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"PRODUCTION OF PLURIPOTENT GRANULOCYTE
COLONY-STIMULATING FACTOR"

5 This is a continuation-in-part of co-pending
U.S. Patent Application Serial No. 768,959, filed August
23, 1985.

Background

10

The present invention pertains in general to
hematopoietic growth factors and to polynucleotides
encoding such factors. The present application pertains
in particular to mammalian pluripotent colony stimulat-
15 ing factors, specifically human pluripotent granulocyte
colony-stimulating factor (hpG-CSF), to fragments and
polypeptide analogs thereof and to polynucleotides
encoding the same.

The human blood-forming (hematopoietic) system
20 replaces a variety of white blood cells (including
neutrophils, macrophages, and basophils/mast cells), red
blood cells (erythrocytes) and clot-forming cells (mega-
karyocytes/platelets). The hematopoietic system of the
average human male has been estimated to produce on the
25 order of 4.5×10^{11} granulocytes and erythrocytes every
year, which is equivalent to an annual replacement of
total body weight. Dexter et al., BioEssays, 2, 154-158
(1985).

It is believed that small amounts of certain
30 hematopoietic growth factors account for the differen-
tiation of a small number of progenitor "stem cells"
into the variety of blood cell lines, for the tremen-
dous proliferation of those lines, and for the ultimate
differentiation of mature blood cells from those
35 lines. Because the hematopoietic growth factors are
present in extremely small amounts, the detection and

identification of these factors has relied upon an array of assays which as yet only distinguish among the different factors on the basis of stimulative effects on cultured cells under artificial conditions. As a
5 result, a large number of names have been coined to denote a much smaller number of factors. As an example of the resultant confusion the terms, IL-3, BPA, multi-CSF, HCGF, MCGF and PSF are all acronyms which are now believed to apply to a single murine hematopoietic
10 growth factor. Metcalf, Science, 229, 16-22 (1985). See also, Burgess, et al. J.Biol.Chem., 252, 1988 (1977), Das, et al. Blood, 58, 600 (1980), Ihle, et al., J.Immunol., 129, 2431 (1982), Nicola, et al., J.Biol.Chem., 258, 9017 (1983), Metcalf, et al.,
15 Int.J.Cancer, 30, 773 (1982), and Burgess, et al. Int.J.Cancer, 26, 647 (1980), relating to various murine growth regulatory glycoproteins.

The application of recombinant genetic techniques has brought some order out of this chaos. For
20 example, the amino acid and DNA sequences for human erythropoietin, which stimulates the production of erythrocytes, have been obtained. (See, Lin, PCT Published Application No. 85/02610, published June 20, 1985.) Recombinant methods have also been applied to
25 the isolation of cDNA for a human granulocyte-macrophage colony-stimulating factor. See, Lee, et al., Proc. Natl. Acad. Sci. (USA), 82, 4360-4364 (1985) and Wong, et al., Science, 228, 810-814 (1985). See also Yokota, et al. Proc. Natl. Acad. Sci. (USA), 81, 1070 (1984),
30 Fung, et al., Nature, 307, 233 (1984), and Gough, et al., Nature, 309, 763 (1984) relating to cloning of murine genes, as well as Kawasaki, et al., Science, 230, 291 (1985) relating to human M-CSF.

A human hematopoietic growth factor, called
35 human pluripotent colony-stimulating factor (hpCSF) or pluripoietin, has been shown to be present in the cul-

ture medium of a human bladder carcinoma cell line
denominated 5637 and deposited under restrictive condi-
tions with the American Type Culture Collection,
Rockville, Maryland as A.T.C.C. Deposit No. HTB-9. The
5 hpCSF purified from this cell line has been reported to
stimulate proliferation and differentiation of pluri-
potent progenitor cells leading to the production of all
major blood cell types in assays using human bone marrow
progenitor cells. Welte et al., Proc. Natl. Acad. Sci.
10 (USA), 82, 1526-1530 (1985). Purification of hpCSF
employed: $(\text{NH}_4)_2\text{SO}_4$ precipitation; anion exchange
chromatography (DEAE cellulose, DE52); gel filtration
(Aca54 column); and C18 reverse phase high performance
liquid chromatography. A protein identified as hpCSF,
15 which is eluted in the second of two peaks of activity
in C18 reverse phase HPLC fractions, was reported to
have a molecular weight (MW) of 18,000 as determined by
sodium dodecyl sulphate (SDS)-polyacrylamide gel elec-
trophoresis (PAGE) employing silver staining. HpCSF was
20 earlier reported to have an isoelectric point of 5.5
[Welte, et al., J. Cell. Biochem., Supp 9A, 116 (1985)]
and a high differentiation activity for the mouse myelo-
monocytic leukemic cell line WEHI-3B D⁺ [Welte, et al.,
UCLA Symposia on Molecular and Cellular Biology, Gale,
25 et al., eds., New Series, 28 (1985)]. Preliminary
studies indicate that the factor identified as hpCSF has
predominately granulocyte colony-stimulating activity
during the first seven days in a human CFU-GM assay.

Another factor, designated human CSF- δ , has
30 also been isolated from human bladder carcinoma cell
line 5637 and has been described as a competitor of
murine ¹²⁵I-labelled granulocyte colony-stimulating
factor (G-CSF) for binding to WEHI-3B D⁺ cells in a
dose-response relationship identical to that of
35 unlabelled murine G-CSF [Nicola, et al., Nature, 314,
625-628 (1985)]. This dose-response relationship had

previously been reported to be unique to unlabelled murine G-CSF and not possessed by such factors as M-CSF, GM-CSF, or multi-CSF [Nicola, et al., Proc. Natl. Acad. Sci. (USA), 81, 3765-3769 (1984)]. CSF- β and G-CSF are also unique among CSF's in that they share a high degree of ability to induce differentiation of WEHI-3B D⁺ cells. Nicola, et al., Immunology Today, 5, 76-80 (1984). At high concentrations, G-CSF stimulates mixed granulocyte/macrophage colony-forming cells [Nicola, et al., (1984) supra], which is consistent with preliminary results indicating the appearance of granulocytic, monocytic, mixed granulocytic/monocytic and eosinophilic colonies (CFU-GEMM) after 14 days incubation of human bone marrow cultures with hpCSF. CSF- β has also been described as stimulating formation of neutrophilic granulocytic colonies in assays which employed mouse bone marrow cells, a property which has been a criterion for identification of a factor as a G-CSF. On the basis of these similarities, human CSF- β has been identified with G-CSF (granulocytic colony stimulating factor). Nicola et al., Nature, 314, 625-628 (1985).

Based upon their common properties, it appears that human CSF- β of Nicola, et al., supra, and the hpCSF of Welte, et al., supra, are the same factor which could properly be referred to as a human pluripotent granulocyte colony-stimulating factor (hpG-CSF). Characterization and recombinant production of hpG-CSF would be particularly desirable in view of the reported ability of murine G-CSF to completely suppress an in vitro WEHI-3B D⁺ leukemic cell population at "quite normal concentrations", and the reported ability of crude, injected preparations of murine G-CSF to suppress established transplanted myeloid leukemias in mice. Metcalf, Science, 229, 16-22 (1985). See also, Sachs, Scientific American, 284(1), 40-47 (1986).

To the extent that hpG-CSF may prove to be therapeutically significant and hence need to be available in commercial scale quantities, isolation from cell cultures is unlikely to provide an adequate source of material. It is noteworthy, for example, that restrictions appear to exist against commercial use of Human Tumor Bank cells such as the human bladder carcinoma cell line 5637 (A.T.C.C. HTB9) which have been reported as sources of natural hpCSF isolates in Welte, et al. (1985, supra).

Summary of the Invention

According to the present invention, DNA sequences coding for all or part of hpG-CSF are provided. Such sequences may include: the incorporation of codons "preferred" for expression by selected non-mammalian hosts; the provision of sites for cleavage by restriction endonuclease enzymes; and the provision of additional initial, terminal or intermediate DNA sequences which facilitate construction of readily expressed vectors. The present invention also provides DNA sequences coding for microbial expression of polypeptide analogs or derivatives of hpG-CSF which differ from naturally-occurring forms in terms of the identity or location of one or more amino acid residues (i.e., deletion analogs containing less than all of the residues specified for hpG-CSF; substitution analogs, such as [Ser¹⁷]hpG-CSF, wherein one or more residues specified are replaced by other residues; and addition analogs wherein one or more amino acid residues is added to a terminal or medial portion of the polypeptide) and which share some or all the properties of naturally-occurring forms.

Novel DNA sequences of the invention include sequences useful in securing expression in procaryotic

or eucaryotic host cells of polypeptide products having at least a part of the primary structural conformation and one or more of the biological properties of naturally occurring pluripotent granulocyte colony-stimulating factor. DNA sequences of the invention are specifically seen to comprise: (a) the DNA sequence set forth in Table VII and Table VIII or their complimentary strands; (b) a DNA sequence which hybridizes (under hybridization conditions such as illustrated herein or more stringent conditions) to the DNA sequences in Table VII or to fragments thereof; and (c) a DNA sequence which, but for the degeneracy of the genetic code, would hybridize to the DNA sequence in Table VII. Specifically comprehended in part (b) are genomic DNA sequences encoding allelic variant forms of hpG-CSF and/or encoding other mammalian species of pluripotent granulocyte colony-stimulating factor. Specifically comprehended by part (c) are manufactured DNA sequences encoding hpG-CSF, fragments of hpG-CSF and analogs of hpG-CSF which DNA sequences may incorporate codons facilitating translation of messenger RNA in microbial hosts. Such manufactured sequences may readily be constructed according to the methods of Alton, et al., PCT published application WO 83/04053.

Also comprehended by the present invention is that class of polypeptides coded for by portions of the DNA complement to the top strand human cDNA or genomic DNA sequences of Tables VII or VIII herein, i.e., "complementary inverted proteins" as described by Tramontano, et al., Nucleic Acids Res., 12, 5049-5059 (1984).

The present invention provides purified and isolated polypeptide products having part or all of the primary structural conformation (i.e., continuous sequence of amino acid residues) and one or more of the biological properties (e.g, immunological properties and

in vitro biological activity) and physical properties (e.g., molecular weight) of naturally-occurring hpG-CSF including allelic variants thereof. These polypeptides are also characterized by being the product of chemical synthetic procedures or of procaryotic or eucaryotic host expression (e.g., by bacterial, yeast, higher plant, insect and mammalian cells in culture) of exogenous DNA sequences obtained by genomic or cDNA cloning or by gene synthesis. The products of typical yeast (e.g., Saccaromyces cerevisiae) or procaryote [e.g., Escherichia coli (E. coli)] host cells are free of association with any mammalian proteins. The products of microbial expression in vertebrate (e.g., non-human mammalian and avian) cells are free of association with any human proteins. Depending upon the host employed, polypeptides of the invention may be glycosylated with mammalian or other eucaryotic carbohydrates or may be non-glycosylated. Polypeptides of the invention may also include an initial methionine amino acid residue (at position -1).

Also comprehended by the invention are pharmaceutical compositions comprising effective amounts of polypeptide products of the invention together with suitable diluents, adjuvants and/or carriers useful in hpG-CSF therapy.

Polypeptide products of the invention may be "labelled" by association with a detectable marker substance (e.g., radiolabelled with ^{125}I) to provide reagents useful in detection and quantification of human hpG-CSF in solid tissue and fluid samples such as blood or urine. DNA products of the invention may also be labelled with detectable markers (such as radiolabels and non-isotopic labels such as biotin) and employed in DNA hybridization processes to locate the human hpG-CSF gene position and/or the position of any related gene family in a chromosomal map. They may also be used for

identifying human hpG-CSF gene disorders at the DNA level and used as gene markers for identifying neighboring genes and their disorders.

Polypeptide products of the present invention
5 may be useful, alone or in combination with other hematopoietic factors or drugs in the treatment of hematopoietic disorders, such as aplastic anemia. They may also be useful in the treatment of hematopoietic deficits arising from chemotherapy or from radiation
10 therapy. The success of bone marrow transplantation, for example, may be enhanced by application of hpG-CSF. Wound healing burn treatment and the treatment of bacterial inflammation may also benefit from the application of hpG-CSF. In addition, hpG-CSF may also be
15 useful in the treatment of leukemia based upon a reported ability to differentiate leukemic cells. Welte, et al., Proc. Natl. Acad. Sci. (USA), 82, 1526-1530 (1985) and Sachs, supra.

Numerous aspects and advantages of the invention
20 tion will be apparent to those skilled in the art upon consideration of the following detailed description which provides illustrations of the practice of the invention in its presently preferred embodiments.

25 Brief Description of the Drawings

The Figure is a partial restriction endo-
nuclease map of the hpG-CSF gene accompanied by arrows
depicting the sequencing strategy used to obtain the
30 genomic sequence.

Detailed Description

According to the present invention, DNA
35 sequences encoding part or all of the polypeptide sequence of hpG-CSF have been isolated and characterized.

The following examples are presented by way of illustration of the invention and are specifically directed to procedures carried out prior to identification of hpG-CSF cDNA and genomic clones, to procedures
5 resulting in such identification, and to the sequencing, development of expression systems based on cDNA, genomic and manufactured genes and verification of expression hpG-CSF and analog products in such systems.

More particularly, Example 1 is directed to
10 amino acid sequencing of hpG-CSF. Example 2 is directed to the preparation of a cDNA library for colony hybridization screening. Example 3 relates to construction of hybridization probes. Example 4 relates to hybridization screening, identification of positive clones, DNA
15 sequencing of a positive cDNA clone and the generation of polypeptide primary structural conformation (amino acid sequence) information. Example 5 is directed to the identification and sequencing of a genomic clone encoding hpG-CSF. Example 6 is directed to the construction of a manufactured gene encoding hpG-CSF
20 wherein E.coli preference codons are employed.

Example 7 is directed to procedures for construction of an E. coli transformation vector incorporating hpG-CSF-encoding DNA, the use of the vector in
25 procaryotic expression of hpG-CSF, and to analysis of properties of recombinant products of the invention. Example 8 is directed to procedures for generating analogs of hpG-CSF wherein cysteine residues are replaced by another suitable amino acid residue by means
30 of mutagenesis performed on DNA encoding hpG-CSF. Example 9 is directed to procedures for the construction of a vector incorporating hpG-CSF analog-encoding DNA derived from a positive cDNA clone, the use of the vector for transfection of COS-1 cells, and the cultured
35 growth of the transfected cells. Example 10 relates to physical and biological properties or recombinant polypeptide products of the invention.

Example 1

(A) Sequencing of Material
Provided By Literature Methods

5

A sample (3-4 μ g, 85-90% pure of SDS, silver stain-PAGE) of hpG-CSF was obtained from Sloan Kettering Institute, New York, New York, as isolated and purified according to Welte, et al., Proc. Natl. Acad. Sci. (USA), 82, 1526-1530 (1985).

10

The N-terminal amino acid sequence of this sample of hpG-CSF was determined in a Run #1 by micro-sequence analysis using an AB407A gas phase sequencer (Applied Biosystems, Foster City, California) to provide the sequence information set out in Table I below. In Tables I-IV single letter codes are employed, "X" designates a residue which was not unambiguously determined and residues in parentheses were only alternatively or tentatively assigned.

20

TABLE I

1	5	10	15
K-P-L-G-P-A-S-K-L-K-Q-(G,V,S)-G-L-X-X-X			

25

A high background was present in every cycle of the run for which results are reported in Table I, indicating that the sample had many contaminating components, probably in the form of chemical residues from purification. The sequence was retained only for reference use.

30

In Run #2, a second sample (5-6 μ g, ~95% pure) was obtained from Sloan Kettering as for Run #1 and a sequencing procedure was performed as for Run #1. This sample was from the same lot of material employed to generate Fig. 4 of Welte, et al., Proc. Natl. Acad. Sci.

35

(USA), 82, 1526-1530 (1985). The results are given in Table II.

TABLE II

5

1 5 10 15 20
T-P-L-G-P-A-S-(S)-L-P-Q-($\frac{S}{X}$)-M- $\{\frac{L}{M}\}$ -X-K-(R)-X-X-(R)-(L)-X-

10

Although more residues were identified, Run #2 did not provide a sufficiently long, unambiguous sequence from which a reasonable number of probes could be constructed to search for hpG-CSF DNA. It was calculated that at least 1536 probes would have been required to attempt isolation of cDNA based on the sequence of Table II. Again, contamination of the sample was believed to be the problem.

Accordingly, a third sample (3-5 μ g, -40% pure) was obtained from Sloan Kettering as above. This preparation was electroblotted after separation by SDS-PAGE in an attempt at further purification. Sequence analysis of this sample yielded no data.

25

(B) Sequencing of Materials
Provided by Revised Methods

In order to obtain a sufficient amount of pure material to perform suitably definitive amino acid sequence analysis, cells of a bladder carcinoma cell line 5637 (subclone 1A6) as produced at Sloan-Kettering were obtained from Dr. E. Platzer. Cells were initially cultured Iscove's medium (GIBCO, Grand Island, New York) in flasks to confluence. When confluent, the cultures were trypsinized and seeded into roller bottles (1-1/2 flasks/bottle) each containing 25 ml of preconditioned

30

35

Iscove's medium under 5% CO₂. The cells were grown overnight at 37°C. at 0.3 rpm.

Cytodex-1 beads (Pharmacia, Uppsala, Sweden) were washed and sterilized using the following procedures. Eight grams of beads were introduced into a bottle and 400 ml of PBS was added. Beads were suspended by swirling gently for 3 hours. After allowing the beads to settle, the PBS was drawn off, the beads were rinsed in PBS and fresh PBS was added. The beads were autoclaved for 15 minutes. Prior to use, the beads were washed in Iscove's medium plus 10% fetal calf serum (FCS) before adding fresh medium plus 10% FCS to obtain treated beads.

After removing all but 30 ml of the medium from each roller bottle, 30 ml of fresh medium plus 10% FCS and 40 ml of treated beads were added to the bottles. The bottles were gassed with 5% CO₂ and all bubbles were removed by suction. The bottles were placed in roller racks at 3 rpm for 1/2 hour before reducing the speed to 0.3 rpm. After 3 hours, an additional flask was trypsinized and added to each roller bottle containing beads.

At 40% to 50% of confluence the roller bottle cultures were washed with 50 ml PBS and rolled for 10 min. before removing the PBS. The cells were cultured for 48 hours in medium A [Iscove's medium containing 0.2% FCS, 10⁻⁸M hydrocortisone, 2mM glutamine, 100 units/ml penicillin, and 100 µg/ml streptomycin]. Next, the culture supernatant was harvested by centrifugation at 3000 rpm for 15 min., and stored at -70°C. The cultures were refed with medium A containing 10% FCS and were cultured for 48 hours. After discarding the medium, the cells were washed with PBS as above and cultured for 48 hours in medium A. The supernatant was again harvested and treated as previously described.

Approximately 30 liters of medium conditioned by 1A6 cells were concentrated to about 2 liters on a Millipore Pellicon unit equipped with 2 cassettes having 10,000 M.W. cutoffs at a filtrate rate of about 200 ml/min. and at a retentate rate of about 1000 ml/min. The concentrate was diafiltered with about 10 liters of 50mM Tris (pH 7.8) using the same apparatus and same flow rates. The diafiltered concentrate was loaded at 40 ml/min. onto a 1 liter DE cellulose column equilibrated in 50mM Tris (pH 7.8). After loading, the column was washed at the same rate with 1 liter of 50mM Tris (pH 7.8) and then with 2 liters of 50mM Tris (pH 7.8) with 50mM NaCl. The column was then sequentially eluted with six 1 liter solutions of 50mM Tris (pH 7.5) containing the following concentrations of NaCl: 75mM; 100mM; 125mM; 150mM; 200mM; and 300mM. Fractions (50 ml) were collected, and active fractions were pooled and concentrated to 65 ml on an Amicon[®] ultrafiltration stirred cell unit equipped with a YM5 membrane. This concentrate was loaded onto a 2 liter Aca54 gel filtration column equilibrated in PBS. The column was run at 80 ml/hr. and 10 ml fractions were collected. Active fractions were pooled and loaded directly onto a C4 high performance liquid chromatography (HPLC) column.

Samples, ranging in volume from 125 ml to 850 ml and containing 1-8 mg of protein, about 10% of which was hpG-CSF, were loaded onto the column at a flow rate ranging from 1 ml to 4 ml per minute. After loading and an initial washing with 0.1M ammonium acetate (pH 6.0-7.0) in 80% 2-propanol at a flow rate of 1/ml/min. One milliliter fractions were collected and monitored for proteins at 220nm, 260nm and 280nm.

As a result of purification, fractions containing hpG-CSF were clearly separated (as fractions 72 and 73 of 80) from other protein-containing fractions. HpG-CSF was isolated (150-300 µg) at a purity of about

85±5% and at a yield of about 50%. From this purified material 9 µg was used in Run #4, an amino acid sequence analysis wherein the protein sample was applied to a TFA-activated glass fiber disc without polybrene.

- 5 Sequence analysis was carried out with an AB 470A sequencer according to the methods of Hewick, et al., J. Biol. Chem., 256, 7990-7997 (1981) and Lai, Anal. Chim. Acta, 163, 243-248 (1984). The results of Run #4 appear in Table III.

10

TABLE III

1	5	10
Thr - Pro - Leu - Gly - Pro - Ala - Ser - Ser - Leu - Pro-		
15	15	20
Gln - Ser - Phe - Leu - Leu - Lys -(Lys)- Leu -(Glu)- Glu-		
	25	30
20 Val - Arg - Lys - Ile -(Gln)- Gly - Val - Gly - Ala - Ala-		
Leu - X - X -		

- 25 In Run #4, beyond 31 cycles (corresponding to residue 31 in Table III) no further significant sequence information was obtained. In order to obtain a longer unambiguous sequence, in a Run #5, 14 µg of hpG-CSF purified from conditioned medium were reduced with 10 µl of β-mercaptoethanol for one hour at 45°C, then thor-
- 30 oughly dried under a vacuum. The protein residue was then redissolved in 5% formic acid before being applied to a polybrenized glass fiber disc. Sequence analysis was carried out as for Run #4 above. The results of Run #5 are given in Table IV.

35

TABLE IV

	1	5	10
5	Thr - Pro - Leu - Gly -	Pro - Ala - Ser - Ser -	Leu - Pro -
		15	20
	Gln - Ser - Phe - Leu -	Leu - Lys - Cys -	Leu - Glu - Gln -
		25	30
10	Val - Arg - Lys - Ile -	Gln - Gly - Asp -	Gly - Ala - Ala -
		35	40
	Leu - Gln - Phe - Lys -	Leu - Gly - Ala -	Thr - Tyr - Lys -
		45	
	Val - Phe - Ser - Thr -	(Arg) - (Phe) -	(Met) -X-

15

The amino acid sequence give in Table IV was sufficiently long (44 residues) and unambiguous to construct probes for obtaining hpG-CSF cDNA as described infra.

20

Example 2

Among standard procedures for isolating cDNA sequences of interest is the preparation of plasmid-borne cDNA "libraries" derived from reverse transcription of mRNA abundant in donor cells selected on the basis of their expression of a target gene. Where substantial portions of the amino acid sequence of a polypeptide are known, labelled, single-stranded DNA probe sequences duplicating a sequence putatively present in the "target" cDNA may be employed in DNA/DNA hybridization procedures carried out on cloned copies of the cDNA which have been denatured to single stranded form. Weissman, et al., U.S. Patent No. 4,394,443; Wallace, et al., Nucleic Acids Res., 6, 3543-3557 (1979), and Reyes, et al., Proc. Natl. Acad. Sci. (USA), 79, 3270-3274

35

(1982), and Jaye, et al., Nucleic Acids Res., 11, 2325-2335 (1983). See also, U.S. Patent No. 4,358,535 to Falkow, et al., relating to DNA/DNA hybridization procedures in effecting diagnosis; and Davis, et al., "A
5 Manual for Genetic Engineering, Advanced Bacterial Genetics", Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y. (1980) at pp. 55-58 and 174-176, relating to colony and plaque hybridization techniques.

Total RNA was extracted from approximately 1
10 gram of cells from a bladder carcinoma cell line 5637 (IA6) using a guanidinium thiocyanate procedure for quantitative isolation of intact RNA. [Chirgwin, et al., Biochemistry, 18, 5294-5299 (1979)].

The sterile aqueous RNA solution contained
15 total RNA from the IA6 cells. To obtain only the messenger RNA from the total RNA solution, the solution was passed through a column containing oligodeoxythymidylate [oligo(dT)] (Collaborative Research, Inc., Waltham, Massachusetts. Poly-Adenylated (poly-A⁺) tails
20 characteristic of messenger RNA adhere to the column while ribosomal RNA is eluted. As a result of this procedure, approximately 90 µg of poly-adenylated messenger RNA (poly-A⁺ mRNA) were isolated. The isolated poly-A⁺ messenger RNA was pre-treated with methyl-
25 mercury hydroxide (Alpha Ventron, Danvers, Massachusetts) at a final concentration of 4 mM for 5 minutes at room temperature prior to use in a cDNA reaction. The methylmercury hydroxide treatment denatured interactions of messenger RNA, both with itself and with
30 contaminating molecules that inhibit translation. Payvar, et al., J.Biol.Chem., 258, 7636-7642 (1979).

According to the Okayama procedure [Okayama, et al., Molecular & Cellular Biology, 2, 161-170 (1982)], a cDNA bank was prepared using mRNA obtained
35 from IA6 cells. The cDNAs were then transformed by incubation into a host microorganism E.coli K-12 strain HB101 for amplification.

Example 3

Hybridization probes designed on the basis of
 5 the hpG-CSF amino terminal sequence of Table IV con-
 sisted of a set of 24 oligonucleotides each being 23
 bases in length and containing three inosine residues.
 The probe oligonucleotides were manufactured according
 to the procedure of Caruthers, et al., Genetic
 10 Engineering, 4, 1-18 (1982) and labeled with γ -³²P ATP
 by kinasing with polynucleotide kinase. The probe oli-
 gonucleotides, corresponding to the messenger RNA for
 residues 23-30 of the sequence of Table IV, are illus-
 trated in Table V.

15

TABLE V

hpG-CSF Probes

20 5' GC IGC ICC ^ATC ICC ^TTG ^GAT ^TTT^{3'}
 _G _C _A
 _T

The assignment of neutrality to I's was based
 on the published work of Takahashi, et al., Proc. Natl.
 25 Acad. Sci. (USA), 82, 1931-1935 (1985) and Ohtsuka, et
 al., J. Biol. Chem., 260, 2605-2608 (1985). However,
 inosine may have a destabilizing effect if base paired
 with a G or T. In Takahashi, et al., inosines may
 appear to have a neutral effect because they average out
 30 as a group to near neutrality (e.g., three having paired
 favorably with C and two not favorable to pairing with
 T).

To test the effect of having I's base pair
 with G's, control experiments were designed using an N-
 35 myc gene sequence and clone. The sequences picked from
 the N-myc gene had the same overall G and C content at

the first two positions of each codon as was prescribed by the hpG-CSF probes. Thus, the N-myc test probes were of the same length, contained I's in the same relative positions and had potentially the same average T_m (62-
5 66°C., not accounting for the 3 or 4 inosine residues included) as the hpG-CSF probes.

Two sets of N-myc test probes were constructed according to the procedure of Caruthers, et al., supra. Set I, as illustrated in Table VI included: 1,
10 a 23 mer with perfect match; 2, in which three third position C's were replaced with I's generating the worst possible case for adding I's; and 3, in which four third position C's were replaced with I's. The second set of test probes was designed to represent a more random
15 distribution of inosine base pairs, that might give an overall neutral base pairing effect. Set II, as illustrated in Table VI, included: 4, containing two I's that will base pair with C's and one with a G; and 5, identical to 4 with the addition of one more I:G base
20 pair.

TABLE VI

N-myc Test Probes

25

1. 5' CAC AAC TAT GCC GCC CCC TCC CC^{3'}

2. 5' CAC AAC TAT GCI GCC CCI TCI CC^{3'}

30

3. 5' CAI AAC TAT GCI GCC CCI TCI CC^{3'}

4. 5' AAC GAG CTG TGI GGC AGI CCI GC^{3'}

5. 5' AAI GAG CTG TGI GGC AGI CCI GC^{3'}

35

Five replica filters containing N-myc DNA sequences and chicken growth hormone DNA sequences (as a negative control) were baked in a vacuum oven for 2 hours at 80°C. prior to hybridization. All filters were hybridized as described in Example 4 for the hpG-CSF probes except the period of hybridization was only 6 hours. Filters were washed three times at room temperature then once at 45°C., 10 minutes each. The filters were monitored with a Geiger counter.

10 The filter representing N-myc probe 3 gave a very weak signal relative to the other four probed filters and was not washed any further. After a 10 minute 50°C. wash, the Geiger counter gave the following percent signal with probe one being normalized to 100%:
15 Probe 2, 20%; Probe 3 (45°C.), 2%; Probe 4, 92%; and Probe 5, 75%. After a 55°C. wash, the percentages were: Probe 2, 16%; Probe 4, 100%; and Probe 5, 80%. A final wash at 60°C. yielded the following percentages: Probe 2, 1.6%; Probe 4, 90%; and Probe 5, 70%.

20 Thus, in the presence of three I's, as in probes 2 and 4, up to a 60-fold difference in signal is observed as the theoretical T_m (I's not included in the calculation) is approached [based upon a worst case I base pairing (Probe 2) and a relatively neutral I base
25 pairing case (Probe 4)].

 The standardization information gained by the N-myc test hybridizations was utilized in washing and monitoring of the hpG-CSF hybridization as indicated below, to gauge the degree of confidence with which the
30 results of less than stringent washing might be accepted.

Example 4

35 According to the procedure of Hanahan, et al., J. Mol. Biol., 166, 557-580 (1983), bacteria containing

recombinants with cDNA inserts as prepared in Example 2 were spread on 24 nitrocellulose filters (Millipore, Bedford, Massachusetts) laid on agar plates. The plates were then incubated to establish approximately 150,000 colonies which were replica plated to 24 other nitrocellulose filters. The replicas were incubated until distinct colonies appeared. The bacteria on the filters were lysed on sheets of Whatman 3 MM paper barely saturated with sodium hydroxide (0.5M) for 10 minutes, then blotted with Tris (1M) for 2 minutes, followed by blotting with Tris (0.5M) containing NaCl (1.5M) for 10 minutes. When the filters were nearly dry, they were baked for 2 hours at 80°C. in a vacuum oven prior to nucleic acid hybridization. [Wahl, et al., Proc. Natl. Acad. Sci. (USA), 76, 3683-3687 (1979)]; and Maniatis, et al., Cell, 81, 163-182 (1976).

The filters were prehybridized for 2 hours at 65°C. in 750 ml of 10X Denhardt's, 0.2% SDS and 6X SSC. The filters were rinsed in 6X SSC, then placed four in a bag and hybridized for 14 hours in 6X SSC and 10X Denhardt's. There was approximately 15 ml of solution per bag containing 50×10^6 cpm of ^{32}P -labeled probe (oligonucleotides).

After hybridization, the filters were washed three times in 6X SSC (1 liter/wash) at room temperature for 10 minutes each. The filters were then washed two times at 45°C. for 15 minutes each, once at 50° for 15 minutes and once at 55°C. for 15 minutes using 1 liter volumes of 6X SSC. The filters were autoradiographed for 2 hours at -70°C. using an intensifying screen and Kodak XAR-2 film. On this autoradiograph, there were 40-50 positive signals detected including 5 very intense signals.

The areas containing the strongest five signals and an additional five positives were scraped from the master plates and replated for a secondary

screening using the same probe mixture under the same conditions. The wash procedure differed in that the high temperature washes consisted of two at 55°C. for 15 minutes each and then one at 60°C. for 15 minutes.

- 5 Based on the N-myc probe study of Example 3, the final wash temperature in the second screening was raised because the aggregate melting temperature for the 24 23-mers was 60-68°C., similar to that of the N-myc probes. Just after the second 55°C. wash, the filters
10 were left damp and an autoradiograph was made. Comparison of this autoradiograph with a second autoradiograph taken for a similar period of time after a final wash at 60°C. showed that only two of the 10 clones being tested did not suffer a substantial loss in signal in rising
15 from 55-60°C. These two clones were later shown to be of nearly identical lengths and restriction endoclease patterns. One clone designated Ppo2, was selected for sequencing.

- Sequencing of the recombinant hpG-CSF cDNA
20 clone, Ppo2, obtained by the above procedure was accomplished by the dideoxy method of Sanger, et al., Proc. Natl. Acad. Sci. (USA) 74, 5463-5467 (1977). The single-stranded DNA phage M-13 was used as a cloning vector for supplying single-stranded DNA templates from
25 the double-stranded cDNA clones. The Sanger, et al., method revealed the sequence as set forth in Table VII accompanied by its amino acid translation and a complementary strand in the polypeptide coding region.

30

35

TABLE VII

HindIII

5' - AGCTTGGACTCAGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG{fNNNNN}

	-12			-10									-1	+1					
	Leu	Trp	His	Ser	Ala	Leu	Trp	Thr	Val	Gln	Glu	Ala	Thr	Pro	Leu	Gly	Pro		
	CTG	TGG	CAC	AGT	GCA	CTC	TGG	ACA	GTG	CAG	GAA	GCC	ACC	CCC	CTG	GGC	CCT		
	GAC	ACC	GTG	TCA	CGT	GAG	ACC	TGT	CAC	GTC	CTT	CGG	TGG	GGG	GAC	CCG	GGA		
				<u>HgiAI</u>												<u>ApaI</u>			
	10											20							
Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu	Leu	Lys	Cys	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln
GCC	AGC	TCC	CTG	CCC	CAG	AGC	TTC	CTG	CTC	AAG	TGC	TTA	GAG	CAA	GTG	AGG	AAG	ATC	CAG
CGG	TCG	AGG	GAC	GGG	GTC	TCG	AAG	GAC	GAG	TTC	ACG	AAT	CTC	GTT	CAC	TCC	TTC	TAG	GTC
	30											40							
Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu
GGC	GAT	GGC	GCA	GCG	CTC	CAG	GAG	AAG	CTG	TGT	GCC	ACC	TAC	AAG	CTG	TGC	CAC	CCC	GAG
CCG	CTA	CCG	CGT	CGC	GAG	GTC	CTC	TTC	GAC	ACA	CGG	TGG	ATG	TTC	GAC	ACG	GTG	GGG	CTC
	50											60							
Glu	Leu	Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	Cys	Pro
GAG	CTG	GTG	CTG	CTC	GGA	CAC	TCT	CTG	GGC	ATC	CCC	TGG	GCT	CCC	CTG	AGC	AGC	TGC	CCC
CTC	GAC	CAC	GAC	GAG	CCT	GTG	AGA	GAC	CCG	TAG	GGG	ACC	CGA	GGG	GAC	TCG	TCG	ACG	GGG
	70											80							
Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	Phe	Leu	Tyr
AGC	CAG	GCC	CTG	CAG	CTG	GCA	GGC	TGC	TTG	AGC	CAA	CTC	CAT	AGC	GGC	CTT	TTC	CTC	TAC
TCG	GTC	CGG	GAC	GTC	GAC	CGT	CCG	ACG	AAC	TCG	GTT	GAG	GTA	TCG	CCG	GAA	AAG	GAG	ATG
	90											100							
Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr
CAG	GGG	CTC	CTG	CAG	GCC	CTG	GAA	GGG	ATC	TCC	CCC	GAG	TTG	GGT	CCC	ACC	TTG	GAC	ACA
GTC	CCC	GAG	GAC	GTC	CGG	GAC	CTT	CCC	TAG	AGG	GGG	CTC	AAC	CCA	GGG	TGG	AAC	CTG	TGT

TABLE VII (cont'd.)

110														120					
Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly
CTG	CAG	CTG	GAC	GTC	GCC	GAC	TTT	GCC	ACC	ACC	ATC	TGG	CAG	CAG	ATG	GAA	GAA	CTG	GGA
GAC	GTC	GAC	CTG	CAG	CGG	CTG	AAA	CGG	TGG	TGG	TAG	ACC	GTC	GTG	TAC	CTT	CTT	GAC	CCT
130														140					
Met	Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	Ala	Phe	Gln
ATG	GCC	CCT	GCC	CTG	CAG	CCC	ACC	CAG	GGT	GCC	ATG	CCG	GCC	TTC	GCC	TCT	GCT	TTC	CAG
TAC	CGG	GGA	CGG	GAC	GTC	GGG	TGG	CTC	CCA	CGG	TAC	GGC	CGG	AAG	CGG	AGA	CGA	AAG	GTC
150														160					
Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln	Ser	Phe	Leu	Glu	Val	Ser	Tyr
CGC	CGG	GCA	GGA	GGG	GTC	CTG	GTT	GCC	TCC	CAT	CTG	CAG	AGC	TTC	CTG	GAG	GTG	TCG	TAC
GCG	GCC	CGT	CCT	CCC	CAG	GAC	CAA	CGG	AGG	GTA	GAC	GTC	TCG	AAG	GAC	CTC	CAC	AGC	ATG
170														174					
Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	OP										
CGC	GTT	CTA	CGC	CAC	CTT	GCC	CAG	CCC	TGA	GCC	AAG	CCC	TCC	CCA	TCC	CAT	GTA	TTT	ATC
CGC	CAA	GAT	GCG	GTG	GAA	CGG	GTC	GGG	ACT										
TCT ATT TAA TAT TTA TGT CTA TTT AAG CCT CAT ATT TAA AGA CAG GGA AGA GCA GAA CGG																			
AGC CCC AGG CCT CTG TGT CCT TCC CTG CAT TTC TGA GTT TCA TTC TCC TGC CTG TAG CAG																			
<u>StuI</u>																			
TGA GAA AAA GCT CCT GTC CTC CCA TCC CCT GGA CTG GGA GGT AGA TAG GTA AAT ACC AAG																			
TAT TTA TTA CTA TGA CTG CTC CCC AGC CCT GGC TCT GCA ATG GGC ACT GGG ATG AGC CGC																			
TGT GAG CCC CTG GTC CTG AGG GTC CCC ACC TGG GAC CCT TGA GAG TAT CAG GTC TCC CAC																			

TABLE VII (cont'd.)

GTG GGA GAC AAG AAA TCC CTG TTT AAT ATT TAA ACA GCA GTG TTC CCC ATC TGG GTC CTT
GCA CCC CTC ACT CTG GCC TCA GCC GAC TGC ACA GCG GCC CCT GCA TCC CCT TGG CTG TGA
GGC CCC TGG ACA AGC AGA GGT GGC CAG AGC TGG GAG GCA TGG CCC TGG GGT CCC ACG AAT
TTG CTG GGG AAT CTC GTT TTT CTT CTT AAG ACT TTT GGG ACA TGG TTT GAC TCC CGA ACA
TCA CCG ACG TGT CTC CTG TTT TTC TGG GTG GCC TCG GGA CAC CTG CCC TGC CCC CAC GAG
GGT CAG GAC TGT GAC TCT TTT TAG GGC CAG GCA GGT GCC TGG ACA TTT GCC TTG CTG GAC
GGG GAC TGG GGA TGT GGG AGG GAG CAG ACA GGA GGA ATC ATG TCA GGC CTG TGT GTG AAA
GGA AGC TCC ACT GTC ACC CTC CAC CTC TTC ACC CCC CAC TCA CCA GTG TCC CCT CCA CTG
TCA CAT TGT AAC TGA ACT TCA GGA TAA TAA AGT GTT TGC CTC CA

[f150-200 base poly A plus 25-30 bases plasmid DNA preceding a PvuII restriction site]-3'

The following characteristics of the sequence of Table VII are of note. At the 5' end of the sequence there are shown bases corresponding to those of the poly G cDNA linker. There then occur about five bases (designated as "N") whose sequence could not readily be
5 determined unambiguously by the Sanger, et al. method due to the preceding multiple G's. The sequence thereafter reveals a series of 12 codons encoding a portion of a putative leader sequence for the polypeptide. Based on correspondence to the amino terminal sequence
10 of natural isolates of hpCSF described in Example 1, the initial threonine residue of the putative "mature" form of hpG-CSF is indicated by +1. Mature hpG-CSF is thereafter revealed to include 174 residues as indicated. Following the "stop" codon (the OP codon,
15 TGA) are approximately 856 bases of an untranslated 3' sequence and multiple A's of the poly A "tail". Unique HgiAi, and ApaI restriction endonuclease recognition sites, as well as two StuI sites (discussed infra with respect to construction of procaryotic and eucaryotic
20 expression systems) are also designated in Table VII. Owing to the lack of asparagine residues in the polypeptide, there are no apparent sites for N-glycosylation. The underscored 6 bases near the end of the 3' untranslated sequence represent a potential
25 polyadenylation site.

It is noteworthy that each of two additional cDNA clones identified by the hybridization procedures described above from among a total of 450,000 clones failed to include DNA encoding the entire leader
30 sequence from the transcription initiation site onward. Indeed, all three hpG-CSF clones terminated in the 5' region at exactly the same site, indicating that secondary structure of the mRNA transcribed severely hinders cDNA formation beyond this site. As a practical
35

matter, therefore, cDNA expression screening such as described in Okayama, et al., Mol. and Cell. Biol., 3, 280-289 (1983) and as actually employed to isolate GM-CSF in Wong, et al., Science, 228, 810-814 (1985) could
5 not have readily applied to isolation of hpCSF DNA because such isolation systems ordinarily rely upon the presence of a full length cDNA transcript in the clones assayed.

The above sequence is not readily susceptible
10 for securing direct expression of hpG-CSF in a microbial host. To secure such expression, the hpG-CSF coding region should be provided with an initial ATG codon and the sequence should be inserted in a transformation vector at a site under control of a suitable promoter/-
15 regulator DNA sequence.

Example 5

In this example, cDNA encoding hpG-CSF as
20 isolated in the previous example was used to screen a genomic clone. A phage lambda human fetal liver genomic library [prepared according to the procedure of Lawn, et al. Cell, 15, 1157-1174 (1978) and obtained from T. Maniatis] was screened using a nick translated probe
25 consisting of two hpG-CSF cDNA fragments isolated by digestion with HgiAI and StuI (HgiAI to StuI, 649 b.p.; StuI to StuI, 639 b.p.). A total of approximately 500,000 phage were plated on 12 (15 cm) petri dishes and plaque lifted and hybridized to probe using the
30 Benton/Davison procedure [Benton, et al., Science, 196, 180 (1977)]. A total of 12 positive clones were observed. Three clones (1-3) yielding the strongest signals upon autoradiography in a secondary screening were grown in 1 liter cultures and mapped by restriction
35 enzyme digestion and Southern blotting using a radio-labeled 24-mer oligonucleotide (kinased with γ -³²P ATP)

5'CTGCACTGTCCAGAGTGCCTGTG3'. The mapping results showed that isolates 1 and 3 were identical and 2 contained 2000 additional bases 5' to the hpG-CSF gene. Therefore, clone 2 was used for further characterization. DNA from clone 2 was digested with R1 to release an 8500 bp hpG-CSF containing fragment which was subsequently subcloned into pBR322 and further mapped by restriction endonuclease digests, Southern Blotting, M13 subcloning and sequencing. The sequence obtained is as set out in Table VIII.

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TABLE VIII

GGGGACAGGCTTGAGAATCCCAAAGGAGAGGGGCAAAGGACACTGCCCCGCAAGTCTGCCAGAGCAGAGAGGGAGACCCCGACTCAGCTGCCACTTCCC	100
CACAGGCTCGTGCCGCTTCCAGGCGTCTATCAGCGGCTCAGCCTTTGTTTCAGCTGTTCTGTTCAAACACTCTGGGGCCATTTCAGGCCTGGGTGGGGCAGC	200
GGGAGGAAGGGAGTTTGAGGGGGGCAAGGCGACGTCAAAGGAGGATCAGAGATTCCACAATTTACAAAACCTTCGCAAACAGCTTTTTGTTCCAACCCC	300
CCTGCATTGTCTTGACACCAAATTTGCATAAATCCTGGGAAGTTATTACTAAGCCTTAGTCGTGGCCCCAGGTAATTCCTCCCAGGCCTCCATGGGGT	400
	-30
	MetAlaGlyProAlaThrGlnSerProM
TATGTATAAAGGGCCCCCTAGAGCTGGGCCCCAAAACAGCCCGGAGCCTGCAGCCCAGCCCCACCCAGACCCATGGCTGGACCTGCCACCCAGAGCCCCA	500
	-20 -18
etLysLeuMetA	
TGAAGCTGATGGGTGAGTGTCTTGGCCCAGGATGGGAGAGCCGCTGCCCTGGCATGGGAGGGAGGCTGGTGTGACAGAGGGGCTGGGGATCCCCGTTCT	600
	-16
	laLeuGlnLeuL
GGGAATGGGGATTAAAGGCACCCAGTGTCCCCGAGAGGGCCTCAGGTGGTAGGGAACAGCATGTCTCCTGAGCCCGCTCTGTCCCCAGCCCTGCAGCTGC	700

TABLE VIII (cont'd.)

-10	-1 +1	10	20	
euLeuTrpHisSerAlaLeuTrpThrValGlnGluAlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysCysLeuGluGlnVa				
TGCTGTGGCACAGTGCACCTCTGGACAGTGCAGGAAGCCACCCCCCTGGGCCCTGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGCTTAGAGCAAGT				800
	30	35		
lArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeu				
GAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAGGAGAAGCTGGTGAGTGAGGTGGGTGAGAGGGCTGTGGAGGGAAGCCCGGTGGGGAGAGCTAAGGGG				900
GATGGAACTGCAGGGCCAACATCCTCTGGAAGGGACATGGGAGAATATTAGGAGCAGTGGAGCTGGGGAAGGCTGGGAAGGGACTTGGGGAGGAGGACCT				1000
TGGTGGGGACAGTGCTCGGGAGGGCTGGCTGGGATGGGAGTGGAGGCATCACATTCAGGAGAAAGGGCAAGGGCCCCCTGTGAGATCAGAGAGTGGGGGTG				1100
CAGGGCAGAGAGGAACTGAACAGCCTGGCAGGACATGGAGGGAGGGGAAAGACCAGAGAGTCGGGGAGGACCCGGGAAGGAGCGGCGACCCGGCCACGGC				1200
	36	40	50	
CysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpA				
GAGTCTCACTCAGCATCCTTCCATCCCCAGTGTGCCACCTACAAGCTGTGCCACCCGAGGAGCTGGTGCTGCTCGGACACTCTCTGGGCATCCCCTGGG				1300

TABLE VIII (cont'd.)

60	70 71		
1aProLeuSerSerCysProSerGlnAlaLeuGlnLeu			
CTCCCCTGAGCAGCTGCCCCAGCCAGGCCCTGCAGCTGGTGAGTGTGAGGAAAGGATAAGGCTAATGAGGAGGGGGAAGGAGAGGAGGAACACCCATGGG			1400
		72	
		AlaGlyCysLeuSerGln	
CTCCCCCATGTCTCCAGGTTCCAAGCTGGGGGCCTGACGTATCTCAGGCAGCACCCCCTAACTCTTCCGCTCTGTCTCACAGGCAGGCTGCTTGAGCCAA			1500
80	90	100	110
LeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValA			
CTCCATAGCGGCCTTTTCCTCTACCAGGGGCTCCTGCAGGCCCTGGAAGGGATCTCCCCGAGTTGGGTCCACCTTGGACACACTGCAGCTGGACGTCG			1600
	120		
1aAspPheAlaThrThrIleTrpGlnGln			
CCGACTTTGCCACCACCATCTGGCAGCAGGTGAGCCTTGTTGGGCAGGGTGGCCAAGGTCGTGCTGGCATTCTGGGCACCACAGCCGGGCCTGTGTATGG			1700
		121	
		MetGluG	
GCCCTGTCCATGCTGTCAGCCCCCAGCATTTTCCTCATTTGTAATAACGCCCACTCAGAAGGGCCCAACCACTGATCACAGCTTTCCCCCACAGATGGAAG			1800

TABLE VIII (cont'd.)

130										140										150										
luLeuGlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAlaSerHi																														
AACTGGGAATGGCCCCTGCCCTGCAGCCCACCCAGGGTGCCATGCCGGCCTTCGCCTCTGCTTTCCAGCGCCGGGCAGGAGGGGTCTGGTTGCCTCCCA																														1900
160										170										174										
sLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnProOP																														
TCTGCAGAGCTTCCTGGAGGTGTCGTACCGCGTTCTACGCCACCTTGCCCAGCCCTGAGCCAAGCCCTCCCCATCCCATGTATTTATCTCTATTTAATAT																														2000
TTATGTCTATTTAAGCCTCATATTTAAAGACAGGGAAGAGCAGAACGGAGCCCCAGGCCTCTGTGTCCTTCCCTGCATTTCTGAGTTTCATTCTCCTGCC																														2100
TGTAGCAGTGAGAAAAAGCTCCTGTCTCTCCCATCCCCTGGACTGGGAGGTAGATAGGTAAATACCAAGTATTTATTACTATGACTGCTCCCCAGCCCTGG																														2200
CTCTGCAATGGGCACTGGGATGAGCCGCTGTGAGCCCCCTGGTCTGAGGGTCCCCACCTGGGACCCTTGAGAGTATCAGGTCTCCCACGTGGGAGACAAG																														2300
AAATCCCTGTTTAATATTTAAACAGCAGTGTTCCCCATCTGGGTCCCTTGCACCCCTCACTCTGGCCTCAGCCGACTGCACAGCGGCCCTGCATCCCCTT																														2400
GGCTGTGAGGCCCTGGACAAGCAGAGGTGGCCAGAGCTGGGAGGCATGGCCCTGGGGTCCCACGAATTTGCTGGGGAATCTCGTTTTTCTTCTTAAGAC																														2500
TTTTGGGACATGGTTTGACTCCCGAACATCACCGACGTGTCTCCTGTTTTTCTGGGTGGCCTCGGGACACCTGCCCTGCCCCACGAGGGTCAGGACTGT																														2600

TABLE VIII (cont'd.)

GACTCTTTTAGGGCCAGGCAGGTGCCTGGACATTTGCCTTGCTGGATGGGGACTGGGGATGTGGGAGGGAGCAGACAGGAGGAATCATGTCAGGCCTGT	2700
GTGTGAAAGGAAGCTCCACTGTCACCTCCACCTCTTCACCCCCCACTCACCAGTGTCCCCTCCACTGTCACATTGTAAGTGAAGTTCAGGATAATAAAG	2800
TGTTTGCCTCCAGTCACGTCCTTCCTCCTTCTTGAGTCCAGCTGGTGCCTGGCCAGGGGCTGGGGAGGTGGCTGAAGGGTGGGAGAGGCCAGAGGGAGGT	2900
CGGGGAGGAGGTCTGGGGAGGAGGTCCAGGGAGGAGGAGGAAAGTTCTCAAGTTCGTCTGACATTCATTCCGTTAGCACATATTTATCTGAGCACCTACT	3000
CTGTGCAGACGCTGGGCTAAGTGCTGGGGACACAGCAGGGAACAAGGCAGACATGGAATCTGCACTCGAG	3070

A restriction endonuclease map (approximately 3.4 Kb) of genomic DNA containing the hpG-CSF gene is detailed in Figure 1. The restriction endonucleases shown in Figure 1 are: NcoI, N; PstI, P; BamHI, B; 5 ApaI, A; XhoI, X; and Kpn, K. The arrows below the map depict the sequencing strategy used to obtain the genomic sequence. The boxed regions are those found in the cDNA clone with the dashed open ended box representing sequence not present in the cDNA clone, but 10 identified by probing mRNA blots. The identification of coding sequences proposed for exon one was carried out by Northern blot analysis. A 24 mer oligonucleotide probe, 5'CAGCAGCTGCAGGGCCATCAGCTT³', spanning the predicted splice junctures for exons 1 and 2 was hybridized 15 to hpG-CSF mRNA in a Northern blot format. The resulting blot shows an mRNA the same size (~1650 bp) as that seen with an exon 2 oligonucleotide probe. This data combined with the ability to direct expression of hpG-CSF from the pSVGM-Ppol vector (Example 9) using the 20 Met initiation codon depicted in Table VIII, defines the coding sequences contained in exon 1. Exons 2-5 are defined by the coding sequences obtained in the cDNA clone (Ppo2) of the hpG-CSF gene (Table VII).

25 Example 6

This example relates to preparation of a manufactured gene encoding hpG-CSF and including E.coli preference codons.

30 Briefly stated, the protocol employed was generally as set out in the disclosure of co-owned Alton, et al., PCT Publication No. WO83/04053, which is incorporated by reference herein. The genes were designed for initial assembly of component oligonucleo- 35 tides into multiple duplexes which, in turn, were assembled into three discrete sections. These sections

were designed for ready amplification and, upon removal from the amplification system, could be assembled sequentially or through a multiple fragment ligation in a suitable expression vector.

5 The construction of Sections I, II and III is illustrated in Table IX through XIV. In the construction of Section I, as illustrated in Tables IX and X, oligonucleotides 1-14 were assembled into 7 duplexes (1 and 8); 2 and 9; 3 and 10; 4 and 11; 5 and 12; 6 and 13; and
10 7 and 14). The 7 duplexes were then ligated to form Section I as shown in Table X. It may also be noted in Table X that Section I includes an upstream XbaI sticky end and a downstream BamHI sticky end useful for ligation to amplification and expression vectors and for
15 ligation to Section II.

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30

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TABLE IX

EChpG-CSFDNA SECTION I

5	CTAGAAAAACCAAGGAGGTAATAAA	1
	TAATGACTCCATTAGGTCCTGCTTCTTCT	2
	CTGCCGCAAAGCTTTCTGCTGAAATGTCTGG	3
	AACAGGTTCGTAAAATCCAGGGTGACGGT	4
	GCTGCACTGCAAGAAAACTGTGCGCTA	5
10	CTTACAAACTGTGCCATCCGGAAGAGC	6
	TGGTACTGCTGGGTCATTCTCTTGG	7
	CATTATTTATTACCTCCTTGGTTTTTT	8
	GCAGAGAAGAAGCAGGACCTAATGGAGT	9
	TGTTCCAGACATTTTCAGCAGAAAGCTTTGCG	10
15	CAGCACCGTCACCCTGGATTTTACGAACC	11
	TAAGTAGCGCACAGTTTTTCTTGCAGTG	12
	ACCAGCTCTTCCGGATGGCACAGTTTG	13
	GATCCCAAGAGAATGACCCAGCAGT	14
20		
25		
30		
35		

TABLE X

EChpG-CSFDNA SECTION I

10	1	20	30	40	2	50	60
CTAGAAAAA	ACCAAGGAGG	TAATAAATAA	TGACTCCATT	AGGTCCTGCT	TCTTCTCTGC		
TTTTT	TGGTTCCTCC	ATTATTTATT	ACTGAGGTAA	TCCAGGACGA	AGAAGAGACG		
	<u>8</u>				<u>9</u>		
<u>XbaI</u>							
70	3	80	90	100	4	110	120
CGCAAAGCTT	TCTGCTGAAA	TGTCTGGAAC	AGGTTTCGTAA	AATCCAGGGT	GACGGTGCTG		
GCGTTTCGAA	AGACGACTTT	ACAGACCTTG	TCCAAGCATT	TTAGGTCCCA	CTGCCACGAC		
	<u>10</u>				<u>11</u>		
130	5	140	150	160	6	170	180
CACTGCAAGA	AAAAGTGTGC	GCTACTTACA	AACTGTGCCA	TCCGGAAGAG	CTGGTACTGC		
GTGACGTTCT	TTTTGACACG	CGATGAATGT	TTGACACGGT	AGGCCTTCTG	GACCATGACG		
	<u>12</u>				<u>13</u>		
7	190	100					
TGGGTCATTC	TCTTGG						
ACCCAGTAAG	AGAACCCTAG						
<u>14</u>							
<u>BamHI</u>							

As illustrated in Tables XI and XII, in the construction of Section II, oligonucleotides 15-30 were assembled into 8 duplexes (15 and 23; 16 and 24; 17 and 25; 18 and 26; 19 and 27; 20 and 28; 21 and 29; and 22 and 30). These 8 duplexes were then ligated to form Section II, as shown in Table XII. As further shown in Table XII, Section II has an upstream BamHI sticky end and a downstream EcoRI sticky end useful for ligation to an amplification vector and for ligation to Section I.

10 Near its downstream end, Section II also includes a downstream SstI site useful in the eventual ligation Sections II and III.

TABLE XI

15	EChpG-CSFDNA SECTION II	
	GATCCCGTGGGCTCCGCTGTCTTCT	15
20	TGTCCATCTCAAGCTCTTCAGCTGGC	16
	TGGTTGTCTGTCTCAACTGCATTCTGGT	17
	CTGTTCCCTGTATCAGGGTCTTCTG	18
	CAAGCTCTGGAAGGTATCTCTCCGGA	19
	ACTGGGTCCGACTCTGGACACTCTGCA	20
25	GCTAGATGTAGCTGACTTTGCTACTACT	21
	ATTTGGCAACAGATGGAAGAGCTCAAAG	22
	GACAAGAAGACAGCGGAGCCACGG	23
	ACCAGCCAGCTGAAGAGCTTGAGATG	24
	ACAGACCAGAATGCAGTTGAGACAGACA	25
30	CTTGCAGAAGACCCTGATACAGGA	26
	CAGTTCCGGAGAGATACCTTCCAGAG	27
	TAGCTGCAGAGTGTCAGAGTCGGACC	28
	AAATAGTAGTAGCAAAGTCAGCTACATC	29
	AATTCTTTGAGCTCTTCCATCTGTTGCC	30
35		

TABLE XII

EChpG-CSFDNA SECTION II

10	15	20	30	40	16	50	60	
GATCCCGTG	GGCTCCGCTG	TCTTCTTGTC	CATCTCAAGC	TCTTCAGCTG	GCTGGTTGTC			
GGCAC	CCGAGGCGAC	AGAAGAACAG	GTAGAGTTCG	AGAAGTCGAC	CGACCAACAG			
	23			24				
BamHI								
70	17	80	90	18	100	110	19	120
TGTCTCAACT	GCATTCTGGT	CTGTTCTTGT	ATCAGGGTCT	TCTGCAAGCT	CTGGAAGGTA			
ACAGAGTTGA	CGTAAGACCA	GACAAGGACA	TAGTCCCAGA	AGACGTTCGA	GACCTTCCAT			
	25			26			27	
130	140	20	150	160	170	21	180	
TCTCTCCGGA	ACTGGGTCCG	ACTCTGGACA	CTCTGCAGCT	AGATGTAGCT	GACTTTGCTA			
AGAGAGGCCT	TGACCCAGGC	TGAGACCTGT	GAGACGTCGA	TCTACATCGA	CTGAAACGAT			
		28					29	
190	200	22	210					
CTACTATTTG	GCAACAGATG	GAAGAGCTCA	AAG					
GATGATAAAC	CGTTGTCTAC	CTTCTCGAGT	TTCTTAA					
		30						
		SstI		EcoRI				

Finally, Section III was constructed as shown in Tables XIII and XIV. For this construction, oligonucleotides 31-42 were assembled into 6 duplexes (31 and 37; 32 and 38; 33 and 39; 34 and 40; 35 and 41; and 36 and 42). The 6 duplexes were then ligated to form Section III as depicted in Table XIV. As also shown in Table XIV, Section III includes an upstream BamHI sticky end and a downstream EcoRI sticky end useful for ligating into an amplification vector, and at least in the case of the EcoRI end, into an expression vector. In addition, Section II has an upstream SstI site useful in the eventual ligation of Sections II and III.

15

TABLE XIII

EChpG-CSFDNA SECTION III

20	GATCCAAAGAGCTCGGTATGGCACCAG	31
	CTCTGCAACCGACTCAAGGTGCTATGCCG	32
	GCATTGCTTCTGCATTCCAGCGTCGTGC	33
	AGGAGGTGTACTGGTTGCTTCTCATCTG	34
	CAATCTTTCCTGGAAGTATCTTACCGTGT	35
25	TCTGCGTCATCTGGCTCAGCCGTAATAG	36
	AGAGCTGGTGCCATACCGAGCTCTTTG	37
	ATGCCGGCATAGCACCTTGAGTCGGTTGC	38
	TCCTGCACGACGCTGGAATGCAGAAGCGA	39
	ATTGCAGATGAGAAGCAACCAGTACACC	40
30	CAGAACACGGTAAGATACTTCCAGGAAAG	41
	AATTCTATTACGGCTGAGCCAGATGACG	42

35

TABLE XIV

EChpG-CSFDNA SECTION III

10	31	20	30	40	32	50	60
GATCCAAAG	AGCTCGGTAT	GGCACCAGCT	CTGCAACCGA	CTCAAGGTGC	TATGCCGGCA		
GTTTC	TCGAGCCATA	CCGTGGTCGA	GACGTTGGCT	GAGTTCCACG	ATACGGCCGT		
		37			38		
<u>BamHI</u>	<u>SstI</u>						
70	33	80	90	100	34	110	120
TTCGCTTCTG	CATTCCAGCG	TCGTGCAGGA	GGTGTACTGG	TTGCTTCTCA	TCTGCAATCT		
AAGCGAAGAC	GTAAGGTCGC	AGCACGTCCT	CCACATGACC	AACGAAGAGT	AGACGTTAGA		
	39				40		
35	130	140	150	36	160	170	
TTCCTGGAAG	TATCTTACCG	TGTTCTGCGT	CATCTGGCTC	AGCCGTAATA	G		
AAGGACCTTC	ATAGAATGGC	ACAAGACGCA	GTAGACCGAG	TCGGCATTAT	CTTAA		
41				42			
					<u>EcoRI</u>		

The XbaI to BamHI fragment formed by Section I is ligated into an M13mp11 phage vector opened with XbaI and BamHI. The vector is then reopened by digestion with BamHI and EcoRI, followed by ligation with the
5 BamHI to EcoRI fragment formed by Section II. At this stage, Sections I and II have been joined in proper orientation. Next, another M13mp11 vector is opened by BamHI to EcoRI digestion and then ligated with the BamHI to EcoRI fragment formed by Section III.

10 The vector containing Sections I and II is digested with XbaI and SstI. Likewise, the vector containing Section III is digested with SstI and EcoRI. Both of the smaller of the two fragments resulting from each digestion are ligated into a a plasmid pCFM1156
15 which is previously opened with XbaI and EcoRI. The product of this reaction is an expression plasmid containing a continuous DNA sequence, as shown in Table XV, encoding the entire hpG-CSF polypeptide with an amino terminal methionine codon (ATG) for E.coli translation
20 initiation.

25

30

35

TABLE XV

											-1	+1								
	C	TAG	AAA	AAA	CCA	AGG	AGG	TAA	TAA	ATA	Met	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu
											ATG	ACT	CCA	TTA	GGT	CCT	GCT	TCT	TCT	CTG
10											20									
CCG	CAA	AGC	TTT	CTG	CTG	AAA	TGT	CTG	GAA	CAG	GTT	CGT	AAA	ATC	CAG	GGT	GAC	GGT	GCT	
Pro	Gln	Ser	Phe	Leu	Leu	Lys	Cys	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	
30											40									
Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu	
GCA	CTG	CAA	GAA	AAA	CTG	TGC	GCT	ACT	TAC	AAA	CTG	TGC	CAT	CCG	GAA	GAG	CTG	GTA	CTG	
50											60									
Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	ala	Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln	Ala	Leu	
CTG	GGT	CAT	TCT	CTT	GGG	ATC	CCG	TGG	GCT	CCG	CTG	TCT	TCT	TGT	CCA	TCT	CAA	GCT	CTT	
70											80									
Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	leu	His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	
CAG	CTG	GCT	GGT	TGT	CTG	TCT	CAA	CTG	CAT	TCT	GGT	CTG	TTC	CTG	TAT	CAG	GGT	CTT	CTG	
90											100									
Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	
CAA	GCT	CTG	GAA	GGT	ATC	TCT	CCG	GAA	CTG	GGT	CCG	ACT	CTG	GAC	ACT	CTG	CAG	CTA	GAT	
110											120									
Val	Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	leu	Gly	Met	Ala	Pro	Ala	
GTA	GCT	GAC	TTT	GCT	ACT	ACT	ATT	TGG	CAA	CAG	ATG	GAA	GAG	CTC	GGT	ATG	GCA	CCA	GCT	
130											140									
Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	Ala	Phe	Gln	Arg	Arg	Ala	Gly	
CTG	CAA	CCG	ACT	CAA	GGT	GCT	ATG	CCG	GCA	TTC	GCT	TCT	GCA	TTC	CAG	CGT	CGT	GCA	GGA	

TABLE XV (cont'd.)

150 160
Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg
GGT GTA CTG GTT GCT TCT CAT CTG CAA TCT TTC CTG GAA GTA TCT TAC CGT GTT CTG CGT

170 174
His Leu Ala Gln Pro
CAT CTG GCT CAG CCG TAA TAG AAT T

Although any suitable vector may be employed to express this DNA, the expression plasmid pCFM1156 may readily be constructed from a plasmid pCFM836, the construction of which is described in published
5 European Patent Application No. 136,490. pCFM836 is first cut with NdeI and then blunt-ended with PoiI such that both existing NdeI sites are destroyed. Next, the vector is digested with ClaI and SacII to remove an existing polylinker before ligation to a substitute
10 polylinker as illustrated in Table XVI. This substitute polylinker may be constructed according to the procedure of Alton, et al., supra. Control of expression in the expression pCFM1156 plasmid is by means of a lambda P_L promoter, which itself may be under the control of a
15 C_{I857} repressor gene (such as is provided in E.coli strain K12ΔHtrp).

20

25

30

35

TABLE XVI

- 1 ATCGATTTGATTCTAGAAGGAGGAATAACATATGGTTAACGCGTTGGAATTCGGTACCAT
TAGCTAAACTAAGATCTTCCTCCTTATTGTATACCAATTGCGCAACCTTAAGCCATGGTA
- 1 Cl1, 12 XbaI, 29 NdeI, 35 HincII, HpaI, 39 MluI, 47 EcoRI, 53 HgiCI KpnI, 57 NcoI StyI,
- 61 GGAAGCTTACTCGAGGATCCGCGGATAAATAAGTAACGATCC
CCTTCGAATGAGCTCCTAGGCGCCTATTTATTCATTGCTAGG
- 63 HindIII, 70 AvaI XhoI, 75 BamHI Xho2, 79 Sac2,

Example 7

This example relates to E. coli expression of an hpG-CSF polypeptide by means of a DNA sequence encoding [Met⁻¹] hpCSF. The sequence employed was partially synthetic and partially cDNA-derived. The synthetic sequence employed E. coli preference codons.

Plasmid Ppo2, containing the hpG-CSF gene shown in Table VII, was digested with HgiAI and StuI providing an approximately 645 base pair fragment including the gene for mature hpCSF (as shown in Table VII) with seven of the leader sequence residue codons at the 5' end and about 100 base pairs of the 3' non-coding region. HgiAI digestion leaves a 5', 4-base sticky end identical to that of PstI, and StuI leaves a blunt end. This allows for ready insertion of the fragment into M13 mp8 (Rf) cut with PstI and with the blunt-end-forming restriction enzyme, HincII. Upon amplification in M13, the hpG-CSF DNA was excised by digestion with ApaI and BamHI which cut, respectively, at the ApaI site spanning the codons for residues +3 to +5 of hpCSF and at a BamHI site "downstream" of the HincII site in the M13 mp8 restriction polylinker. In order to allow for E. coli expression of the hpG-CSF polypeptide, a synthetic fragment was prepared as set out in Table XVII below.

TABLE XVII

30	5' - C TAG AAA AAA CCA AGG AGG TAA TAA ATA
	3' - TTT TTT GGT TCC TCC ATT ATT TAT
	<u>XbaI</u>
	-1 +1
	Met Thr Pro Leu
	ATG ACA CCT CTG GGC C - 5'
35	TAC TGT GGA GAC -3'
	<u>ApaI</u>

As may be determined from analysis of Table XVII, the linker includes an ApaI sticky end, codons specifying the initial three residues of the amino terminal of hpG-CSF ("restoring" the Thr¹, Pro², Leu³- specifying codons deleted upon ApaI digestion of the M13 DNA described above and employing codons preferentially expressed in E. coli), a translation initiating ATG, a sequence of 24 base pairs providing a ribosome binding site, and an XbaI sticky end.

The expression vector employed for E. coli expression was that described as pCFM536 in European Patent Application No. 136,490, by Morris, published April 10, 1985. (See also, A.T.C.C. 39934, E. coli JM103 harboring pCFM536). Briefly, plasmid pCFM536 was digested with XbaI and BamHI. The hpG-CSF fragment (ApaI/BamHI) and linker (XbaI/ApaI) described above were then ligated thereinto to form a plasmid designated p536Ppo2.

Plasmid p536Ppo2 was transformed into a phage resistant variant of the E. coli AM7 strain which has previously been transformed with plasmid pMW1 (A.T.C.C. No. 39933) harboring a CI^{857} gene. Transformation was verified on the basis of the antibiotic (amp) resistance marker gene carried on the pCFM536 progenitor plasmid. Cultures of cells in LB broth (ampicillin 50 μ g/ml) were maintained at 28°C. and upon growth of cells in culture to A600 = 0.5, hpCSF expression was induced by raising the culture temperature to 42°C. for 3 hours. The final O.D. of the culture was A600 = 1.2.

The level of expression of hpG-CSF by the transformed cells was estimated on a SDS-poly acrylamide gel stained with coomassie blue dye to be 3-5% of total cellular protein.

Cells were harvested by centrifugation at 3500 g for 10 minutes in a JS-4.2 rotor. Cells at 25% (w/v) in water were broken by passing 3 times through a

French Pressure Cell at 10,000 p.s.i. The broken cell suspension was centrifuged at 10,000 g for 15 minutes in a JA-20 rotor. The pellet was resuspended in water and solubilized at about 5 mg/ml total protein in 1% lauric acid, 50 mM Tris, pH 8.7. The solubilized pellet material was centrifuged at 15,000 g for 10 minutes and to the supernatant CuSO_4 was added to 20 mM. After 1 hour, this sample was loaded onto a C4 HPLC column for purification according to the procedures of example 1 (B) with adjustments made for volume and concentration.

A second purification procedure was developed to yield larger quantities of hpG-CSF formulated in a nonorganic-containing buffer. This material is suitable for in vivo studies. One hundred and fifty grams of cell paste was resuspended in about 600 ml of 1 mM DTT and passed 4 times through a Manton Gualin Homogenizer at about 7000 PSI. The broken cell suspension was centrifuged at 10,000 g for 30 minutes and the pellet was resuspended in 400 ml of 1% deoxycholate (DOC), 5 mM EDTA, 5 mM DTT, and 50 mM Tris, pH 9. This suspension was mixed at room temperature for 30 minutes and centrifuged at 10,000 g for 30 minutes. The pellet was resuspended in about 400 ml of water and centrifuged at 10,000 g for 30 minutes. The pellet was solubilized in 100 ml of 2% Sarkosyl and 50 mM at pH 8. CuSO_4 was added to 20 μM and the mixture was stirred 16 hours at room temperature, and then centrifuged at 20,000 g for 30 minutes. To the supernatant was added 300 ml acetone. This mixture was put on ice for 20 minutes and then centrifuged at 5000 g for 30 minutes. The pellet was dissolved in 250 ml of 6 M guanidine and 40 mM sodium acetate at pH 4, and put over a 1,200 ml G-25 column equilibrated and run in 20 mM sodium acetate at pH 5.4. The hpG-CSF peak (about 400 ml) was pooled and put on a 15 ml CM-cellulose column equilibrated in 20 mM

sodium acetate at pH 5.4. After loading, the column was washed with 60 ml of 20 mM sodium acetate at pH 5.4 and with 25 mM sodium chloride, and then the column was eluted with 200 ml of 20 mM sodium acetate at pH 5.4 and with 37 mM sodium chloride. 150 ml of this eluent was concentrated to 10 ml and applied to a 300 ml G-75 column equilibrated and run in 20 mM sodium acetate and 100 mM sodium chloride at pH 5.4. The peak fractions comprising 35 ml were pooled and filter sterilized. The final concentration of hpG-CSF was 1.5 mg/ml, is greater than 95% pure as determined by analysis on a gel, and contained less than 0.5 ng of pyrogen per 0.5 mg of hpG-CSF. The pyrogen level was determined using a Limulus Amebocyte Lysate (LAL) test kit (M. A. Bioproducts, Walkersville, Maryland).

Example 8

This example relates to the use of recombinant methods to generate analogs of hpG-CSF wherein cysteine residues present at positions 17, 36, 42, 64 and 74 were individually replaced by a suitable amino acid residue.

Site directed mutagenesis procedures according to Souza, et al., published PCT Application No. WO85/00817, published February 28, 1985, were carried out on [Met⁻¹] encoding DNA of plasmid p536Ppo2, described infra, using synthetic oligonucleotides ranging in size from 20 to 23 bases as set out in Table XVIII below. Oligonucleotide No. 1 allowed for formation of a gene encoding [Ser¹⁷]hpG-CSF; oligonucleotide No. 2 allowed for formation of [Ser³⁶]hpG-CSF, and so on.

TABLE XVIII

<u>Oligonucleotide</u>	<u>Sequence</u>
5 1.	5'-CTG CTC AAG TCC TTA GAG CAA GT-3'
2.	3'-GAG AAG CTG TCT GCC ACC TACA-3'
3.	5'-TAC AAG CTG TCC CAC CCC GAG-3'
4.	5'-TGA GCA GCT CCC CCA GCC AG-3'
5.	5'-CTG GCA GGC TCC TTG AGC CAA-3'
10	

The Cys to Ser site directed mutagenesis restrictions were carried out using M13 mp10 containing an XbaI-BamHI hpG-CSF fragment isolated from p536Ppo2 as a template. DNA from each M13mp10 clone containing a Cys-Ser substitution was treated with XbaI and BamHI. The resulting fragment was cloned into expression vector pCFM746 and expression products were isolated as in Example 7.

The plasmid pCFM746 may be constructed by cleaving a plasmid pCFM736 (the construction of which from deposited and publically available materials is described in Morris, published PCT Application No. WO85/00829, published February 28, 1985) with ClaI and BamHI to remove an existing polylinker and by substituting the following polylinker.

TABLE XIX

30	<u>ClaI</u>
	5' CGATTGATTCTAGAATTCGTTAACGGTACCATGGAA
	3' TAAACTAAGATCTTAAGCAATTGCCATGGTACCTT
	GCTTACTCGAGGATCCGCGGATAAATAAGTAAC ^{3'}
35	CGAATGAGCTCCTAGGCGCCTATTTATTCATTGCTAG ^{5'}
	<u>Sau3a</u>

In a purification procedure for Cys to Ser analogs according to the present invention, about 10-15 g of cell paste was resuspended in 40 ml of 1 mM DTT and passed 3 times through a French Pressure Cell at 10,000 psi. The broken cell suspension was centrifuged at 1,000 g for 30 minutes. The pellet was resuspended in 1% DOC, 5 mM EDTA, 5 mM DTT, 50 mM Tris, pH 9 and allowed to mix 30 minutes at room temperature. The mixture was centrifuged at 10,000 g for 30 minutes, resuspended in 40 ml H₂O, and recentrifuged as 10,000 g for 30 minutes. The pellet was dissolved in 10 ml of 2% Sarkosyl, 50 mM DTT, 50 mM Tris, pH 8. After mixing for 1 hour, the mixture was clarified by centrifugation at 20,000 g for 30 minutes, and then applied to a 300 ml G-75 column equilibrated and run in 1% Sarkosyl, 50 mM Tris, pH 8. Fractions containing the analog were pooled and allowed to air oxidize by standing with exposure to air for at least one day. Final concentrations ranged from 0.5 - 5 mg/ml.

Example 9

In this example, a mammalian cell expression system was devised to ascertain whether an active polypeptide product of hpG-CSF DNA could be expressed in and secreted by mammalian cells (COS-1, A.T.C.C. CRL-1650). This system was designed to provide for secretion of a polypeptide analog of hpGCSF via expression and secretory processing of a partially synthetic, partially cDNA-derived construction encoding [Ala¹] hpG-CSF preceded by a leader polypeptide having the sequence of residues attributed to human GM-CSF in Wong, et al., Science, 228, 810-815 (1985) and Lee, et al., Proc. Natl. Acad. Sci. (USA), 82, 4360-4364 (1985).

5 autonomous replication in both E. coli and mammalian cells, with mammalian cell expression of inserted exogenous DNA under control of a viral promoter/regulator DNA sequence. This vector, designated pSVDM-19, harbored in E. coli 101, was deposited August 23, 10 1985, with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, Maryland, and received the accession No. A.T.C.C. 53241.

The specific manipulations involved in the expression vector construction were as follows. A leader-encoding DNA sequence was synthesized as set out in Table XX below.

20

TABLE XX

-17

HindIII

Met Trp

25 5' - A GCT TCC AAC ACC ATG TGG
 3' - AGG TTG TGG TAC ACC

-10

	Leu	Gln	Ser	Leu	Leu	Leu	Leu	Gly	Thr	Val
	CTG	CAG	AGC	CTG	CTG	CTC	TTG	GGC	ACT	GTG
30	GAC	GTC	TCG	GAC	GAC	GAG	AAC	CCG	TGA	CAC

-1 +1

Ala Cys Ser Ile Ser Ala Pro Leu
GCC TGC AGC ATC TCT GCA CCC CTG GGC G -3'
35 CGG ACG TCG TAG AGA CGT GGG GAC -5'

Apa I

As indicated in Table XX, the sequence includes HindIII and ApaI sticky ends and codons for the 17 amino acid residues attributed to the "leader" of human GM-CSF. There follow codons specifying an alanine residue, a proline residue and a leucine residue. The proline and leucine residues duplicate the amino acids present at positions +2 and +3 of hpG-CSF, while the alanine residue is duplicative of the initial amino terminal (+1) residue of GM-CSF rather than hpG-CSF. Replacement of threonine by alanine was designed to be facilitative of proper host cell "processing off" of the GM-CSF leader by cellular mechanisms ordinarily involved in GM-CSF secretory processing.

Plasmid pSVDM-19 was digested with KpnI and the site was blunt ended with Klenow enzyme. Thereafter the DNA was cut with HindIII. The resulting large fragment was combined and ligated with the HindIII/PvuII fragment shown in Table VII (isolated from plasmid Ppo2 as the second largest fragment resulting from HindIII digestion and partial digestion with PvuII) to form plasmid pSV-Ppo1. The manufactured GM-CSF leader sequence fragment of Table VIII was then ligated into pSV-Ppo1 (following its cleavage with HindIII and ApaI) to yield plasmid pSVGM-Ppo1.

Calcium phosphate precipitates (1-5 μ g) of plasmid pSVGM-Ppo1 DNA was transformed into duplicate 60 mm plates of COS-1 cells essentially as described in Wigler, et al., Cell, 14, 725-731 (1978). As a control, plasmid pSVDM-19 was also transformed into COS-1 cells. Tissue culture supernatants were harvested 5 days post-transfection and assayed for hpG-CSF activity. Yields of [Ala¹]hpG-CSF from the culture supernatant were on the order of 1 to 2.5 μ g/ml.

Following successful expression of the [Ala¹]hpG-CSF product encoded plasmid pSVGM-Ppo1 in

COS-1 cells, another vector was constructed which included the human GM-CSF leader sequence but had a codon for a threonine residue (naturally occurring at position 1 of hpG-CSF) replacing the codon for alanine at that position. Briefly, an oligonucleotide was synthesized (5' CAGCATCTCTACACCTCTGGG) for site-directed mutagenesis (SDM). The HindIII to BamHI hpG-CSF fragment in pSVGM-Ppo1 was ligated into M13mp10 for the SDM. The newly synthesized hpG-CSF gene containing a Thr codon in position one was isolated by cleavage with HindIII and EcoRI. The fragment was then cloned into pSVDM-19 prepared by cleavage with the same two restriction endonucleases. The resulting vector pSVGM-Ppo(Thr) was transformed into COS cells and the yields of hpG-CSF measured in the culture supernates ranged from 1 to 5 µg/ml.

Finally, the genomic sequence whose isolation is described in Example 5 was employed to form an expression vector for mammalian cell expression of hpG-CSF. More specifically, pSVDM-19 was digested with KpnI and HindIII and the large fragment used in a four-way ligation with a synthetic linker with HindIII and NcoI sticky ends, as shown in Table XXI. An NcoI-BamHI fragment containing exon 1 isolated from pBR322 (8500 hpG-CSF), a genomic subclone, and a BamHI-KpnI fragment containing exons 2-5 isolated from the plasmid pBR322 (8500 hpG-CSF genomic subclone). The resulting mammalian expression vector, pSV/ghG-CSF produced 1 to 2.5 µg/ml of hpG-CSF from transformed COS cells.

TABLE XXI

HindIII
5' AGCTTCCAACAC
AGGTTGTGGTAC^{5'}
NcoI

Example 10

This example relates to physical and biological properties or recombinant polypeptide products of the invention.

1. Molecular Weight

Recombinant hpG-CSF products of E. coli expression as in Example 7 had an apparent molecular weight of 18.8 kD when determined in reducing SDS-PAGE (as would be predicted from the deduced amino acid analysis of Table VII., whereas natural isolates purified as described in Example 1 had an apparent molecular weight of 19.6 kD. The presence of N-glycans associated with the natural isolates could effectively be ruled out on the basis of the lack of asparagine residues in the primary sequence of hpG-CSF in Table VII and therefore a procedure was devised to determine if O-glycans were responsible for molecular weight differences between natural isolates and the non-glycosylated recombinant products. Approximately 5 µg of the natural isolate material was treated with neuraminidase (Calbiochem, LaJolla, California), a 0.5 µg sample was removed, and the remaining material was incubated with 4 mU O-Glycanase (endo-x-n-acetylgalactoseaminidase, Genzyme, Boston, Massachusetts) at 37°C. Aliquots were removed after 1/2, 2 and 4 hours of incubation. These samples were subjected to SDS-PAGE side by side with the E. coli derived recombinant material. After neuraminidase treatment, the apparent molecular weight of the isolate shifted from 19.6 kD to 19.2 kD, suggestive of removal of a sialic acid residue. After 2 hours of treatment with O-glycanase, the molecular weight shifted to 18.8 kD -- identical to the apparent molecular weight of the E. coli derived material. The sensitivity of the carbohydrate structure to neuraminidase and O-glycanase

suggests the following structure for the carbohydrate component: N-acetylneuraminic acid- α (2-6)(galactose β (1-3) N-acetylgalactosamine-R, wherein R is serine or threonine.

5

2. ^3H -Thymidine Uptake

Proliferation induction of human bone marrow cells was assayed on the basis of increased incorporation of ^3H -thymidine. Human bone marrow from
10 healthy donors was subjected to a density cut with Ficoll-Hypaque (1.077g/ml, Pharmacia) and low density cells were suspended in Iscove's medium (GIBCO) containing 10% fetal bovine serum and glutamine pen-strep. Subsequently, 2×10^4 human bone marrow cells were incubated with either control medium or the recombinant E. coli material of Example 7 in 96 flat bottom well plates at 37°C . in 5% CO_2 in air for 2 days. The samples were assayed in duplicate and the concentration varied over a 10,000 fold range. Cultures were then pulsed for 4
20 hours with $0.5 \mu\text{Ci/well}$ of ^3H -Thymidine (New England Nuclear, Boston, Massachusetts). ^3H -Thymidine uptake was measured as described in Ventua, et al., Blood, 61, 781 (1983). In this assay human hpG-CSF isolates can induce ^3H -Thymidine incorporation into human bone marrow
25 cells at levels approximately 4-10 times higher than control supernatants. The E. coli-derived hpG-CSF material of Example 6 had similar properties.

A second human bone marrow cell proliferation study was carried out using culture medium of trans-
30 fected COS-1 cells as prepared in Example 9 and yielded similar results, indicating that encoded polypeptide products were indeed secreted into culture medium as active materials.

35

3. WEHI-3B D⁺ Differentiation Induction

Capacity of recombinant, E. coli-derived materials to induce differentiation of the murine myelomonocytic leukemic cell line WEHI-3B D⁺ was assayed in semi-solid agar medium as described in Metcalf, Int. J. Cancer, 25, 225 (1980). The recombinant hpG-CSF product and media controls were incubated with ~60 WEHI-3B D⁺ cells/well at 37°C. in 5% CO₂ in air for 7 days. The samples were incubated in 24 flat bottom well plates and the concentration varied over a 2000-fold range. Colonies were classified as undifferentiated, partially differentiated or wholly differentiated and colony cell counts were counted microscopically. The E. coli recombinant material was found to induce differentiation.

4. CFU-GM, BFU-E and CFU-GEMM Assays

Natural isolates of pluripotent human G-CSF (hpG-CSF) and the recombinant pluripotent human G-CSF (rhG-CSF) were found to cause human bone marrow cells to proliferate and differentiate. These activities were measured in CFU-GM [Broxmeyer, et al., Exp.Hematol., 5, 87, (1971)] BFU-E and CFU-GEMM assays [Lu, et al., Blood, 61, 250 (1983)] using low density, non-adherent bone marrow cells from healthy human volunteers. A comparison of CFU-GM, BFU-E and CFU-GEMM biological activities using either 500 units of hpG-CSF or rhG-CSF are shown in Table XXII below.

All the colony assays were performed with low density non-adherent bone marrow cells. Human bone marrow cells were subject to a density cut with Ficoll-Hypaque (density, 1.077 g/cm³; Pharmacia). The low density cells were then resuspended in Iscove's modified Dulbecco's medium containing fetal calf serum and placed for adherence on Falcon tissue culture dishes (No. 3003, Becton Dickenson, Cockeysville, MD.) for 1-1/2 hours at 37°C.

TABLE XXII

	<u>CFU-GM</u>	<u>BFU-E</u>	<u>CFU-GEMM</u>
5			
Medium	0±0	26±1	0±0
natural			
hpG-CSF	83±5.4	83±6.7	4±0
rhG-CSF	87±5	81±0.1	6±2

10

Medium control consisted of Iscove's modified Dulbecco medium plus 10% FCS, 0.2 mM hemin and 1 unit of recombinant erythropoietin.

15 For the CFU-GM assay target cells were plated at 1×10^5 in 1 ml of 0.3% agar culture medium that included supplemented McCoy's 5A medium and 10% heat inactivated fetal calf serum. Cultures were scored for colonies (greater than 40 cells per aggregate) and mor-
20 phology assessed on day 7 of culture. The number of colonies is shown as the mean ±SEM as determined from quadruplicate plates.

For the BFU-E and CFU-GEMM assays, cells (1×10^5) were added to a 1 ml mixture of Iscove's modi-
25 fied Dulbecco medium (Gibco), 0.8% methylcellulose, 30% fetal calf serum 0.05 nM 2-mercaptoethanol, 0.2 mM hemin and 1 unit of recombinant erythropoietin. Dishes were incubated in a humidified atmosphere of 5% CO₂ and 5% O₂. Low oxygen tension was obtained using an oxyreducer
30 from Reming Bioinstruments (Syracuse, N.Y.). Colonies were scored after 14 days of incubation. The number of colonies is shown as the mean ±SEM, as determined from duplicate plates.

Colonies formed in the CFU-GM assay were all
35 found to be chloracetate esterase positive and non-specific esterase (alpha-naphthyl acetate esterase)

negative, consistent with the colonies being granulocyte in type. Both natural hpG-CSF and rhpG-CSF were found to have a specific activity of approximately 1×10^8 U/mg pure protein, when assayed by serial dilution in a CFU-GM assay. The BFU-E and CFU-GEMM data in Table XXII are representative of three separate experiments and similar to the data reported previously for natural hpG-CSF. It is important to note that the rhpG-CSF is extremely pure and free of other potential mammalian growth factors by virtue of its production in E.coli. Thus rhpG-CSF is capable of supporting mixed colony formation (CFU-GEMM) and BFU-E when added in the presence of recombinant erythropoietin.

5. Cell Binding Assays

It was previously reported that WEHI-3B(D⁺) cells and human leukemic cells from newly diagnosed leukemias will bind ¹²⁵I-labeled murine G-CSF and that this binding can be complete for by addition of unlabeled G-CSF or human CSF- α . The ability of natural hpG-CSF and rhpG-CSF to compete for binding of ¹²⁵I-hpG-CSF to human and murine leukemic cells was tested. Highly purified natural hpG-CSF (>95% pure; 1 μ g) was iodinated [Tejedor, et al., Anal.Biochem., 127, 143 (1982)] was separated from reactants by gel filtration and ion exchange chromatography. The specific activity of the natural ¹²⁵I-hpG-CSF was approximately μ Ci/ μ g protein. Murine WEHI-3B(D⁺) and two human peripheral blood myeloid leukemic cell preparations (ANLL, one classified as M4, the other as M5B) were tested for their ability to bind ¹²⁵I-hpG-CSF.

The murine and freshly obtained human peripheral blood myeloid leukemic cells were washed three times with PBS/1% BSA. WEHI-3B(D⁺) cells (5×10^6) or fresh leukemic cells (3×10^6) were incubated in duplicate in PBS/1% BSA (100 μ l) in the absence or presence

- of various concentrations (volume: 10 μ l) of unlabeled hpG-CSF, rhpG-CSF or GM-CSF and in the presence of 125 I-hpG-CSF (approx. 100,000 cpm or 1 ng) at 0°C. for 90 min. (total volume: 120 μ l). Cells were then
- 5 resuspended and layered over 200 μ l ice cold FCS in a 350 μ l plastic centrifuge tube and centrifuged (1000 g; 1 min.). The pellet was collected by cutting off the end of the tube and pellet and supernatant counted separately in a gamma counter (Packard).
- 10 Specific binding (cpm) was determined as total binding in the absence of a competitor (mean of duplicates) minus binding (cpm) in the presence of 100-fold excess of unlabeled hpG-CSF (non-specific binding). The non-specific binding was maximally 2503 cpm for
- 15 WEHI-3B(D⁺) cells, 1072 cpm for ANLL (M4) cells and 1125 cpm for ANLL (M5B) cells. Experiments one and two were run on separate days using the same preparation of 125 I-hpG-CSF and display internal consistency in the percent inhibition noted for 2000 units of hpG-CSF.
- 20 Data obtained are reported in Table XXIII below.

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TABLE XXIII

<u>Competitor</u>	<u>(U/ml)</u>	<u>WEHI-3B(D⁺)</u>		<u>ANLL (M4)</u>		<u>ANLL (M5B)</u>	
		<u>cpm</u>	<u>% Inhib.</u>	<u>cpm</u>	<u>% Inhib.</u>	<u>cpm</u>	<u>% Inhib.</u>
<u>Exp. 1</u>							
none	0	6,608	-	1,218	-	122	-
natural							
hpG-CSF:	10,000	685	90				
	2,000	1,692	74	34	97	-376	0
	200	2,031	69				
rhpg-CSF:	10,000	0	100				
	2,000	1,185	82	202	83	0	0
	200	2,330	65				
<u>Exp. 2</u>							
none	0	2,910	0				
natural							
hpG-CSF:	2,000	628	78				
GM-CSF:	2,000	3,311	0				

As shown in Table XXIII, ^{125}I -hpG-CSF demonstrated binding to the WEHI-3B(D^+) leukemic cells. The binding was inhibited in a dose dependent manner by unlabeled natural hpG-CSF or rhpG-CSF, but not by GM-CSF. In addition, binding of natural hpG-CSF to human myelomonocytic leukemic cells (ANLL, M4) was observed. The binding to these cells is paralleled in response to natural hpG-CSF in liquid cultures by differentiation into mature macrophages as judged by morphology. The absence of binding of natural ^{125}I -hpG-CSF to monocytic leukemic cells from another patient (ANLL, M5B) suggests that certain leukemias may differentially express or lack receptors for hpG-CSF. The ability of rhpG-CSF to compete for the binding of natural ^{125}I -hpG-CSF, similar to natural hpG-CSF, suggests that the receptors recognize both forms equally well.

These studies demonstrating the binding of natural ^{125}I -labeled hpG-CSF to leukemic cells are paralleled in culture by the ability of natural hpG-CSF to induce granulocytic and monocytic differentiation of light density bone marrow cells obtained from one patient with an acute promyelocytic leukemia (M3) and a second patient with an acute myeloblastic leukemia (M2). Cells from each patient were cultured for four days in medium alone or in the presence of 1×10^5 units of rhpG-CSF. Cells from the M3 control cultures incubated in medium alone were still promyelocyte in type; while cells cultured in the presence of rhpG-CSF showed mature cells of the myeloid type including a metamyelocyte, giant band form and segmented neutrophils and monocyte. The actual differentials for this patient, on 100 cells evaluated for the control, 100% promyelocytes, and for the rhpG-CSF treated cells, 22% blasts plus promyelocytes, 7% myelocytes, 35% metamyelocytes, 20% band forms plus segmented neutrophils, 14% monocytes and

2% macrophages. Of note is the fact that one of the polymorphonuclear granulocytes still contained a prominent auer rod, suggesting that at least this cell represented a differentiated cell belonging to the leukemic clone. Cells from the second patient with a myeloblastic leukemia (M2) were also cultured for four days in the presence of absence of rhpG-CSF. Visual analysis of M2 cells cultured in medium alone revealed large "blast-like" cells, some of which had nucleoli. Some of the M2 cells, when treated with rhpG-CSF, differentiated to mature segmented neutrophils displaying residual auer rods in the center neutrophil suggesting differentiation occurring in a cell belonging to the leukemic clone. The actual differentiation of 100 cells evaluated morphologically revealed that control cells consisted of 100% blasts. The rhpG-CSF treated cells consisted of 43% blasts, 1% myelocytes, 15% metamyelocytes, 28% band forms plus segmented neutrophils, 2% promonocytes and 11% monocytes. The leukemic cells were also examined for differentiation at four other concentrations of rhpG-CSF (5×10^3 , 1×10^4 , 2.5×10^4 and 5×10^4 U/ml, data not shown). Even at the lowest concentration of rhpG-CSF tested (5×10^3 U/ml), there was significant differentiation (cells differentiated beyond myelocytes) of the M3 (50%) and M2 (37%) leukemic cells.

6. Immunoassay

To prepare polyclonal antibodies for immunoassay use the antigen employed was pluripotent G-CSF purified from the human bladder carcinoma cell line 5637 (1A6) as prepared in Example 1 (B). This material was judged to be 85% pure based on silver nitrate staining of polyacrylamide gels. Six week-old Balb/C mice were immunized with multiple-site subcutaneous injections of antigen. The antigen was resuspended in PBS and emulsified with equal volumes of Freund's complete adjuvant.

The dose was 5 to 7 μ g of antigen per mouse per injection. A booster immunization was administered 18 days later with the same amount of antigen emulsified with an equal volume of Freund's incomplete adjuvant. 4 days
5 later mouse serum was taken to test for the antibody specific to human pluripotent G-CSF.

Dynatech Immulon II Removawell strips in holders (Dynateck Lab., Inc., Alexandria, Virginia) were coated with hpG-CSF 5 μ g/ml in 50mM carbonate-bicarbonate buffer, pH 9.2. Wells were coated with 0.25 μ g
10 in a volume of 50 μ l. Antigen coated plates were incubated 2 hours at room temperature and overnight at 4°C. The solution was decanted and the plates were incubated 30 minutes with PBS containing 5% BSA to block
15 the reactive surface. This solution was decanted and the diluted preimmune or test sera were added to the wells and incubated for 2 hours at room temperature. Sera were diluted with PBS, pH 7.0 containing 1% BSA. The serum solution was decanted and plates were washed
20 three times with Wash Solution (KPL, Gaithersburg, Maryland). Approximately 200,000 cpm of iodinated rabbit anti-mouse IgG (NEN, Boston, Massachusetts) in 50 μ l PBS, pH 7.0 containing 1% BSA was added to each well. After incubating 1-1/2 hours at room temperature,
25 the solution was decanted and plates were washed 5 times with Wash Solution. Wells were removed from holder and counted in a Beckman 5500 gamma counter. High-titered mouse sera showed greater than 12-fold higher reactivity than the corresponding preimmune sera at a dilution of
30 1:100.

The immunological properties of E. coli-derived hpG-CSF were determined by reactivity to high-titered mouse serum specific to mammalian-cell derived hpG-CSF. 0.25 μ g of 90% pure E. coli-derived protein
35 was coated to Immulon II Removawells in a volume of 50 μ l and mouse serum was assayed as described above.

High-titered mouse sera showed a 24-fold higher reactivity to the E. coli-derived material than did the corresponding preimmune sera at a dilution of 1:100.

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7. Serine Analog Bioassays

[Ser¹⁷]hpG-CSF, [Ser³⁶]hpG-CSF, [Ser⁴²]hpG-CSF, [Ser⁶⁴]hpG-CSF, and [Ser⁷⁴]hpG-CSF products prepared according to Example 9 were assay for
10 hpG-CSF activity in the ³H-thymidine uptake, CFU-GM, and WEHI3B D⁺ assays. In each assay, the [Ser¹⁷] analog had activity comparable to that of recombinant molecules having the native structure. The remaining analogs had on the order of 100-fold lesser activity in the ³H-
15 thymidine uptake assay, 250-fold lesser activity in the CFU-GM assay, and 500-fold lesser activity in the WEHI-3B D⁺ assay. This data is supportive of the proposition that cysteines at positions 36, 42, 64 and 74 may be needed for full biological activity.

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8. In vivo Bioassay

Alzet[®] osmotic pumps (Alzet Corp., Palo Alto, CA; Model 2001) were connected to indwelling right jugular vein catheters and implanted subcutaneously in
25 seven male Syrian golden hamster. Four of the pumps contained a buffer [20 mM sodium acetate (pH 5.4) and 37 mM sodium chloride] and 1.5 mg/ml E.coli-derived hpG-CSF while 3 contained buffer alone. The claimed pumping rate for the osmotic pumps was 1 microliter/hr.
30 for up to seven days. At the third day after implantation of the pumps, the mean granulocyte count of the four treated hamsters was six-fold higher than that of the three (buffer) controls and the increased granulocyte count was reflected in a four-fold increase in
35 total lymphocytes. Erythrocyte count was unchanged by treatment. These results indicate that the recombinant

material produces a specific enhancement of production and/or release of granulocytes in a mammal.

In addition to naturally-occurring allelic forms of hpG-CSF, the present invention also embraces
5 other hpG-CSF products such as polypeptide analogs of hpG-CSF and fragments of hpG-CSF. Following the procedures of the above-noted published application by Alton, et al. (WO/83/04053) one may readily design and manufacture genes coding for microbial expression of polypep-
10 tides having primary conformations which differ from that herein specified for in terms of the identity or location of one or more residues (e.g., substitutions, terminal and intermediate additions and deletions). Alternately, modifications of cDNA and genomic genes may
15 be readily accomplished by well-known site-directed mutagenesis techniques and employed to generate analogs and derivatives of. Such products would share at least one of the biological properties of hpG-CSF but may differ in others. As examples, projected products of
20 the invention include those which are foreshortened by e.g., deletions; or those which are more stable to hydrolysis (and, therefore, may have more pronounced or longer lasting effects than naturally-occurring); or which have been altered to delete one or more a poten-
25 tial sites for o-glycosylation (which may result in higher activities for yeast-produced products); or which have one or more cysteine residues deleted or replaced by, e.g., alanine or serine residues and are potentially more easily isolated in active form from microbial
30 systems; or which have one or more tyrosine residues replaced by phenylalanine and may bind more or less readily to hpG-CSF receptors on target cells. Also comprehended are polypeptide fragments duplicating only a part of the continuous amino acid sequence or
35 secondary conformations within hpG-CSF, which fragments may possess one activity of (e.g., receptor binding) and

not others (e.g., colony growth stimulating activity). It is noteworthy that activity is not necessary for any one or more of the products of the invention to have therapeutic utility [see, Weiland, et al., Blut, 44, 173-175 (1982)] or utility in other contexts, such as in assays of hpG-CSF antagonism. Competitive antagonists may be quite useful in, for example, cases of overproduction of hpG-CSF.

According to another aspect of the present invention, the DNA sequence described herein which encodes hpG-CSF polypeptides is valuable for the information which it provides concerning the amino acid sequence of the mammalian protein which has heretofore been unavailable despite analytical processing of isolates of naturally-occurring products. The DNA sequences are also conspicuously valuable as products useful in effecting the large scale microbial synthesis of hpG-CSF by a variety of recombinant techniques. Put another way, DNA sequences provided by the invention are useful in generating new and useful viral and circular plasmid DNA vectors, new and useful transformed and transfected microbial procaryotic and eucaryotic host cells (including bacterial and yeast cells and mammalian cells grown in culture), and new and useful methods for cultured growth of such microbial host cells capable of expression of hpG-CSF and its related products. DNA sequences of the invention are also conspicuously suitable materials for use as labelled probes in isolating hpG-CSF and related protein encoding human genomic DNA as well as cDNA and genomic DNA sequences of other mammalian species. DNA sequences may also be useful in various alternative methods of protein synthesis (e.g., in insect cells) or in genetic therapy in humans and other mammals. DNA sequences of the invention are expected to be useful in developing transgenic mammalian species which may serve as eucaryotic "hosts" for pro-

duction of hpG-CSF and hpG-CSF products in quantity.
See, generally, Palmiter, et al., Science, 222(4625),
809-814 (1983).

Of applicability to hpG-CSF fragments and
5 polypeptide analogs of the invention are reports of the
immunological activity of synthetic peptides which sub-
stantially duplicate the amino acid sequence extant in
naturally-occurring proteins, glycoproteins and nucleo-
10 weight polypeptides have been shown to participate in
immune reactions which are similar in duration and
extent to the immune reactions of physiologically signi-
ficant proteins such as viral antigens, polypeptide
hormones, and the like. Included among the immune reac-
15 tions of such polypeptides is the provocation of the
formation of specific antibodies in immunologically
active animals. See, e.g., Lerner, et al., Cell, 23,
309-310 (1981); Ross, et al., Nature, 294, 654-656
(1981); Walter, et al., Proc. Natl. Acad. Sci. (USA),
20 77, 5197-5200 (1980); Lerner, et al., Proc. Natl. Acad.
Sci. (USA), 78, 3403-3407 (1981); Walter, et al., Proc.
Natl. Acad. Sci. (USA), 78, 4882-4886 (1981); Wong, et
al., Proc. Natl. Acad. Sci. (USA), 78, 7412-7416 (1981);
Green, et al., Cell, 28, 477-487 (1982); Nigg, et al.,
25 Proc. Natl. Acad. Sci. (USA), 79, 5322-5326 (1982);
Baron, et al., Cell, 28, 395-404 (1982); Dreesman, et
al., Nature, 295, 185-160 (1982); and Lerner,
Scientific American, 248, No. 2, 66-74 (1983). See,
also, Kaiser, et al., Science, 223, 249-255 (1984)
30 relating to biological and immunological activities of
synthetic peptides which approximately share secondary
structures of peptide hormones but may not share their
primary structural conformation.

While the present invention has been described
35 in terms of preferred embodiments, it is understood that
variations and modifications will occur to those skilled

in the art. Therefore, it is intended that the appended claims cover all such equivalent variations which come within the scope of the invention as claimed.

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CLAIMS:

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1. A polypeptide which: a) has part or all of the primary structure and one or more of the biological properties typical of naturally-occurring human pluripotent granulocyte colony-stimulating factor (hpG-CSF) of the sequence set forth in Table VIII, b) is a non-naturally occurring polypeptide; and c) is the product of procaryotic or eucaryotic expression of an exogenous DNA sequence.
2. A polypeptide according to Claim 1 wherein the exogenous DNA sequence is a cDNA sequence.
3. A polypeptide according to Claim 1 wherein the exogenous DNA sequence is a genomic DNA sequence.
4. A polypeptide according to Claim 1 wherein the exogenous DNA sequence is carried on an autonomously replicating DNA plasmid or viral vector.
5. A polypeptide according to Claim 1 further characterized by being covalently associated with a detectable label substance.
6. A polypeptide according to Claim 5 wherein said detectable label is a radiolabel.
7. A DNA sequence which codes upon expression in a procaryotic or eucaryotic host cell for a polypeptide product having at least a part of the primary structure and one or more of the biological properties of naturally-occurring pluripotent granulocyte colony-stimulating factor, said DNA sequence being selected

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from among:

(a) the DNA sequence set out in Table VI or the complementary stands thereof;

(b) DNA sequences which hybridize to the DNA sequences defined in (a) or fragments thereof; and

(c) DNA sequences which, but for the degeneracy of the genetic code, would hybridize to the DNA sequences defined in (a) or (b) and which sequences code for a polypeptide having the same amino acid sequence.

8. A procaryotic or eucaryotic host cell transformed or transfected with a DNA sequence according to Claim 7 in a manner allowing the host cell to express said polypeptide product.

9. A host cell according to Claim 8 wherein the host is E. coli.

10. A host cell according to Claim 8 wherein the host cell is a mammalian cell.

11. A non-naturally occurring polypeptide product of the expression of a DNA sequence of Claim 7 in a procaryotic or eucaryotic host.

12. A cDNA sequence according to Claim 7.

13. A genomic DNA sequence according to Claim 7.

14. A DNA sequence according to Claim 7 and including one or more codons preferred for expression in E. coli cells.

15. A DNA sequence according to Claim 7 and coding for

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expression of human pluripotent granulocyte colony-stimulating factor.

16. A DNA sequence according to Claim 15 and including one or more codons preferred for expression in yeast cells.

17. A DNA sequence according to Claim 12 or 13 coding for expression of human pluripotent granulocyte colony-stimulating factor.

18. A DNA sequence according to Claim 7 covalently associated with a detectable label substance.

19. A DNA sequence according to Claim 18 wherein the detectable label is a radiolabel.

20. A single-stranded DNA sequence according to Claim 18.

21. A biologically functional plasmid or viral DNA vector including a DNA sequence according to Claim 7.

22. A procaryotic or eucaryotic host cell stably transformed or transfected with a DNA vector according to Claim 21.

23. A process for the production of a polypeptide having part or all of the primary structure and one or more of the biological properties of naturally occurring pluripotent granulocyte colony-stimulating factor, which process is characterized by culturing under suitable nutrient conditions, procaryotic or eucaryotic host cells transformed or transfected with a DNA sequence according to Claim 7 in a manner allowing the



host cell to express said polypeptide, and isolating desired polypeptide products of the expression of DNA sequence.

24. A process for the production of a polypeptide having the primary structure of human pluripotent granulocyte colony-stimulating factor, which process is characterized by culturing under suitable nutrient conditions, procaryotic or eucaryotic host cells transformed or transfected with a DNA sequence set forth in Table VIII in a manner allowing the host cells to express said polypeptide, and isolating desired polypeptide products of the expression of the DNA sequence.

25. A pharmaceutical composition comprising an effective amount of a polypeptide according to Claim 1 and/or produced by the process of Claim 23 or 24 and a pharmaceutically acceptable diluent, adjuvant or carrier.

26. A pharmaceutical composition according to Claim 25 further characterized by being free of association with any human protein.

27. Use of a polypeptide according to Claim 1 for the manufacture of a medicament for providing hematopoietic therapy to a mammal.

28. Use of a polypeptide according to Claim 1 for the manufacture of a medicament for arresting proliferation of leukemic cells.





29. A polypeptide according to Claim 1 preceded by a methionine residue.

30. A polypeptide having the hematopoietic biological properties of naturally occurring pluripotent granulocyte colony-stimulating factor, said polypeptide having an amino acid sequence selected from the polypeptide sequence set forth in Table VIII or any allelic variants, derivatives, deletion analogs, substitution analogs, or addition analogs thereof, and characterized by being non-naturally occurring and by being the product of procaryotic or eucaryotic expression of an exogenous DNA sequence.

31. A pharmaceutical composition comprising an effective amount of the polypeptide according to Claim 29 and a pharmaceutically acceptable diluent, adjuvant or carrier.