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(54) **DIAGNOSTIC METHODS BASED ON HUMAN BTG-2 AND BTG-3 POLYPEPTIDES**

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(57) **ABSTRACT**

The present invention relates to novel antiproliferative genes. More specifically, isolated nucleic acid molecules are provided encoding the human B-cell translocation genes 2 and 3 (BTG-2 and BTG-3). BTG-2 and BTG-3 polypeptides are also provided, as are vectors, host cells and recombinant methods for producing the same.

4 Claims, 6 Drawing Sheets

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1 GGCACGAGATTTTGTGGCGTAGAGCTATGCAGCTTGAAATCCAAGTAGCACTAAATTTTA
M Q L E I Q V A L N F I

61 TTATTTTCGTATTTGTACAATAAGCTTCCCAGGAGACGTGTCAACATTTTGGTGAAGAAC
I S Y L Y N K L P R R R V N I F G E E L

121 TTGAAAGACTTCTTAAGAAGAAATATGAAGGGCACTGGTATCCTGAAAAGCCATACAAAG
E R L L K K K Y E G H W Y P E K P Y K G

181 GATCGGGGTTTAGATGTATACACATAGGGGAGAAAGTGGACCCAGTGATTGAACAAGCAT
S G F R C I H I G E K V D P V I E Q A S

241 CCAAAGAGAGTGGTTTGGACATTGATGATGTTTCGTGGCAATCTGCCACAGGATCTTAGTG
K E S G L D I D D V R G N L P Q D L S V

301 TTTGGATCGACCCATTTGAGGTTTCTTACCAAATTGGTGAAAAGGGACCAGTGAAGGTGC
W I D P F E V S Y Q I G E K G P V K V L

361 TTTACGTGGATGATAATAATGAAAATGGATGTGAGTTGGATAAGGAGATCAAAAACAGCT
Y V D D N N E N G C E L D K E I K N S F

421 TTAACCCAGAGGCCAGGTTTTTATGCCATAAGTGACCCAGCCTCATCAGTGTCCAGCT
N P E A Q V F M P I S D P A S S V S S S

481 CTCCATCGCCTCCTTTTGGTCACTCTGCTGCTGTAAGCCCTACCTTCATGCCCCGGTCCA
P S P P F G H S A A V S P T F M P R S T

541 CTCAGCCTTTAACCTTTACCACTGCCACTTTTGTGCCACCAAGTTCGGCTCTACCAAAA
Q P L T F T T A T F A A T K F G S T K M

601 TGAAAAATAGTGGCCGTAGCAACAAGGTTGCACGTACTTCTCCCATCAACCTCGGCTTGA
K N S G R S N K V A R T S P I N L G L N

661 ATGTGAATGACCTCTTGAAGCAGAAAGCCATCTCTTCTCAATGCACTCTCTGTATGGGC
V N D L L K Q K A I S S S M H S L Y G L

721 TTGGCTTGGGTAGCCAGCAGCAGCCACAGCAACAGCAGCAGCCAGCCAGCCGCCACCGC
G L G S Q Q Q P Q Q Q Q Q P A Q P P P P

781 CACCACCACCACCACAGCAGCAACAACAGCAGAAAACCTCTGCTCTTTCTCCTAATGCCA
P P P P Q Q Q Q Q Q K T S A L S P N A K

FIG. 1A

841 AGGAATTTATTTTTCTAATATGCAGGGTCAAGGTAGTAGTACCAATGGAATGTTCCCAG
E F I F P N M Q G Q G S S T N G M F P G

901 GTGACAGCCCCCTTAACCTCAGTCCTCTCCAGTACAGTAATGCCTTTGATGTGTTTGCAG
D S P L N L S P L Q Y S N A F D V F A A

961 CCTATGGAGGCCTCAATGAGAAGTCTTTTGTAGATGGCTTGAATTTTAGCTTAAATAACA
Y G G L N E K S F V D G L N F S L N N M

1021 TGCAGTATTCTAACCAGCAATTCAGCCTGTTATGGCTAACTAAAAAAAAAGAAAATGTAT
Q Y S N Q Q F Q P V M A N

1081 CGTACAAGTTAAAATGCACGGGCCAAGGGGGGATTTTTTTTTTTCACCTCCTTGAGAATTT
1141 TTTTTTTAAGCTTATAGTAAGGATACATTC AAGCTTGGTTAAAAAATAATAATAAAAC
1201 ATGCATCATTTTTTCATTTGCCAACCAAGCACAAAGTTATTTTATGCTGCCTGTATATTTT
1261 AAAGTATACTCTCAGATATGCCCTCTTACAGTATTTAAGATATTAGCAAAGGACATGGC
1321 TTGATTTTTTTTTATAAAAAATTGGCACTAATAAGTGGGTTTATTGGTCTTTTCTAATTGT
1381 ATAATTTAATTTAGTACCAAAGTTTGTAAAAATATCAGAGGATATATATATATTGTATCCT
1441 ACGACATGGTATTGCATTTATATCTTTTTACTACAGTGATCTGTGACAGCAGCAGCCTCA
1501 TGTTGTATTTTTTTTACTGAAATTGTA AAAATATCCATCTTAAAGACATCAACTATTCTAA
1561 AAATTGTGTACAGGATATTCCTTTAGTGGTGGGAATTTAAAATGTGCGAATACTTGCTTTCT
1621 CCAAAAAAATGTATTTTCTGTAAAAGTTTAAAGATTTTGGCTATATATTJGGAAGGAA
1681 AATGTAATCGTAAATATTAATTTTGTACCTATATTGTGCAATACTTGAAAAAACGGTAT
1741 AAAAGTATTTTGAGTCAGTGTCTTACATGTTAAGAGGGACTGAAATAGTTTATATTAAGT
1801 TTGTATTAAAATTCCTTTAAAATTA AAAAAAAAAAAAAAAAAAAAAA

FIG. 1B

1 GGAATTCGGCAGGAGCAACCCTCAACGACGAAAAGGACTTCGGTCCCCTGGCCCGGCGAC
61 GCCCGGGAAGGAAAGGAGAGCGACCTCCGCCCGCGCTCAGGCCACCCTGGAGGGAGAAG
121 CCGCCCCGCGCSSGSGTTAGAGCGCCCCGCGCCCCGTAGACCCGAAGCCGCTGGAGCC
181 CAAGGCTGTACACGTGCCCTGTGCTGATTCTCTGCCTAGGAAAGGACCATGCAGCTAGAG
M Q L E

241 ATCAAAGTGGCCCTGAACTTCATCATCTCCTACTTGTACAACAAGCTGCCCCGGCGCCGG
I K V A L N F I I S Y L Y N K L P R R R

301 GCAGACCTGTTTGGGGAGGAGCTAGAGCGGCTTTTGAAAAGGAAATATGAAGGCCACTGG
A D L F G E E L E R L L K R K Y E G H W

361 TACCCTGAGAAGCCACTGAAAGGCTCTGGCTTCCGCTGTGTTACATTGGGGAGATGGTG
Y P E K P L K G S G F R C V H I G E M V

421 GACCCCGTGGTGGAGCTGGCCGCCAAGCGGAGTGGCCTGGCGGTGGAAGATGTGCGGGCC
D P V V E L A A K R S G L A V E D V R A

481 AATGTGCCTGAGGAGCTGAGTGTCTGGATTGATCCCTTTGAGGTGTCCTACCAGATTGGT
N V P E E L S V W I D P F E V S Y Q I G

541 GAGAAGGGAGCTGTGAAAGTGCTGTACCTGGATGACAGTGAGGGTTGCGGTGCCCCAGAG
E K G A V K V L Y L D D S E G C G A P E

601 CTGGACAAGGAGATCAAGAGCAGCTTCAACCCTGACGCCAGGTGTTTCGTGCCCATTTGGC
L D K E I K S S F N P D A Q V F V P I G

661 AGCCAGGACAGCTCCCTGTCCAACCTCCCCATCGCCATCCTTTGGCCAGTCACCCAGCCCT
S Q D S S L S N S P S P S F G Q S P S P

721 ACCTTCATTCCCCGCTCCGCTCAGCCCATCACCTTACCACCGCCTCCTTCGCTGCCACC
T F I P R S A Q P I T F T T A S F A A T

781 AAATTTGGCTCCACTAAGATGAAGAAGGGGGGCGGGGCAGCAAGTGGTGGGGGTGTAGCC
K F G S T K M K K G G G A A S G G G V A

841 AGCAGTGGGGCGGGTGGCCAGCAGCCACCACAGCAGCCTCGCATGGCCCGCTCACCCACC
S S G A G G Q Q P P Q Q P R M A R S P T

FIG.2A

901 AACAGCCTGCTGAAGCACAAGAGCCTCTCTCTGTCTATGCATTCACTGAACTTCATCAGG
N S L L K H K S L S L S M H S L N F I T

961 GCCAACCCGGCCCTCAGTCCCAGCTCTCACCCAATGCCAAGGAGTTCGTGTACAACGGT
A N P A P Q S Q L S P N A K E F V Y N G

1021 GGTGGCTCACCCAGCCTCTTCTTTGATGCGGCCGATGGCCAGGGCAGCGGCACCCAGGC
G G S P S L F F D A A D G Q G S G T P G

1081 CCGTTTGGAGGCAGTGGGGCTGGCACCTGCAACAGCAGCAGCTTTGACATGGCCCAGGTA
P F G G S G A G T C N S S S F D M A Q V

1141 TTTGGAGGTGGTGCCAACAGCCTCTTCCTGGAGAAGACACCCTTTGTGGAAGGCCTCAGC
F G G G A N S L F L E K T P F V E G L S

1201 TACAACCTGAACACCATGCAGTATCCCAGCCAGCAGTTCCAGCCCGTGGTGCTGGCCAAC
Y N L N T M Q Y P S Q Q F Q P V V L A N

1261 TGACCATCTACCTGGCCCGTGGGGCAGGAGCACCCAAGACCACAGAAAAGAGAAAGGAA
1321 AGGCCAAAAAAAAAAAAAAAAAAAAA 1343

FIG.2B

	1				50
BTG2	MQLEIQVALN	FIISYLYNK.	.LPRRRVNIF	GEELERLLKK
BTG3	MQLEIKVALN	FIISYLYNK.	.LPRRRADLF	GEELERLLKR
BTG1	MHPFYTRAA	MIGEIAAAVS	FISKFLRTKG	LTSERQLQTF	SQSLQELLAE
Consensus	-----	MQLEI-VALN	FIISYLYNK-	-LPRRR---	F GEELERLLK-
	51				100
BTG2	KYEGHWYPEK	PYKSGGFRCI	HIGEKVDPVI	EQASKESGLD	IDDVRGNLPQ
BTG3	KYEGHWYPEK	PLKSGGFRCV	HIGEMVDPVV	ELAAKRSGLA	VEDVRANVPE
BTG1	HYKHHWFPEK	PCKGSGYRCI	RINHKMDPLI	GQAAQRIGLS	SQELFRLLPS
Consensus	KYEGHWYPEK	P-KSGGFRCI	HIGEKVDPVI	EQAAKRSGL-	--DVR-NLP-
	101				150
BTG2	DLSVWIDPFE	VSYQIGEKGP	VKVLYVDDNN	ENGC.ELD..	KEIKNSFNPE
BTG3	ELSVWIDPFE	VSYQIGEKGA	VKVLYLDDSE	GCGAPELD..	KEIKSSFNP
BTG1	ELTLWVDPYE	VSYRIGEDGS	ICVLYEASPA	GGSTQNSTNV	QMVDSRISCK
Consensus	ELSVWIDPFE	VSYQIGEKG-	VKVLY-DD--	G-G--ELD--	KEIKSSFNP-
	151				200
BTG2	AQVFMPISDP	ASSVSSSPSP	PFGHSAAVSP	TFMPRSTQPL	TFTTATFAAT
BTG3	AQVFVPIGSQ	DSSLSNSPSP	SFGQSP..SP	TFIPRSAQPI	TFTTASFAAT
BTG1	EELLLG....RTSPSK	NYNMMTVSG.
Consensus	AQVF-PI---	-SS-S-SPSP	-FG-S---SP	TF-PRS-QP-	TFTTA-FAAT
	201				250
BTG2	KFGSTKMKNS	GRSNKVARTS	PINLGLN...V	NDLLKQKAIS
BTG3	KFGSTKMKKG	GGAASGGGVA	SSGAGGQOPP	QQPRMARSPT	N\$LLKHKSLS
BTG1
Consensus	KFGSTKMK--	G-----	----G----	-----	N-LLK-K--S
	251				300
BTG2	SSMHSLYGLG	LGSQQQPQQQ	QOPAQP PPPP	PPPQQQQQK	TSALSPNAKE
BTG3	LSMHSLNFIT	ANPAPQSQ..LSPNAKE
BTG1
Consensus	-SMHSL----	-----Q-Q--	-----	-----	---LSPNAKE

FIG.3A

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          301                                     350
BTG2  FI..... ..FPNMQGQG SSTNGMFPGD SPL..NLSPL QYSNAFDVFA
BTG3  FVYNGGGSPS LFFDAADGQG SGTGPFPGGS GAGTCNSSF DMAQVFGGGA
BTG1  .....
Consensus F----- --F---GQG S-T-G-F-G- -----N-S-- -----F---A

          351                                     385
BTG2  AYGGLNEKSF VDGLNFSLNN MQYSNQQFQP .VMAN
BTG3  NSLFLEKTPF VEGLSYNLNT MQYPSQQFQP VVLAN
BTG1  .....
Consensus ----L----F V-GL---LN- MQY--QQFQP -V-AN
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FIG.3B

DIAGNOSTIC METHODS BASED ON HUMAN BTG-2 AND BTG-3 POLYPEPTIDES

The present application is a divisional of U.S. application Ser. No. 09/843,846, filed Apr. 30, 2001 (now U.S. Pat. No. 6,689,360), which is herein incorporated by reference, which is a divisional of U.S. application Ser. No. 09/221,844, filed Dec. 29, 1998 (now U.S. Pat. No. 6,258,777), which is herein incorporated by reference; said U.S. patent application Ser. No. 09/221,844 is a divisional of U.S. application Ser. No. 08/718,738, filed Sep. 18, 1996 (now U.S. Pat. No. 6,013,469), which is herein incorporated by reference; said U.S. patent application Ser. No. 08/718,738 is a continuation-in-part (CIP) of U.S. patent application Ser. No. 08/463,382, filed Jun. 5, 1995, now abandoned, which is herein incorporated by reference; U.S. patent application Ser. No. 08/718,738 is also a CIP of U.S. patent application Ser. No. 08/460,104, filed Jun. 2, 1995, now abandoned, which is herein incorporated by reference; said U.S. patent application Ser. Nos. 08/463,382 and 08/460,104 are CIPs of International Application No. PCT/US95/03323, filed Mar. 17, 1995, which is herein incorporated by reference.

BACKGROUND OF THE INVENTION

1. Field of the Invention

The present invention relates to novel antiproliferative genes. More specifically, isolated nucleic acid molecules are provided encoding the human B-cell translocation genes 2 and 3 (BTG-2 and BTG-3). BTG-2 and BTG-3 polypeptides are also provided, as are vectors, host cells and recombinant methods for producing the same.

2. Related Art

In normal tissues, homeostasis is maintained through negative and positive growth controls which effect the proliferation and differentiation related to cellular genetic programs. An alteration of this subtle balance can result in developmental abnormalities or in neoplasia. Proto-oncogenes, genes that promote cell division, were the first growth-inducing elements to be identified and more than sixty of them have been described so far (Bishop, J. M., *Cell* 64:235:248 (1991)). The genes that negatively regulate cell proliferation are crucial to counteract the growth-inducing elements and are likely to have the same importance as proto-oncogenes in controlling cell division (Marshall, C. J., *Cell* 64:313-326 (1991)), especially since the loss of their function has been reported to be associated with irregular cellular differentiation and proliferation or with alteration of embryonic development (Weinberg, R. A., *Science* 254: 1138-1146 (1991)).

The polynucleotides and polypeptides of the present invention are thought to be members of a family of anti-proliferative genes. BTG-1 is a member of this group and has been cloned and expressed. (Rovault, J. P. et al., *The EMBO Journal* 11(4):1663-1670 (1992)). BTG-1 was shown to negatively regulate NIH3T3 cell proliferation when over-or inappropriately expressed. BTG stands for B-cell translocation gene, and the BTG-1 gene has been shown to be involved in a chromosomal translocation [t(8; 12)(q24;22)] in B-cell chronic lymphocytic leukemia.

The BTG-1 open reading frame is 60% homologous to PC3, an immediate early gene induced by nerve growth factor in rat PC12 cells. Sequence and Northern blot analyses indicate that BTG-1 and PC3 are not cognate genes but are thought to be members of this new family of anti-proliferation genes. The BTG-1 gene is preferentially expressed in quiescent cells during the early sub-phases of

G₁ in a serum-dependent manner and it is then down-regulated to reach a minimum level as the cells enter the S phase. This suggests a functional link between BTG-1 and the cell cycle process. BTG-1 is expressed in tissues (lymphoid, liver, placenta) containing non-dividing cells likely to re-enter the cell cycle upon different stimuli, whereas the expression of BTG-1 is barely detectable in fully differentiated tissues such as brain and muscle.

The BTG-1 gene was shown to be highly conserved in evolution and a similar 1.8 Kb transcript can be detected in murine and chicken tissue by using a human BTG-1 DNA probe (Rimokh, R. et al., *Genes Chrom. Cancer* 3:24-36 (1991)).

The BTG-2 and BTG-3 genes and gene products have been putatively identified as members of this family as a result of amino acid sequence homology to BTG-1.

SUMMARY OF THE INVENTION

The present invention provides isolated nucleic acid molecules comprising a polynucleotide encoding the BTG-2 or BTG-3 polypeptide having the amino acid sequences shown in FIG. 1A-1B (SEQ ID NO:2) and FIG. 2A-2B (SEQ ID NO:4), respectively, or having the amino acid sequences encoded by the cDNA clones deposited in bacterial hosts as ATCC™ Deposit Number 97025 on Jan. 17, 1995 (BTG-2) and ATCC™ Deposit Number 97010 on Jan. 5, 1995 (BTG-3). For BTG-2, the nucleotide sequence determined by sequencing the deposited cDNA clone contains an open reading frame encoding a polypeptide of about 345 amino acid residues, with a predicted leader sequence of about 25 amino acid residues such that the mature protein comprises about 320 amino acids. The amino acid sequence of the predicted mature BTG-2 protein is shown in FIG. 1A-1B, amino acid residues from about 26 to about 345 (SEQ ID NO:2).

For BTG-3, the nucleotide sequence determined by sequencing the deposited cDNA clone contains an open reading frame encoding a polypeptide of about 344 amino acid residues, with a predicted leader sequence of about 18 amino acid residues such that the mature protein comprises about 326 amino acids. The amino acid sequence of the predicted mature BTG-3 protein is shown in FIG. 2A-2B, amino acid residues from about 19 to about 344 (SEQ ID NO:4).

Thus, one aspect of the invention provides an isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence encoding the BTG-2 or BTG-3 polypeptide having the complete amino acid sequence in FIG. 1A-1B (SEQ ID NO:2) and FIG. 2A-2B (SEQ ID NO:4), respectively; (b) a nucleotide sequence encoding the mature BTG-2 or mature BTG-3 polypeptide having the amino acid sequence at positions from about 26 to about 345 in FIG. 1A-1B (SEQ ID NO:2) and from about 19 to about 344 in FIG. 2A-2B (SEQ ID NO:4), respectively; (c) a nucleotide sequence encoding the BTG-2 or BTG-3 polypeptide having the complete amino acid sequence encoded by the cDNA clone contained in ATCC™ Deposit No. 97025 and 97010, respectively; (d) a nucleotide sequence encoding the mature BTG-2 or mature BTG-3 polypeptide having the amino acid sequence encoded by the cDNA clone contained in ATCC™ Deposit No. 97025 and 97010, respectively; and (e) a nucleotide sequence complementary to any of the nucleotide sequences in (a), (b), (c) or (d) above.

Further embodiments of the invention include isolated nucleic acid molecules that comprise a polynucleotide having a nucleotide sequence at least 90% identical, and more preferably at least 95%, 96%, 97%, 98% or 99% identical, to any of the nucleotide sequences in (a), (b), (c), (d) or (e), above, or a polynucleotide which hybridizes under stringent hybridization conditions to a polynucleotide in (a), (b), (c), (d) or (e), above. This polynucleotide which hybridizes does not hybridize under stringent hybridization conditions to a polynucleotide having a nucleotide sequence consisting of only A residues or of only T residues. An additional nucleic acid embodiment of the invention relates to an isolated nucleic acid molecule comprising a polynucleotide which encodes the amino acid sequence of an epitope-bearing portion of a BTG-2 or BTG-3 polypeptide having an amino acid sequence in (a), (b), (c) or (d), above.

The present invention also relates to recombinant vectors, which include the isolated nucleic acid molecules of the present invention, and to host cells containing the recombinant vectors, as well as to methods of making such vectors and host cells and for using them for production of BTG-2 or BTG-3 polypeptides or peptides by recombinant techniques.

The invention further provides an isolated BTG-2 or BTG-3 polypeptide having an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of the BTG-2 or BTG-3 polypeptide having the complete 345 and 344 amino acid sequences shown in FIG. 1A-1B (SEQ ID NO:2) and FIG. 2A-2B (SEQ ID NO:4), respectively; (b) the amino acid sequence of the predicted mature BTG-2 or BTG-3 polypeptide (without the leader) having the amino acid sequence at positions from about 26 to about 345 in FIG. 1A-1B (SEQ ID NO:2) and from about 19 to about 344 in FIG. 2A-2B (SEQ ID NO:4), respectively; (c) the amino acid sequence of the BTG-2 or BTG-3 polypeptide having the complete amino acid sequence, including the leader, encoded by the cDNA clone contained in ATCC™ Deposit No. 97025 and 97010, respectively; and (d) the amino acid sequence of the mature BTG-2 or BTG-3 polypeptide having the amino acid sequence encoded by the cDNA clone contained in ATCC™ Deposit No. 97025 and 97010, respectively. The polypeptides of the present invention also include polypeptides having an amino acid sequence with at least 90% similarity, and more preferably at least 95% similarity to those described in (a), (b), (c) or (d) above, as well as polypeptides having an amino acid sequence at least 80% identical, more preferably at least 90% identical, and still more preferably 95%, 96%, 97%, 98% or 99% identical to those above.

An additional embodiment of this aspect of the invention relates to a peptide or polypeptide which has the amino acid sequence of an epitope-bearing portion of a BTG-2 or BTG-3 polypeptide having an amino acid sequence described in (a), (b), (c) or (d), above. Peptides or polypeptides having the amino acid sequence of an epitope-bearing portion of a BTG-2 or BTG-3 polypeptide of the invention include portions of such polypeptides with at least six or seven, preferably at least nine, and more preferably at least about 30 amino acids to about 50 amino acids, although epitope-bearing polypeptides of any length up to and including the entire amino acid sequence of a polypeptide of the invention described above also are included in the invention.

In another embodiment, the invention provides an isolated antibody that binds specifically to a BTG-2 or BTG-3 polypeptide having an amino acid sequence described in (a), (b), (c) or (d) above. Such antibodies are useful diagnostically or therapeutically as describe below.

In accordance with yet a further aspect of the present invention, there is provided a process for utilizing such polypeptides, or polynucleotides encoding such polypeptides for therapeutic purposes, for example, to treat disease states characterized by aberrant cellular proliferation, and to modulate cellular growth.

In accordance with yet another aspect of the present invention, there are provided antagonists to such polypeptides, which may be used to inhibit the action of such polypeptides, for example, in the treatment of diseases related to chromosomal translocation, for example, lymphocytic leukemia.

In accordance with still another aspect of the present invention, there are provided diagnostic assays for detecting diseases related to the under-expression of the polypeptides of the present invention and mutations in the nucleic acid sequences encoding such polypeptides.

In accordance with yet a further aspect of the present invention, there is provided a process for utilizing such polypeptides, or polynucleotides encoding such polypeptides, for in vitro purposes related to scientific research, synthesis of DNA and manufacture of DNA vectors.

BRIEF DESCRIPTION OF THE FIGURES

FIG. 1A-1B is an illustration of the cDNA and corresponding deduced amino acid sequence of BTG-2. One-letter abbreviations for amino acids are used. Sequencing was performed, for both BTG-2 and BTG-3, using a 373 Automated DNA sequencer (Applied Biosystems, Inc.). Sequencing accuracy is predicted to be greater than 97% accurate.

FIG. 2A-2B shows the cDNA and corresponding deduced amino acid sequence of the putative BTG-3.

FIG. 3A-3B is an amino acid sequence alignment between BTG-1, BTG-2 and BTG-3 proteins.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides isolated nucleic acid molecules comprising a polynucleotide encoding a BTG-2 or BTG-3 polypeptide having the amino acid sequence shown in FIG. 1A-1B (SEQ ID NO:2) and FIG. 2A-2B (SEQ ID NO:4), respectively, which were determined by sequencing cloned cDNAs. The BTG-2 and BTG-3 proteins of the present invention share sequence homology with each other and with BTG-1 (FIG. 3A-3B) (SEQ ID NO:17 (BTG-I sequence) and SEQ ID NO:18 (consensus sequence)). The nucleotide sequences shown in FIG. 1A-1B (SEQ ID NO:1) and FIG. 2A-2B (SEQ ID NO:3) were obtained by sequencing the above described cDNA clones, which were deposited at the American Type Culture Collection, 10801 University Blvd., Manassas, Va. 20110-2209, USA, and given the accession numbers indicated above. The deposited clones are contained in the PBLUESCRIPT™ SK(-) plasmid (STRATAGENE™, LaJolla, Calif.).

Nucleic Acid Molecules

Unless otherwise indicated, all nucleotide sequences determined by sequencing a DNA molecule herein were determined using an automated DNA sequencer (such as the Model 373 from Applied Biosystems, Inc.), and all amino acid sequences of polypeptides encoded by DNA molecules determined herein were predicted by translation of a DNA sequence determined as above. Therefore, as is known in the art for any DNA sequence determined by this automated

approach, any nucleotide sequence determined herein may contain some errors. Nucleotide sequences determined by automation are typically at least about 90% identical, more typically at least about 95% to at least about 99.9% identical to the actual nucleotide sequence of the sequenced DNA molecule. The actual sequence can be more precisely determined by other approaches including manual DNA sequencing methods well known in the art. As is also known in the art, a single insertion or deletion in a determined nucleotide sequence compared to the actual sequence will cause a frame shift in translation of the nucleotide sequence such that the predicted amino acid sequence encoded by a determined nucleotide sequence will be completely different from the amino acid sequence actually encoded by the sequenced DNA molecule, beginning at the point of such an insertion or deletion.

Unless otherwise indicated, each "nucleotide sequence" set forth herein is presented as a sequence of deoxyribonucleotides (abbreviated A, G, C and T). However, by "nucleotide sequence" of a nucleic acid molecule or polynucleotide is intended, for a DNA molecule or polynucleotide, a sequence of deoxyribonucleotides, and for an RNA molecule or polynucleotide, the corresponding sequence of ribonucleotides (A, G, C and U), where each thymidine deoxyribonucleotide (T) in the specified deoxyribonucleotide sequence is replaced by the ribonucleotide uridine (U). For instance, reference to an RNA molecule having the sequence of SEQ ID NO:1 or SEQ ID NO:3 set forth using deoxyribonucleotide abbreviations is intended to indicate an RNA molecule having a sequence in which each deoxyribonucleotide A, G or C of SEQ ID NO:1 or SEQ ID NO:3 has been replaced by the corresponding ribonucleotide A, G or C, and each deoxyribonucleotide T has been replaced by a ribonucleotide U.

Using the information provided herein, such as the nucleotide sequence in FIG. 1A-1B or FIG. 2A-2B, a nucleic acid molecule of the present invention encoding a BTG-2 or BTG-3 polypeptide may be obtained using standard cloning and screening procedures, such as those for cloning cDNAs using mRNA as starting material. Illustrative of the invention, the nucleic acid molecules described in FIG. 1A-1B (SEQ ID NO:1) and FIG. 2A-2B (SEQ ID NO:3) were discovered in cDNA libraries derived from a human endometrial tumor and a human synovial carcinoma, respectively. For BTG-2, the gene can also be identified in cDNA libraries from the following tissues: liver, lymphoid and placenta. For BTG-3, the gene can also be identified in cDNA libraries from the following tissues: synovial sarcoma, cerebellum, embryonic, and placenta.

The determined nucleotide sequence of the BTG-2 cDNA of FIG. 1A-1B (SEQ ID NO:1) contains an open reading frame encoding a protein of about 345 amino acid residues and a predicted leader sequence of about 25 amino acid residues. The amino acid sequence of the predicted mature BTG-2 protein is shown in FIG. 1A-1B (SEQ ID NO:2), amino acid residue from about 26 to about 345. The BTG-2 protein shown in FIG. 1A-1B (SEQ ID NO:2) is about 49% identical and about 72% similar to BTG-1 over a 91 amino acid stretch (FIG. 3A-3B).

The determined nucleotide sequence of the BTG-3 cDNA of FIG. 2A-2B (SEQ ID NO:3) contains an open reading frame encoding a protein of about 344 amino acid residues and a predicted leader sequence of about 18 amino acid residues. The amino acid sequence of the predicted mature BTG-3 protein is shown in FIG. 2A-2B (SEQ ID NO:4), amino acid residue from about 19 to about 344. The BTG-3 protein shown in FIG. 2A-2B (SEQ ID NO:4) is about 41%

identical and about 74% similar to BTG-1 over an 85 amino acid stretch (FIG. 3A-3B). Over the same stretch of 85 amino acids, BTG-2 and BTG-3 are 83% identical and 87% similar to each other. In addition, BTG-2 is approximately 143 amino acids longer at the carboxy terminus as compared to BTG-1, while BTG-3 is approximately 162 amino acids longer at the carboxy terminus. Both BTG-2 and BTG-3 contain unique regions rich in the amino acids proline and glutamine.

As indicated, the present invention also provides mature forms of the BTG-2 and BTG-3 proteins. According to the signal hypothesis, proteins secreted by mammalian cells have a signal or secretory leader sequence which is cleaved from the mature protein once export of the growing protein chain across the rough endoplasmic reticulum has been initiated. Most mammalian cells and even insect cells cleave secreted proteins with the same specificity. However, in some cases, cleavage of a secreted protein is not entirely uniform, which results in two or more mature species on the protein. Further, it has long been known that the cleavage specificity of a secreted protein is ultimately determined by the primary structure of the complete protein, that is, it is inherent in the amino acid sequence of the polypeptide. Therefore, the present invention provides nucleotide sequences encoding the mature BTG-2 and BTG-3 polypeptides having the amino acid sequences encoded by the cDNA clones contained in the hosts identified as ATCC™ Deposit No. 97025 and 97010, respectively.

By the mature BTG-2 and BTG-3 polypeptides having the amino acid sequences encoded by the deposited cDNA clones is meant the mature forms of these proteins produced by expression in a mammalian cell (e.g., COS cells, as described below) of the complete open reading frame encoded by the human DNA, sequence of the clones contained in the vectors in the deposited hosts. As indicated below, the mature BTG-2 and BTG-3 polypeptides having the amino acid sequences encoded by the deposited cDNA clones may or may not differ from the predicted "mature" BTG-2 and BTG-3 polypeptides shown in FIG. 1A-1B and FIG. 2A-2B, respectively. This depends on the accuracy of the predicted cleavage site based on computer analysis.

Methods for predicting whether a protein has a secretory leader as well as the cleavage point for that leader sequence are available because it is known that much of the cleavage specificity for a secretory protein resides in certain amino acid residues within the signal sequence and the N-terminus of the mature protein, particularly residues immediately surrounding the cleavage site. For instance, the method of McGeoch (Virus Res. 3:271-286 (1985)) uses the information from a short N-terminal charged region and a subsequent uncharged region of the complete (uncleaved) protein. The method of von Heinje (Nucleic Acids Res. 14:4683-4690 (1986)) uses the information from the residues surrounding the cleavage site, typically residues -13 to +2 where +1 indicates the amino acid terminus of the mature protein. The accuracy of predicting the cleavage points of known mammalian secretory proteins for each of these methods is in the range of 75-80%. von Heinje, supra. However, the two methods do not always produce the same predicted cleavage point(s) for a given protein.

Thus, in view of above, as one of ordinary skill would appreciate, the actual leader sequence of the BTG-2 protein of the present invention is predicted to be about 25 amino acids in length, but may be anywhere in the range of about 15 to about 35 amino acids. Similarly, the actual leader sequence of the BTG-3 protein of the present invention is predicted to be about 18 amino acids in length, but may be

anywhere in the range of about 8 to about 28 amino acids. Further, due to possible sequencing errors as discussed above, the full-length BTG-2 protein is predicted to be about 345 amino acids in length, but may be in the range of about 335 to about 355 amino acids. Similarly, the full-length BTG-3 protein is predicted to be about 344 amino acids in length, but may be in the range of about 335 to about 355 amino acids.

As indicated, nucleic acid molecules of the present invention may be in the form of RNA, such as mRNA, or in the form of DNA, including, for instance, cDNA and genomic DNA obtained by cloning or produced synthetically. The DNA may be double-stranded or single-stranded. Single-stranded DNA or RNA may be the coding strand, also known as the sense strand, or it may be the non-coding strand, also referred to as the anti-sense strand.

By "isolated" nucleic acid molecule(s) is intended a nucleic acid molecule, DNA or RNA, which has been removed from its native environment. For example, recombinant DNA molecules contained in a vector are considered isolated for the purposes of the present invention. Further examples of isolated DNA molecules include recombinant DNA molecules maintained in heterologous host cells or purified (partially or substantially) DNA molecules in solution. Isolated RNA molecules include in vivo or in vitro RNA transcripts of the DNA molecules of the present invention. Isolated nucleic acid molecules according to the present invention further include such molecules produced synthetically.

Isolated nucleic acid molecules of the present invention include DNA molecules shown in FIG. 1A-1B (SEQ ID NO:1) and FIG. 2A-2B (SEQ ID NO:3); DNA molecules comprising the coding sequence for the mature BTG-2 and BTG-3 proteins shown in FIG. 1A-1B (SEQ ID NO:2) and FIG. 2A-2B (SEQ ID NO:3), respectively; and DNA molecules which comprise a sequence substantially different from those described above but which, due to the degeneracy of the genetic code, still encode the BTG-2 or BTG-3 protein. Of course, the genetic code is well known in the art. Thus, it would be routine for one skilled in the art to generate such degenerate variants.

In another aspect, the invention provides isolated nucleic acid molecules encoding the BTG-2 or BTG-3 polypeptide having an amino acid sequence encoded by the above-described deposited cDNA clones. Preferably, these nucleic acid molecules will encode the mature polypeptides encoded by the deposited cDNA clones. The invention further provides isolated nucleic acid molecules having a sequence complementary to one of the above sequences. Such isolated molecules, particularly DNA molecules, are useful as probes for gene mapping, by in situ hybridization with chromosomes, and for detecting expression of the BTG-2 or BTG-3 gene in human tissue, for instance, by Northern blot analysis.

The present invention is further directed to fragments of the isolated nucleic acid molecules described herein. By a fragment of an isolated nucleic acid molecule having the nucleotide sequence of one of the deposited cDNAs or the nucleotide sequence shown in FIG. 1A-1B (SEQ ID NO:1) or FIG. 2A-2B (SEQ ID NO:2) is intended fragments at least about 15 nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nucleotides in length which are useful as diagnostic probes and primers as discussed herein. Of course, larger fragments 50-1500 nucleotides in length are also useful according to the present invention as are fragments corresponding to most, if not all, of the nucleotide

sequences of the deposited cDNAs or as shown in FIG. 1A-1B (SEQ ID NO:1) or FIG. 2A-2B (SEQ ID NO:2). By a fragment at least 20 nucleotides in length, for example, is intended fragments which include 20 or more contiguous bases from the nucleotide sequences of the deposited cDNA or the nucleotide sequence as shown in FIG. 1A-1B (SEQ ID NO:1) or FIG. 2A-2B (SEQ ID NO:2). Since the BTG-2 and BTG-3 genes have been deposited and the nucleotide sequences shown in FIG. 1A-2B (SEQ ID NO:1) and FIG. 2A-2B (SEQ ID NO:3) are provided, generating such DNA fragments would be routine to the skilled artisan. For example, restriction endonuclease cleavage or shearing by sonication could easily be used to generate fragments of various sizes. Alternatively, such fragments could be generated synthetically.

Preferred nucleic acid fragments of the present invention include nucleic acid molecules encoding epitope-bearing portions of the BTG-2 or BTG-3 protein. Methods for generating such epitope-bearing portions of the BTG-2 or BTG-3 protein are described in detail below.

In another aspect, the invention provides an isolated nucleic acid molecule comprising a polynucleotide which hybridizes under stringent hybridization conditions to a portion of the polynucleotide in a nucleic acid molecule of the invention described above, for instance, the cDNA clone contained in ATCC™ Deposit No. 97025 or 97010. By "stringent hybridization conditions" is intended overnight incubation at 42° C. in a solution comprising: 50% formamide, 5×SSC (750 mM NaCl, 75 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5× Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1×SSC at about 65° C.

By a polynucleotide which hybridizes to a "portion" of a polynucleotide is intended a polynucleotide (either DNA or RNA) hybridizing to at least about 15 nucleotides (nt), and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably about 30-70 nt of the reference polynucleotide. These are useful as diagnostic probes and primers as discussed above and in more detail below.

Of course, polynucleotides hybridizing to a larger portion of the reference polynucleotide (e.g., the deposited cDNA clone), for instance, a portion 50-750 nt in length, or even to the entire length of the reference polynucleotide, are also useful as probes according to the present invention, as are polynucleotides corresponding to most, if not all, of the nucleotide sequence of the deposited cDNAs or the nucleotide sequence as shown in FIG. 1A-1B (SEQ ID NO:1) or FIG. 2A-2B (SEQ ID NO:3). By a portion of a polynucleotide of "at least 20 nucleotides in length," for example, is intended 20 or more contiguous nucleotides from the nucleotide sequence of the reference polynucleotide. As indicated, such portions are useful diagnostically either as a probe according to conventional DNA hybridization techniques or as primers for amplification of a target sequence by the polymerase chain reaction (PCR), as described, for instance, in *Molecular Cloning, A Laboratory Manual*, 2nd. edition, Sambrook, J., Fritsch, E. F. and Maniatis, T., eds., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989), the entire disclosure of which is hereby incorporated herein by reference. Of course, a polynucleotide which hybridizes only to a poly A sequence (such as the 3' terminal poly(A) tract of the BTG-2 or BTG-3 cDNA shown in FIG. 1A-1B (SEQ ID NO:1)) and FIG. 2A-2B (SEQ ID NO:2), respectively, or to a complementary stretch of T (or U) residues, would not be included in a polynucleotide of the

invention used to hybridize to a portion of a nucleic acid of the invention, since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone).

As indicated, nucleic acid molecules of the present invention which encode a BTG-2 or BTG-3 polypeptide may include, but are not limited to those encoding the amino acid sequence of the mature polypeptide, by itself; the coding sequence for the mature polypeptide and additional sequences, such as those encoding the leader or secretory sequence, such as a pre-, or pro- or prepro-protein sequence; the coding sequence of the mature polypeptide, with or without the aforementioned additional coding sequences, together with additional, non-coding sequences, including for example, but not limited to introns and non-coding 5' and 3' sequences, such as the transcribed, non-translated sequences that play a role in transcription, mRNA processing, including splicing and polyadenylation signals, for example—ribosome binding and stability of mRNA; an additional coding sequence which codes for additional amino acids, such as those which provide additional functionalities. Thus, the sequence encoding the polypeptide may be fused to a marker sequence, such as a sequence encoding a peptide which facilitates purification of the fused polypeptide. In certain preferred embodiments of this aspect of the invention, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (Qiagen, Inc.), among others, many of which are commercially available. As described in Gentz et al., *Proc. Natl. Acad. Sci. USA* 86:821–824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion protein. The “HA” tag is another peptide useful for purification which corresponds to an epitope derived from the influenza hemagglutinin protein, which has been described by Wilson et al., *Cell* 37: 767 (1984). As discussed below, other such fusion proteins include the BTG-2 or BTG-2 protein fused to Fc at the N- or C-terminus.

The present invention further relates to variants of the nucleic acid molecules of the present invention, which encode portions, analogs or derivatives of the BTG-2 or BTG-3 protein. Variants may occur naturally, such as a natural allelic variant. By an “allelic variant” is intended one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. *Genes II*, Lewin, B., ed., John Wiley & Sons, New York (1985). Non-naturally occurring variants may be produced using art-known mutagenesis techniques.

Such variants include those produced by nucleotide substitutions, deletions or additions. The substitutions, deletions or additions may involve one or more nucleotides. The variants may be altered in coding regions, non-coding regions, or both. Alterations in the coding regions may produce conservative or non-conservative amino acid substitutions, deletions or additions. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of the BTG-2 or BTG-3 protein or portions thereof. Also especially preferred in this regard are conservative substitutions.

Further embodiments of the invention include isolated nucleic acid molecules comprising a polynucleotide having a nucleotide sequence at least 90% identical, and more preferably at least 95%, 96%, 97%, 98% or 99% identical to: (a) a nucleotide sequence encoding the BTG-2 or BTG-3 polypeptide having the complete amino acid sequence in FIG. 1A–1B (SEQ ID NO:2) and FIG. 2A–2B (SEQ ID NO:4), respectively; (b) a nucleotide sequence encoding the

mature BTG-2 or mature BTG-3 polypeptide having the amino acid sequence at positions from about 26 to about 345 in FIG. 1A–1B (SEQ ID NO:2) and from about 19 to about 344 in FIG. 2A–2B (SEQ ID NO:4), respectively; (c) a nucleotide sequence encoding the BTG-2 or BTG-3 polypeptide having the complete amino acid sequence encoded by the cDNA clone contained in ATCC™ Deposit No. 97025 and 97010, respectively; (d) a nucleotide sequence encoding the mature BTG-2 or mature BTG-3 polypeptide having the amino acid sequence encoded by the cDNA clone contained in ATCC™ Deposit No. 97025 and 97010, respectively; and (e) a nucleotide sequence complementary to any of the nucleotide sequences in (a), (b), (c) or (d) above.

By a polynucleotide having a nucleotide sequence at least, for example, 95% “identical” to a reference nucleotide sequence encoding a BTG-2 or BTG-3 polypeptide is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the BTG-2 or BTG-3 polypeptide. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. These mutations of the reference sequence may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular nucleic acid molecule is at least 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the nucleotide sequence shown in FIG. 1A–1B or FIG. 3A–3B or to the nucleotide sequence of one of the deposited cDNA clones can be determined conventionally using known computer programs such as the Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, Wis. 53711. Bestfit uses the local homology algorithm of Smith and Waterman, *Advances in Applied Mathematics* 2:482–489 (1981), to find the best segment of homology between two sequences. When using Bestfit or any other sequence alignment program to determine whether a particular sequence is, for instance, 95% identical to a reference sequence according to the present invention, the parameters are set, of course, such that the percentage of identity is calculated over the full length of the reference nucleotide sequence and that gaps in homology of up to 5% of the total number of nucleotides in the reference sequence are allowed.

The present application is directed to nucleic acid molecules at least 90%, 95%, 96%, 97%, 98% or 99% identical to the nucleic acid sequence shown in FIG. 1A–1B (SEQ ID NO:1) or FIG. 3A–3B (SEQ ID NO:3) or to the nucleic acid sequence of one of the deposited cDNAs, irrespective of whether they encode a polypeptide having BTG-2 or BTG-3 activity. This is because even where a particular nucleic acid molecule does not encode a polypeptide having BTG-2 or BTG-3 activity, one of skill in the art would still know how to use the nucleic acid molecule, for instance, as a hybridization probe or a polymerase chain reaction (PCR) primer. Uses of the nucleic acid molecules of the present invention that do not encode a polypeptide having BTG-2 or BTG-3

activity include, inter alia, (1) isolating the BTG-2 or BTG-3 gene or allelic variants thereof in a cDNA library; (2) in situ hybridization (e.g., "FISH") to metaphase chromosomal spreads to provide precise chromosomal location of the BTG-2 or BTG-3 gene, as described in Verma et al., *Human Chromosomes: A Manual of Basic Techniques*, Pergamon Press, New York (1988); and Northern Blot analysis for detecting BTG-2 or BTG-3 mRNA expression in specific tissues.

Preferred, however, are nucleic acid molecules having sequences at least 90%, 95%, 96%, 97%, 98% or 99% identical to the nucleic acid sequence shown in FIG. 1A-1B (SEQ ID NO:1) or FIG. 2A-2B (SEQ ID NO:3) or to the nucleic acid sequence of one of the deposited cDNAs which do, in fact, encode a polypeptide having BTG-2 or BTG-3 protein activity. By "a polypeptide having BTG-2 or BTG-3 activity" is intended polypeptides exhibiting activity similar, but not necessarily identical, to an activity of the BTG-2 or BTG-3 protein of the invention (either the full-length protein or, preferably, the mature protein), as measured in a particular biological assay. For example, the BTG-2 and BTG-3 proteins are antiproliferative agents. In fact, exogenously expressed BTG-2 protein has been shown to suppress growth of NIH3T3 cells (Matsuda et al., *Oncogene* 12:705-713 (1996)). Thus, BTG-2 or BTG-3 protein activity can be assayed by measuring the ability of a candidate polypeptide to suppress growth of certain cell types in vitro, such as NIH3T3 cells.

Of course, due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the nucleic acid molecules having a sequence at least 90%, 95%, 96%, 97%, 98%, or 99% identical to the nucleic acid sequence of the deposited cDNA or the nucleic acid sequence shown in FIG. 1A-1B (SEQ ID NO:1) will encode a polypeptide "having BTG-2 or BTG-3 protein activity." In fact, since degenerate variants of these nucleotide sequences all encode the same polypeptide, this will be clear to the skilled artisan even without performing the above described comparison assay. It will be further recognized in the art that, for such nucleic acid molecules that are not degenerate variants, a reasonable number will also encode a polypeptide having BTG-2 or BTG-3 protein activity. This is because the skilled artisan is fully aware of amino acid substitutions that are either less likely or not likely to significantly affect protein function (e.g., replacing one aliphatic amino acid with a second aliphatic amino acid).

For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie, J. U. et al., "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions," *Science* 247:1306-1310 (1990), wherein the authors indicate that there are two main approaches for studying the tolerance of an amino acid sequence to change. The first method relies on the process of evolution, in which mutations are either accepted or rejected by natural selection. The second approach uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene and selections or screens to identify sequences that maintain functionality. As the authors state, these studies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at a certain position of the protein. For example, most buried amino acid residues require nonpolar side chains, whereas few features of surface side chains are

generally conserved. Other such phenotypically silent substitutions are described in Bowie, J. U. et al., supra, and the references cited therein.

Vectors and Host Cells

The present invention also relates to vectors which include the isolated DNA molecules of the present invention, host cells which are genetically engineered with the recombinant vectors, and the production of BTG-2 and BTG-3 polypeptides or fragments thereof by recombinant techniques.

Recombinant constructs may be introduced into host cells using well known techniques such infection, transduction, transfection, transvection, electroporation and transformation. The vector may be, for example, a phage, plasmid, viral or retroviral vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells.

The polynucleotides may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus, it may be packaged in vitro using an appropriate packaging cell line and then transduced into host cells.

Preferred are vectors comprising cis-acting control regions to the polynucleotide of interest. Appropriate trans-acting factors may be supplied by the host, supplied by a complementing vector or supplied by the vector itself upon introduction into the host.

In certain preferred embodiments in this regard, the vectors provide for specific expression, which may be inducible and/or cell type-specific. Particularly preferred among such vectors are those inducible by environmental factors that are easy to manipulate, such as temperature and nutrient additives.

Expression vectors useful in the present invention include chromosomal-, episomal- and virus-derived vectors, e.g., vectors derived from bacterial plasmids, bacteriophage, yeast episomes, yeast chromosomal elements, viruses such as baculoviruses, papova viruses, vaccinia viruses, adenoviruses, fowl pox viruses, pseudorabies viruses and retroviruses, and vectors derived from combinations thereof, such as cosmids and phagemids.

The DNA insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the *E. coli* lac, trp and tac promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination and, in the transcribed region, a ribosome binding site for translation. The coding portion of the mature transcripts expressed by the constructs will preferably include a translation initiating at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase or neomycin resistance for eukaryotic cell culture and tetracycline or ampicillin resistance genes for culturing in *E. coli* and other bacteria. Representative examples of appropriate hosts include, but are not limited to, bacterial cells, such as *E. coli*, *Streptomyces* and *Salmonella typhimurium* cells; fungal cells, such as yeast cells; insect cells such as *Drosophila* S2 and *Spodoptera* Sf9

cells; animal cells such as CHO, COS and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9, available from Qiagen; pBS vectors, Phagescript vectors, Bluescript vectors, pNH8A, pNH16a, pNH18A, pNH46A, available from STRATAGENE™; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from PHARMACIA™. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from STRATAGENE™; and pSVK3, pBPV, pMSG and pSVL available from PHARMACIA™. Other suitable vectors will be readily apparent to the skilled artisan.

Among known bacterial promoters suitable for use in the present invention include the *E. coli* lacI and lacZ promoters, the T3 and T7 promoters, the gpt promoter, the lambda PR and PL promoters and the trp promoter. Suitable eukaryotic promoters include the CMV immediate early promoter, the HSV thymidine kinase promoter, the early and late SV40 promoters, the promoters of retroviral LTRs, such as those of the Rous sarcoma virus (RSV), and metallothionein promoters, such as the mouse metallothionein-I promoter.

Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection or other methods. Such methods are described in many standard laboratory manuals, such as Davis et al., *Basic Methods In Molecular Biology* (1986).

Transcription of the DNA encoding the polypeptides of the present invention by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp that act to increase transcriptional activity of a promoter in a given host cell-type. Examples of enhancers include the SV40 enhancer, which is located on the late side of the replication origin at bp 100 to 270, the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers.

For secretion of the translated protein into the lumen of the endoplasmic reticulum, into the periplasmic space or into the extracellular environment, appropriate secretion signals may be incorporated into the expressed polypeptide. The signals may be endogenous to the polypeptide or they may be heterologous signals.

The polypeptide may be expressed in a modified form, such as a fusion protein, and may include not only secretion signals, but also additional heterologous functional regions. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence in the host cell, during purification, or during subsequent handling and storage. Also, peptide moieties may be added to the polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to polypeptides to engender secretion or excretion, to improve stability and to facilitate purification, among others, are familiar and routine techniques in the art. A preferred fusion protein comprises a heterologous region from immunoglobulin that is useful to solubilize proteins. For example, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many

cases, the Fc part in a fusion protein is thoroughly advantageous for use in therapy and diagnosis and thus results, for example, in improved pharmacokinetic properties (EP-A 0232 262). On the other hand, for some uses it would be desirable to be able to delete the Fc part after the fusion protein has been expressed, detected and purified in the advantageous manner described. This is the case when Fc portion proves to be a hindrance to use in therapy and diagnosis, for example when the fusion protein is to be used as antigen for immunizations. In drug discovery, for example, human proteins, such as, hIL5- has been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. See, D. Bennett et al., *Journal of Molecular Recognition*, Vol. 8:52-58 (1995) and K. Johanson et al., *The Journal of Biological Chemistry*, Vol. 270, No. 16:9459-9471 (1995).

The BTG-2 and BTG-3 proteins can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification. Polypeptides of the present invention include naturally purified products, products of chemical synthetic procedures, and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect and mammalian cells. Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes.

BTG-2 and BTG-3 Polypeptides and Fragments

The invention further provides an isolated BTG-2 or BTG-3 polypeptide having the amino acid sequence encoded by the deposited cDNAs, or the amino acid sequence in FIG. 1A-1B (SEQ ID NO:2) or FIG. 2A-2B (SEQ ID NO:4), or a peptide or polypeptide comprising a portion of the above polypeptides. The terms "peptide" and "oligopeptide" are considered synonymous (as is commonly recognized) and each term can be used interchangeably as the context requires to indicate a chain of at least to amino acids coupled by peptidyl linkages. The word "polypeptide" is used herein for chains containing more than ten amino acid residues. All oligopeptide and polypeptide formulas or sequences herein are written from left to right and in the direction from amino terminus to carboxy terminus.

It will be recognized in the art that some amino acid sequences of the BTG-2 or BTG-3 polypeptide can be varied without significant effect of the structure or function of the protein. If such differences in sequence are contemplated, it should be remembered that there will be critical areas on the protein which determine activity. In general, it is possible to replace residues which form the tertiary structure, provided that residues performing a similar function are used. In other instances, the type of residue may be completely unimportant if the alteration occurs at a non-critical region of the protein.

Thus, the invention further includes variations of the BTG-2 or BTG-3 polypeptide which show substantial BTG-2 or BTG-3 polypeptide activity or which include regions of BTG-2 or BTG-3 protein such as the protein

portions discussed below. Such mutants include deletions, insertions, inversions, repeats, and type substitutions (for example, substituting one hydrophilic residue for another, but not strongly hydrophilic for strongly hydrophobic as a rule). Small changes or such "neutral" amino acid substitutions will generally have little effect on activity.

Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe, Tyr. Examples of conservative amino acid substitutions known to those skilled in the art are set forth below:

Aromatic:	phenylalanine tryptophan tyrosine
Hydrophobic:	leucine isoleucine valine
Polar:	glutamine asparagine
Basic:	arginine lysine histidine
Acidic:	aspartic acid glutamic acid
Small:	alanine serine threonine methionine glycine

As indicated in detail above, further guidance concerning which amino acid changes are likely to be phenotypically silent (i.e., are not likely to have a significant deleterious effect on a function) can be found in Bowie, J. U., et al., "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions," *Science* 247:1306-1310 (1990).

The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of the BTG-2 or BTG-3 polypeptide can be substantially purified by the one-step method described in Smith and Johnson, *Gene* 67:31-40 (1988).

The polypeptides of the present invention include the BTG-2 or BTG-3 polypeptide encoded by the deposited cDNA clones (ATCC™ Nos. 97025 and 97010, respectively) including the leader, the mature polypeptide encoded by the deposited the cDNA clones minus the leader (i.e., the mature protein), the BTG-2 polypeptide of FIG. 1A-1B (SEQ ID NO:2) including the leader, the BTG-3 polypeptide of FIG. 2A-2B (SEQ ID NO:4) including the leader, the BTG-2 polypeptide of FIG. 1A-1B (SEQ ID NO:2) minus the leader, the BTG-3 polypeptide of FIG. 2A-2B (SEQ ID NO:4) minus the leader, as well as polypeptides which have at least 90% similarity, more preferably at least 95% similarity, and still more preferably at least 96%, 97%, 98% or 99% similarity to those described above. Further polypeptides of the present invention include polypeptides at least 80% identical, more preferably at least 90% or 95% identical, still more preferably at least 96%, 97%, 98% or 99% identical to the BTG-2 or BTG-3 polypeptide encoded by the deposited cDNA clones (ATCC™ Nos. 97025 and 97010, respectively), to the BTG-2 polypeptide of FIG.

1A-1B (SEQ ID NO:2), to the BTG-3 polypeptide of FIG. 2A-2B (SEQ ID NO:4) and also include portions of such BTG-2 or BTG-3 polypeptides with at least 30 amino acids and more preferably at least 50 amino acids.

By "% similarity" for two polypeptides is intended a similarity score produced by comparing the amino acid sequences of the two polypeptides using the Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, Wis. 53711) and the default settings for determining similarity. Bestfit uses the local homology algorithm of Smith and Waterman (*Advances in Applied Mathematics* 2:482489, 1981) to find the best segment of similarity between two sequences.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a reference amino acid sequence of a BTG-2 or BTG-3 polypeptide is intended that the amino acid sequence of the polypeptide is identical to the reference sequence except that the polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the reference amino acid of the BTG-2 or BTG-3 polypeptide. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a reference amino acid sequence, up to 5% of the amino acid residues in the reference sequence may be deleted or substituted with another amino acid, or a number of amino acids up to 5% of the total amino acid residues in the reference sequence may be inserted into the reference sequence. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequence shown in FIG. 1A-1B (SEQ ID NO:2), FIG. 2A-2B (SEQ ID NO:4) or to the amino acid sequence encoded by deposited cDNA clones can be determined conventionally using known computer programs such the Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, Wis. 53711. When using Bestfit or any other sequence alignment program to determine whether a particular sequence is, for instance, 95% identical to a reference sequence according to the present invention, the parameters are set, of course, such that the percentage of identity is calculated over the full length of the reference amino acid sequence and that gaps in homology of up to 5% of the total number of amino acid residues in the reference sequence are allowed.

The BTG-2 or BTG-3 polypeptide of the present invention could be used as a molecular weight marker on SDS-PAGE gels or on molecular sieve gel filtration columns using methods well known to those of skill in the art.

As described in detail below, the polypeptides of the present invention can also be used to raise polyclonal and monoclonal antibodies, which are useful in assays for detecting BTG-2 or BTG-3 protein expression as described below or as agonists and antagonists capable of enhancing or inhibiting BTG-2 or BTG-3 protein function. Further, such polypeptides can be used in the yeast two-hybrid system to "capture" BTG-2 or BTG-3 protein binding proteins which are also candidate agonist and antagonist according to the present invention. The yeast two hybrid system is described in Fields and Song, *Nature* 340:245-246 (1989).

In another aspect, the invention provides a peptide or polypeptide comprising an epitope-bearing portion of a polypeptide of the invention. The epitope of this polypeptide portion is an immunogenic or antigenic epitope of a polypeptide of the invention. An "immunogenic epitope" is defined as a part of a protein that elicits an antibody response when the whole protein is the immunogen. These immunogenic epitopes are believed to be confined to a few loci on the molecule. On the other hand, a region of a protein molecule to which an antibody can bind is defined as an "antigenic epitope." The number of immunogenic epitopes of a protein generally is less than the number of antigenic epitopes. See, for instance, Geysen et al., *Proc. Natl. Acad. Sci. USA* 81:3998-4002 (1983).

As to the selection of peptides or polypeptides bearing an antigenic epitope (i.e., that contain a region of a protein molecule to which an antibody can bind), it is well known in that art that relatively short synthetic peptides that mimic part of a protein sequence are routinely capable of eliciting an antiserum that reacts with the partially mimicked protein. See, for instance, Sutcliffe, J. G., Shinnick, T. M., Green, N. and Learner, R. A. (1983) Antibodies that react with predetermined sites on proteins. *Science* 219:660-666. Peptides capable of eliciting protein-reactive sera are frequently represented in the primary sequence of a protein, can be characterized by a set of simple chemical rules, and are confined neither to immunodominant regions of intact proteins (i.e., immunogenic epitopes) nor to the amino or carboxyl terminals. Peptides that are extremely hydrophobic and those of six or fewer residues generally are ineffective at inducing antibodies that bind to the mimicked protein; longer, peptides, especially those containing proline residues, usually are effective. Sutcliffe et al., *supra*, at 661. For instance, 18 of 20 peptides designed according to these guidelines, containing 8-39 residues covering 75% of the sequence of the influenza virus hemagglutinin HA1 polypeptide chain, induced antibodies that reacted with the HA1 protein or intact virus; and 12/12 peptides from the MuLV polymerase and 18/18 from the rabies glycoprotein induced antibodies that precipitated the respective proteins.

Antigenic epitope-bearing peptides and polypeptides of the invention are therefore useful to raise antibodies, including monoclonal antibodies, that bind specifically to a polypeptide of the invention. Thus, a high proportion of hybridomas obtained by fusion of spleen cells from donors immunized with an antigen epitope-bearing peptide generally secrete antibody reactive with the native protein. Sutcliffe et al., *supra*, at 663. The antibodies raised by antigenic epitope-bearing peptides or polypeptides are useful to detect the mimicked protein, and antibodies to different peptides may be used for tracking the fate of various regions of a protein precursor which undergoes post-translational processing. The peptides and anti-peptide antibodies may be used in a variety of qualitative or quantitative assays for the mimicked protein, for instance in competition assays since it has been shown that even short peptides (e.g., about 9 amino acids) can bind and displace the larger peptides in immunoprecipitation assays. See, for instance, Wilson et al., *Cell* 37:767-778 (1984) at 777. The anti-peptide antibodies of the invention also are useful for purification of the mimicked protein, for instance, by adsorption chromatography using methods well known in the art.

Antigenic epitope-bearing peptides and polypeptides of the invention designed according to the above guidelines preferably contain a sequence of at least seven, more preferably at least nine and most preferably between about 15 to about 30 amino acids contained within the amino acid

sequence of a polypeptide of the invention. However, peptides or polypeptides comprising a larger portion of an amino acid sequence of a polypeptide of the invention, containing about 30 to about 50 amino acids, or any length up to and including the entire amino acid sequence of a polypeptide of the invention, also are considered epitope-bearing peptides or polypeptides of the invention and also are useful for inducing antibodies that react with the mimicked protein. Preferably, the amino acid sequence of the epitope-bearing peptide is selected to provide substantial solubility in aqueous solvents (i.e., the sequence includes relatively hydrophilic residues and highly hydrophobic sequences are preferably avoided); and sequences containing proline residues are particularly preferred.

The epitope-bearing peptides and polypeptides of the invention may be produced by any conventional means for making peptides or polypeptides including recombinant means using nucleic acid molecules of the invention. For instance, a short epitope-bearing amino acid sequence may be fused to a larger polypeptide which acts as a carrier during recombinant production and purification, as well as during immunization to produce anti-peptide antibodies. Epitope-bearing peptides also may be synthesized using known methods of chemical synthesis. For instance, Houghten has described a simple method for synthesis of large numbers of peptides, such as 10-20 mg of 248 different 13 residue peptides representing single amino acid variants of a segment of the HA1 polypeptide which were prepared and characterized (by ELISA-type binding studies) in less than four weeks. Houghten, R. A. (1985) General method for the rapid solid-phase synthesis of large numbers of peptides: specificity of antigen-antibody interaction at the level of individual amino acids. *Proc. Natl. Acad. Sci. USA* 82:5131-5135. This "Simultaneous Multiple Peptide Synthesis (SMPS)" process is further described in U.S. Pat. No. 4,631,211 to Houghten et al. (1986). In this procedure the individual resins for the solid-phase synthesis of various peptides are contained in separate solvent-permeable packets, enabling the optimal use of the many identical repetitive steps involved in solid-phase methods. A completely manual procedure allows 500-1000 or more syntheses to be conducted simultaneously. Houghten et al., *supra*, at 5134.

Epitope-bearing peptides and polypeptides of the invention are used to induce antibodies according to methods well known in the art. See, for instance, Sutcliffe et al., *supra*; Wilson et al., *supra*; Chow, M. et al., *Proc. Natl. Acad. Sci. USA* 82:910-914; and Bittle, F. J. et al., *J. Gen. Virol.* 66:2347-2354 (1985). Generally, animals may be immunized with free peptide; however, anti-peptide antibody titer may be boosted by coupling of the peptide to a macromolecular carrier, such as keyhole limpet hemacyanin (KLH) or tetanus toxoid. For instance, peptides containing cysteine may be coupled to carrier using a linker such as m-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS), while other peptides may be coupled to carrier using a more general linking agent such as glutaraldehyde. Animals such as rabbits, rats and mice are immunized with either free or carrier-coupled peptides, for instance, by intraperitoneal and/or intradermal injection of emulsions containing about 100 g peptide or carrier protein and Freund's adjuvant. Several booster injections may be needed, for instance, at intervals of about two weeks, to provide a useful titer of anti-peptide antibody which can be detected, for example, by ELISA assay using free peptide adsorbed to a solid surface. The titer of anti-peptide antibodies in serum from an immunized animal may be increased by selection of anti-peptide antibodies, for instance, by adsorption to the peptide

on a solid support and elution of the selected antibodies according to methods well known in the art.

Immunogenic epitope-bearing peptides of the invention, i.e., those parts of a protein that elicit an antibody response when the whole protein is the immunogen, are identified according to methods known in the art. For instance, Geysen et al., supra, discloses a procedure for rapid concurrent synthesis on solid supports of hundreds of peptides of sufficient purity to react in an enzyme-linked immunosorbent assay. Interaction of synthesized peptides with antibodies is then easily detected without removing them from the support. In this manner a peptide bearing an immunogenic epitope of a desired protein may be identified routinely by one of ordinary skill in the art. For instance, the immunologically important epitope in the coat protein of foot-and-mouth disease virus was located by Geysen et al. with a resolution of seven amino acids by synthesis of an overlapping set of all 208 possible hexapeptides covering the entire 213 amino acid sequence of the protein. Then, a complete replacement set of peptides in which all 20 amino acids were substituted in turn at every position within the epitope were synthesized, and the particular amino acids conferring specificity for the reaction with antibody were determined. Thus, peptide analogs of the epitope-bearing peptides of the invention can be made routinely by this method. U.S. Pat. No. 4,708,781 to Geysen (1987) further describes this method of identifying a peptide bearing an immunogenic epitope of a desired protein.

Further still, U.S. Pat. No. 5,194,392 to Geysen (1990) describes a general method of detecting or determining the sequence of monomers (amino acids or other compounds) which is a topological equivalent of the epitope (i.e., a "mimotope") which is complementary to a particular paratope (antigen binding site) of an antibody of interest. More generally, U.S. Pat. No. 4,433,092 to Geysen (1989) describes a method of detecting or determining a sequence of monomers which is a topographical equivalent of a ligand which is complementary to the ligand binding site of a particular receptor of interest. Similarly, U.S. Pat. No. 5,480,971 to Houghten, R. A. et al. (1996) on Peralkylated Oligopeptide Mixtures discloses linear C₁-C-alkyl peralkylated oligopeptides and sets and libraries of such peptides, as well as methods for using such oligopeptide sets and libraries for determining the sequence of a peralkylated oligopeptide that preferentially binds to an acceptor molecule of interest. Thus, non-peptide analogs of the epitope-bearing peptides of the invention also can be made routinely by these methods.

The entire disclosure of each document cited in this section on "Polypeptides and Peptides" is hereby incorporated herein by reference.

As one of skill in the art will appreciate, BTG-2 or BTG-3 polypeptides of the present invention and the epitope-bearing fragments thereof described above can be combined with parts of the constant domain of immunoglobulins (IgG), resulting in chimeric polypeptides. These fusion proteins facilitate purification and show an increased half-life in vivo. This has been shown, e.g., for chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins (EPA 394,827; Trauneker et al., *Nature* 331:84-86 (1988)). Fusion proteins that have a disulfide-linked dimeric structure due to the IgG part can also be more efficient in binding and neutralizing other molecules than the monomeric BTG-2 or BTG-3 protein or protein fragment alone (Fountoulakis et al., *J Biochem* 270:3958-3964 (1995)).

Diagnostic and Therapeutic Uses

The BTG-2 and BTG-3 polypeptides have an anti-proliferative ability and may be employed to treat diseases or pathological conditions associated with aberrant cellular proliferation. The polypeptides may be employed as a tumor/growth suppression regulator. They may also be employed to inhibit cancer cell proliferation.

BTG-2 and BTG-3 may also be employed to prevent uncontrolled wound healing which would otherwise cause scarring. Restenosis, which is re-occlusion of arterial walls after balloon angioplasty, may also be treated with BTG-2 and BTG-3 since arteries re-occlude through cell proliferation. Similarly angiogenesis of tumors may be inhibited.

The BTG-2 and BTG-3 genes and gene products may also be employed for modulation of cellular growth. Due to their anti-proliferative effect they could be selectively administered or possibly inhibited when it is desirable to have certain cells proliferate. An example would be a disorder related to the underproduction of certain cells, where proliferation and differentiation of these cells would help to treat the disorder.

The polynucleotides and polypeptides encoded by such polynucleotides may also be utilized for in vitro purposes related to scientific research, synthesis of DNA and manufacture of DNA vectors and for designing therapeutics and diagnostics for the treatment of human disease.

The nucleic acid sequences of the present invention may be employed as part of a diagnostic assay for detecting susceptibility to diseases associated with aberrant cellular proliferation. Since, the polypeptides of the present invention are encoded by anti-proliferative genes, a disruption in the transcription of the genes and corresponding lack of production of the gene product will likely be involved in aberrant cellular proliferation associated with a malignant phenotype.

Individuals carrying mutations in the genes may be detected at the DNA level by a variety of techniques. Nucleic acids for diagnosis may be obtained from a patient's cells, including but not limited to blood, urine, saliva, tissue biopsy and autopsy material. The genomic DNA may be used directly for detection or may be amplified enzymatically by using PCR (Saiki et al., *Nature* 324:163-166 (1986)) prior to analysis. RNA or cDNA may also be used for the same purpose. As an example, PCR primers complementary to the nucleic acid encoding the polypeptides of the present invention can be used to identify and analyze mutations. For example, deletions and insertions can be detected by a change in size of the amplified product in comparison to the normal genotype. Point mutations can be identified by hybridizing amplified DNA to radiolabeled RNA of the present invention or alternatively, radiolabeled antisense DNA sequences. Perfectly matched sequences can be distinguished from mismatched duplexes by RNase A digestion or by differences in melting temperatures.

Genetic testing based on DNA sequence differences may be achieved by detection of alteration in electrophoretic mobility of DNA fragments in gels with or without denaturing agents. Small sequence deletions and insertions can be visualized by high resolution gel electrophoresis. DNA fragments of different sequences may be distinguished on denaturing formamide gradient gels in which the mobilities of different DNA fragments are retarded in the gel at different positions according to their specific melting or partial melting temperatures (see, e.g., Myers et al., *Science* 230:1242 (1985)).

Sequence changes at specific locations may also be revealed by nuclease protection assays, such as RNase and

SI protection or the chemical cleavage method (e.g., Cotton et al., *Proc. Natl. Acad. Sci. (USA)* 85:4397-4401 (1985)).

Thus, the detection of a specific DNA sequence may be achieved by methods such as hybridization, RNase protection, chemical cleavage, direct DNA sequencing or the use of restriction enzymes, (e.g., Restriction Fragment Length Polymorphisms (RFLP)) and Southern blotting of genomic DNA.

In addition to more conventional gel-electrophoresis and DNA sequencing, mutations can also be detected by in situ analysis.

The present invention also relates to a diagnostic assay for detecting altered levels of the proteins of the present invention in various tissues since an over-expression of the proteins compared to normal control tissue samples may detect the presence of a disease or susceptibility to a disease, for example, abnormal cellular proliferation and differentiation. Assays used to detect levels of these proteins in a sample derived from a host are well-known to those of skill in the art and include radioimmunoassays, competitive-binding assays, Western Blot analysis, ELISA assays and "sandwich" assay. An ELISA assay (Coligan et al., *Current Protocols in Immunology* 1(2), Chapter 6, (1991)) initially comprises preparing an antibody specific to the antigens to the polypeptides of the present invention, preferably a monoclonal antibody. In addition a reporter antibody is prepared against the monoclonal antibody. To the reporter antibody is attached a detectable reagent such as radioactivity, fluorescence or, in this example, a horseradish peroxidase enzyme. A sample is removed from a host and incubated on a solid support, e.g. a polystyrene dish, that binds the proteins in the sample. Any free protein binding sites on the dish are then covered by incubating with a non-specific protein, for example, bovine serum albumen. Next, the monoclonal antibody specific to the polypeptides of the present invention is incubated in the dish during which time the monoclonal antibodies attach to any proteins attached to the polystyrene dish. All unbound monoclonal antibody is washed out with buffer. The reporter antibody linked to horseradish peroxidase is now placed in the dish resulting in binding of the reporter antibody to any monoclonal antibody bound to the proteins of the present invention. Unattached reporter antibody is then washed out. Peroxidase substrates are then added to the dish and the amount of color developed in a given time period is a measurement of the amount of protein present in a given volume of patient sample when compared against a standard curve.

A competition assay may be employed wherein antibodies specific to the polypeptides of the present invention are attached to a solid support. Labeled polypeptides and a sample derived from the host are then passed over the solid support and the amount of label detected, for example by liquid scintillation chromatography, can be correlated to a quantity of the polypeptides of the present invention in the sample.

A "sandwich" assay is similar to an ELISA assay. In a "sandwich" assay the polypeptides of the present invention are passed over a solid support and bind to antibodies attached to a solid support. A second antibody is then bound to the polypeptides. A third antibody which is labeled and specific to the second antibody is then passed over the solid support and binds to the second antibody and an amount can then be quantified.

This invention provides a method for identification of the receptors for the polypeptides of the present invention. The gene encoding the receptor can be identified by numerous

methods known to those of skill in the art, for example, ligand panning and FACS sorting (Coligan, et al., *Current Protocols in Immun.* 1(2), Chapter 5, (1991)). Preferably, expression cloning is employed wherein polyadenylated RNA is prepared from a cell responsive to the polypeptides, and a cDNA library created from this RNA is divided into pools and used to transfect COS cells or other cells that are not responsive to the polypeptides. Transfected cells which are grown on glass slides are exposed to the labeled polypeptides. The polypeptides can be labeled by a variety of means including iodination or inclusion of a recognition site for a site-specific protein kinase. Following fixation and incubation, the slides are subjected to auto-radiographic analysis. Positive pools are identified and sub-pools are prepared and re-transfected using an iterative sub-pooling and re-screening process, eventually yielding a single clones that encodes the putative receptor.

As an alternative approach for receptor identification, the labeled polypeptides can be photo-affinity linked with cell membrane or extract preparations that express the receptor molecule. Cross-linked material is resolved by PAGE analysis and exposed to X-ray film. The labeled complex containing the receptors of the polypeptides can be excised, resolved into peptide fragments, and subjected to protein micro-sequencing. The amino acid sequence obtained from micro-sequencing would be used to design a set of degenerate oligonucleotide probes to screen a cDNA library to identify the genes encoding the putative receptors.

Agonists and Antagonists

The present invention further provides a method of identifying agonist and antagonist compounds to the genes and gene products of the present invention. An example of such an assay comprises contacting a mammalian cell or membrane preparation expressing the receptors of the polypeptides with labeled polypeptides, eg. by radioactivity, in the presence of a compound to be screened. The ability of the compound to block and enhance the interaction of the polypeptides of the present invention with its receptor is then measured, for example, by liquid scintillation chromatography.

This invention provides a method of screening drugs to identify those which enhance or inhibit interaction of the polypeptides with their receptors. As an example, a mammalian cell or membrane preparation expressing the receptor would be incubated with labeled polypeptides in the presence of the drug. The ability of the drug to enhance or block this interaction could then be measured.

Alternatively, the response of a known second messenger system following interaction of the polypeptides and their receptors would be measured and compared in the presence or absence of the drug. Such second messenger systems include but are not limited to, cAMP guanylate cyclase, ion channels or phosphoinositide hydrolysis.

Potential antagonists to BTG-2 or BTG-3 polypeptides include an antibody, or in some cases, an oligopeptide, which binds to the polypeptide. Alternatively, a potential antagonist may be a closely related protein which binds to the receptor sites, however, they are inactive forms of the polypeptide and thereby prevent their action since receptor sites are occupied.

Another potential antagonist is an antisense construct prepared using antisense technology. Antisense technology can be used to control gene expression through triple-helix formation or antisense DNA or RNA, both of which methods are based on binding of a polynucleotide to DNA or RNA. For example, the 5' coding portion of the polynucleotide

sequence, which encodes for the mature polypeptides of the present invention, is used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription (triple helix -see Lee et al., *Nucl. Acids Res.* 6:3073 (1979); Cooney et al, *Science* 241:456 (1988); and Dervan et al., *Science* 251: 1360 (1991)), thereby preventing transcription and the production of BTG-2 and/or BTG-3. The antisense RNA oligonucleotide hybridizes to the mRNA in vivo and blocks translation of the mRNA molecule into the polypeptides (Antisense—Okano, *J. Neurochem.* 56:560 (1991); *Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression*, CRC Press, Boca Raton, Fla. (1988)). The oligonucleotides described above can also be delivered to cells such that the antisense RNA or DNA may be expressed in vivo to inhibit production of the polypeptides of the present invention.

Potential antagonists also include a small molecule which binds to and occupies the active site of the polypeptides thereby making them inaccessible to substrate such that normal biological activity is prevented. Examples of small molecules include but are not limited to small peptides or peptide-like molecules.

The antagonists may be employed to treat leukemia, which results from oncogene activation in hemopoietic cells due to a chromosomal translocation. The polypeptides of the present invention may have a direct or indirect function in the activation of a cellular oncogene resulting in leukemia.

The antagonists may be employed in a composition with a pharmaceutically acceptable carrier, e.g., as hereinafter described.

Modes of Administration

The polypeptides and agonists or antagonists of the present invention may be employed in combination with a suitable pharmaceutical carrier. Such compositions comprise a therapeutically effective amount of the polypeptide, and a pharmaceutically acceptable carrier or excipient. Such a carrier includes but is not limited to saline, buffered saline, dextrose, water, glycerol, ethanol, and combinations thereof. The formulation should suit the mode of administration.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. In addition, the polypeptides and agonists or antagonists of the present invention may be employed in conjunction with other therapeutic compounds.

The pharmaceutical compositions may be administered in a convenient manner such as by the topical, intravenous, intramuscular or subcutaneous routes. The pharmaceutical compositions are administered in an amount which is effective for treating and/or prophylaxis of the specific indication. In general, they are administered in an amount of at least about 10 µg/kg body weight and in most cases they will be administered in an amount not in excess of about 8 mg/Kg body weight per day. In most cases, the dosage is from about 10 µg/kg to about 1 mg/kg body weight daily, taking into account the routes of administration, symptoms, etc.

Gene Therapy

The polypeptides of the present invention, and agonists and antagonists which are polypeptides, may also be employed in accordance with the present invention by

expression of such polypeptides in vivo, which is often referred to as "gene therapy."

Thus, for example, cells from a patient may be engineered with a polynucleotide (DNA or RNA) encoding a polypeptide ex vivo, with the engineered cells then being provided to a patient to be treated with the polypeptide. Such methods are well-known in the art. For example, cells may be engineered by procedures known in the art by use of a retroviral particle containing RNA encoding a polypeptide of the present invention.

Similarly, cells may be engineered in vivo for expression of a polypeptide in vivo by, for example, procedures known in the art. As known in the art, a producer cell for producing a retroviral particle containing RNA encoding the polypeptide of the present invention may be administered to a patient for engineering cells in vivo and expression of the polypeptide in vivo. These and other methods for administering a polypeptide of the present invention by such method should be apparent to those skilled in the art from the teachings of the present invention. For example, the expression vehicle for engineering cells may be other than a retrovirus, for example, an adenovirus which may be used to engineer cells in vivo after combination with a suitable delivery vehicle.

Retroviruses from which the retroviral vectors hereinabove mentioned may be derived include, but are not limited to, Moloney Murine Leukemia Virus, spleen necrosis virus, retroviruses such as Rous Sarcoma Virus, Harvey Sarcoma Virus, avian leukosis virus, gibbon ape leukemia virus, human immunodeficiency virus, adenovirus, Myeloproliferative Sarcoma Virus, and mammary tumor virus. In one embodiment, the retroviral plasmid vector is derived from Moloney Murine Leukemia Virus.

The vector includes one or more promoters. Suitable promoters which may be employed include, but are not limited to, the retroviral LTR; the SV40 promoter; and the human cytomegalovirus (CMV) promoter described in Miller et al., *Biotechniques* 7(9):980-990 (1989), or any other promoter (e.g., cellular promoters such as eukaryotic cellular promoters including, but not limited to, the histone, pol III, and β-actin promoters). Other viral promoters which may be employed include, but are not limited to, adenovirus promoters, thymidine kinase (TK) promoters, and B19 parvovirus promoters. The selection of a suitable promoter will be apparent to those skilled in the art from the teachings contained herein.

The nucleic acid sequence encoding the polypeptide of the present invention is under the control of a suitable promoter. Suitable promoters which may be employed include, but are not limited to, adenoviral promoters, such as the adenoviral major late promoter; or heterologous promoters, such as the cytomegalovirus (CMV) promoter; the respiratory syncytial virus (RSV) promoter; inducible promoters, such as the MMT promoter, the metallothionein promoter; heat shock promoters; the albumin promoter; the ApoAI promoter; human globin promoters; viral thymidine kinase promoters, such as the Herpes Simplex thymidine kinase promoter; retroviral LTRs (including the modified retroviral LTRs hereinabove described); the β-actin promoter; and human growth hormone promoters. The promoter also may be the native promoter which controls the gene encoding the polypeptide.

The retroviral plasmid vector is employed to transduce packaging cell lines to form producer cell lines. Examples of packaging cells which may be transfected include, but are not limited to, the PE501, PA317, ψ-2, ψ-AM, PA12, T19-14X, VT-19-17-H2, ψCRE, ψCRIP, GP+E-86, GP+envAm12, and DAN cell lines as described in Miller, Human

Gene Therapy, Vol. 1 (1990), pp. 5–14, which is incorporated herein by reference in its entirety. The vector may transduce the packaging cells through any means known in the art. Such means include, but are not limited to, electroporation, the use of liposomes, and CaPO₄ precipitation. In one alternative, the retroviral plasmid vector may be encapsulated into a liposome, or coupled to a lipid, and then administered to a host.

The producer cell line generates infectious retroviral vector particles which include the nucleic acid sequence(s) encoding the polypeptides. Such retroviral vector particles then may be employed, to transduce eukaryotic cells, either in vitro or in vivo. The transduced eukaryotic cells will express the nucleic acid sequence(s) encoding the polypeptide. Eukaryotic cells which may be transduced include, but are not limited to, embryonic stem cells, embryonic carcinoma cells, as well as hematopoietic stem cells, hepatocytes, fibroblasts, myoblasts, keratinocytes, endothelial cells, and bronchial epithelial cells.

Chromosome Assay

The sequences of the present invention are also valuable for chromosome identification. The sequence is specifically targeted to and can hybridize with a particular location on an individual human chromosome. Moreover, there is a current need for identifying particular sites on the chromosome. Few chromosome marking reagents based on actual sequence data (repeat polymorphisms) are presently available for marking chromosomal location. The mapping of DNAs to chromosomes according to the present invention is an important first step in correlating those sequences with genes associated with disease.

Briefly, sequences can be mapped to chromosomes by preparing PCR primers (preferably 15–25 bp) from the cDNA. Computer analysis of the 3' untranslated region is used to rapidly select primers that do not span more than one exon in the genomic DNA, thus complicating the amplification process. These primers are then used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the primer will yield an amplified fragment.

PCR mapping of somatic cell hybrids is a rapid procedure for assigning a particular DNA to a particular chromosome. Using the present invention with the same oligonucleotide primers, sublocalization can be achieved with panels of fragments from specific chromosomes or pools of large genomic clones in an analogous manner. Other mapping strategies that can similarly be used to map to its chromosome include in situ hybridization, prescreening with labeled flow-sorted chromosomes and preselection by hybridization to construct chromosome specific-cDNA libraries.

Fluorescence in situ hybridization (FISH) of a cDNA clone to a metaphase chromosomal spread can be used to provide a precise chromosomal location in one step. This technique can be used with cDNA as short as 500 or 600 bases. For a review of this technique, see Verma et al., *Human Chromosomes: A Manual of Basic Techniques*, Pergamon Press, New York (1988).

Once a sequence has been mapped to a precise chromosomal location, the physical position of the sequence on the chromosome can be correlated with genetic map data. Such data are found, for example, in V. McKusick, *Mendelian Inheritance in Man* (available on-line through Johns Hopkins University Welch Medical Library). The relationship between genes and diseases that have been mapped to the

same chromosomal region are then identified through linkage analysis (coinheritance of physically adjacent genes).

Next, it is necessary to determine the differences in the cDNA or genomic sequence between affected and unaffected individuals. If a mutation is observed in some or all of the affected individuals but not in any normal individuals, then the mutation is likely to be the causative agent of the disease.

With current resolution of physical mapping and genetic mapping techniques, a cDNA precisely localized to a chromosomal region associated with the disease could be one of between 50 and 500 potential causative genes. (This assumes 1 megabase mapping resolution and one gene per 20 kb).

Antibodies

The polypeptides, their fragments or other derivatives, or analogs thereof, or cells expressing them can be used as an immunogen to produce antibodies thereto. These antibodies can be, for example, polyclonal or monoclonal antibodies. The present invention also includes chimeric, single chain, and humanized antibodies, as well as Fab fragments, or the product of an Fab expression library. Various procedures known in the art may be used for the production of such antibodies and fragments.

Antibodies generated against the polypeptides corresponding to a sequence of the present invention can be obtained by direct injection of the polypeptides into an animal or by administering the polypeptides to an animal, preferably a nonhuman. The antibody so obtained will then bind the polypeptides itself. In this manner, even a sequence encoding only a fragment of the polypeptides can be used to generate antibodies binding the whole native polypeptides. Such antibodies can then be used to isolate the polypeptide from tissue expressing that polypeptide.

For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the hybridoma technique (Kohler and Milstein, *Nature* 256:495–497 (1975)), the trioma technique, the human B-cell hybridoma technique (Kozbor et al., *Immunology Today* 4:72 (1983)), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole et al., in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc. (1985), pp. 77–96).

Techniques described for the production of single chain antibodies (U.S. Pat. No. 4,946,778) can be adapted to produce single chain antibodies to immunogenic polypeptide products of this invention. Also, transgenic mice may be used to express humanized antibodies to immunogenic polypeptide products of this invention.

The present invention will be further described with reference to the following examples; however, it is to be understood that the present invention is not limited to such examples. All parts or amounts, unless otherwise specified, are by weight.

In order to facilitate understanding of the following examples certain frequently occurring methods and/or terms will be described.

“Plasmids” are designated by a lower case p preceded and/or followed by capital letters and/or numbers. The starting plasmids herein are either commercially available, publicly available on an unrestricted basis, or can be constructed from available plasmids in accord with published procedures. In addition, equivalent plasmids to those described are known in the art and will be apparent to the ordinarily skilled artisan.

“Digestion” of DNA refers to catalytic cleavage of the DNA with a restriction enzyme that acts only at certain

sequences in the DNA. The various restriction enzymes used herein are commercially available and their reaction conditions, cofactors and other requirements were used as would be known to the ordinarily skilled artisan. For analytical purposes, typically 1 µg of plasmid or DNA fragment is used with about 2 units of enzyme in about 20 µl of buffer solution. For the purpose of isolating DNA fragments for plasmid construction, typically 5 to 50 µg of DNA are digested with 20 to 250 units of enzyme in a larger volume. Appropriate buffers and substrate amounts for particular restriction enzymes are specified by the manufacturer. Incubation times of about 1 hour at 37° C. are ordinarily used, but may vary in accordance with the supplier's instructions. After digestion the reaction is electrophoresed directly on a polyacrylamide gel to isolate the desired fragment.

Size separation of the cleaved fragments is performed using 8 percent polyacrylamide gel described by Goeddel, D. et al., *Nucleic Acids Res.* 8:4057 (1980).

"Oligonucleotides" refers to either a single stranded polydeoxynucleotide or two complementary polydeoxynucleotide strands which may be chemically synthesized. Such synthetic oligonucleotides have no 5' phosphate and thus will not ligate to another oligonucleotide without adding a phosphate with an ATP in the presence of a kinase. A synthetic oligonucleotide will ligate to a fragment that has not been dephosphorylated.

"Ligation" refers to the process of forming phosphodiester bonds between two double stranded nucleic acid fragments (Sambrook, J. et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Laboratory Press, Cold Spring Harbor, N.Y. (1989), p. 146). Unless otherwise provided, ligation may be accomplished using known buffers and conditions with 10 units of T4 DNA ligase ("ligase") per 0.5 µg of approximately equimolar amounts of the DNA fragments to be ligated.

Unless otherwise stated, transformation was performed as described in the method of Graham, F. and Van der Eb, A., *Virology*, 52:456-457 (1973).

Having generally described the invention, the same will be more readily understood by reference to the following examples, which are provided by way of illustration and are not intended as limiting.

EXAMPLE 1

Cloning and Expression of BTG-2 Using the Baculovirus Expression System

The DNA sequence encoding the full length BTG-2 protein, ATCC™ #97025, is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' end sequences of the gene:

The 5' primer has the sequence 5' CAGTGGATCCGC-CACCA**AT**GCAGCTTCAAATCCAAGTAGCAC 3' (SEQ ID No. 5) and contains a Bam HI restriction enzyme site (in bold) followed by 6 nucleotides resembling an efficient signal for the initiation of translation in eukaryotic cells (Kozak, M., *J. Mol. Biol.*, 196:947-950 (1987) and just behind the first 26 nucleotides of the BTG-2 gene (the initiation codon for translation "ATG" is underlined).

The 3' primer has the sequence 5' CAGTGGTACCATA-CATTTTCTTTTTTTAGTTAGCCAT 3' (SEQ ID No. 6) and contains the cleavage site for the restriction endonuclease Asp718 and 25 nucleotides complementary to the 3' non-translated sequence of the BTG-2 gene. The amplified sequences are isolated from a 1% agarose gel using a commercially available kit ("GENECLEAN™," BIO 101

Inc., La Jolla, Calif.). The fragment is then digested with the endonucleases Bam HI and Asp718 and purified again on a 1% agarose gel. This fragment is designated F2.

The vector pRG1 (modification of pVL941 vector, discussed below) is used for the expression of the BTG-2 protein using the baculovirus expression system (for review see: Summers, M. D. and Smith, G. E., *A manual of methods for baculovirus vectors and insect cell culture procedures*, Texas Agricultural Experimental Station Bulletin No. 1555 (1987)). This expression vector contains the strong polyhedrin promoter of the *Autographa californica* nuclear polyhidrosis virus (AcMNPV) followed by the recognition sites for the restriction endonucleases. The polyadenylation site of the simian virus (SV)40 is used for efficient polyadenylation. For an easy selection of recombinant viruses the beta-galactosidase gene from *E. coli* is inserted in the same orientation as the polyhedrin promoter followed by the polyadenylation signal of the polyhedrin gene. The polyhedrin sequences are flanked at both sides by viral sequences for the cell-mediated homologous recombination of co-transfected wild-type viral DNA. Many other baculovirus vectors could be used in place of pRG1 such as pAc373, pVL941 and pAcIM1 (Luckow, V. A. and Summers, M. D., *Virology* 170:31-39).

The plasmid is digested with the restriction enzymes Bam HI and Asp718 and dephosphorylated using calf intestinal phosphatase by procedures known in the art. The DNA is then isolated from a 1% agarose gel using the commercially available kit ("GENECLEAN™" BIO 101 Inc., La Jolla, Calif.). This vector DNA is designated V2.

Fragment F2 and the dephosphorylated plasmid V2 are ligated with T4 DNA ligase. *E. coli* HB101 cells are then transformed and bacteria identified that contained the plasmid (pBac BTG-2) with the BTG-2 gene using the respective restriction enzymes. The sequence of the cloned fragment is confirmed by DNA sequencing.

5 µg of the plasmid pBac BTG-2 is co-transfected with 1.0 µg of a commercially available linearized baculovirus ("BACULOGOLD™ baculovirus DNA", Pharmingen, San Diego, Calif.) using the lipofection method (Felgner et al., *Proc. Natl. Acad. Sci. (USA)* 84:7413-7417 (1987)).

1 µg of BACULOGOLD™ virus DNA and 5 µg of the plasmid pBac BTG-2 are mixed in a sterile well of a microtiter plate containing 50 µl of serum free Grace's medium (Life Technologies Inc., Gaithersburg, Md.). Afterwards 10 µl LIPOFECTIN™ plus 90 µl Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to the Sf9 insect cells (ATCC™ CRL 1711) seeded in a 35 mm tissue culture plate with 1 ml Grace's medium without serum. The plate is rocked back and forth to mix the newly added solution. The plate is then incubated for 5 hours at 27° C. After 5 hours the transfection solution is removed from the plate and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. The plate is put back into an incubator and cultivation continued at 27° C. for four days.

After four days the supernatant is collected and a plaque assay performed similar as described by Summers and Smith (supra). As a modification an agarose gel with "Blue Gal" (Life Technologies Inc., Gaithersburg) is used which allows an easy isolation of blue stained plaques. (A detailed description of a "plaque assay" can also be found in the user's guide for insect cell culture and baculovirology distributed by Life Technologies Inc., Gaithersburg, page 9-10).

Four days after the serial dilution the viruses are added to the cells and blue stained plaques are picked with the tip of an Eppendorf pipette. The agar containing the recombinant viruses is then resuspended in an Eppendorf tube containing 200 μ l of Grace's medium. The agar is removed by a brief centrifugation and the supernatant containing the recombinant baculovirus is used to infect Sf9 cells seeded in 35 mm dishes. Four days later the supernatants of these culture dishes are harvested and then stored at 4° C.

Sf9 cells are grown in Grace's medium supplemented with 10% heat-inactivated FBS. The cells are infected with the recombinant baculovirus V-BTG-2 at a multiplicity of infection (MOI) of 2. Six hours later the medium is removed and replaced with SF900 II medium minus methionine and cysteine (Life Technologies Inc., Gaithersburg). 42 hours later 5 μ Ci of ³⁵S-methionine and 5 μ Ci ³⁵S cysteine (Amersham) are added. The cells are further incubated for 16 hours before they are harvested by centrifugation and the labeled proteins visualized by SDS-PAGE and autoradiography.

EXAMPLE 2

Cloning and Expression of BTG-3 Using the Baculovirus Expression System

The DNA sequence encoding the full length BTG-3 protein, ATCC™ #97010, is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' end sequences of the gene:

The 5' primer has the sequence 5' CAGTGGATCCGC-CACCAATGCAGCTAGAGATCAAAGTGGCCC 3' (SEQ ID No:7) and contains a Bam HI restriction enzyme site (in bold) followed by 6 nucleotides resembling an efficient signal for the initiation of translation in eukaryotic cells (Kozak, M., *J. Mol. Biol.* 196:947-950 (1987)) and just behind the first 228 nucleotides of the BTG-3 gene (the initiation codon for translation "ATG" is underlined).

The 3' primer has the sequence 5' CAGTGGTAC-CACGGGCCAGGTAGATGGTCCAGTTGGCCAGCAC 3' (SEQ ID No:8) and contains the cleavage site for the restriction endonuclease Asp718 and 25 nucleotides complementary to the 3' non-translated sequence of the BTG-3 gene. The amplified sequences are isolated from a 1% agarose gel using a commercially available kit ("GENECLEAN™," BIO 101 Inc., La Jolla, Calif.). The fragment is then digested with the endonucleases Bam HI and Asp718 and purified again on a 1% agarose gel. This fragment is designated F2.

The vector pRG1 (modification of pVL941 vector, discussed below) is used for the expression of the BTG-3 protein using the baculovirus expression system (for review see: Summers, M. D. and Smith, G. E. 1987, A manual of methods for baculovirus vectors and insect cell culture procedures, Texas Agricultural Experimental Station Bulletin No. 1555). This expression vector contains the strong polyhedrin promoter of the *Autographa californica* nuclear polyhedrosis virus (AcMNPV) followed by the recognition sites for the restriction endonucleases Bam HI and Asp718. The polyadenylation site of the simian virus (SV)40 is used for efficient polyadenylation. For an easy selection of recombinant viruses the beta-galactosidase gene from *E. coli* is inserted in the same orientation as the polyhedrin promoter followed by the polyadenylation signal of the polyhedrin gene. The polyhedrin sequences are flanked at both sides by viral sequences for the cell-mediated homologous recombination of co-transfected wild-type viral DNA. Many other

baculovirus vectors could be used in place of pRG1 such as pAc373, pVL941 and pAcIM1 (Luckow, V. A. and Summers, M. D., *Virology* 170:31-39).

The plasmid is digested with the respective restriction enzymes and dephosphorylated using calf intestinal phosphatase by procedures known in the art. The DNA is then isolated from a 1% agarose gel using the commercially available kit ("GENECLEAN™" BIO 101 Inc., La Jolla, Calif.). This vector DNA is designated V2.

Fragment F2 and the dephosphorylated plasmid V2 are ligated with T4 DNA ligase. *E. coli* HB101 cells are then transformed and bacteria identified that contained the plasmid (pBac BTG-3) with the BTG-3 gene using the enzymes Bam HI and Asp718. The sequence of the cloned fragment is confirmed by DNA sequencing.

5 μ g of the plasmid pBac BTG-3 is co-transfected with 1.0 μ g of a commercially available linearized baculovirus ("BACULOGOLD™ baculovirus DNA", Pharmingen, San Diego, Calif.) using the lipofection method (Feigner et al., *Proc. Natl. Acad. Sci. (USA)* 84:7413-7417 (1987)).

1 μ g of BACULOGOLD™ virus DNA and 5 μ g of the plasmid pBac BTG-3 are mixed in a sterile well of a microtiter plate containing 50 μ l of serum free Grace's medium (Life Technologies Inc., Gaithersburg, Md.). Afterwards 10 μ l LIPOFECTIN™ plus 90 μ l Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to the Sf9 insect cells (ATCC™ CRL 1711) seeded in a 35 mm tissue culture plate with 1 ml Grace's medium without serum. The plate is rocked back and forth to mix the newly added solution. The plate is then incubated for 5 hours at 27° C. After 5 hours the transfection solution is removed from the plate and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. The plate is put back into an incubator and cultivation continued at 27° C. for four days.

After four days the supernatant is collected and a plaque assay performed similar as described by Summers and Smith (supra). As a modification an agarose gel with "Blue Gal" (Life Technologies Inc., Gaithersburg) is used which allows an easy isolation of blue stained plaques. (A detailed description of a "plaque assay" can also be found in the user's guide for insect cell culture and baculovirology distributed by Life Technologies Inc., Gaithersburg, page 9-10).

Four days after the serial dilution the viruses are added to the cells and blue stained plaques are picked with the tip of an Eppendorf pipette. The agar containing the recombinant viruses is then resuspended in an Eppendorf tube containing 200 μ l of Grace's medium. The agar is removed by a brief centrifugation and the supernatant containing the recombinant baculovirus is used to infect Sf9 cells seeded in 35 mm dishes. Four days later the supernatants of these culture dishes are harvested and then stored at 4° C.

Sf9 cells are grown in Grace's medium supplemented with 10% heat-inactivated FBS. The cells are infected with the recombinant baculovirus V-BTG-3 at a multiplicity of infection (MOI) of 2. Six hours later the medium is removed and replaced with SF900 II medium minus methionine and cysteine (Life Technologies Inc., Gaithersburg). 42 hours later 5 μ Ci of ³⁵S-methionine and 5 μ Ci ³⁵S cysteine (Amersham) are added. The cells are further incubated for 16 hours before they are harvested by centrifugation and the labeled proteins visualized by SDS-PAGE and autoradiography.

Expression of Recombinant BTG-2 in COS Cells

The expression of plasmid, BTG-2 HA is derived from a vector pcDNA1/Amp (Invitrogen) containing: 1) SV40 origin of replication, 2) ampicillin resistance gene, 3) *E. coli* replication origin, 4) CMV promoter followed by a polylinker region, a SV40 intron and polyadenylation site. A DNA fragment encoding the entire BTG-2 precursor and a HA tag fused in frame to its 3' end is cloned into the polylinker region of the vector, therefore, the recombinant protein expression is directed under the CMV promoter. The HA tag correspond to an epitope derived from the influenza hemagglutinin protein as previously described (Wilson, I. et al., *Cell* 37:767 (1984)). The fusion of HA tag to the target protein allows easy detection of the recombinant protein with an antibody that recognizes the HA epitope.

The plasmid construction strategy is described as follows:

The DNA sequence encoding BTG-2, ATCC™ #97025, is constructed by PCR using two primers: the 5' primer 5' GGCCCAAGCTTGCCCGCCATGCAGCT-TGAAATCCAAGTAG 3' (SEQ ID No:9) contains a Hind III site followed by 23 nucleotides of BTG-2 coding sequence starting from the initiation codon; the 3' sequence 5' ATCGTCTAGATTAGTTAGCCATAACAG-GCTGGAATTGCTGGTTAGAAATAC TGCATGTTATT-TAAGCTAAAATTCAAGCCATCTA 3' (SEQ ID No:10) contains complementary sequences to XbaI site, translation stop codon, HA tag and the last 68 nucleotides of the BTG-2 coding sequence (not including the stop codon). Therefore, the PCR product contains a Hind III site, BTG-2 coding sequence followed by HA tag fused in frame, a translation termination stop codon next to the HA tag, and an XbaI site. The PCR amplified DNA fragment and the vector, pcDNA1/Amp, are digested with Hind III and XbaI restriction enzyme and ligated. The ligation mixture is transformed into *E. coli* strain SURE (STRATAGENE™ Cloning Systems, La Jolla, Calif.) the transformed culture is plated on ampicillin media plates and resistant colonies are selected. Plasmid DNA is isolated from transformants and examined by restriction analysis for the presence of the correct fragment. For expression of the recombinant BTG-2, COS cells are transfected with the expression vector by DEAE-DEXTRAN method (Sambrook, J. et al., *Molecular Cloning. A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989)). The expression of the BTG-2 HA protein is detected by radiolabelling and immunoprecipitation method (E. Harlow, D. Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1988)). Cells are labeled for 8 hours with ³⁵S-cysteine two days post transfection. Culture media are then collected and cells are lysed with detergent (RIPA buffer (150 mM NaCl, 1% NP-40, 0.1% SDS, 1% NP-40, 0.5% DOC, 50 mM Tris, pH 7.5). Wilson, I. et al., *Cell* 37:767 (1984)). Both cell lysate and culture media are precipitated with a HA specific monoclonal antibody. Proteins precipitated are analyzed on 15% SDS-PAGE gels.

EXAMPLE 4

Expression of Recombinant BTG-3 in COS Cells

The expression of plasmid, BTG-3 HA is derived from a vector pcDNA1/Amp (Invitrogen) containing: 1) SV40 origin of replication, 2) ampicillin resistance gene, 3) *E. coli* replication origin, 4) CMV promoter followed by a

polylinker region, a SV40 intron and polyadenylation site. A DNA fragment encoding the entire BTG-3 precursor and a HA tag fused in frame to its 3' end is cloned into the polylinker region of the vector, therefore, the recombinant protein expression is directed under the CMV promoter. The HA tag corresponds to an epitope derived from the influenza hemagglutinin protein as previously described (Wilson, I. et al., *Cell* 37:767 (1984)). The infusion of HA tag to the target protein allows easy detection of the recombinant protein with an antibody that recognizes the HA epitope.

The plasmid construction strategy is described as follows:

The DNA sequence encoding BTG-3, ATCC™ #97010, is constructed by PCR using two primers: the 5' primer 5' GGCCCAAGCTTGCCCGCCATGCAGCT-ATGCAGCTAGAGATCAAAGTGGC 3' (SEQ ID No. 11) contains a Hind III site followed by 23 nucleotides of BTG-3 coding sequence starting from the initiation codon; the 3' sequence 5' ATCGTCTAGATCAAGCGTAGTCTGG-GACGTCGTATGGGTAGGTTG TAGCTGAGGCCCTT-CACAAAGGGTGTCTTCTCCAGG 3' (SEQ ID No:12) contains complementary sequences to an XbaI site, translation stop codon, HA tag and the last 68 nucleotides of the BTG-3 coding sequence (not including the stop codon). Therefore, the PCR product contains a Hind III site, BTG-3 coding sequence followed by HA tag fused in frame, a translation termination stop codon next to the HA tag, and an XbaI site. The PCR amplified DNA fragment and the vector, pcDNA1/Amp, are digested with Hind III and XbaI restriction enzymes and ligated. The ligation mixture is transformed into *E. coli* strain SURE (STRATAGENE™ Cloning Systems, La Jolla, Calif.) the transformed culture is plated on ampicillin media plates and resistant colonies are selected. Plasmid DNA is isolated from transformants and examined by restriction analysis for the presence of the correct fragment. For expression of the recombinant BTG-3, COS cells are transfected with the expression vector by DEAE-DEXTRAN method (Sambrook, J. et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989)). The expression of the BTG-3 HA protein is detected by radiolabelling and immunoprecipitation method (E. Harlow, D. Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1988)). Cells are labeled for 8 hours with ³⁵S-cysteine two days post transfection. Culture media is then collected and cells are lysed with detergent (RIPA buffer (150 mM NaCl, 1% NP-40, 0.1% SDS, 1% NP-40, 0.5% DOC, 50 mM Tris, pH 7.5) (Wilson, I. et al., *Cell* 37:767 (1984)). Both cell lysate and culture media are precipitated with a HA specific monoclonal antibody. Proteins precipitated are analyzed on 15% SDS-PAGE gels.

EXAMPLE 5

Bacterial Expression and Purification of BTG-2

The DNA sequence encoding BTG-2, ATCC™ #97025, is initially amplified using PCR oligonucleotide primers corresponding to the 5' and 3' end sequences of the processed BTG-2 gene (minus the signal peptide sequence) and the vector sequences 3' to the BTG-2 gene. Additional nucleotides corresponding to NcoI and Bgl II restriction enzyme sites were added to the 5' and 3' end sequences respectively. The 5' oligonucleotide primer has the sequence ATCGC-CATGGGACAGCTTGAAATCCAAGTAGCACTA 3' (SEQ ID No:13) contains a Nco I restriction enzyme site followed by 24 nucleotides of BTG-2 coding sequence. The

3' sequence 5' ATCGAGATCTTTAGTTAGCCATAACAG-GCTGGAAT 3' (SEQ ID No:14) contains complementary sequences to a Bgl II restriction site and the last 21 nucleotides of BTG-2. The restriction enzyme sites correspond to the restriction enzyme sites on the bacterial expression vector pQE-60 (Qiagen, Inc. Chatsworth, Calif.). pQE-60 encodes antibiotic resistance (Amp^r), a bacterial origin of replication (ori), an IPTG-regulatable promoter operator (P/O), a ribosome binding site (RBS), a 6-His tag and restriction enzyme sites. pQE-60 is then digested with Nco I and Bgl II. The amplified sequences are ligated into pQE-60 and are inserted in frame with the sequence encoding for the histidine tag and the RBS. The ligation mixture is then used to transform *E. coli* strain M15/rep 4 (Qiagen, Inc.) by the procedure described in Sambrook, J. et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989). M15/rep4 contains multiple copies of the plasmid pREP4, which expresses the lacI repressor and also confers kanamycin resistance (Kan^r). Transformants are identified by their ability to grow on LB plates and ampicillin/kanamycin resistant colonies are selected. Plasmid DNA is isolated and confirmed by restriction analysis. Clones containing the desired constructs are grown overnight (O/N) in liquid culture in LB media supplemented with both Amp (100 µg/ml) and Kan (25 µg/ml). The O/N culture is used to inoculate a large culture at a ratio of 1:100 to 1:250. The cells are grown to an optical density 600 (O.D.⁶⁰⁰) of between 0.4 and 0.6. IPTG ("Isopropyl-B-D-thiogalactopyranoside") is then added to a final concentration of 1 mM. IPTG induces by inactivating the lacI repressor, clearing the P/O leading to increased gene expression. Cells are grown an extra 3 to 4 hours. Cells are then harvested by centrifugation. The cell pellet is solubilized in the chaotropic agent 6 Molar Guanidine HCl. After clarification, solubilized BTG-2 is purified from this solution by chromatography on a Nickel-Chelate column under conditions that allow for tight binding by proteins containing the 6-His tag (Hochuli, E. et al., *J Chromatography* 411:177-184 (1984)). BTG-2 (95% pure) is eluted from the column in 6 molar guanidine HCl pH 5.0 and for the purpose of renaturation adjusted to 3 molar guanidine HCl, 100 mM sodium phosphate, 10 mmolar glutathione (reduced) and 2 mmolar glutathione (oxidized). After incubation in this solution for 12 hours the protein is dialyzed to 10 mmolar sodium phosphate.

EXAMPLE 6

Bacterial Expression and Purification of BTG-3

The DNA sequence encoding BTG-3, ATCC™ #97010 is initially amplified using PCR oligonucleotide primers corresponding to the 5' and 3' end sequences of the processed BTG-3 gene. Additional nucleotides corresponding to NcoI and Bgl II restriction enzyme sites are added to the 5' and 3' sequences respectively. The 5' oligonucleotide primer has the sequence 5' ATCGCCATGGGACAGCTAGAGATCAAAGTGGCCCTG3' (SEQ ID No:15) contains an NcoI restriction enzyme site followed by 24 nucleotides of BTG-3 coding sequence. The 3' sequence 5' ATCGAGATCTGTTG-GCCAGCACCACGGGCTGG 3' (SEQ ID NO:16) contains complementary sequences to a Bgl II restriction site and the last 21 nucleotides of BTG-3 coding sequence. The restriction enzyme sites correspond to the restriction enzyme sites on the bacterial expression vector pQE-60 (Qiagen, Inc. Chatsworth, Calif.). pQE-60 encodes antibiotic resistance (Amp^r), a bacterial origin of replication (ori), an IPTG-

regulatable promoter operator (P/O), a ribosome binding site (RBS), a 6-His tag and restriction enzyme sites. pQE-60 is then digested with Nco I and Bgl II. The amplified sequences are ligated into pQE-60 and are inserted in frame with the sequence encoding for the histidine tag and the RBS. The ligation mixture is then used to transform *E. coli* strain M15/rep 4 (Qiagen, Inc.) by the procedure described in Sambrook, J. et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989) (160860). M15/rep4 contains multiple copies of the plasmid pREP4, which expresses the lacI repressor and also confers kanamycin resistance (Kan^r). Transformants are identified by their ability to grow on LB plates and ampicillin/kanamycin resistant colonies are selected. Plasmid DNA is isolated and confirmed by restriction analysis. Clones containing the desired constructs are grown overnight (O/N) in liquid culture in LB media supplemented with both Amp (100 µg/ml) and Kan (25 µg/ml). The O/N culture is used to inoculate a large culture at a ratio of 1:100 to 1:250. The cells are grown to an optical density 600 (O.D.⁶⁰⁰) of between 0.4 and 0.6. IPTG ("Isopropyl-B-D-thiogalactopyranoside") is then added to a final concentration of 1 mM. IPTG induces by inactivating the lacI repressor, clearing the P/O leading to increased gene expression. Cells are grown an extra 3 to 4 hours. Cells are then harvested by centrifugation. The cell pellet is solubilized in the chaotropic agent 6 Molar Guanidine HCl. After clarification, solubilized BTG-3 is purified from this solution by chromatography on a Nickel-Chelate column under conditions that allow for tight binding by proteins containing the 6-His tag (Hochuli, E. et al., *J Chromatography* 411:177-184 (16084)). BTG-3 (95% pure) is eluted from the column in 6 molar guanidine HCl pH 5.0 and for the purpose of renaturation adjusted to 3 molar guanidine HCl, 100 mM sodium phosphate, 10 mmolar glutathione (reduced) and 2 mmolar glutathione (oxidized). After incubation in this solution for 12 hours the protein is dialyzed to 10 mmolar sodium phosphate.

EXAMPLE 7

Fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in tissue-culture medium and separated into small pieces. Small chunks of the tissue are placed on a wet surface of a tissue culture flask, approximately ten pieces are placed in each flask. The flask is turned upside down, closed tight and left at room temperature overnight. After 24 hours at room temperature, the flask is inverted and the chunks of tissue remain fixed to the bottom of the flask and fresh media (e.g., Ham's F12 media, with 10% FBS, penicillin and streptomycin, is added. This is then incubated at 37° C. for approximately one week. At this time, fresh media is added and subsequently changed every several days. After an additional two weeks in culture, a monolayer of fibroblasts emerge. The monolayer is trypsinized and scaled into larger flasks.

pmV-7 (Kirschmeier, P. T. et al, *DNA* 7:219-25 (1988)) flanked by the long terminal repeats of the Moloney murine sarcoma virus, is digested with EcoRI and HindIII and subsequently treated with calf intestinal phosphatase. The linear vector is fractionated on agarose gel and purified, using glass beads.

The cDNA encoding a polypeptide of the present invention is amplified using PCR primers which correspond to the 5' and 3' end sequences respectively. The 5' primer containing an EcoRI site and the 3' primer further includes a HindIII site. Equal quantities of the Moloney murine sarcoma virus

linear backbone and the amplified EcoRI and HindIII fragment are added together, in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions appropriate for ligation of the two fragments. The ligation mixture is used to transform bacteria HB101, which are then plated onto agar-containing kanamycin for the purpose of confirming that the vector had the gene of interest properly inserted.

The amphotropic pA317 or GP+am12 packaging cells are grown in tissue culture to confluent density in Dulbecco's Modified Eagles Medium (DMEM) with 10% calf serum (CS), penicillin and streptomycin. The MSV vector containing the gene is then added to the media and the packaging cells are transduced with the vector. The packaging cells now produce infectious viral particles containing the gene (the packaging cells are now referred to as producer cells).

Fresh media is added to the transduced producer cells, and subsequently, the media is harvested from a 10 cm plate of confluent producer cells. The spent media, containing the infectious viral particles, is filtered through a millipore filter to remove detached producer cells and this media is then used to infect fibroblast cells. Media is removed from a sub-confluent plate of fibroblasts and quickly replaced with

the media from the producer cells. This media is removed and replaced with fresh media. If the titer of virus is high, then virtually all fibroblasts will be infected and no selection is required. If the titer is very low, then it is necessary to use a retroviral vector that has a selectable marker, such as neo or his.

The engineered fibroblasts are then injected into the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads. The fibroblasts now produce the protein product.

It will be clear that the invention may be practiced otherwise than as particularly described in the foregoing description and examples.

Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, within the scope of the appended claims, the invention may be practiced otherwise than as particularly described.

The entire disclosure of all publications (including patents, patent applications, journal articles, laboratory manuals, books, or other documents) cited herein are hereby incorporated by reference.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(iii) NUMBER OF SEQUENCES: 18

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1843 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 27..1061

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

GGCACGAGAT TTTGTGGCGT AGAGCT ATG CAG CTT GAA ATC CAA GTA GCA CTA	53
Met Gln Leu Glu Ile Gln Val Ala Leu	
1 5	
AAT TTT ATT ATT TCG TAT TTG TAC AAT AAG CTT CCC AGG AGA CGT GTC	101
Asn Phe Ile Ile Ser Tyr Leu Tyr Asn Lys Leu Pro Arg Arg Arg Val	
10 15 20 25	
AAC ATT TTT GGT GAA GAA CTT GAA AGA CTT CTT AAG AAG AAA TAT GAA	149
Asn Ile Phe Gly Glu Glu Leu Glu Arg Leu Leu Lys Lys Lys Tyr Glu	
30 35 40	
GGG CAC TGG TAT CCT GAA AAG CCA TAC AAA GGA TCG GGG TTT AGA TGT	197
Gly His Trp Tyr Pro Glu Lys Pro Tyr Lys Gly Ser Gly Phe Arg Cys	
45 50 55	
ATA CAC ATA GGG GAG AAA GTG GAC CCA GTG ATT GAA CAA GCA TCC AAA	245
Ile His Ile Gly Glu Lys Val Asp Pro Val Ile Glu Gln Ala Ser Lys	
60 65 70	
GAG AGT GGT TTG GAC ATT GAT GAT GTT CGT GGC AAT CTG CCA CAG GAT	293
Glu Ser Gly Leu Asp Ile Asp Asp Val Arg Gly Asn Leu Pro Gln Asp	
75 80 85	
CTT AGT GTT TGG ATC GAC CCA TTT GAG GTT TCT TAC CAA ATT GGT GAA	341
Leu Ser Val Trp Ile Asp Pro Phe Glu Val Ser Tyr Gln Ile Gly Glu	

-continued

90	95	100	105	
AAG GGA CCA GTG Lys Gly Pro Val	AAG GTG CTT TAC Lys Val Leu Tyr	GTG GAT GAT AAT AAT GAA AAT GGA Val Asp Asp Asn Asn Glu Asn Gly		389
	110	115	120	
TGT GAG TTG GAT AAG GAG ATC AAA AAC AGC TTT AAC CCA GAG GCC CAG Cys Glu Leu Asp Lys Glu Ile Lys Asn Ser Phe Asn Pro Glu Ala Gln		130	135	437
125				
GTT TTT ATG CCC ATA AGT GAC CCA GCC TCA TCA GTG TCC AGC TCT CCA Val Phe Met Pro Ile Ser Asp Pro Ala Ser Ser Val Ser Ser Ser Pro		145	150	485
140				
TCG CCT CCT TTT GGT CAC TCT GCT GCT GTA AGC CCT ACC TTC ATG CCC Ser Pro Pro Phe Gly His Ser Ala Ala Val Ser Pro Thr Phe Met Pro		160	165	533
155				
CGG TCC ACT CAG CCT TTA ACC TTT ACC ACT GCC ACT TTT GCT GCC ACC Arg Ser Thr Gln Pro Leu Thr Phe Thr Thr Ala Thr Phe Ala Ala Thr		180	185	581
170	175		185	
AAG TTC GGC TCT ACC AAA ATG AAA AAT AGT GGC CGT AGC AAC AAG GTT Lys Phe Gly Ser Thr Lys Met Lys Asn Ser Gly Arg Ser Asn Lys Val		195	200	629
190				
GCA CGT ACT TCT CCC ATC AAC CTC GGC TTG AAT GTG AAT GAC CTC TTG Ala Arg Thr Ser Pro Ile Asn Leu Gly Leu Asn Val Asn Asp Leu Leu		210	215	677
205				
AAG CAG AAA GCC ATC TCT TCC TCA ATG CAC TCT CTG TAT GGG CTT GGC Lys Gln Lys Ala Ile Ser Ser Ser Met His Ser Leu Tyr Gly Leu Gly		225	230	725
220				
TTG GGT AGC CAG CAG CAG CCA CAG CAA CAG CAG CAG CCA GCC CAG CCG Leu Gly Ser Gln Gln Gln Pro Gln Gln Gln Gln Gln Pro Ala Gln Pro		240	245	773
235				
CCA CCG CCA CCA CCA CCA CCA CAG CAG CAA CAA CAG CAG AAA ACC TCT Pro Pro Pro Pro Pro Pro Pro Gln Gln Gln Gln Gln Gln Lys Thr Ser		260	265	821
250	255		265	
GCT CTT TCT CCT AAT GCC AAG GAA TTT ATT TTT CCT AAT ATG CAG GGT Ala Leu Ser Pro Asn Ala Lys Glu Phe Ile Phe Pro Asn Met Gln Gly		275	280	869
270				
CAA GGT AGT AGT ACC AAT GGA ATG TTC CCA GGT GAC AGC CCC CTT AAC Gln Gly Ser Ser Thr Asn Gly Met Phe Pro Gly Asp Ser Pro Leu Asn		290	295	917
285				
CTC AGT CCT CTC CAG TAC AGT AAT GCC TTT GAT GTG TTT GCA GCC TAT Leu Ser Pro Leu Gln Tyr Ser Asn Ala Phe Asp Val Phe Ala Ala Tyr		305	310	965
300				
GGA GGC CTC AAT GAG AAG TCT TTT GTA GAT GGC TTG AAT TTT AGC TTA Gly Gly Leu Asn Glu Lys Ser Phe Val Asp Gly Leu Asn Phe Ser Leu		320	325	1013
315				
AAT AAC ATG CAG TAT TCT AAC CAG CAA TTC CAG CCT GTT ATG GCT AAC Asn Asn Met Gln Tyr Ser Asn Gln Gln Phe Gln Pro Val Met Ala Asn		340	345	1061
330	335		345	
TAAAAAAG AAAATGTATC GTACAAGTTA AAATGCACGG GCCAAGGGGG GATTTTTT				1121
TTCACCTCCT TGAGAATTTT TTTTTTTAAG CTTATAGTAA GGATACATTC AAGCTTGG				1181
AAAAAATAA TAATAAACA TGCATCATT TTCATTTGCC AACCAAGCAC AAAGTTAT				1241
TATGCTGCCT GTATATTTTA AAGTATACTC TCAGATATGC CCTCTTACAG TATTTTAA				1301
TATTAGCAAA GGACATGGCT TGATTTTTTT TTATAAAAAT TGGCACTAAT AAGTGGGT				1361
ATTGGTCTTT TCTAATGTGA TAATTTAATT TAGTACCAA GTTTGTAAAA TATCAGAG				1421
TATATATATA TTGTATCCTA CGACATGGTA TTGCATTAT ATCTTTTAC TACAGTGA				1481
TGTGACAGCA CGACCTCAT GTTGTATTTT TTTTACTGAA ATTGTAAAAT ATCCATCT				1541
AAGACATCAA CTATTCTAAA AATTGTGTAC AGGATATTC TTTAGTGGTG GAATTTAA				1601

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GTGCGAATAC TTGCTTTCTC CAAAAAATG TATTTTCTGT TAAAAGTTA AAGATTTT	1661
CTATATATTA TGGAAGGAAA ATGTAATCGT AAATATTAAT TTTGTACCTA TATTGTGC	1721
TACTTGAAAA AAACGGTATA AAAGTATTTT GAGTCAGTGT CTTACATGTT AAGAGGGA	1781
GAAATAGTTT ATATTAAGTT TGTATTAAAA TTCTTTAAAA TTAATAAAAA AAAAAAAA	1841
AA	1843

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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

Met	Gln	Leu	Glu	Ile	Gln	Val	Ala	Leu	Asn	Phe	Ile	Ile	Ser	Tyr	Leu	1	5	10	15
Tyr	Asn	Lys	Leu	Pro	Arg	Arg	Arg	Val	Asn	Ile	Phe	Gly	Glu	Glu	Leu	20	25	30	
Glu	Arg	Leu	Leu	Lys	Lys	Lys	Tyr	Glu	Gly	His	Trp	Tyr	Pro	Glu	Lys	35	40	45	
Pro	Tyr	Lys	Gly	Ser	Gly	Phe	Arg	Cys	Ile	His	Ile	Gly	Glu	Lys	Val	50	55	60	
Asp	Pro	Val	Ile	Glu	Gln	Ala	Ser	Lys	Glu	Ser	Gly	Leu	Asp	Ile	Asp	65	70	75	80
Asp	Val	Arg	Gly	Asn	Leu	Pro	Gln	Asp	Leu	Ser	Val	Trp	Ile	Asp	Pro	85	90	95	
Phe	Glu	Val	Ser	Tyr	Gln	Ile	Gly	Glu	Lys	Gly	Pro	Val	Lys	Val	Leu	100	105	110	
Tyr	Val	Asp	Asp	Asn	Asn	Glu	Asn	Gly	Cys	Glu	Leu	Asp	Lys	Glu	Ile	115	120	125	
Lys	Asn	Ser	Phe	Asn	Pro	Glu	Ala	Gln	Val	Phe	Met	Pro	Ile	Ser	Asp	130	135	140	
Pro	Ala	Ser	Ser	Val	Ser	Ser	Ser	Pro	Ser	Pro	Pro	Phe	Gly	His	Ser	145	150	155	160
Ala	Ala	Val	Ser	Pro	Thr	Phe	Met	Pro	Arg	Ser	Thr	Gln	Pro	Leu	Thr	165	170	175	
Phe	Thr	Thr	Ala	Thr	Phe	Ala	Ala	Thr	Lys	Phe	Gly	Ser	Thr	Lys	Met	180	185	190	
Lys	Asn	Ser	Gly	Arg	Ser	Asn	Lys	Val	Ala	Arg	Thr	Ser	Pro	Ile	Asn	195	200	205	
Leu	Gly	Leu	Asn	Val	Asn	Asp	Leu	Leu	Lys	Gln	Lys	Ala	Ile	Ser	Ser	210	215	220	
Ser	Met	His	Ser	Leu	Tyr	Gly	Leu	Gly	Leu	Gly	Ser	Gln	Gln	Gln	Pro	225	230	235	240
Gln	Gln	Gln	Gln	Gln	Pro	Ala	Gln	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	245	250	255	
Gln	Gln	Gln	Gln	Gln	Gln	Lys	Thr	Ser	Ala	Leu	Ser	Pro	Asn	Ala	Lys	260	265	270	
Glu	Phe	Ile	Phe	Pro	Asn	Met	Gln	Gly	Gln	Gly	Ser	Ser	Thr	Asn	Gly	275	280	285	
Met	Phe	Pro	Gly	Asp	Ser	Pro	Leu	Asn	Leu	Ser	Pro	Leu	Gln	Tyr	Ser	290	295	300	

-continued

Asn Ala Phe Asp Val Phe Ala Ala Tyr Gly Gly Leu Asn Glu Lys Ser
 305 310 315 320
 Phe Val Asp Gly Leu Asn Phe Ser Leu Asn Asn Met Gln Tyr Ser Asn
 325 330 335
 Gln Gln Phe Gln Pro Val Met Ala Asn
 340 345

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1343 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 229..1260

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

GGAATTCGGC ACGAGCAACC CTCACGACG AAAAGGACTT CGGTCCCCTG GCCCGGCGAC 60
 GCCCGGGAAG GAAAGGAGAG CGACCTCCGC CCCCGCTCA GCCCACCTG GAGGGAGAA 120
 CCGCCCCGCG CSSGSGTTAG AGCGCCCCGC CGCCCCGTAG ACCCGAAGCC GCCTGGAGC 180
 CAAGGCTGTA CACGTGCCCT GTGCTGATTC TCTGCCTAGG AAAGGACC ATG CAG CTA 237
 Met Gln Leu
 1
 GAG ATC AAA GTG GCC CTG AAC TTC ATC ATC TCC TAC TTG TAC AAC AAG 285
 Glu Ile Lys Val Ala Leu Asn Phe Ile Ile Ser Tyr Leu Tyr Asn Lys
 5 10 15
 CTG CCC CGG CGC CGG GCA GAC CTG TTT GGG GAG GAG CTA GAG CGG CTT 333
 Leu Pro Arg Arg Arg Ala Asp Leu Phe Gly Glu Glu Leu Glu Arg Leu
 20 25 30 35
 TTG AAA AGG AAA TAT GAA GGC CAC TGG TAC CCT GAG AAG CCA CTG AAA 381
 Leu Lys Arg Lys Tyr Glu Gly His Trp Tyr Pro Glu Lys Pro Leu Lys
 40 45 50
 GGC TCT GGC TTC CGC TGT GTT CAC ATT GGG GAG ATG GTG GAC CCC GTG 429
 Gly Ser Gly Phe Arg Cys Val His Ile Gly Glu Met Val Asp Pro Val
 55 60 65
 GTG GAG CTG GCC GCC AAG CGG AGT GGC CTG GCG GTG GAA GAT GTG CGG 477
 Val Glu Leu Ala Ala Lys Arg Ser Gly Leu Ala Val Glu Asp Val Arg
 70 75 80
 GCC AAT GTG CCT GAG GAG CTG AGT GTC TGG ATT GAT CCC TTT GAG GTG 525
 Ala Asn Val Pro Glu Glu Leu Ser Val Trp Ile Asp Pro Phe Glu Val
 85 90 95
 TCC TAC CAG ATT GGT GAG AAG GGA GCT GTG AAA GTG CTG TAC CTG GAT 573
 Ser Tyr Gln Ile Gly Glu Lys Gly Ala Val Lys Val Leu Tyr Leu Asp
 100 105 110 115
 GAC AGT GAG GGT TGC GGT GCC CCA GAG CTG GAC AAG GAG ATC AAG AGC 621
 Asp Ser Glu Gly Cys Gly Ala Pro Glu Leu Asp Lys Glu Ile Lys Ser
 120 125 130
 AGC TTC AAC CCT GAC GCC CAG GTG TTC GTG CCC ATT GGC AGC CAG GAC 669
 Ser Phe Asn Pro Asp Ala Gln Val Phe Val Pro Ile Gly Ser Gln Asp
 135 140 145
 AGC TCC CTG TCC AAC TCC CCA TCG CCA TCC TTT GGC CAG TCA CCC AGC 717
 Ser Ser Leu Ser Asn Ser Pro Ser Pro Ser Phe Gly Gln Ser Pro Ser
 150 155 160
 CCT ACC TTC ATT CCC CGC TCC GCT CAG CCC ATC ACC TTC ACC ACC GCC 765
 Pro Thr Phe Ile Pro Arg Ser Ala Gln Pro Ile Thr Phe Thr Thr Ala

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165	170	175	
TCC TTC GCT GCC ACC AAA TTT GGC TCC ACT AAG ATG AAG AAG GGG GGC Ser Phe Ala Ala Thr Lys Phe Gly Ser Thr Lys Met Lys Lys Gly Gly 180 185 190 195			813
GGG GCA GCA AGT GGT GGG GGT GTA GCC AGC AGT GGG GCG GGT GGC CAG Gly Ala Ala Ser Gly Gly Val Ala Ser Ser Gly Ala Gly Gly Gln 200 205 210			861
CAG CCA CCA CAG CAG CCT CGC ATG GCC CGC TCA CCC ACC AAC AGC CTG Gln Pro Pro Gln Gln Pro Arg Met Ala Arg Ser Pro Thr Asn Ser Leu 215 220 225			909
CTG AAG CAC AAG AGC CTC TCT CTG TCT ATG CAT TCA CTG AAC TTC ATC Leu Lys His Lys Ser Leu Ser Leu Ser Met His Ser Leu Asn Phe Ile 230 235 240			957
ACG GCC AAC CCG GCC CCT CAG TCC CAG CTC TCA CCC AAT GCC AAG GAG Thr Ala Asn Pro Ala Pro Gln Ser Gln Leu Ser Pro Asn Ala Lys Glu 245 250 255			1005
TTC GTG TAC AAC GGT GGT GGC TCA CCC AGC CTC TTC TTT GAT GCG GCC Phe Val Tyr Asn Gly Gly Ser Pro Ser Leu Phe Phe Asp Ala Ala 260 265 270 275			1053
GAT GGC CAG GGC AGC GGC ACC CCA GGC CCG TTT GGA GGC AGT GGG GCT Asp Gly Gln Gly Ser Gly Thr Pro Gly Pro Phe Gly Gly Ser Gly Ala 280 285 290			1101
GGC ACC TGC AAC AGC AGC AGC TTT GAC ATG GCC CAG GTA TTT GGA GGT Gly Thr Cys Asn Ser Ser Ser Phe Asp Met Ala Gln Val Phe Gly Gly 295 300 305			1149
GGT GCC AAC AGC CTC TTC CTG GAG AAG ACA CCC TTT GTG GAA GGC CTC Gly Ala Asn Ser Leu Phe Leu Glu Lys Thr Pro Phe Val Glu Gly Leu 310 315 320			1197
AGC TAC AAC CTG AAC ACC ATG CAG TAT CCC AGC CAG CAG TTC CAG CCC Ser Tyr Asn Leu Asn Thr Met Gln Tyr Pro Ser Gln Gln Phe Gln Pro 325 330 335			1245
GTG GTG CTG GCC AAC TGACCATCTA CCTGGCCCGT GGGGGCAGGA GCACCCAAGA Val Val Leu Ala Asn 340			1300
CCACAGAAAA GAGAAAGGAA AGGCCAAAAA AAAAAAAAAAA AAA			1343

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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

Met Gln Leu Glu Ile Lys Val Ala Leu Asn Phe Ile Ile Ser Tyr Leu
1 5 10 15

Tyr Asn Lys Leu Pro Arg Arg Arg Ala Asp Leu Phe Gly Glu Glu Leu
20 25 30

Glu Arg Leu Leu Lys Arg Lys Tyr Glu Gly His Trp Tyr Pro Glu Lys
35 40 45

Pro Leu Lys Gly Ser Gly Phe Arg Cys Val His Ile Gly Glu Met Val
50 55 60

Asp Pro Val Val Glu Leu Ala Ala Lys Arg Ser Gly Leu Ala Val Glu
65 70 75 80

Asp Val Arg Ala Asn Val Pro Glu Glu Leu Ser Val Trp Ile Asp Pro
85 90 95

Phe Glu Val Ser Tyr Gln Ile Gly Glu Lys Gly Ala Val Lys Val Leu

-continued

100	105	110
Tyr Leu Asp Asp Ser Glu Gly Cys Gly Ala Pro Glu Leu Asp Lys Glu 115 120 125		
Ile Lys Ser Ser Phe Asn Pro Asp Ala Gln Val Phe Val Pro Ile Gly 130 135 140		
Ser Gln Asp Ser Ser Leu Ser Asn Ser Pro Ser Pro Ser Phe Gly Gln 145 150 155 160		
Ser Pro Ser Pro Thr Phe Ile Pro Arg Ser Ala Gln Pro Ile Thr Phe 165 170 175		
Thr Thr Ala Ser Phe Ala Ala Thr Lys Phe Gly Ser Thr Lys Met Lys 180 185 190		
Lys Gly Gly Gly Ala Ala Ser Gly Gly Gly Val Ala Ser Ser Gly Ala 195 200 205		
Gly Gly Gln Gln Pro Pro Gln Gln Pro Arg Met Ala Arg Ser Pro Thr 210 215 220		
Asn Ser Leu Leu Lys His Lys Ser Leu Ser Leu Ser Met His Ser Leu 225 230 235 240		
Asn Phe Ile Thr Ala Asn Pro Ala Pro Gln Ser Gln Leu Ser Pro Asn 245 250 255		
Ala Lys Glu Phe Val Tyr Asn Gly Gly Gly Ser Pro Ser Leu Phe Phe 260 265 270		
Asp Ala Ala Asp Gly Gln Gly Ser Gly Thr Pro Gly Pro Phe Gly Gly 275 280 285		
Ser Gly Ala Gly Thr Cys Asn Ser Ser Ser Phe Asp Met Ala Gln Val 290 295 300		
Phe Gly Gly Gly Ala Asn Ser Leu Phe Leu Glu Lys Thr Pro Phe Val 305 310 315 320		
Glu Gly Leu Ser Tyr Asn Leu Asn Thr Met Gln Tyr Pro Ser Gln Gln 325 330 335		
Phe Gln Pro Val Val Leu Ala Asn 340		

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

CAGTGGATCC GCCACCATGC AGCTTGAAAT CCAAGTAGCA C

41

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

CAGTGGTACC ATACATTTTC TTTTTTTTAG TTAGCCAT

38

(2) INFORMATION FOR SEQ ID NO: 7:

-continued

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

CAGTGGATCC GCCACCATGC AGCTAGAGAT CAAAGTGGCC C 41

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

CAGTGGTACC ACGGGCCAGG TAGATGGTCA GTTGCCAGC AC 42

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

GGCCCAAGCT TGCCGCCATG CAGCTTGAAA TCCAAGTAG 39

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

ATCGTCTAGA TTAGTTAGCC ATAACAGGCT GGAATTGCTG GTTAGAATAC TGCATGTTAT 60

TTAAGCTAAA ATTCAAGCCA TCTA 84

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

GGCCCAAGCT TGCCGCCATG CAGCTAGAGA TCAAAGTGGC 40

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

-continued

(A) LENGTH: 81 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1 2:

ATCGTCTAGA TCAAGCGTAG TCTGGGACGT CGTATGGGTA GGTGTAGCT GAGGCCTTCC 60
 ACAAAGGGTG TCTTCTCCAG G 81

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

ATCGCCATGG GACAGCTTGA AATCCAAGTA GCACTA 36

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cD NA

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

ATCGAGATCT TTAGTTAGCC ATAACAGGCT GGAAT 35

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cD NA

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

ATCGCCATGG GACAGCTAGA GATCAAAGTG GCCCTG 36

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

ATCGAGATCT GTTGGCCAGC ACCACGGGCT GG 32

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 171 amino acids
 (B) TYPE: amino acid

-continued

(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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

Met His Pro Phe Tyr Thr Arg Ala Ala Thr Met Ile Gly Glu Ile Al
1 5 10 15
Ala Ala Val Ser Phe Ile Ser Lys Phe Leu Arg Thr Lys Gly Leu Th
20 25 30
Ser Glu Arg Gln Leu Gln Thr Phe Ser Gln Ser Leu Gln Glu Leu Le
35 40 45
Ala Glu His Tyr Lys His His Trp Phe Pro Glu Lys Pro Cys Lys Gl
50 55 60
Ser Gly Tyr Arg Cys Ile Arg Ile Asn His Lys Met Asp Pro Leu Il
65 70 75 80
Gly Gln Ala Ala Gln Arg Ile Gly Leu Ser Ser Gln Glu Leu Phe Ar
85 90 95
Leu Leu Pro Ser Glu Leu Thr Leu Trp Val Asp Pro Tyr Glu Val Se
100 105 110
Tyr Arg Ile Gly Glu Asp Gly Ser Ile Cys Val Leu Tyr Glu Ala Se
115 120 125
Pro Ala Gly Gly Ser Thr Gln Asn Ser Thr Asn Val Gln Met Val As
130 135 140
Ser Arg Ile Ser Cys Lys Glu Leu Leu Leu Gly Arg Thr Ser Pr
145 150 155 160
Ser Lys Asn Tyr Asn Met Met Thr Val Ser Gly
165 170

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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

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

-continued

Thr Thr Ala Phe Ala Ala Thr Lys Phe Gly Ser Thr Lys Met Lys Gl
 145 150 155 160

Gly Asn Leu Leu Lys Lys Ser Ser Met His Ser Leu Gln Gln Leu Se
 165 170 175

Pro Asn Ala Lys Glu Phe Phe Gly Gln Gly Ser Thr Gly Phe Gly As
 180 185 190

Ser Phe Ala Leu Phe Val Gly Leu Leu Asn Met Gln Tyr Gln Gln Ph
 195 200 205

Gln Pro Val Ala Asn
 210

What is claimed is:

1. A method for diagnosing aberrant cellular proliferation associated with a malignant phenotype comprising:
 - a) measuring by radioimmunoassay, competitive-binding assay, Western blot analysis, ELISA assay, or sandwich assay the amount of BTG-2 protein in a sample obtained from a patient, using an antibody that specifically binds the amino acid sequence of SEQ ID NO:2; and
 - b) comparing the amount of BTG-2 protein to a normal control tissue sample,
 wherein under-expression of the BTG-2 protein in the sample obtained from the patient relative to the normal control tissue sample is diagnostic of aberrant cellular proliferation associated with a malignant phenotype, and wherein said BTG-2 protein consists of the amino acid sequence of SEQ ID NO:2, or a fragment thereof.
2. The method of claim 1, wherein said sample obtained from a patient is blood, urine, saliva, tissue biopsy or autopsy material.
3. A method for diagnosing aberrant cellular proliferation associated with a malignant phenotype comprising:

- a) measuring by radioimmunoassay, competitive-binding assay, Western blot analysis, ELISA assay, or sandwich assay the amount of BTG-3 protein in a sample obtained from a patient, using an antibody that specifically binds the amino acid sequence of SEQ ID NO:4; and
- b) comparing the amount of BTG-3 protein to a normal control tissue sample, wherein under-expression of the BTG-3 protein in the sample obtained from the patient relative to the normal control tissue sample is diagnostic of aberrant cellular proliferation associated with a malignant phenotype, and wherein said BTG-3 protein consists of the amino acid sequence of SEQ ID NO:4, or a fragment thereof.
4. The method of claim 3, wherein said sample obtained from a patient is blood, urine, saliva, tissue biopsy or autopsy material.

* * * * *

UNITED STATES PATENT AND TRADEMARK OFFICE
CERTIFICATE OF CORRECTION

PATENT NO. : 7,049,081 B2
APPLICATION NO. : 10/739043
DATED : May 23, 2006
INVENTOR(S) : Kunsch et al.

Page 1 of 1

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

Title Page:

On page 1, INID code (56) - "Other Publications", delete "Marshall, C.J., "Tumor suppressor genes," Cell, 86:313-326 (1991)" and insert --Marshall, C.J., "Tumor suppressor genes," Cell, 64:313-326 (1991)--.

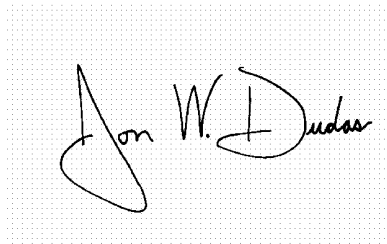
In the Claims:

Claim 1, at column 53, delete "or a fragment thereof." and insert --or mature form thereof.--

Claim 3, at column 54, delete "or a fragment thereof." and insert --or mature form thereof.--

Signed and Sealed this

Fifteenth Day of August, 2006

A handwritten signature in black ink on a light gray grid background. The signature reads "Jon W. Dudas" in a cursive style.

JON W. DUDAS

Director of the United States Patent and Trademark Office

专利名称(译)	基于人BTG-2和BTG-3多肽的诊断方法		
公开(公告)号	US7049081	公开(公告)日	2006-05-23
申请号	US10/739043	申请日	2003-12-19
[标]申请(专利权)人(译)	人类基因科学公司		
申请(专利权)人(译)	人类基因组科学, INC.		
当前申请(专利权)人(译)	人类基因组科学, INC.		
[标]发明人	KUNSCH CHARLES A CHOPRA ARVIND ROSEN CRAIG A		
发明人	KUNSCH, CHARLES A. CHOPRA, ARVIND ROSEN, CRAIG A.		
IPC分类号	G01N33/53 A61K38/17 C07K14/00 C07K14/82		
CPC分类号	C07K14/82 C12N2799/026		
代理机构(译)	人类基因组科学, INC.		
优先权	08/463382 1995-06-05 US 08/460104 1995-06-02 US PCT/US1995/003323 1995-03-17 WO		
其他公开文献	US20040131597A1		
外部链接	Espacenet USPTO		

摘要(译)

本发明涉及新的抗增殖基因。更具体地, 提供了分离的核酸分子, 其编码人B细胞易位基因2和3 (BTG-2和BTG-3)。还提供了BTG-2和BTG-3多肽, 以及载体, 宿主细胞和用于产生它们的重组方法。

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1  GGCACGAGATTTTGTGGCGTAGAGCTATGCAGCTTGAATCCAAGTAGCACTAAATTTTA
61  TTATTTTCGTATTTGTACAATAAGCTTCCCAGGAGACGTGTCAACATTTTGGTGAAGAAC
   I S Y L Y N K L P R R V N I F G E E L
121  TTGAAGACTTCTTAGAAGAAATATGAAAGGCGACTGGTATCCTGAAAAGCCATACAAG
   E R L L K K K Y E G H W Y P E K P Y K G
181  GATCGGGTTTAGATGTATACACATAGGGGAGAAAGTGGACCCAGTGATTGAACAAGCAT
   S G F R C I H I G E K V D P V I E Q A S
241  CCAAAGAGAGTGGTTTGGACATTGATGATGTTTCGTGGCAATCTGCCACAGGATCTTAGTG
   K E S G L D I D D V R G N L F Q D L S V
301  TTTGGATCGACCATTTGAGGTTTCTTACCAAATTTGGTAAAAGGACCAAGTGAAGGTGC
   W I D P F E V S Y Q I G E K G P V K V L
361  TTTACGTGGATGATAATAATGAAAATGGATGTGAGTTGGATAAGGAGATCAAAAACAGCT
   Y V D D N N E N G C E L D K E I K N S F
421  TTAACCCAGAGGCCAGGTTTATGCCATAAGTGACCCAGCCTCATCAGTGTCCAGCT
   N P E A Q V F M P I S D P A S S V S S S
481  CTCCATCGCCTCCTTTTGGTCACTCTGCTGCTGTAAAGCCCTACCTTCATGCCCCGGTCCA
   P S P P F G H S A A V S P T F M P R S T
541  CTCAGCCTTTAACCTTTACCCTGCCACTTTTGTGCCACCAAGTTCGGCTCTACCAAAA
   Q P L T F T T A T F A A T K F G S T K M
601  TGAATAATAGTGGCCGTAGCAACAAGTTGCAGCTACTTCTCCATCAACCTCGGCTTGA
   K N S G R S N K V A R T S P I N L G L N
661  ATGTGAATGACCTTTGAAGCAGAAAGCCATCTCTCCTCAATGCACCTCTGTATGGGC
   V N D L L K Q K A I S S S M H S L Y G L
721  TTGGCTTGGTAGCCAGCAGCAGCCACAGCAACAGCAGCAGCCAGCCAGCCAGCCAGCCAGC
   G L G S Q Q Q P Q Q Q Q Q P A Q P P P P
781  CACCACCACCACAGCAGCAACAACAGCAAAAACCTCTGCTTTTCTCTAATGCCA
   P P P Q Q Q Q Q Q K T S A L S P N A K

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FIG. 1A