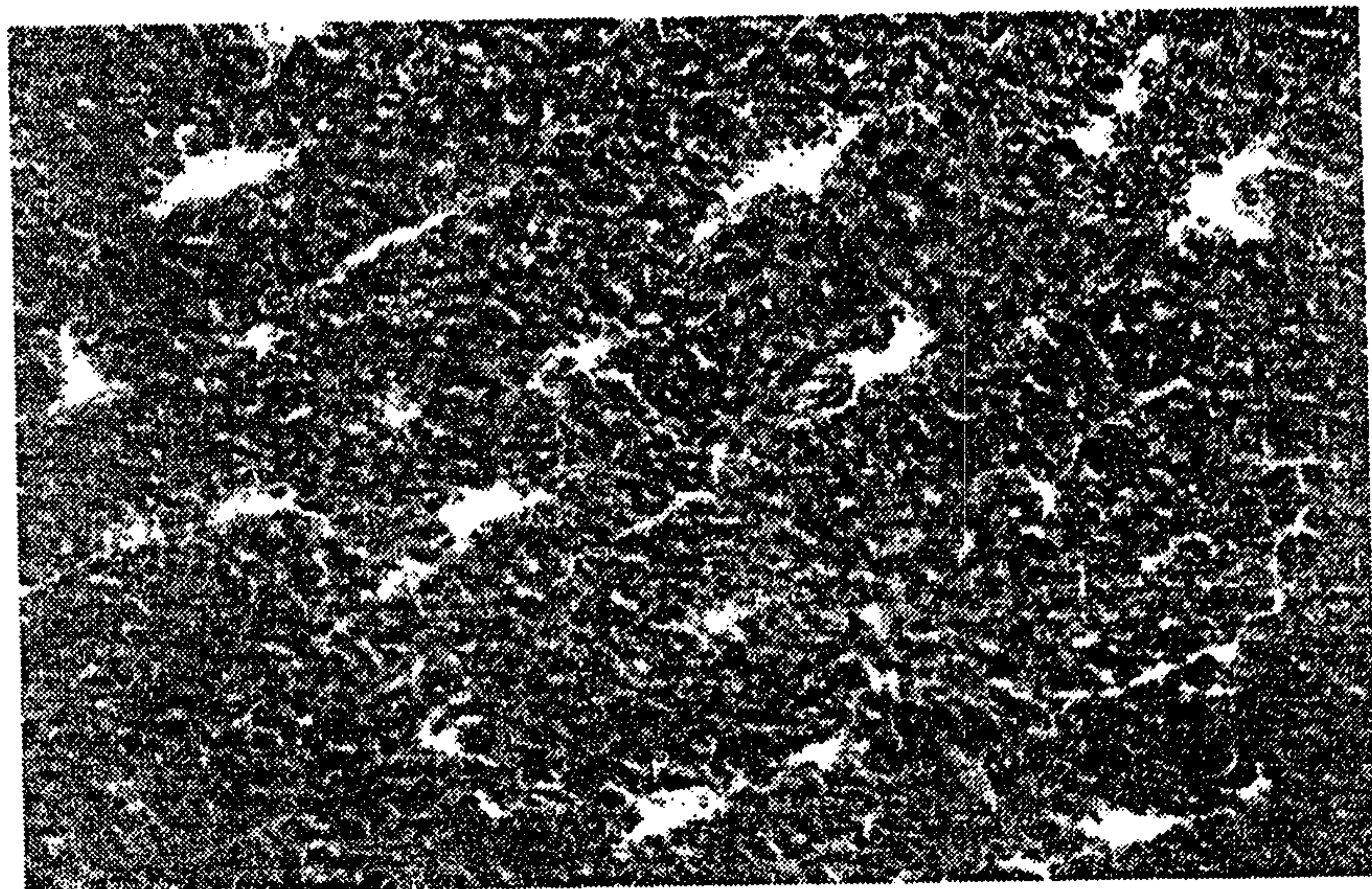


Fig. 4B

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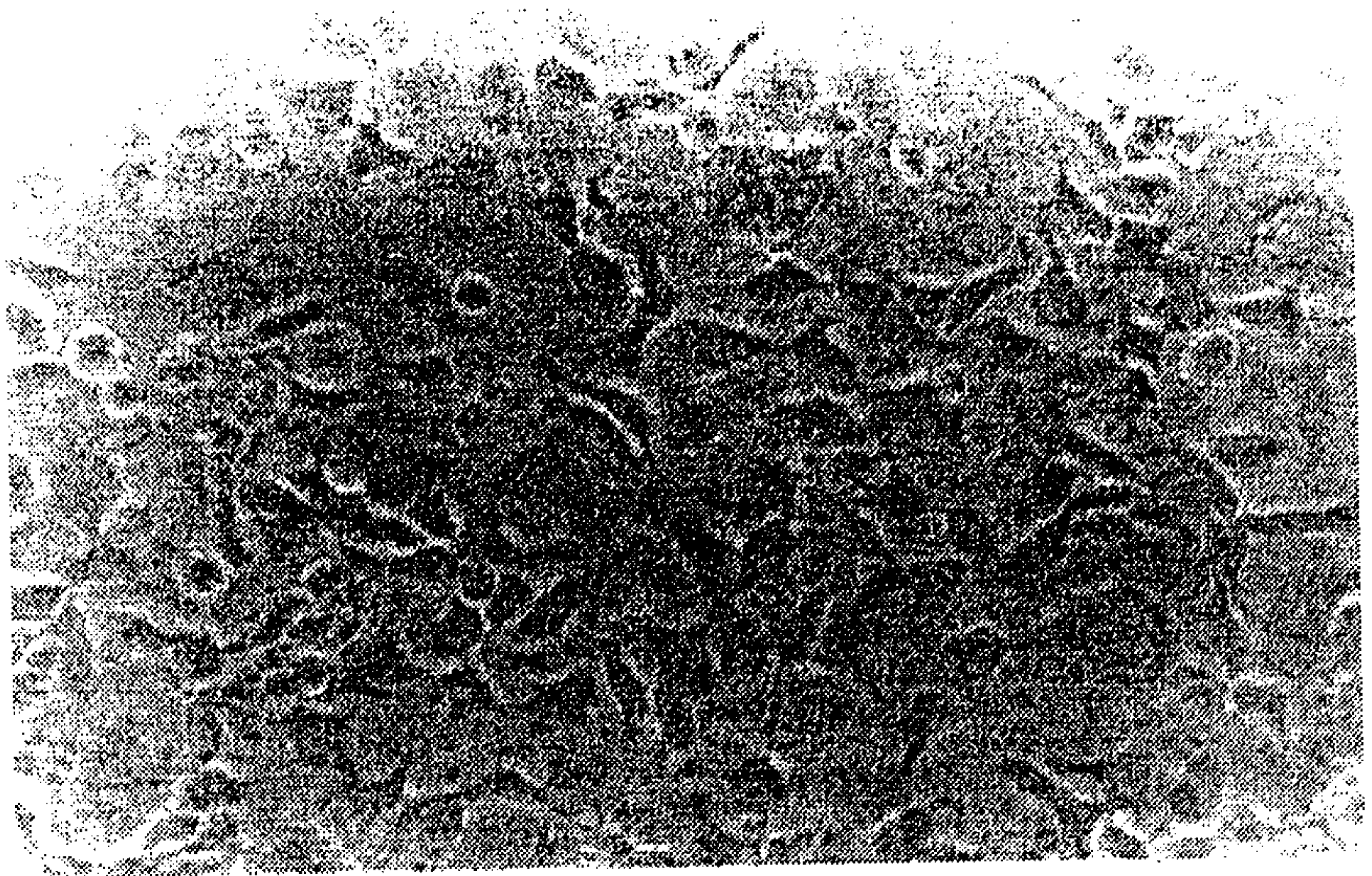


Fig. 5A

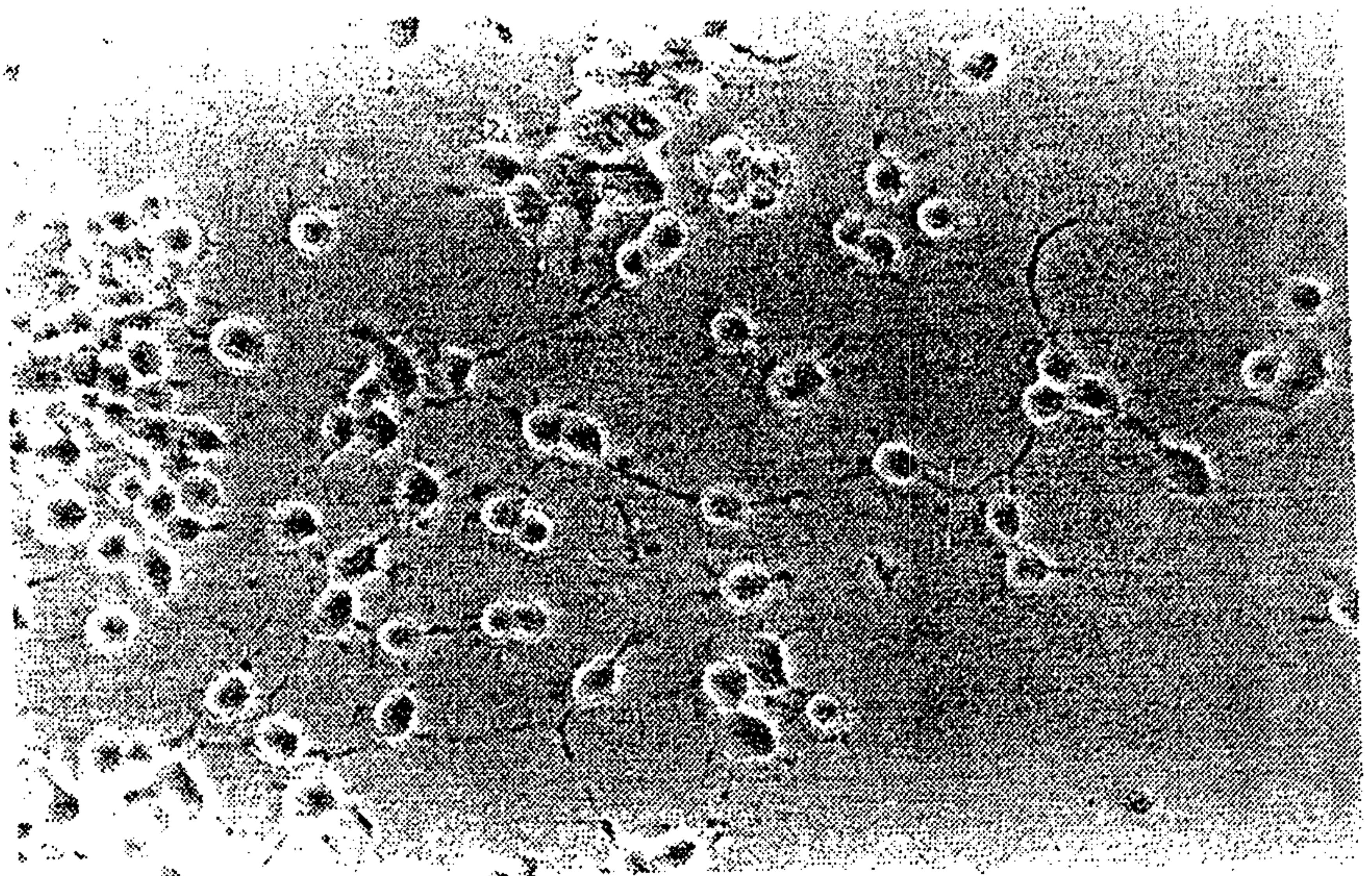


Fig. 5B

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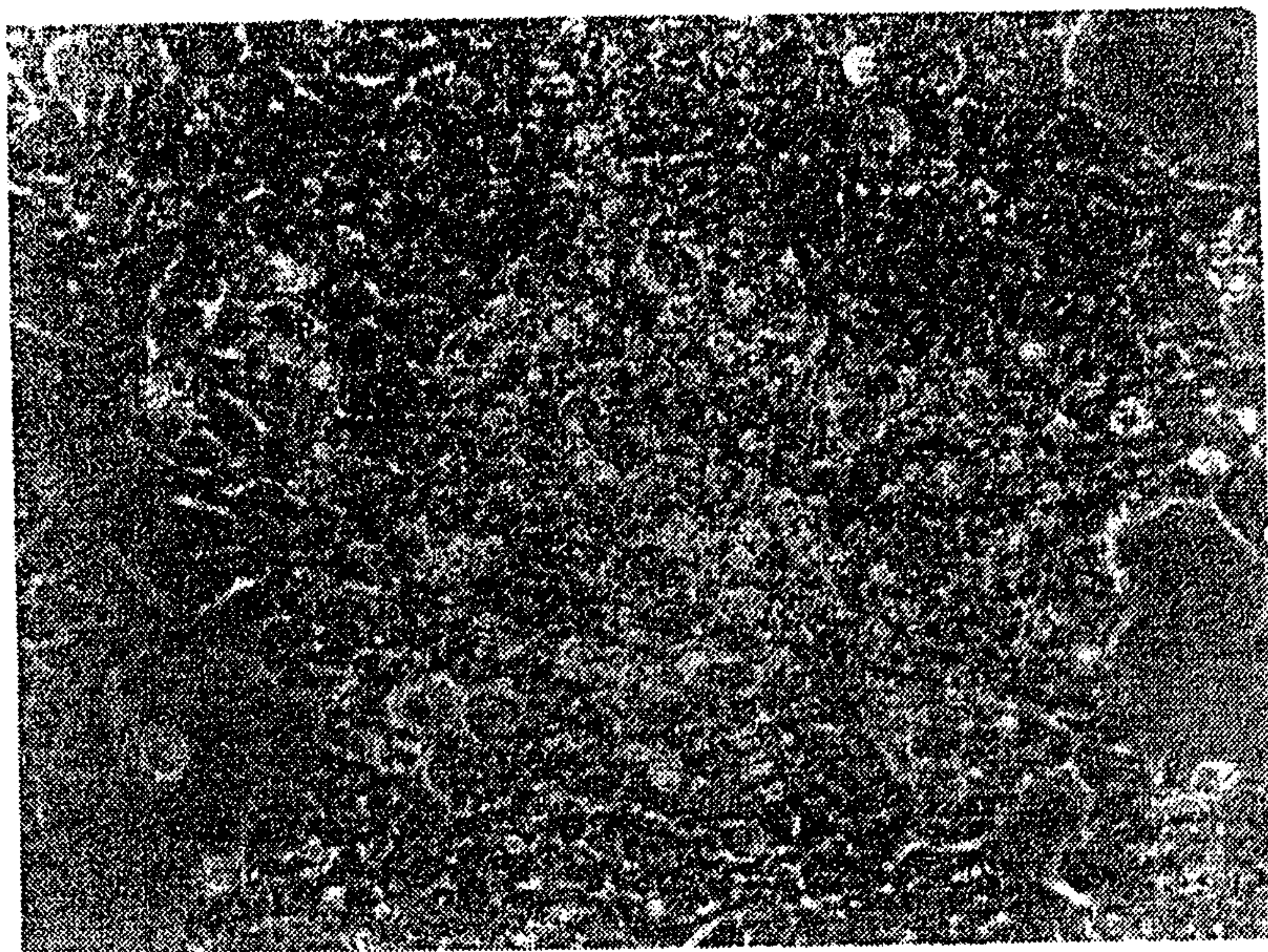


Fig. 6A

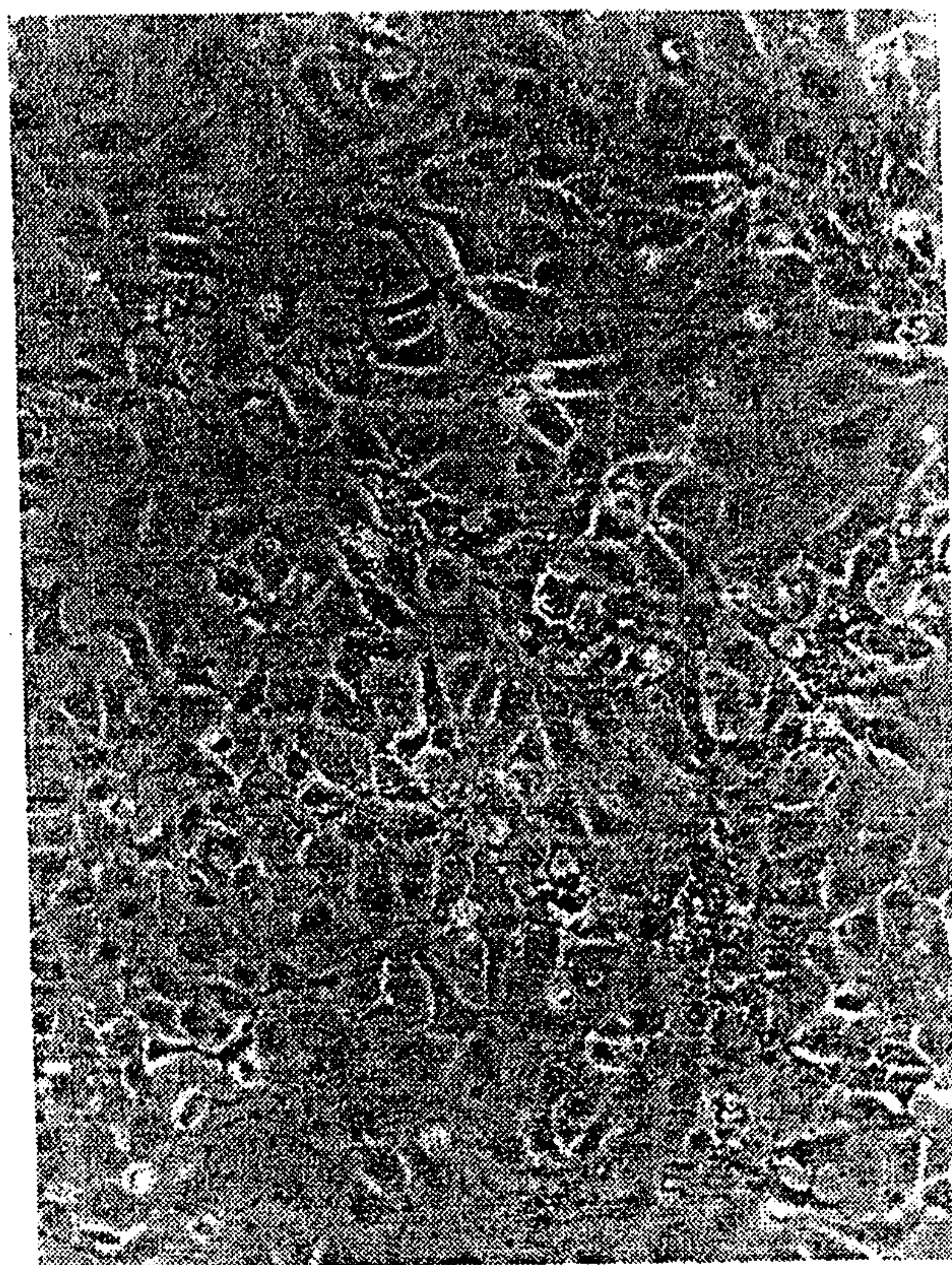


Fig. 6B

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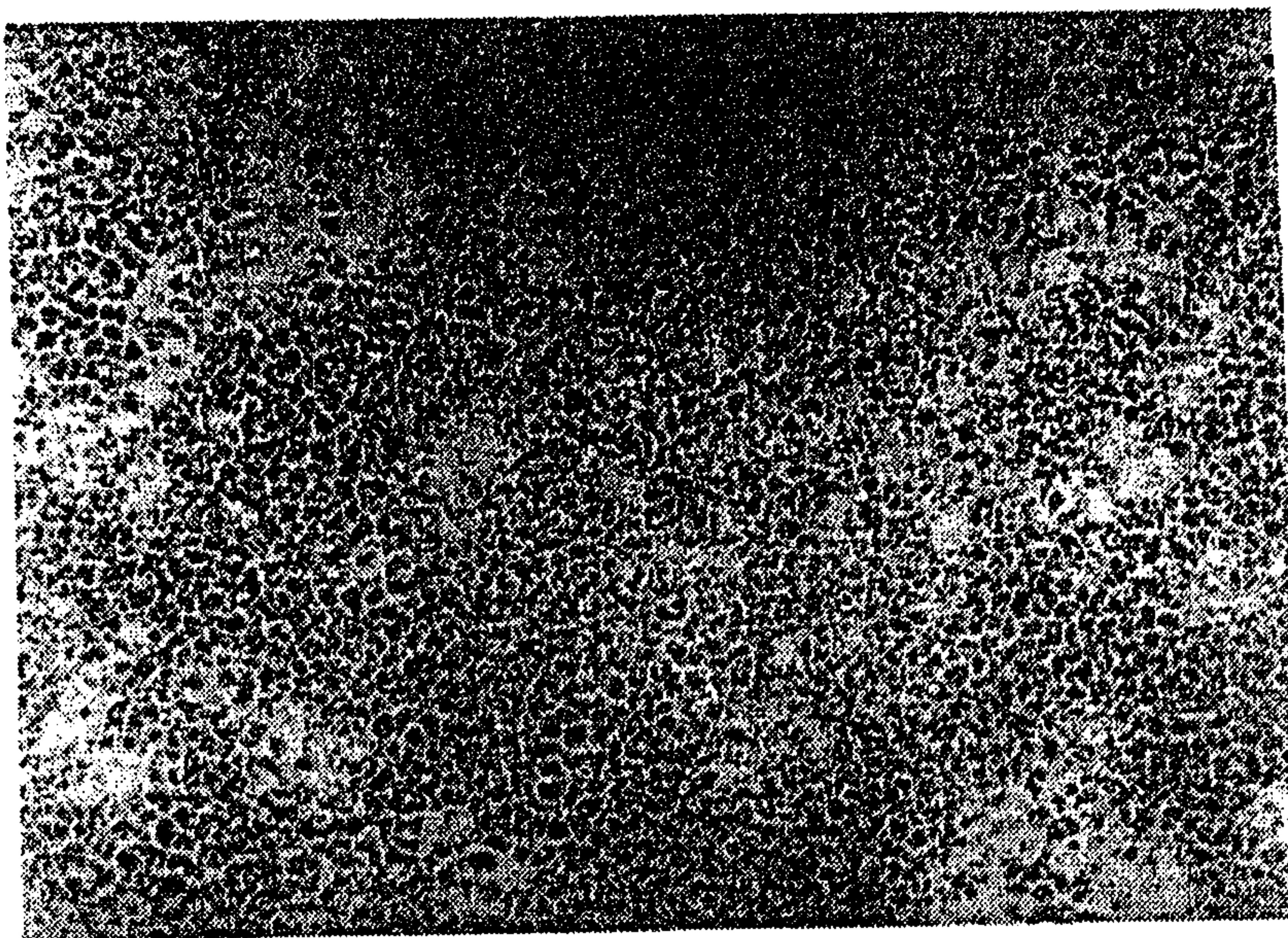


Fig. 6C

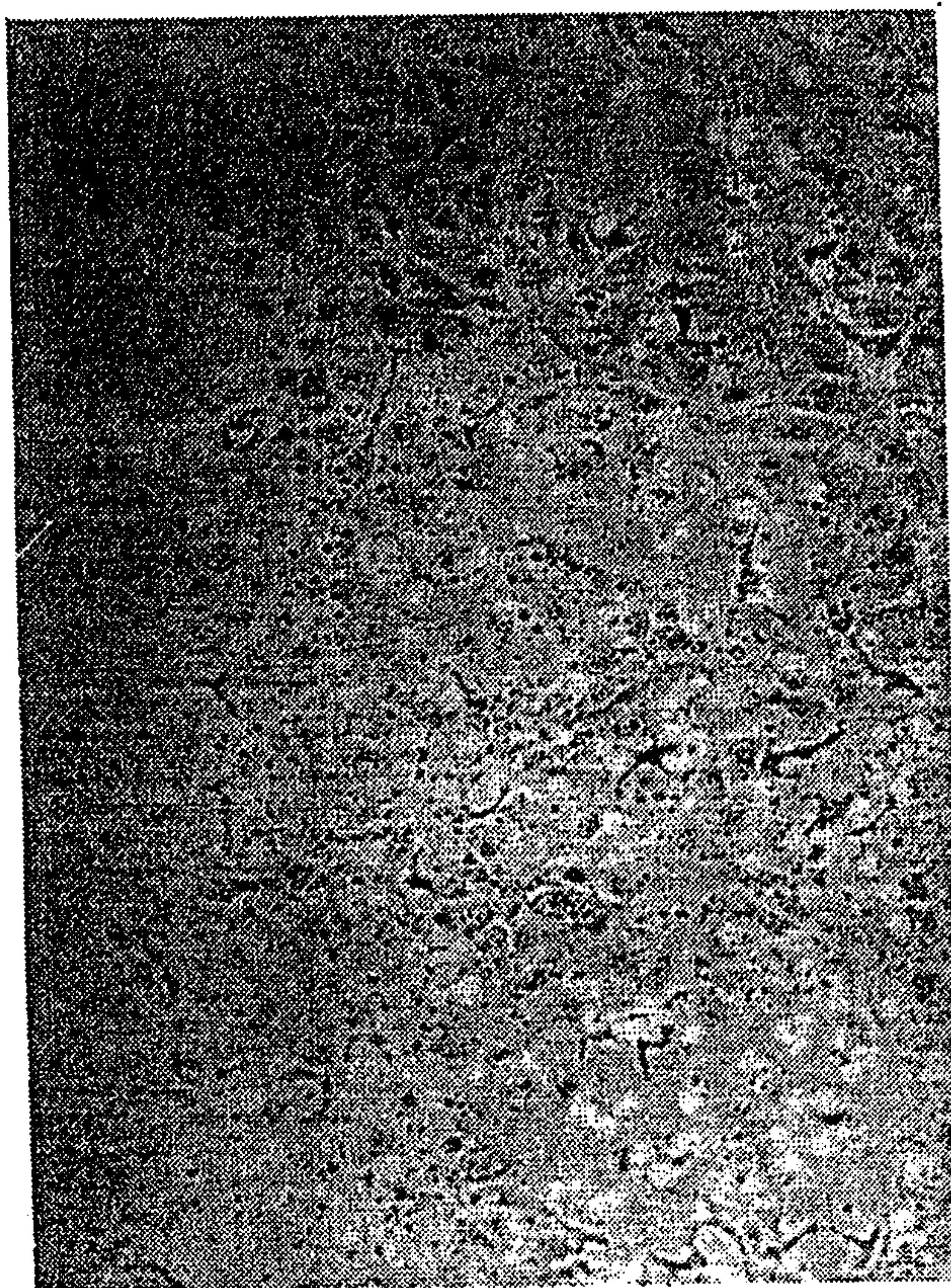


Fig. 6D

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Fig. 7

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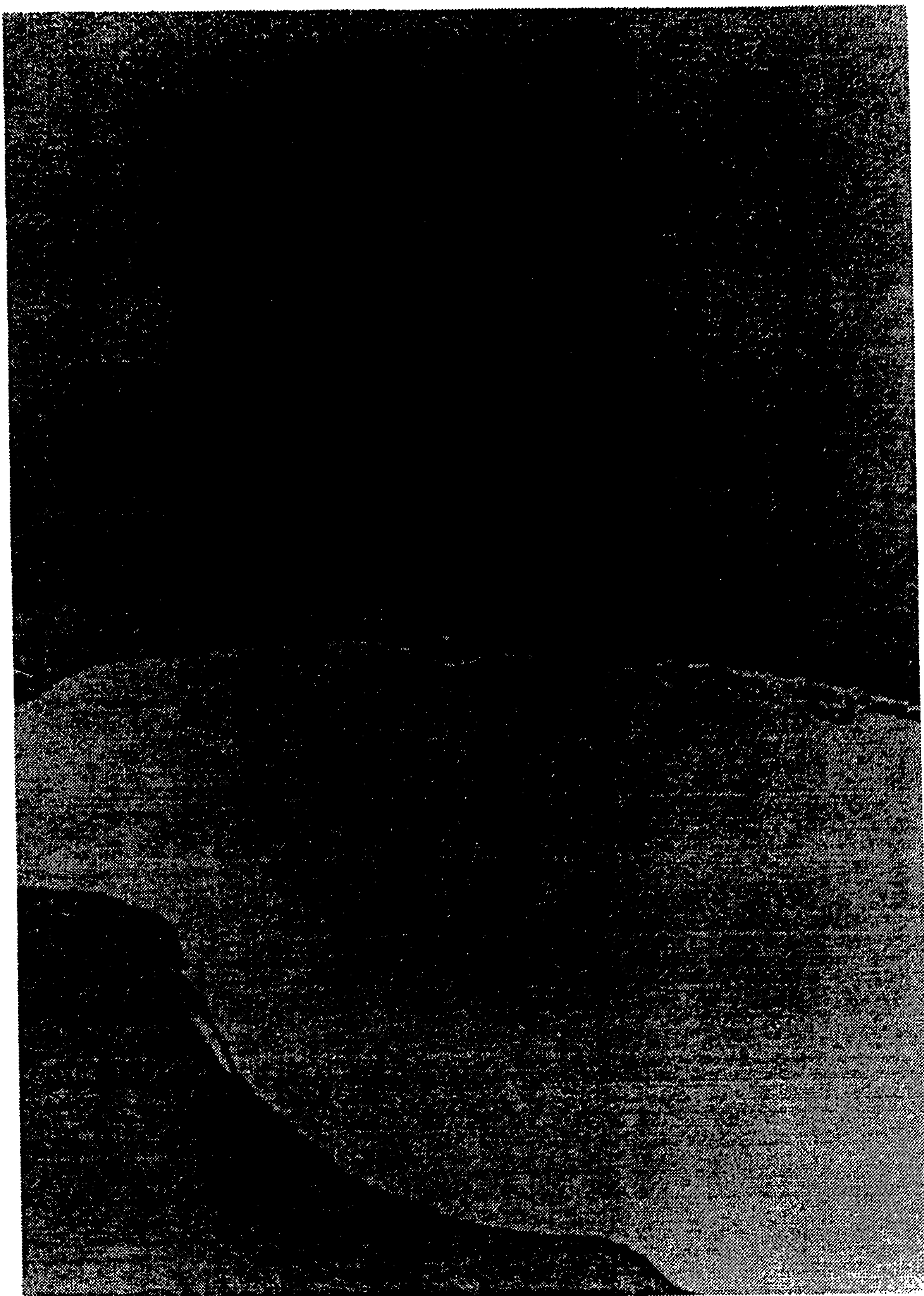


Fig. 8A

10/11



Fig. 8B

11/11

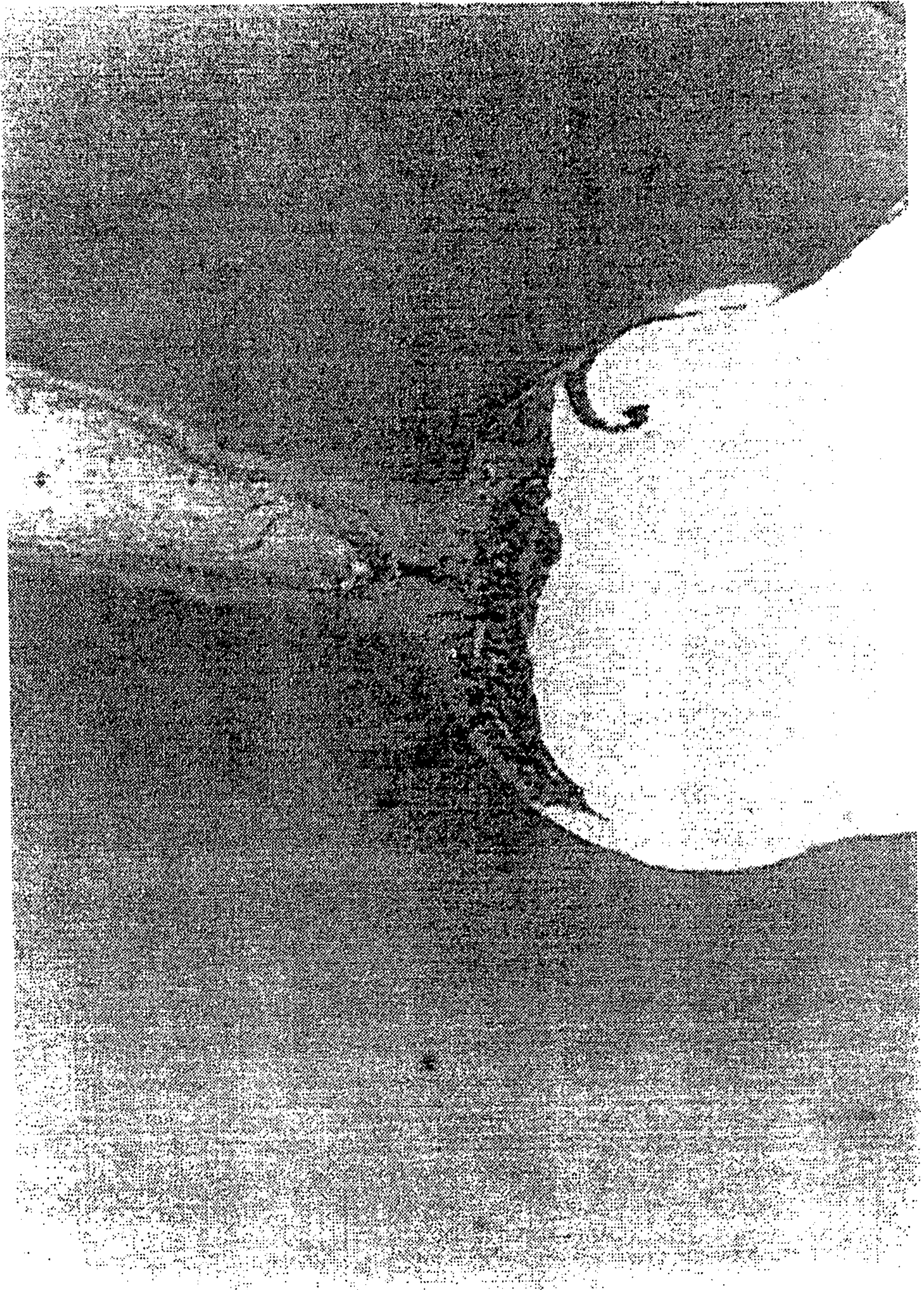


Fig. 8C