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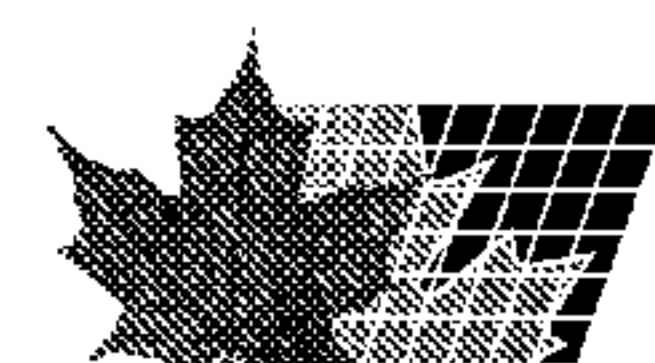
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(57) **Abrégé/Abstract:**

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ANGIOGENESIS ASSOCIATES PROTEINS, AND NUCLEIC ACIDS ENCODING THE SAME

RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/191,134 filed 03/22/2000.

BACKGROUND

Cities have roads and alleys, plants have xylem and phloem, and people have arteries, veins and lymphatics. Without these byways, the vertebrate animal cells would starve or drown in their metabolic refuse. Not only do blood vessels deliver food and oxygen and carry away metabolic wastes, but they also transport signaling substances that apprise cells of situations remote to them but to which they need to respond. Hormonal messages are a common signal.

All blood vessels are ensheathed by a basal lamina and a delicate monolayer of remarkably plastic endothelial cells lining the luminal walls. Depending on location and function, smooth muscle and connective tissue may also be present.

Not only do healthy cells depend on the blood resources transported by the circulatory system, but so, too, unwanted cells: tumorigenic and malignant cells. These cells colonize and proliferate if they are able to divert blood resources to themselves. Angiogenesis, the type of blood vessel formation where new vessels emerge from the proliferation of preexisting vessels (Risau, 1995; Risau and Flamme, 1995), is exploited not only by usual processes, such as in wound healing or myocardial infarction repair, but also by tumors themselves and in cancers, diabetic retinopathy, macular degeneration, psoriasis, and rheumatoid arthritis. Regardless of the process, whether pathological or usual physiological, endothelial cells mediate angiogenesis in a multi-step fashion: (1) endothelia receive an extracellular cue, (2) the signaled cells breach the basal lamina sheath, abetted by proteases they secrete, (3) the cells then migrate to the signal and proliferate, and finally, (4) the cells form a tube, a morphogenic event (Alberts *et al.*, 1994). The complexity of this process indicates complex changes in cellular physiology and morphology, gene expression, and signaling. Angiogenic accomplices that are cues

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include basic fibroblast growth factors (bFGF), angiopoietins (such as ANG1) and various forms of vascular endothelial growth factor (VEGF).

The molecular events and the order in which they occur and the pathways that are required for this process are of fundamental importance to understand angiogenesis. *In vitro* models are useful for identifying alterations in gene expression that occur during angiogenesis. A particularly fruitful model systems involves the supsension in a three-dimensional type I collagen gel and various stimuli, such as phorbol myristate acetate (PMA), basic fibroblast growth factor (bFGF), and VEGF. The combination of the stimuli and the collagen gel results in the formation of a three-dimensional tubular network of endothelial cells with interconnecting luminal structures. In this model, endothelial differentiation into tubelike structures is completely blocked by inhibitors of new mRNA or protein synthesis. Furthermore, the cells progress through differentiation in a coordinated and synchronized manner, thus optimizing the profile of gene expression (Kahn *et al.*, 2000; Yang *et al.*, 1999).

Tumor cells exploit angiogenesis to facilitate tumor growth. Controlling angiogenesis, by controlling the activity or expression of genes and proteins associated with angiogenesis, provides a way to prevent tumor growth, or even destroy tumors.

SUMMARY

The invention is based in part upon the discovery of novel nucleic acid sequences encoding novel polypeptides. Nucleic acids encoding the polypeptides disclosed in the invention, and derivatives and fragments thereof, will hereinafter be collectively designated as "AAP" nucleic acid or polypeptide sequences. AAP, or angiogenesis associated polypeptides (AAP) comprises kelch-like polypeptide (KLP), human ortholog of mouse BAZF (hBAZF), hmt-elongation factor G (hEF-G), human ortholog of rat TRG (hTRG), human myosin X (hMX1) and its splice variant (hMX2), nuclear hormone receptor (NHR), and human mitochondrial protein (hMP).

The invention is based in part upon the discovery of novel nucleic acid sequences encoding novel polypeptides. Nucleic acids encoding the polypeptides disclosed in the invention, and derivatives and fragments thereof, will hereinafter be collectively designated as "AAP" nucleic acid or polypeptide sequences."

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In a first aspect, the present invention is an isolated polypeptide having at least 80% sequence identity to the sequence SEQ ID NOS:2, 4, 6, 8, 10, 12, 14 or 16, polynucleotides encoding the same, and antibodies that specifically bind the same.

In a second aspect, the present invention is an isolated polynucleotide having at least 80% sequence identity to the sequence SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15, or a complement thereof.

In a third aspect, the present invention is a transgenic non-human animal, having a disrupted *AAP* gene or a transgenic non-human animal expressing an exogenous polynucleotide having at least 80% sequence identity to the sequence SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15, or a complement of said polynucleotide.

In a fourth aspect, the present invention is a method of screening a sample for a mutation in an *AAP* gene.

In a fifth aspect, the present invention is a method of modulating angiogenesis comprising modulating the activity of at least one AAP polypeptide.

In a sixth aspect, the present invention is a method of increasing, as well as decreasing angiogenesis, comprising modulating the activity of at least one AAP polypeptide. Activity modulation of AAP polypeptides may be over-expressing or eliminating expression of the gene, or impairing a AAP polypeptide's function by contact with specific antagonists or agonists, such as antibodies or aptamers.

In a seventh aspect, the present invention is a method of treating various pathologies, including tumors, cancers, myocardial infarctions and the like.

In an eighth aspect, the present invention is a method of measuring a AAP transcriptional and translational up-regulation or down-regulation activity of a compound.

In a ninth aspect, the invention is a method of screening a tissue sample for tumorigenic potential.

In a tenth aspect, the invention is a method of determining the clinical stage of tumor which compares the expression of at least one AAP in a sample with expression of said at least one gene in control samples.

Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and

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materials are described below. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

DETAILED DESCRIPTION

A model of angiogenesis-the suspension of endothelial cells in type I collagen gels with various stimuli-was used to identify a molecular fingerprint or transcriptional profile of endothelial differentiation into tubelike structures, using amplification and an imaging approach called GeneCalling (Shimkets *et al.*, 1999). This method was previously shown to provide a comprehensive sampling of cDNA populations in conjunction with the sensitive detection of quantitative differences in mRNA abundance for both known and novel genes. Many differentially expressed cDNA fragments were found. The identification and differential expression of these genes was confirmed by a second independent method employing real-time quantitative polymerase chain reaction (PCR). Although some of the identified cDNA fragments were genes known to play some role in angiogenesis, many other differentially expressed genes were unexpected. The inventors have identified the unexpected genes and polypeptides that are expressed in response to this model of angiogenesis, collectively referred to as angiogenesis associated polypeptides (AAP). AAP are kelch-like polypeptide (KLP), human ortholog of mouse BAZF (hBAZF), hmt-elongation factor G (hEF-G), human ortholog of rat TRG (hTRG), human myosin X (hMX1) and its splice variant (hMX2), nuclear hormone receptor (NHR), and human mitochondrial protein (hMP).

Definitions

Unless defined otherwise, all technical and scientific terms have the same meaning as is commonly understood by one of skill in the art to which this invention belongs. The definitions below are presented for clarity.

The recommendations of (Demerec *et al.*, 1966) where these are relevant to genetics are adapted herein. To distinguish between genes (and related nucleic acids) and the proteins that they encode, the abbreviations for genes are indicated by *italicized* (or underlined) text while abbreviations for the proteins start with a capital letter and are not italicized. Thus, *AAP* or AAP refers to the nucleotide sequence that encodes AAP.

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“Isolated,” when referred to a molecule, refers to a molecule that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that interfere with diagnostic or therapeutic use.

“Container” is used broadly to mean any receptacle for holding material or reagent. Containers may be fabricated of glass, plastic, ceramic, metal, or any other material that can hold reagents. Acceptable materials will not react adversely with the contents.

1. *Nucleic acid-related definitions*

(a) *control sequences*

Control sequences are DNA sequences that enable the expression of an operably-linked coding sequence in a particular host organism. Prokaryotic control sequences include promoters, operator sequences, and ribosome binding sites. Eukaryotic cells utilize promoters, polyadenylation signals, and enhancers.

(b) *operably-linked*

Nucleic acid is operably-linked when it is placed into a functional relationship with another nucleic acid sequence. For example, a promoter or enhancer is operably-linked to a coding sequence if it affects the transcription of the sequence, or a ribosome-binding site is operably-linked to a coding sequence if positioned to facilitate translation. Generally, “operably-linked” means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by conventional recombinant DNA methods.

(c) *isolated nucleic acids*

An isolated nucleic acid molecule is purified from the setting in which it is found in nature and is separated from at least one contaminant nucleic acid molecule. Isolated *AAP* molecules are distinguished from the specific *AAP* molecule, as it exists in cells. However, an isolated *AAP* molecule includes *AAP* molecules contained in cells that ordinarily express an *AAP* where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

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2. *Protein-related definitions*

(a) *purified polypeptide*

When the molecule is a purified polypeptide, the polypeptide will be purified (1) to obtain at least 15 residues of N-terminal or internal amino acid sequence using a sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or silver stain. Isolated polypeptides include those expressed heterologously in genetically-engineered cells or expressed *in vitro*, since at least one component of an AAP natural environment will not be present. Ordinarily, isolated polypeptides are prepared by at least one purification step.

(b) *active polypeptide*

An active AAP or AAP fragment retains a biological and/or an immunological activity of the native or naturally-occurring AAP. Immunological activity refers to the ability to induce the production of an antibody against an antigenic epitope possessed by a native AAP; biological activity refers to a function, either inhibitory or stimulatory, caused by a native AAP that excludes immunological activity. A biological activity of AAP includes, for example, modulating angiogenesis.

(c) *Abs*

Antibody may be single anti-AAP monoclonal Abs (including agonist, antagonist, and neutralizing Abs), anti-AAP antibody compositions with polyepitopic specificity, single chain anti-AAP Abs, and fragments of anti-AAP Abs. A "monoclonal antibody" refers to an antibody obtained from a population of substantially homogeneous Abs, *i.e.*, the individual Abs comprising the population are identical except for naturally-occurring mutations that may be present in minor amounts

(d) *epitope tags*

An epitope tagged polypeptide refers to a chimeric polypeptide fused to a "tag polypeptide". Such tags provide epitopes against which Abs can be made or are available, but do not interfere with polypeptide activity. To reduce anti-tag antibody reactivity with endogenous epitopes, the tag polypeptide is preferably unique. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 and 50 amino acid residues, preferably between 8 and 20 amino acid residues). Examples of epitope tag sequences include HA from *Influenza A* virus and FLAG.

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The novel *AAP* of the invention include the nucleic acids whose sequences are provided in Tables 1, 3, 5, 7, 9, 11, 13 and 15, or a fragment thereof. The invention also includes a mutant or variant *AAP*, any of whose bases may be changed from the corresponding base shown in Tables 1, 3, 5, 7, 9, 11, 13 and 15 while still encoding a protein that maintains the activities and physiological functions of the AAP fragment, or a fragment of such a nucleic acid. The invention further includes nucleic acids whose sequences are complementary to those just described, including complementary nucleic acid fragments. The invention additionally includes nucleic acids or nucleic acid fragments, or complements thereto, whose structures include chemical modifications. Such modifications include, by way of nonlimiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as anti-sense binding nucleic acids in therapeutic applications in a subject. In the mutant or variant nucleic acids, and their complements, up to 20% or more of the bases may be so changed.

The novel AAP of the invention include the protein fragments whose sequences are provided in Tables 2, 4, 6, 8, 10, 12, 14 and 16. The invention also includes an AAP mutant or variant protein, any of whose residues may be changed from the corresponding residue shown in Tables 2, 4, 6, 8, 10, 12, 14 and 16 while still encoding a protein that maintains its native activities and physiological functions, or a functional fragment thereof. In the mutant or variant AAP, up to 20% or more of the residues may be so changed. The invention further encompasses Abs and antibody fragments, such as F_{ab} or $(F_{ab})'_2$, that bind immunospecifically to any of the AAP of the invention.

The AAP nucleic acids are shown in Tables 1, 3, 5, 7, 9, 11, 13 and 15, and the corresponding polypeptides are shown in Tables 2, 4, 6, 8, 10, 12, 14 and 16, respectively. Start and stop codons in the polynucleotide sequences are indicated in **boldface** and with underlining. SEQ ID NO:3 lacks a stop codon. The sequences of *hMX1* and *hMX2* do not have start codons (see Table 17); consequently, hMX1 and hMX2 polypeptides do not start with a Met. For any lacking polynucleotide sequence, one of skill in the art may retrieve the full length sequence by, for example, probing cDNA or genomic libraries with probes designed according to the sequences of the instant invention.

Table 1 KLP nucleotide sequence (SEQ ID NO:1)

ctggcctaga	tactacaact	gaactttttt	tcttttttagt	tactccacag	gatccgctga	60
acataggatg	ttgccacaaa	atctacctcg	tgtattttttc	tctttcactc	atgagctgca	120
caattgcaga	tttgagcaca	atgtctgcag	actgtgttga	aaaactctga	agaacctaat	180
taacacagga	tgacctagga	gtgattctaa	gtctgtgtaa	caagatatta	ctcattagtg	240
aatgtgtcag	tcttggtact	gaatgctgca	gataacagca	agtaggttct	cctttatttc	300
tgaagtattc	acttgacctt	ccatcagtaa	gacggacttt	tctaactctgt	tcctggagat	360
attaatggaa	tacagtc <u>atg</u>	tccactcaag	acgagaggca	gatcaatact	gaatatgctg	420
tgtcattggt	ggaacagttg	aaactgtttt	atgaacagca	gttgtttact	gacatagtgt	480
taattgttga	gggcactgaa	ttcccttgtc	ataagatggg	tcttgcaaca	tgtagctctt	540
atttcagggc	catgtttatg	agtggactaa	gtgaaagcaa	acaaacccat	gtacacctga	600
ggaatgtcga	tgctgccacc	ttacagataa	taataactta	tgcatacacg	ggtaacttgg	660
caatgaatga	cagcactgta	gaacagcttt	atgaaacagc	ttgcttccta	caggtagaag	720
atgtgttaca	acgttgtcga	gaatatttaa	ttaaaaaaat	aaatgcagag	aattgtgtac	780
gattgttgag	ttttgctgat	ctcttcagtt	gtgaggaatt	aaaacagagt	gctaaaagaa	840
tggtggagca	caagttcact	gctgtgtatc	atcaggacgc	gttcatgcag	ctgtcacatg	900
acctactgat	agatattctc	agtagtgaca	atttaaattgt	agaaaaggaa	gaaaccgttc	960
gagaagctgc	tatgctgtgg	ctagagtata	acacagaatc	acgatcccag	tatttgtctt	1020
ctgttcttag	ccaaatcaga	attgatgcac	tttcagaagt	aacacagaga	gcttggtttc	1080
aaggtctgcc	acccaatgat	aagtcagtgg	tggttcaagg	tctgtataag	tccatgcca	1140
agtttttcaa	accaagactt	gggatgacta	aagaggaaat	gatgattttc	attgaagcat	1200
cttcagaaaa	tccttgtagt	ctttactctt	ctgtctgtta	cagcccccaa	gcagaaaaag	1260
tttacaagtt	atgtagccca	ccagctgatt	tgcataaggt	tgggaccggt	gtaactcctg	1320
ataatgatat	ctacatagca	gggggtcaag	ttcctctgaa	aaacacaaaa	acaaatcaca	1380
gtaaaacaag	caaacttcag	actgccttca	gaactgtgaa	ttgcttttat	tggtttgatg	1440
cacagcaaaa	tacctggttt	ccaaagaccc	caatgctttt	tgtccgcata	aagccatctt	1500
tggtttgctg	tgaaggctat	atctatgcaa	ttggaggaga	tagcgtaggt	ggagaactta	1560
atcggaggac	cgtagaaaga	tacgacactg	agaaagatga	gtggacgatg	gtaagccctt	1620
taccttgctg	ttggcaatgg	agtgcagcag	ttgtgggttca	tgactgcatt	tatgtgatga	1680
cactgaacct	catgtactgt	tattttccaa	ggctctgactc	atgggtagaa	atggccatga	1740
gacagactag	taggtccttt	gcttcagctg	cagcttttgg	tgataaaatt	ttctatatatg	1800
gagggttgca	tattgctacc	aattccggca	taagactccc	ctctggcact	gtagatgggt	1860
cttcagtaac	tgtggaaatt	tatgatgtga	ataaaaaatga	gtggaaaatg	gcagccaaca	1920
tccttgctaa	gaggtactct	gacccctgtg	ttagagctgt	tgtgatctca	aattctctat	1980
gtgtgtttat	gcgagaaacc	cacttaaattg	agcgagctaa	atacgtcacc	taccaatatg	2040
acctggaact	tgaccgggtgg	tctctgcggc	agcatatatc	tgaacgtgta	ctgtgggact	2100
tggggagaga	ttttcgatgc	actgtgggga	aactctatcc	atcctgcctt	gaagagtctc	2160
catggaaacc	accaacttat	cttttttcaa	cggatgggac	agaagagttt	gaactggatg	2220

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gagaaatggt tgcactacca cctgtat <u>agt</u> ggggaagttc agggagtgca cgcctgagtt	2280
atgtgctttg tcatttttctt tgctaaacaa aagaggctat gaaagaacta aatatgagta	2340
cataaaattc tatctttgat aaattttatt tttatgccct acttaatat tgcatacagta	2400
taatatatat cagtgagtct tacagaaaga tatgcttcca taatatgaaa tagattattc	2460
aataattgag aaactttatg tgtaatcatg agagtataag aatctggatt atctaacatt	2520
gtagccctg tgtatgtaca gttcaaaaag ttcatttata aaagtagttt cctgttc	2577

Table 2 KLP polypeptide sequence (SEQ ID NO:2)

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

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

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530						535						540				
Glu	Arg	Ala	Lys	Tyr	Val	Thr	Tyr	Gln	Tyr	Asp	Leu	Glu	Leu	Asp	Arg	
545					550					555					560	
Trp	Ser	Leu	Arg	Gln	His	Ile	Ser	Glu	Arg	Val	Leu	Trp	Asp	Leu	Gly	
				565					570					575		
Arg	Asp	Phe	Arg	Cys	Thr	Val	Gly	Lys	Leu	Tyr	Pro	Ser	Cys	Leu	Glu	
			580					585					590			
Glu	Ser	Pro	Trp	Lys	Pro	Pro	Thr	Tyr	Leu	Phe	Ser	Thr	Asp	Gly	Thr	
		595					600					605				
Glu	Glu	Phe	Glu	Leu	Asp	Gly	Glu	Met	Val	Ala	Leu	Pro	Pro	Val		
610						615					620					

Table 3 hBAZF nucleotide sequence (SEQ ID NO:3)

caagggagcg	agggtgtcgt	agagggcaga	atgaacaaga	agaattagga	gggaggctgc	60
gtgtgccggg	gctaggggct	ggaagtccctg	gctctagttg	cacctcggaa	ggaaaaggca	120
aacagaggag	ggaaggcgctc	ttaggactgc	ctggatccag	agcactttcc	tcggcctcta	180
caggcctgtg	tcgctatggg	ttcccccgcc	gccccggagg	gagcgctggg	ctacgtccgc	240
gagttcactc	gccactcctc	cgacgtgctg	ggcaacctca	acgagctgcg	cctgcgcggg	300
atcctcactg	acgtcacgct	gctggttggc	gggcaacccc	tcagagcaca	caaggcagtt	360
ctcatcgct	gcagtggctt	cttctattca	attttccggg	gccgtgcggg	agtcgggggtg	420
gacgtgctct	ctctgcccgg	gggtcccga	gcgagaggct	tcgcccctct	attggacttc	480
atgtacactt	cgcgctgcg	cctctctcca	gccactgcac	cagcagtcct	agcggccgcc	540
acctatattgc	agatggagca	cgtgggtccag	gcatgccacc	gcttcatcca	ggccagctat	600
gaacctctgg	gcatctccct	gcgccccctg	gaagcagaac	ccccaacacc	cccaacggcc	660
cctccaccag	gtagtcccag	gcgctccgaa	ggacaccag	accacacctac	tgaatctcga	720
agctgcagtc	aaggcccccc	cagtccagcc	agccctgacc	ccaaggcctg	caactggaaa	780
aagtacaagt	acatcgtgct	aaactctcag	gcctcccaag	cagggagcct	ggtcggggag	840
agaagttctg	gtcaaccttg	cccccaagcc	aggctcccca	gtggagacga	ggcctccagc	900
agcagcagca	gcagcagcag	cagcagcagt	gaagaaggac	ccattcctgg	tccccagagc	960
aggctctctc	caactgctgc	cactgtgcag	ttcaaattgtg	gggctccagc	cagtaccccc	1020
tacctcctca	catcccaggc	tcaagacacc	tctggatcac	cctctgaacg	ggctcgtcca	1080
ctaccgggga	gtgaattttt	cagctgccag	aactgtgagg	ctgtggcagg	gtgctcatcg	1140
gggctggact	ccttggttcc	tggggacgaa	gacaaaccct	ataagtgtca	gctgtgccgg	1200
tcttcgttcc	gctacaaggg	caaccttgcc	agtcaccgta	cagtgcacac	aggggaaaag	1260
ccttaccact	gctcaatctg	cggagcccgt	tttaaccggc	cagcaaaccct	gaaaacgcac	1320
agccgcatcc	attcggggaga	gaagccgtat	aagtgtgaga	cgtgcggctc	gcgctttgta	1380

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caggtacgga gccagcctcc aagtggcttc caaggcaaac ctgcaagagg tgggggtgggc	1440
caaaagggag ggttctgttc ctcccagagg caggacttga agtctcctcc ctcccaggtg	1500
gcacatctgc gggcgcacgt gctgatccac accggggaga agccctaccc ttgccctacc	1560
tgcggaaccc gcttccgcca cctgcagacc ctcaagagcc acgttcgcat ccacaccgga	1620
gagaagcctt accactgcga cccctgtggc ctgcatttcc ggcacaagag tcaactgcgg	1680
ctgcatctgc gccagaaaca cggagctgct accaacacca aagtgcacta ccacattctc	1740
gggggggcc	1749

Table 4 hBAZF polypeptide sequence (SEQ ID NO:4)

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

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

Table 5 hEF-G nucleotide sequence (SEQ ID NO:5)

tctttttcct	cgcgctccttt	gccccggaag	tgctcttaca	acattggctg	ccggcgtgac	60
tttgaccgct	tcccgggtgcg	ttaccggcag	ctgaaccac	ccggcgccac	gggactttga	120
cgcgctgctct	gcgcttgcca	<u>tg</u> agactcct	gggagctgca	gccgtcgcg	ctctggggcg	180
cggaagggcc	cccgcctccc	taggctggca	gaggaagcag	gttaattgga	aggcctgccg	240
atgggtcttca	tcaggggtga	ttcctaata	aaaaatacga	aatattggaa	tctcagctca	300
cattgattct	gggaaaacta	cattaacaga	acgagtcctt	tactacactg	gcagaattgc	360
aaagatgcat	gaggtgaaag	gtaaagatgg	agttgggtgct	gtcatggatt	ccatggaact	420
agagagacaa	agaggaatca	ctattcagtc	agcagccact	ttcaccatgt	ggaaagatgt	480
caatattaac	attatagata	ctcctgggca	tgtggacttc	acaatagaag	tggaaagggc	540
cctgagagtg	ttggatgggtg	cagtccttgt	tctctgtgct	gttggagggg	tacagtgcc	600
gaccatgact	gtcaatcgtc	agatgaagcg	ctacaacggt	ccgtttctaa	cttttattaa	660
caaattggac	cgaatgggct	ccaaccacgc	cagggccctg	cagcaaata	ggctctaaact	720
aatcataat	acagcgttta	tgcagatacc	catgggtttg	gagggttaatt	ttaaaggtat	780
tgtagatctt	attgaggaac	gagccatcta	ttttgatgga	gacttttagtc	agattgttcg	840
atatgggtgag	attccagctg	aattaagggc	ggcggccact	gaccaccggc	aggagctaat	900
tgaatgtgtt	gccaattcag	atgaacagct	tggtgagatg	tttctggaag	aaaaaatccc	960
ctcgatttct	gatttaaagc	tagcaattcg	aagagctact	ctgaaaagat	catttactcc	1020
tgtatttttg	ggaagcgcct	tgaagaacaa	aggagttagc	cctcttttag	atgctgtttt	1080
agaataacctc	ccaaatccat	ctgaagtcca	gaactatgct	attctcaata	aaaaggatga	1140
ctcaaaagag	aaaaccaaaa	tcctaataga	ctccagtaga	cacaattccc	accattttgt	1200
aggcctggct	tttcccctgg	aggtaggtcg	atttggaaca	ttaacttatg	ttcgcagtta	1260
tcaggggagag	ctaaagaagg	gtgacaccat	ctataacaca	aggacaagaa	agaaagtacg	1320
gttgcaacgg	ctggctcgca	tgcatgccga	catgatggag	gcaagtacag	aggaagtata	1380
tgccggagac	atctgtgcat	tgtttggcat	tgactgtgct	agtggagaca	cattcacaga	1440
caaagccaac	agcggccttt	ctatggagtc	aattcatggt	cctgatcctg	tcattttcaat	1500
agcaatgaag	ccttctaaca	agaacgatct	ggaaaaattt	tcaaaaggta	ttggcagggtt	1560
tacaagagaa	gatcccacat	ttaaagtata	ctttgacact	gagaacaaag	agacagttat	1620
atctggaatg	ggagaattac	acctggaaat	ctatgctcag	aggctggaaa	gagagtatgg	1680
ctgtccttgt	atcacaggaa	agccaaaagt	tgcccttcga	gagaccatta	ctgcccctgt	1740
ccggtttgac	tttacacata	aaaaacaatc	aggtgggtgca	ggccagtatg	gaaaagtaat	1800
aggtgtcctg	gagcctctgg	accagagga	ctacactaaa	ttggaatttt	cagatgaaac	1860
attcggatca	aatattccaa	agcagtttgt	gcctgctgta	gaaaaggggt	ttttagatgc	1920
ctgcgagaag	ggccctcttt	ctgggtcaca	gctctctggg	ctccggtttg	tcctgcaaga	1980
tggagcacac	cacatgggtg	attctaata	aatctctttc	atccgagcag	gagaaggtgc	2040
tcttaaacia	gccttggcaa	atgcaacatt	atgtattctt	gaacctatta	tggctgtgga	2100
agttgtagct	ccaaatgaat	ttcaggggaca	agtaattgca	ggaattaacc	gacgccatgg	2160

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ggtaatcact	gggcaagatg	gagttgagga	ctatttttaca	ctgtatgcag	atgtccctct	2220
aaatgatatg	tttggttatt	ccactgaact	taggtcatgc	acagagggaa	agggagaata	2280
cacaatggag	tatagcaggt	atcagccatg	tttaccatcc	acacaagaag	acgtcattaa	2340
taagtatttg	gaagctacag	gtcaacttcc	tgtaaataaaa	ggaaaagcca	agaact <u>taact</u>	2400
ttgcttactg	tgagttgact	gactctaatt	gaatctgcgt	ggttttgata	ctttgatgga	2460
ttccagtgga	ataaattcag	gctgctgaaa	caagaaattc	tgagcccagg	aagcgggctc	2520
ttctttcttc	aaaagaagcc	cttcttggtc	atattcagga	gcttctgtta	tattcaaagg	2580
taattctatg	tctatctcaa	ctctattgat	tggtttttata	gttcattgaa	aatcctcaaa	2640
taaaatataa	ttattactga	aatatgttta	atattttaagg	ggaaaagaga	ctaatttcag	2700
ttatactttt	aagcttagaa	tgtatgttca	tttccaaatt	ttgtatcata	agagttttca	2760
acatagagaa	aagctgaaaa	aatgcaaaga	ataaccacat	actttccatc	taccttcctt	2820
tgtaaacggg	ttgttttatca	tataataatt	tgttttgtca	tatttgcttt	cactgtctat	2880
tatctgttta	agtctcataa	ctctattttt	agtttgctga	agacttgaaa	gtgaatcgca	2940
tatatcatga	cacttcttgg	agtgtcatta	atgggcaggc	ttttctgttg	aagagtggat	3000
tccgtatggt	cttcatagag	agtgtttttc	agattcttca	ttgggatatt	aaaatattag	3060
ccaaatttcn	ctctgtttta	tatatgncag	tttattttcag	tttgtggttt	ctgcaaattt	3120
gtaactgcct	ctgttttagg	agtataagta	ttacttcctt	gtggtctatt	gtgaagtaaa	3180
aagtagaccc	ttgcatatac	tattcttggt	tgtgttcac	ttaatgtttt	tgtacagcta	3240
aatcaaagt	aatttataga	gttagtttca	tcaacctaat	gaatgctagt	taaatttgaa	3300
ttccttgga	tttatcgtat	attgtattca	ctgagattat	gaagggacaa	atgttaatat	3360
tttgtttcca	gaaaaagttg	ggctttccca	agcagttcta	ttaccgggtt	cagaattgct	3420
tcacccaaaa	atcatctgat	ggtatagatg	gatcctagtc	cttttcatta	cctgatggta	3480
gaaataaaat	aattgatttt	a				3501

Table 6 hEF-G polypeptide (SEQ ID NO:6)

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

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100							105					110				
Asp	Val	Asn	Ile	Asn	Ile	Ile	Asp	Thr	Pro	Gly	His	Val	Asp	Phe	Thr	
		115					120					125				
Ile	Glu	Val	Glu	Arg	Ala	Leu	Arg	Val	Leu	Asp	Gly	Ala	Val	Leu	Val	
	130					135					140					
Leu	Cys	Ala	Val	Gly	Gly	Val	Gln	Cys	Gln	Thr	Met	Thr	Val	Asn	Arg	
145					150					155					160	
Gln	Met	Lys	Arg	Tyr	Asn	Val	Pro	Phe	Leu	Thr	Phe	Ile	Asn	Lys	Leu	
				165					170					175		
Asp	Arg	Met	Gly	Ser	Asn	Pro	Ala	Arg	Ala	Leu	Gln	Gln	Met	Arg	Ser	
			180					185					190			
Lys	Leu	Asn	His	Asn	Thr	Ala	Phe	Met	Gln	Ile	Pro	Met	Gly	Leu	Glu	
		195					200					205				
Gly	Asn	Phe	Lys	Gly	Ile	Val	Asp	Leu	Ile	Glu	Glu	Arg	Ala	Ile	Tyr	
	210					215					220					
Phe	Asp	Gly	Asp	Phe	Ser	Gln	Ile	Val	Arg	Tyr	Gly	Glu	Ile	Pro	Ala	
225					230					235					240	
Glu	Leu	Arg	Ala	Ala	Ala	Thr	Asp	His	Arg	Gln	Glu	Leu	Ile	Glu	Cys	
				245				250						255		
Val	Ala	Asn	Ser	Asp	Glu	Gln	Leu	Gly	Glu	Met	Phe	Leu	Glu	Glu	Lys	
			260					265					270			
Ile	Pro	Ser	Ile	Ser	Asp	Leu	Lys	Leu	Ala	Ile	Arg	Arg	Ala	Thr	Leu	
		275					280					285				
Lys	Arg	Ser	Phe	Thr	Pro	Val	Phe	Leu	Gly	Ser	Ala	Leu	Lys	Asn	Lys	
	290					295					300					
Gly	Val	Gln	Pro	Leu	Leu	Asp	Ala	Val	Leu	Glu	Tyr	Leu	Pro	Asn	Pro	
305					310					315					320	
Ser	Glu	Val	Gln	Asn	Tyr	Ala	Ile	Leu	Asn	Lys	Lys	Asp	Asp	Ser	Lys	
				325					330					335		
Glu	Lys	Thr	Lys	Ile	Leu	Met	Asn	Ser	Ser	Arg	His	Asn	Ser	His	Pro	
			340					345					350			
Phe	Val	Gly	Leu	Ala	Phe	Pro	Leu	Glu	Val	Gly	Arg	Phe	Gly	Gln	Leu	
		355					360					365				
Thr	Tyr	Val	Arg	Ser	Tyr	Gln	Gly	Glu	Leu	Lys	Lys	Gly	Asp	Thr	Ile	
	370					375						380				
Tyr	Asn	Thr	Arg	Thr	Arg	Lys	Lys	Val	Arg	Leu	Gln	Arg	Leu	Ala	Arg	
385					390					395					400	
Met	His	Ala	Asp	Met	Met	Glu	Ala	Ser	Thr	Glu	Glu	Val	Tyr	Ala	Gly	
				405					410					415		

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Asp	Ile	Cys	Ala	Leu	Phe	Gly	Ile	Asp	Cys	Ala	Ser	Gly	Asp	Thr	Phe	420	425	430	
Thr	Asp	Lys	Ala	Asn	Ser	Gly	Leu	Ser	Met	Glu	Ser	Ile	His	Val	Pro	435	440	445	
Asp	Pro	Val	Ile	Ser	Ile	Ala	Met	Lys	Pro	Ser	Asn	Lys	Asn	Asp	Leu	450	455	460	
Glu	Lys	Phe	Ser	Lys	Gly	Ile	Gly	Arg	Phe	Thr	Arg	Glu	Asp	Pro	Thr	465	470	475	480
Phe	Lys	Val	Tyr	Phe	Asp	Thr	Glu	Asn	Lys	Glu	Thr	Val	Ile	Ser	Gly	485	490	495	
Met	Gly	Glu	Leu	His	Leu	Glu	Ile	Tyr	Ala	Gln	Arg	Leu	Glu	Arg	Glu	500	505	510	
Tyr	Gly	Cys	Pro	Cys	Ile	Thr	Gly	Lys	Pro	Lys	Val	Ala	Phe	Arg	Glu	515	520	525	
Thr	Ile	Thr	Ala	Pro	Val	Pro	Phe	Asp	Phe	Thr	His	Lys	Lys	Gln	Ser	530	535	540	
Gly	Gly	Ala	Gly	Gln	Tyr	Gly	Lys	Val	Ile	Gly	Val	Leu	Glu	Pro	Leu	545	550	555	560
Asp	Pro	Glu	Asp	Tyr	Thr	Lys	Leu	Glu	Phe	Ser	Asp	Glu	Thr	Phe	Gly	565	570	575	
Ser	Asn	Ile	Pro	Lys	Gln	Phe	Val	Pro	Ala	Val	Glu	Lys	Gly	Phe	Leu	580	585	590	
Asp	Ala	Cys	Glu	Lys	Gly	Pro	Leu	Ser	Gly	His	Lys	Leu	Ser	Gly	Leu	595	600	605	
Arg	Phe	Val	Leu	Gln	Asp	Gly	Ala	His	His	Met	Val	Asp	Ser	Asn	Glu	610	615	620	
Ile	Ser	Phe	Ile	Arg	Ala	Gly	Glu	Gly	Ala	Leu	Lys	Gln	Ala	Leu	Ala	625	630	635	640
Asn	Ala	Thr	Leu	Cys	Ile	Leu	Glu	Pro	Ile	Met	Ala	Val	Glu	Val	Val	645	650	655	
Ala	Pro	Asn	Glu	Phe	Gln	Gly	Gln	Val	Ile	Ala	Gly	Ile	Asn	Arg	Arg	660	665	670	
His	Gly	Val	Ile	Thr	Gly	Gln	Asp	Gly	Val	Glu	Asp	Tyr	Phe	Thr	Leu	675	680	685	
Tyr	Ala	Asp	Val	Pro	Leu	Asn	Asp	Met	Phe	Gly	Tyr	Ser	Thr	Glu	Leu	690	695	700	
Arg	Ser	Cys	Thr	Glu	Gly	Lys	Gly	Glu	Tyr	Thr	Met	Glu	Tyr	Ser	Arg	705	710	715	720

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Tyr	Gln	Pro	Cys	Leu	Pro	Ser	Thr	Gln	Glu	Asp	Val	Ile	Asn	Lys	Tyr
				725					730					735	
Leu	Glu	Ala	Thr	Gly	Gln	Leu	Pro	Val	Lys	Lys	Gly	Lys	Ala	Lys	Asn
				740				745						750	

Table 7 hTRG nucleotide sequence (SEQ ID NO:7)

gccgcgggag	caggcggagg	cggaggcggc	gggggcagga	ggatgtcgca	gccgccgctg	60
ctccccgcct	cggcggagac	tcggaagttc	acccggggcg	tgagtaagcc	gggcacggcg	120
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acaaaacaat	ttgaaacctg	cagtaaaact	cccatcacgt	ttgaagtgga	ggaatttggtg	1920

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ccctgcatac	caaaacacac	tcagccttac	accatctaca	ccaatcacct	ttacgtttat	1980
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aagcggaggg	attttgagag	gctggcccat	ctgtatgaca	cgctgcaccg	ggcctacagc	5340
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cccatcgagg	tggccattga	cgagatgagt	aagaagggtg	cggagctccg	gcagctgtgc	5940
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gtgtgattac	atctcatggc	ccgtgtgtgg	ggacttgctt	tgtcattttgc	aaactcagga	6420
tgctttccaa	agccaatcac	tggggagacc	gagcacaggg	aggaccaagg	ggaaggggag	6480

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agaaaggaaa	taaagaacaa	cgttatttct	taacagactt	tctataggag	ttgtaagaag	6540
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cagttttaag	aatttcatcc	ttttgccaaa	atggtggagt	atgtaattgg	taaatcataa	7320
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tcactgccct	gctgtaatta	aacattctgt	accacatctg	tattaaaaag	acattgctga	7500
ccatta						7506

Table 8 hTRG polypeptide sequence (SEQ ID NO:8)

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

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Leu	Asp	Lys	Leu	Pro	Val	His	Val	Tyr	Glu	Val	Asp	Glu	Glu	Val	Asp	
145					150					155					160	
Lys	Asp	Glu	Asp	Ala	Ala	Ser	Leu	Gly	Ser	Gln	Lys	Gly	Gly	Ile	Thr	
				165					170					175		
Lys	His	Gly	Trp	Leu	Tyr	Lys	Gly	Asn	Met	Asn	Ser	Ala	Ile	Ser	Val	
			180					185					190			
Thr	Met	Arg	Ser	Phe	Lys	Arg	Arg	Phe	Phe	His	Leu	Ile	Gln	Leu	Gly	
		195					200					205				
Asp	Gly	Ser	Tyr	Lys	Phe	Glu	Phe	Leu	Lys	Asp	Leu	Gln	Lys	Glu	Pro	
	210					215					220					
Lys	Gly	Ser	Ile	Phe	Leu	Gly	Phe	Leu	Tyr	Gly	Val	Ser	Phe	Arg	Asn	
225					230					235					240	
Asn	Lys	Val	Arg	Arg	Phe	Ala	Phe	Glu	Leu	Lys	Met	Gln	Asp	Lys	Ser	
				245					250					255		
Ser	Tyr	Leu	Leu	Ala	Ala	Asp	Ser	Glu	Val	Glu	Met	Glu	Glu	Trp	Ile	
			260					265					270			
Thr	Ile	Leu	Asn	Lys	Ile	Leu	Gln	Leu	Asn	Phe	Glu	Ala	Ala	Met	Gln	
		275					280					285				
Glu	Lys	Arg	Asn	Gly	Asp	Ser	His	Glu	Asp	Asp	Glu	Gln	Ser	Lys	Leu	
	290					295					300					
Glu	Gly	Ser	Gly	Ser	Gly	Leu	Asp	Ser	Tyr	Leu	Pro	Glu	Leu	Ala	Lys	
305					310					315					320	
Ser	Ala	Arg	Glu	Ala	Glu	Ile	Lys	Leu	Lys	Ser	Glu	Ser	Arg	Val	Lys	
				325					330					335		
Leu	Phe	Tyr	Leu	Asp	Pro	Asp	Ala	Gln	Lys	Leu	Asp	Phe	Ser	Ser	Ala	
			340					345					350			
Glu	Pro	Glu	Val	Lys	Ser	Phe	Glu	Glu	Lys	Phe	Gly	Lys	Arg	Ile	Leu	
		355					360					365				
Val	Lys	Cys	Asn	Asp	Leu	Ser	Phe	Asn	Leu	Gln	Cys	Cys	Val	Ala	Glu	
		370				375					380					
Asn	Glu	Glu	Gly	Pro	Thr	Thr	Asn	Val	Glu	Pro	Phe	Phe	Val	Thr	Leu	
385					390					395					400	
Ser	Leu	Phe	Asp	Ile	Lys	Tyr	Asn	Arg	Lys	Ile	Ser	Ala	Asp	Phe	His	
				405					410					415		
Val	Asp	Leu	Asn	His	Phe	Ser	Val	Arg	Gln	Met	Ile	Ala	Thr	Thr	Ser	
			420					425					430			
Pro	Ala	Leu	Met	Asn	Gly	Ser	Gly	Pro	Glu	Thr	Gln	Ser	Ala	Leu	Arg	
		435					440					445				

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Gly	Ile	Leu	His	Glu	Ala	Ala	Met	Gln	Tyr	Pro	Lys	Gln	Gly	Ile	Phe	
450						455					460					
Ser	Val	Thr	Cys	Pro	His	Pro	Asp	Ile	Phe	Leu	Val	Ala	Arg	Ile	Glu	
465					470					475					480	
Lys	Val	Leu	Gln	Gly	Ser	Ile	Thr	His	Cys	Ala	Glu	Pro	Tyr	Met	Lys	
				485					490					495		
Ser	Ser	Asp	Ser	Ser	Lys	Val	Ala	Gln	Lys	Val	Leu	Lys	Asn	Ala	Lys	
			500					505					510			
Gln	Ala	Cys	Gln	Arg	Leu	Gly	Gln	Tyr	Arg	Met	Pro	Phe	Ala	Trp	Ala	
		515					520					525				
Ala	Arg	Thr	Leu	Phe	Lys	Asp	Ala	Ser	Gly	Asn	Leu	Asp	Lys	Asn	Ala	
						535					540					
Arg	Phe	Ser	Ala	Ile	Tyr	Arg	Gln	Asp	Ser	Asn	Lys	Leu	Ser	Asn	Asp	
545					550					555					560	
Asp	Met	Leu	Lys	Leu	Leu	Ala	Asp	Phe	Arg	Lys	Pro	Glu	Lys	Met	Ala	
				565					570					575		
Lys	Leu	Pro	Val	Ile	Leu	Gly	Asn	Leu	Asp	Ile	Thr	Ile	Asp	Asn	Val	
			580					585					590			
Ser	Ser	Asp	Phe	Pro	Asn	Tyr	Val	Asn	Ser	Ser	Tyr	Ile	Pro	Thr	Lys	
		595					600					605				
Gln	Phe	Glu	Thr	Cys	Ser	Lys	Thr	Pro	Ile	Thr	Phe	Glu	Val	Glu	Glu	
		610				615					620					
Phe	Val	Pro	Cys	Ile	Pro	Lys	His	Thr	Gln	Pro	Tyr	Thr	Ile	Tyr	Thr	
625					630					635					640	
Asn	His	Leu	Tyr	Val	Tyr	Pro	Lys	Tyr	Leu	Lys	Tyr	Asp	Ser	Gln	Lys	
				645					650					655		
Ser	Phe	Ala	Lys	Ala	Arg	Asn	Ile	Ala	Ile	Cys	Ile	Glu	Phe	Lys	Asp	
			660					665					670			
Ser	Asp	Glu	Glu	Asp	Ser	Gln	Pro	Leu	Lys	Cys	Ile	Tyr	Gly	Arg	Pro	
		675					680					685				
Gly	Gly	Pro	Val	Phe	Thr	Arg	Ser	Ala	Phe	Ala	Ala	Val	Leu	His	His	
	690					695					700					
His	Gln	Asn	Pro	Glu	Phe	Tyr	Asp	Glu	Ile	Lys	Ile	Glu	Leu	Pro	Thr	
705					710					715					720	
Gln	Leu	His	Glu	Lys	His	His	Leu	Leu	Leu	Thr	Phe	Phe	His	Val	Ser	
				725					730					735		
Cys	Asp	Asn	Ser	Ser	Lys	Gly	Ser	Thr	Lys	Lys	Arg	Asp	Val	Val	Glu	
			740					745					750			
Thr	Gln	Val	Gly	Tyr	Ser	Trp	Leu	Pro	Leu	Leu	Lys	Asp	Gly	Arg	Val	

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755	760	765
Val Thr Ser Glu Gln His Ile Pro Val Ser Ala Asn Leu Pro Ser Gly 770 775 780		
Tyr Leu Gly Tyr Gln Glu Leu Gly Met Gly Arg His Tyr Gly Pro Glu 785 790 795 800		
Ile Lys Trp Val Asp Gly Gly Lys Pro Leu Leu Lys Ile Ser Thr His 805 810 815		
Leu Val Ser Thr Val Tyr Thr Gln Asp Gln His Leu His Asn Phe Phe 820 825 830		
Gln Tyr Cys Gln Lys Thr Glu Ser Gly Ala Gln Ala Leu Gly Asn Glu 835 840 845		
Leu Val Lys Tyr Leu Lys Ser Leu His Ala Met Glu Gly His Val Met 850 855 860		
Ile Ala Phe Leu Pro Thr Ile Leu Asn Gln Leu Phe Arg Val Leu Thr 865 870 875 880		
Arg Ala Thr Gln Glu Glu Val Ala Val Asn Val Thr Arg Val Ile Ile 885 890 895		
His Val Val Ala Gln Cys His Glu Glu Gly Leu Glu Ser His Leu Arg 900 905 910		
Ser Tyr Val Lys Tyr Ala Tyr Lys Ala Glu Pro Tyr Val Ala Ser Glu 915 920 925		
Tyr Lys Thr Val His Glu Glu Leu Thr Lys Ser Met Thr Thr Ile Leu 930 935 940		
Lys Pro Ser Ala Asp Phe Leu Thr Ser Asn Lys Leu Leu Lys Tyr Ser 945 950 955 960		
Trp Phe Phe Phe Asp Val Leu Ile Lys Ser Met Ala Gln His Leu Ile 965 970 975		
Glu Asn Ser Lys Val Lys Leu Leu Arg Asn Gln Arg Phe Pro Ala Ser 980 985 990		
Tyr His His Ala Val Glu Thr Val Val Asn Met Leu Met Pro His Ile 995 1000 1005		
Thr Gln Lys Phe Arg Asp Asn Pro Glu Ala Ser Lys Asn Ala Asn 1010 1015 1020		
His Ser Leu Ala Val Phe Ile Lys Arg Cys Phe Thr Phe Met Asp 1025 1030 1035		
Arg Gly Phe Val Phe Lys Gln Ile Asn Asn Tyr Ile Ser Cys Phe 1040 1045 1050		
Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu Tyr Lys Phe Glu Phe		

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1055	1060	1065
Leu Arg Val Val Cys Asn His Glu His Tyr Ile Pro Leu Asn Leu 1070 1075 1080		
Pro Met Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr Gln Asp Leu 1085 1090 1095		
Gln Leu Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn His Phe 1100 1105 1110		
Leu Val Gly Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln Glu 1115 1120 1125		
Phe Arg Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu 1130 1135 1140		
Leu Ile Lys His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His 1145 1150 1155		
Gln Ala Arg Ile Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu 1160 1165 1170		
Ile Glu Asn Val Gln Arg Ile Asn Val Arg Asp Val Ser Pro Phe 1175 1180 1185		
Pro Val Asn Ala Gly Met Thr Val Lys Asp Glu Ser Leu Ala Leu 1190 1195 1200		
Pro Ala Val Asn Pro Leu Val Thr Pro Gln Lys Gly Ser Thr Leu 1205 1210 1215		
Asp Asn Ser Leu His Lys Asp Leu Leu Gly Ala Ile Ser Gly Ile 1220 1225 1230		
Ala Ser Pro Tyr Thr Thr Ser Thr Pro Asn Ile Asn Ser Val Arg 1235 1240 1245		
Asn Ala Asp Ser Arg Gly Ser Leu Ile Ser Thr Asp Ser Gly Asn 1250 1255 1260		
Ser Leu Pro Glu Arg Asn Ser Glu Lys Ser Asn Ser Leu Asp Lys 1265 1270 1275		
His Gln Gln Ser Ser Thr Leu Gly Asn Ser Val Val Arg Cys Asp 1280 1285 1290		
Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu Met Cys Phe Leu 1295 1300 1305		
Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe Thr Tyr Trp 1310 1315 1320		
Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr Ile Ser 1325 1330 1335		
Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr Ile 1340 1345 1350		

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Ala Arg Thr Gly Met Met His	Ala Arg Leu Gln Gln	Leu Gly Ser
1355	1360	1365
Leu Asp Asn Ser Leu Thr Phe	Asn His Ser Tyr Gly	His Ser Asp
1370	1375	1380
Ala Asp Val Leu His Gln Ser	Leu Leu Glu Ala Asn	Ile Ala Thr
1385	1390	1395
Glu Val Cys Leu Thr Ala Leu	Asp Thr Leu Ser Leu	Phe Thr Leu
1400	1405	1410
Ala Phe Lys Asn Gln Leu Leu	Ala Asp His Gly His	Asn Pro Leu
1415	1420	1425
Met Lys Lys Val Phe Asp Val	Tyr Leu Cys Phe Leu	Gln Lys His
1430	1435	1440
Gln Ser Glu Thr Ala Leu Lys	Asn Val Phe Thr Ala	Leu Arg Ser
1445	1450	1455
Leu Ile Tyr Lys Phe Pro Ser	Thr Phe Tyr Glu Gly	Arg Ala Asp
1460	1465	1470
Met Cys Ala Ala Leu Cys Tyr	Glu Ile Leu Lys Cys	Cys Asn Ser
1475	1480	1485
Lys Leu Ser Ser Ile Arg Thr	Glu Ala Ser Gln Leu	Leu Tyr Phe
1490	1495	1500
Leu Met Arg Asn Asn Phe Asp	Tyr Thr Gly Lys Lys	Ser Phe Val
1505	1510	1515
Arg Thr His Leu Gln Val Ile	Ile Ser Val Ser Gln	Leu Ile Ala
1520	1525	1530
Asp Val Val Gly Ile Gly Gly	Thr Arg Phe Gln Gln	Ser Leu Ser
1535	1540	1545
Ile Ile Asn Asn Cys Ala Asn	Ser Asp Arg Leu Ile	Lys His Thr
1550	1555	1560
Ser Phe Ser Ser Asp Val Lys	Asp Leu Thr Lys Arg	Ile Arg Thr
1565	1570	1575
Val Leu Met Ala Thr Ala Gln	Met Lys Glu His Glu	Asn Asp Pro
1580	1585	1590
Glu Met Leu Val Asp Leu Gln	Tyr Ser Leu Ala Lys	Ser Tyr Ala
1595	1600	1605
Ser Thr Pro Glu Leu Arg Lys	Thr Trp Leu Asp Ser	Met Ala Arg
1610	1615	1620
Ile His Val Lys Asn Gly Asp	Leu Ser Glu Ala Ala	Met Cys Tyr
1625	1630	1635

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Val 1640	His	Val	Thr	Ala	Leu	Val 1645	Ala	Glu	Tyr	Leu	Thr	Arg	Lys	Glu	1650
Ala 1655	Val	Gln	Trp	Glu	Pro	Pro 1660	Leu	Leu	Pro	His	Ser	His	Ser	Ala	1665
Cys 1670	Leu	Arg	Arg	Ser	Arg	Gly 1675	Gly	Val	Phe	Arg	Gln	Gly	Cys	Thr	1680
Ala 1685	Phe	Arg	Val	Ile	Thr	Pro 1690	Asn	Ile	Asp	Glu	Glu	Ala	Ser	Met	1695
Met 1700	Glu	Asp	Val	Gly	Met	Gln 1705	Asp	Val	His	Phe	Asn	Glu	Asp	Val	1710
Leu 1715	Met	Glu	Leu	Leu	Glu	Gln 1720	Cys	Ala	Asp	Gly	Leu	Trp	Lys	Ala	1725
Glu 1730	Arg	Tyr	Glu	Leu	Ile	Ala 1735	Asp	Ile	Tyr	Lys	Leu	Ile	Ile	Pro	1740
Ile 1745	Tyr	Glu	Lys	Arg	Arg	Asp 1750	Phe	Glu	Arg	Leu	Ala	His	Leu	Tyr	1755
Asp 1760	Thr	Leu	His	Arg	Ala	Tyr 1765	Ser	Lys	Val	Thr	Glu	Val	Met	His	1770
Ser 1775	Gly	Arg	Arg	Leu	Leu	Gly 1780	Thr	Tyr	Phe	Arg	Val	Ala	Phe	Phe	1785
Gly 1790	Gln	Ala	Ala	Gln	Tyr	Gln 1795	Phe	Thr	Asp	Ser	Glu	Thr	Asp	Val	1800
Glu 1805	Gly	Phe	Phe	Glu	Asp	Glu 1810	Asp	Gly	Lys	Glu	Tyr	Ile	Tyr	Lys	1815
Glu 1820	Pro	Lys	Leu	Thr	Pro	Leu 1825	Ser	Glu	Ile	Ser	Gln	Arg	Leu	Leu	1830
Lys 1835	Leu	Tyr	Ser	Asp	Lys	Phe 1840	Gly	Ser	Glu	Asn	Val	Lys	Met	Ile	1845
Gln 1850	Asp	Ser	Gly	Lys	Val	Asn 1855	Pro	Lys	Asp	Leu	Asp	Ser	Lys	Tyr	1860
Ala 1865	Tyr	Ile	Gln	Val	Thr	His 1870	Val	Ile	Pro	Phe	Phe	Asp	Glu	Lys	1875
Glu 1880	Leu	Gln	Glu	Arg	Lys	Thr 1885	Glu	Phe	Glu	Arg	Ser	His	Asn	Ile	1890
Arg 1895	Arg	Phe	Met	Phe	Glu	Met 1900	Pro	Phe	Thr	Gln	Thr	Gly	Lys	Arg	1905
Gln 1910	Gly	Gly	Val	Glu	Glu	Gln 1915	Cys	Lys	Arg	Arg	Thr	Ile	Leu	Thr	1920
Ala 1925	Ile	His	Cys	Phe	Pro	Tyr 1930	Val	Lys	Lys	Arg	Ile	Pro	Val	Met	1935

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1925	1930	1935
Tyr Gln His His Thr Asp	Leu Asn Pro Ile Glu	Val Ala Ile Asp
1940	1945	1950
Glu Met Ser Lys Lys Val	Ala Glu Leu Arg Gln	Leu Cys Ser Ser
1955	1960	1965
Ala Glu Val Asp Met Ile	Lys Leu Gln Leu Lys	Leu Gln Gly Ser
1970	1975	1980
Val Ser Val Gln Val Asn	Ala Gly Pro Leu Ala	Tyr Ala Arg Ala
1985	1990	1995
Phe Leu Asp Asp Thr Asn	Thr Lys Arg Tyr Pro	Asp Asn Lys Val
2000	2005	2010
Lys Leu Leu Lys Glu Val	Phe Arg Gln Phe Val	Glu Ala Cys Gly
2015	2020	2025
Gln Ala Leu Ala Val Asn	Glu Arg Leu Ile Lys	Glu Asp Gln Leu
2030	2035	2040
Glu Tyr Gln Glu Glu Met	Lys Ala Asn Tyr Arg	Glu Met Ala Lys
2045	2050	2055
Glu Leu Ser Glu Ile Met	His Glu Gln Ile Cys	Pro Leu Glu Glu
2060	2065	2070
Lys Thr Ser Val Leu Pro	Asn Ser Leu His Ile	Phe Asn Ala Ile
2075	2080	2085
Ser Gly Thr Pro Thr Ser	Thr Met Val His Gly	Met Thr Ser Ser
2090	2095	2100
Ser Ser Val Val		
2105		

Table 9 hMX1 nucleotide sequence (SEQ ID NO:9)

ttttgtttac agggaaacacg ggtctggctg agagaaaatg gccagcattt tccaagtact	60
gtaaattcct gtgcagaagg catcgtcgtc ttccggacag actatgggtca ggtattcact	120
tacaagcaga gcacaattac ccaccagaag gtgactgcta tgcacccac gaacgaggag	180
ggcgtggatg acatggcgtc cttgacagag ctccatggcg gctccatcat gtataactta	240
ttccagcgggt ataagagaaa tcaaatatgg acctacatcg gctccatcct ggcctctgtg	300
aaccctacc agcccatcgc cgggctgtac gagcctgcca ccatggagca gtacagccgg	360
cgccacctgg gcgagctgcc cccgcacatc ttccgcatcg ccaacgagtg ctaccgctgc	420
ctgtggaagc gccacgacaa ccagtgcac ctcacaaagg gtgaaagtgg ggcaggtaaa	480
accgaaagca ctaaattgat cctcaagttt ctgtcagtc tcaagtcaaca gtctttggaa	540

ttgtccttaa	aggagaagac	atcctgtgtt	gaacgagcta	ttcttgaaag	cagccccatc	600
atggaagctt	tcggcaatgc	gaagaccgtg	tacaacaaca	actctagtcg	ctttgggaag	660
tttgttcagc	tgaacatctg	tcagaaagga	aatattcagg	gcgggagaat	tgtagattgt	720
atcctctctt	cccagaaccg	agtagtaagg	caaaatcccc	gggaaaggaa	ttatcacata	780
ttttatgcac	tgctggcagg	gctggaacat	gaagaaagag	aagaatttta	tttatctacg	840
ccagaaaact	accactactt	gaatcagtct	ggatgtgtag	aagacaagac	aatcagtgac	900
caggaatcct	ttagggaagt	tattacggca	atggacgtga	tgcagttcag	caaggaggaa	960
gttcgggaag	tgtcgaggct	gcttgctggt	atactgcata	ttgggaacat	agaatttatc	1020
actgctggtg	gggcacaggt	ttccttcaaa	acagctttgg	gcagatctgc	ggagttactt	1080
gggctggacc	caacacagct	cacagatgct	ttgacccaga	gatcaatggt	cctcagggga	1140
gaagagatcc	tcacgcctct	caatgttcaa	caggcagtag	acagcaggga	ctccctggcc	1200
atggctctgt	atgcgtgctg	ctttgagtgg	gtaatcaaga	agatcaacag	caggatcaaa	1260
ggcaatgagg	acttcaagtc	tattggcata	ctcgacatct	ttggatttga	aaactttgag	1320
gttaatcact	ttgaacagtt	caatataaac	tatgcaaacg	agaaacttca	ggagtacttc	1380
aacaagcata	ttttttcttt	agaacaacta	gaatatagca	gggaaggatt	agtgtgggaa	1440
gatattgact	ggatagacaa	tggagaatgc	ctggacttga	ttgagaagaa	acttggcctc	1500
ctagccctta	tcaatgaaga	aagccatttt	cctcaagcca	cagacagcac	cttattggag	1560
aagctacaca	gtcagcatgc	gaataaccac	ttttatgtga	agcccagagt	tgcagttaac	1620
aatttttgag	tgaagcacta	tgctggagag	gtgcaatatg	atgtccgagg	tatcttggag	1680
aagaacagag	atacatttcg	agatgacctt	ctcaatttgc	taagagaaag	ccggtttgac	1740
tttatctacg	atctttttga	acatgtttca	agccgcaaca	accaggatac	cttgaaatgt	1800
ggaagcaaac	atcggcggcc	tacagtcagc	tcacagttca	aggttgactc	actgcattcc	1860
ttaatggcaa	cgctaagctc	ctctaatact	ttctttgttc	gctgtatcaa	gccaaacatg	1920
cagaagatgc	cagaccagtt	tgaccaggcg	gttggtgctga	accagctgcg	gtactcaggg	1980
atgctggaga	ctgtgagaat	ccgcaaagct	gggtatgcgg	tccgaagacc	ctttcaggac	2040
ttttacaaaa	ggtataaagt	gctgatgagg	aatctggctc	tgcctgagga	cgtccgaggg	2100
aagtgcacga	gcctgctgca	gctctatgat	gcctccaaca	gcgagtggca	gctggggaag	2160
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gtgagccacg	cggccatggt	gattcgggcc	catgtcttgg	gcttcttagc	acggaaacaa	2280
tacagaaagg	tcctttattg	tgtggtgata	atacagaaga	attacagagc	attccttctg	2340
aggaggagat	ttttgcacct	gaaaaaggca	gccatagttt	tccagaagca	actcagaggt	2400
cagattgctc	ggagagttta	cagacaattg	ctggcagaga	aaaggagca	agaagaaaag	2460
aagaaacagg	aagaggaaga	aaagaagaaa	cgggaggaag	aagaaagaga	aagagagaga	2520
gagcgaagag	aagccgagct	ccgcgcccag	caggaagaag	aaacgaggaa	gcagcaagaa	2580
ctcgaagcct	tgcagaagag	ccagaaggaa	gctgaactga	cccgtgaact	ggagaaacag	2640
aaggaaaata	agcaggtgga	agagatcctc	cgtctggaga	aagaaatcga	ggacctgcag	2700
cgcataagag	agcagcagga	gctgtcgctg	accgaggctt	ccctgcagaa	gctgcaggag	2760
cggcgggacc	aggagctccg	caggctggag	gaggaagcgt	gcagggcggc	ccaggagttc	2820

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ctcgagtc	ccc	tcaatttcga	cgagatcgac	gagtgtgtcc	ggaatatcga	gcggtccctg	2880
tcgggggg	gaa	gcgaattttc	cagcgagctg	gctgagagcg	catgcgagga	gaagcccaac	2940
ttcaacttca	gccagcccta	cccagaggag	gaggtcgatg	agggcttcga	agccgacgac		3000
gacgccttca	aggactcccc	caaccccagc	gagcacggcc	actcagacca	gcgaacaagt		3060
ggcatccgga	ccagcgatga	ctcttcagag	gaggacccat	acatgaacga	cacggtggtg		3120
cccaccagcc	ccagtgcgga	cagcacgggtg	ctgctcgccc	catcagtgc	ggactccggg		3180
agcctacaca	actcctccag	cggcgagtcc	acctactgca	tgccccagaa	cgctggggac		3240
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acttccggca	gcagcgtgac	cttctccaac	tcctacggca	gccagtggtc	ccccgactac		3360
cgctgctctg	tggggaccta	caacagctcg	ggtgcctacc	ggttcagctc	tgagggggcg		3420
cagtcctcgt	ttgaagatag	tgaagaggac	tttgattcca	ggtttgatac	agatgatgag		3480
ctttcatacc	ggcgtgactc	tgtgtacagc	tgtgtcactc	tgccgtat	ttt	ccacagcttt	3540
ctgtacatga	aaggtggcct	gatgaactct	tggaaacgcc	gctggtgcgt	cctcaaggat		3600
gaaaccttct	tgtggttccg	ctccaagcag	gaggccctca	agcaaggctg	gctccacaaa		3660
aaaggggggg	gctcctccac	gctgtccagg	agaaattgga	agaagcgctg	gtttgtcctc		3720
cgccagtcca	agctgatgta	ctttgaaaac	gacagcgagg	agaagctcaa	gggcaccgta		3780
gaagtgcgaa	cggcaaaaaga	gatcatagat	aacaccacca	aggagaatgg	gatcgacatc		3840
attatggccg	ataggacttt	ccacctgatt	gcagagtccc	cagaagatgc	cagccagtgg		3900
ttcagcgtgc	tgagtcaggt	ccacgcgtcc	acggaccagg	agatccagga	gatgcatgat		3960
gagcaggcaa	acccacagaa	tgctgtgggc	accttggtatg	tggggctgat	tgattctgtg		4020
tgtgcctctg	acagccctga	tagaccaac	tcgtttgtga	tcatcacggc	caaccgggtg		4080
ctgcactgca	acgccgacac	gccggaggag	atgcaccact	ggataaccct	gctgcagagg		4140
tccaaagggg	acaccagagt	ggagggccag	gaattcatcg	tgagaggatg	gttgcacaaa		4200
gaggtgaaga	acagtccaaa	gatgtcttca	ctgaaactga	agaaacgggtg	gtttgtactc		4260
accacaaatt	ccctggatta	ctacaagagt	tcagagaaga	acgcgctcaa	actggggacc		4320
ctggtcctca	acagcctctg	ctctgtcgtc	ccccagatg	agaagatatt	caaagagaca		4380
ggctactgga	acgtcaccgt	gtacggggcg	aagcactgtt	accggctcta	caccaagctg		4440
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atcgacaccc	ccaccagca	gctgattcaa	gatatacagg	agaactgcct	gaactcggat		4560
gtggtggaac	agatttataa	gcggaacccg	atccttcgat	acacccatca	ccccttgcac		4620
tccccgctcc	tgccccttcc	gtatggggac	ataaatctca	acttgctgaa	agacaaaggc		4680
tataccaccc	ttcaggatga	ggccatcaag	atattcaatt	ccctgcagca	actggagtcc		4740
atgtctgacc	caattccaat	aatccagggc	atcctacaga	cagggcatga	cctgcgacct		4800
ctgcggggacg	agctgtactg	ccagcttatc	aaacagacca	acaaagtgcc	ccaccccggc		4860
agtgtgggca	acctgtacag	ctggcagatc	ctgacatgcc	tgagctgcac	cttcctgccc		4920
agtcgagggga	ttctcaagta	tctcaagttc	catctgaaaa	ggatacggga	acagtttcca		4980
ggaaccgaga	tggaaaaata	cgctctcttc	acttacgaat	ctcttaagaa	aaccaa	aatgc	5040
cgagagtttg	tgcccttccc	agatgaaata	gaagctctga	tccacaggca	ggaaatgaca		5100

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tccacggtct attgccatgg cggcggctcc tgcaagatca ccatcaactc ccacaccacc	5160
gctggggagg tgggtggagaa gctgatccga ggccctggcca tggaggacag caggaacatg	5220
tttgctttgt ttgaatacaa cggccacgtc gacaaagcca ttgaaagtcg aaccgtcgta	5280
gctgatgtct tagccaagtt tgaaaagctg gctgccacat ccgaggttgg ggacctgcca	5340
tggaaattct acttcaaact ttactgcttc ctggacacag acaacgtgcc aaaagacagt	5400
gtggagtttg catttatgtt tgaacaggcc cacgaagcgg ttatccatgg ccaccatcca	5460
gccccggaag aaaacctcca ggttcttgct gccctgcgac tccagtatct gcagggggat	5520
tatactctgc acgtgccat cccacctctc gaagaggttt attccctgca gagactcaag	5580
gcccgcataca gccagtcaac caaaaccttc accccttggtg aacggctgga gaagaggcgg	5640
acgagcttcc tagaggggac cctgaggcgg agcttccgga caggatccgt ggtccggcag	5700
aaggctcgagg aggagcagat gctggacatg tggattaagg aagaagtctc ctctgctcga	5760
gccagtatca ttgacaagtg gaggaaatth cagggaatga accaggaaca ggccatggcc	5820
aagtacatgg ccttgatcaa ggagtggcct ggctatggct cgacgctgtt tgatgtggag	5880
tgcaaggaag gtggcttccc tcaggaactc tggttgggtg tcagcgcgga cgccgtctcc	5940
gtctacaagc gtggagaggg aagaccactg gaagtcttcc agtatgaaca catcctctct	6000
tttggggcac ccctggcgaa tacgtataag atcgtggctg atgagaggga gctgctcttt	6060
gaaaccagtg aggtagtgga tgtggccaag ctcatgaaag cctacatcag catgatcgtg	6120
aagaagcgct acagcacgac acgctccgcc agcagccagg gcagctccag g	6171

Table 10 hMX1 polypeptide sequence (SEQ ID NO:10)

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

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His 130	Ile	Phe	Ala	Ile	Ala	Asn 135	Glu	Cys	Tyr	Arg	Cys 140	Leu	Trp	Lys	Arg
His 145	Asp	Asn	Gln	Cys	Ile 150	Leu	Ile	Lys	Gly	Glu 155	Ser	Gly	Ala	Gly	Lys 160
Thr	Glu	Ser	Thr	Lys 165	Leu	Ile	Leu	Lys	Phe 170	Leu	Ser	Val	Ile	Ser	Gln 175
Gln	Ser	Leu	Glu 180	Leu	Ser	Leu	Lys	Glu 185	Lys	Thr	Ser	Cys	Val	Glu	Arg 190
Ala	Ile	Leu 195	Glu	Ser	Ser	Pro	Ile 200	Met	Glu	Ala	Phe	Gly 205	Asn	Ala	Lys
Thr 210	Val	Tyr	Asn	Asn	Asn	Ser 215	Ser	Arg	Phe	Gly	Lys 220	Phe	Val	Gln	Leu
Asn 225	Ile	Cys	Gln	Lys	Gly 230	Asn	Ile	Gln	Gly	Gly 235	Arg	Ile	Val	Asp	Cys 240
Ile	Leu	Ser	Ser	Gln 245	Asn	Arg	Val	Val	Arg 250	Gln	Asn	Pro	Gly	Glu	Arg 255
Asn	Tyr	His	Ile 260	Phe	Tyr	Ala	Leu 265	Leu	Ala	Gly	Leu	Glu	His 270	Glu	Glu
Arg	Glu	Glu	Phe 275	Tyr	Leu	Ser	Thr 280	Pro	Glu	Asn	Tyr	His 285	Tyr	Leu	Asn
Gln 290	Ser	Gly	Cys	Val	Glu	Asp 295	Lys	Thr	Ile	Ser	Asp 300	Gln	Glu	Ser	Phe
Arg 305	Glu	Val	Ile	Thr	Ala 310	Met	Asp	Val	Met	Gln 315	Phe	Ser	Lys	Glu	Glu 320
Val	Arg	Glu	Val	Ser 325	Arg	Leu	Leu	Ala	Gly 330	Ile	Leu	His	Leu	Gly	Asn 335
Ile	Glu	Phe	Ile 340	Thr	Ala	Gly	Gly	Ala 345	Gln	Val	Ser	Phe	Lys	Thr	Ala 350
Leu	Gly	Arg	Ser 355	Ala	Glu	Leu	Leu	Gly 360	Leu	Asp	Pro	Thr 365	Gln	Leu	Thr
Asp 370	Ala	Leu	Thr	Gln	Arg	Ser 375	Met	Phe	Leu	Arg	Gly 380	Glu	Glu	Ile	Leu
Thr 385	Pro	Leu	Asn	Val	Gln 390	Gln	Ala	Val	Asp	Ser 395	Arg	Asp	Ser	Leu	Ala 400
Met	Ala	Leu	Tyr	Ala 405	Cys	Cys	Phe	Glu	Trp 410	Val	Ile	Lys	Lys	Ile	Asn 415
Ser	Arg	Ile	Lys 420	Gly	Asn	Glu	Asp	Phe 425	Lys	Ser	Ile	Gly	Ile	Leu	Asp 430
Ile	Phe	Gly	Phe	Glu	Asn	Phe	Glu	Val	Asn	His	Phe	Glu	Gln	Phe	Asn

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435	440	445
Ile Asn Tyr Ala Asn Glu Lys Leu Gln Glu Tyr Phe Asn Lys His Ile 450 455 460		
Phe Ser Leu Glu Gln Leu Glu Tyr Ser Arg Glu Gly Leu Val Trp Glu 465 470 475 480		
Asp Ile Asp Trp Ile Asp Asn Gly Glu Cys Leu Asp Leu Ile Glu Lys 485 490 495		
Lys Leu Gly Leu Leu Ala Leu Ile Asn Glu Glu Ser His Phe Pro Gln 500 505 510		
Ala Thr Asp Ser Thr Leu Leu Glu Lys Leu His Ser Gln His Ala Asn 515 520 525		
Asn His Phe Tyr Val Lys Pro Arg Val Ala Val Asn Asn Phe Gly Val 530 535 540		
Lys His Tyr Ala Gly Glu Val Gln Tyr Asp Val Arg Gly Ile Leu Glu 545 550 555 560		
Lys Asn Arg Asp Thr Phe Arg Asp Asp Leu Leu Asn Leu Leu Arg Glu 565 570 575		
Ser Arg Phe Asp Phe Ile Tyr Asp Leu Phe Glu His Val Ser Ser Arg 580 585 590		
Asn Asn Gln Asp Thr Leu Lys Cys Gly Ser Lys His Arg Arg Pro Thr 595 600 605		
Val Ser Ser Gln Phe Lys Val Asp Ser Leu His Ser Leu Met Ala Thr 610 615 620		
Leu Ser Ser Ser Asn Pro Phe Phe Val Arg Cys Ile Lys Pro Asn Met 625 630 635 640		
Gln Lys Met Pro Asp Gln Phe Asp Gln Ala Val Val Leu Asn Gln Leu 645 650 655		
Arg Tyr Ser Gly Met Leu Glu Thr Val Arg Ile Arg Lys Ala Gly Tyr 660 665 670		
Ala Val Arg Arg Pro Phe Gln Asp Phe Tyr Lys Arg Tyr Lys Val Leu 675 680 685		
Met Arg Asn Leu Ala Leu Pro Glu Asp Val Arg Gly Lys Cys Thr Ser 690 695 700		
Leu Leu Gln Leu Tyr Asp Ala Ser Asn Ser Glu Trp Gln Leu Gly Lys 705 710 715 720		
Thr Lys Val Phe Leu Arg Glu Ser Leu Glu Gln Lys Leu Glu Lys Arg 725 730 735		
Arg Glu Glu Glu Val Ser His Ala Ala Met Val Ile Arg Ala His Val 740 745 750		

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Leu Gly Phe Leu Ala Arg Lys Gln Tyr Arg Lys Val Leu Tyr Cys Val	755	760	765
Val Ile Ile Gln Lys Asn Tyr Arg Ala Phe Leu Leu Arg Arg Arg Phe	770	775	780
Leu His Leu Lys Lys Ala Ala Ile Val Phe Gln Lys Gln Leu Arg Gly	785	790	795
Gln Ile Ala Arg Arg Val Tyr Arg Gln Leu Leu Ala Glu Lys Arg Glu	805	810	815
Gln Glu Glu Lys Lys Lys Gln Glu Glu Glu Glu Lys Lys Lys Arg Glu	820	825	830
Glu Glu Glu Arg Glu Arg Glu Arg Glu Arg Arg Glu Ala Glu Leu Arg	835	840	845
Ala Gln Gln Glu Glu Glu Thr Arg Lys Gln Gln Glu Leu Glu Ala Leu	850	855	860
Gln Lys Ser Gln Lys Glu Ala Glu Leu Thr Arg Glu Leu Glu Lys Gln	865	870	875
Lys Glu Asn Lys Gln Val Glu Glu Ile Leu Arg Leu Glu Lys Glu Ile	885	890	895
Glu Asp Leu Gln Arg Met Lys Glu Gln Gln Glu Leu Ser Leu Thr Glu	900	905	910
Ala Ser Leu Gln Lys Leu Gln Glu Arg Arg Asp Gln Glu Leu Arg Arg	915	920	925
Leu Glu Glu Glu Ala Cys Arg Ala Ala Gln Glu Phe Leu Glu Ser Leu	930	935	940
Asn Phe Asp Glu Ile Asp Glu Cys Val Arg Asn Ile Glu Arg Ser Leu	945	950	955
Ser Gly Gly Ser Glu Phe Ser Ser Glu Leu Ala Glu Ser Ala Cys Glu	965	970	975
Glu Lys Pro Asn Phe Asn Phe Ser Gln Pro Tyr Pro Glu Glu Glu Val	980	985	990
Asp Glu Gly Phe Glu Ala Asp Asp Asp Ala Phe Lys Asp Ser Pro Asn	995	1000	1005
Pro Ser Glu His Gly His Ser Asp Gln Arg Thr Ser Gly Ile Arg	1010	1015	1020
Thr Ser Asp Asp Ser Ser Glu Glu Asp Pro Tyr Met Asn Asp Thr	1025	1030	1035
Val Val Pro Thr Ser Pro Ser Ala Asp Ser Thr Val Leu Leu Ala	1040	1045	1050

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Pro 1055	Ser	Val	Gln	Asp	Ser	Gly 1060	Ser	Leu	His	Asn	Ser 1065	Ser	Ser	Gly
Glu 1070	Ser	Thr	Tyr	Cys	Met	Pro 1075	Gln	Asn	Ala	Gly	Asp 1080	Leu	Pro	Ser
Pro 1085	Asp	Gly	Asp	Tyr	Asp	Tyr 1090	Asp	Gln	Asp	Asp	Tyr 1095	Glu	Asp	Gly
Ala 1100	Ile	Thr	Ser	Gly	Ser	Ser 1105	Val	Thr	Phe	Ser	Asn 1110	Ser	Tyr	Gly
Ser 1115	Gln	Trp	Ser	Pro	Asp	Tyr 1120	Arg	Cys	Ser	Val	Gly 1125	Thr	Tyr	Asn
Ser 1130	Ser	Gly	Ala	Tyr	Arg	Phe 1135	Ser	Ser	Glu	Gly	Ala 1140	Gln	Ser	Ser
Phe 1145	Glu	Asp	Ser	Glu	Glu	Asp 1150	Phe	Asp	Ser	Arg	Phe 1155	Asp	Thr	Asp
Asp 1160	Glu	Leu	Ser	Tyr	Arg	Arg 1165	Asp	Ser	Val	Tyr	Ser 1170	Cys	Val	Thr
Leu 1175	Pro	Tyr	Phe	His	Ser	Phe 1180	Leu	Tyr	Met	Lys	Gly 1185	Gly	Leu	Met
Asn 1190	Ser	Trp	Lys	Arg	Arg	Trp 1195	Cys	Val	Leu	Lys	Asp 1200	Glu	Thr	Phe
Leu 1205	Trp	Phe	Arg	Ser	Lys	Gln 1210	Glu	Ala	Leu	Lys	Gln 1215	Gly	Trp	Leu
His 1220	Lys	Lys	Gly	Gly	Gly	Ser 1225	Ser	Thr	Leu	Ser	Arg 1230	Arg	Asn	Trp
Lys 1235	Lys	Arg	Trp	Phe	Val	Leu 1240	Arg	Gln	Ser	Lys	Leu 1245	Met	Tyr	Phe
Glu 1250	Asn	Asp	Ser	Glu	Glu	Lys 1255	Leu	Lys	Gly	Thr	Val 1260	Glu	Val	Arg
Thr 1265	Ala	Lys	Glu	Ile	Ile	Asp 1270	Asn	Thr	Thr	Lys	Glu 1275	Asn	Gly	Ile
Asp 1280	Ile	Ile	Met	Ala	Asp	Arg 1285	Thr	Phe	His	Leu	Ile 1290	Ala	Glu	Ser
Pro 1295	Glu	Asp	Ala	Ser	Gln	Trp 1300	Phe	Ser	Val	Leu	Ser 1305	Gln	Val	His
Ala 1310	Ser	Thr	Asp	Gln	Glu	Ile 1315	Gln	Glu	Met	His	Asp 1320	Glu	Gln	Ala
Asn 1325	Pro	Gln	Asn	Ala	Val	Gly 1330	Thr	Leu	Asp	Val	Gly 1335	Leu	Ile	Asp
Ser	Val	Cys	Ala	Ser	Asp	Ser	Pro	Asp	Arg	Pro	Asn	Ser	Phe	Val

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1340						1345						1350					
Ile	Ile	Thr	Ala	Asn	Arg	Val	Leu	His	Cys	Asn	Ala	Asp	Thr	Pro			
1355						1360					1365						
Glu	Glu	Met	His	His	Trp	Ile	Thr	Leu	Leu	Gln	Arg	Ser	Lys	Gly			
1370						1375					1380						
Asp	Thr	Arg	Val	Glu	Gly	Gln	Glu	Phe	Ile	Val	Arg	Gly	Trp	Leu			
1385						1390					1395						
His	Lys	Glu	Val	Lys	Asn	Ser	Pro	Lys	Met	Ser	Ser	Leu	Lys	Leu			
1400						1405					1410						
Lys	Lys	Arg	Trp	Phe	Val	Leu	Thr	His	Asn	Ser	Leu	Asp	Tyr	Tyr			
1415						1420					1425						
Lys	Ser	Ser	Glu	Lys	Asn	Ala	Leu	Lys	Leu	Gly	Thr	Leu	Val	Leu			
1430						1435					1440						
Asn	Ser	Leu	Cys	Ser	Val	Val	Pro	Pro	Asp	Glu	Lys	Ile	Phe	Lys			
1445						1450					1455						
Glu	Thr	Gly	Tyr	Trp	Asn	Val	Thr	Val	Tyr	Gly	Arg	Lys	His	Cys			
1460						1465					1470						
Tyr	Arg	Leu	Tyr	Thr	Lys	Leu	Leu	Asn	Glu	Ala	Thr	Arg	Trp	Ser			
1475						1480					1485						
Ser	Val	Ile	Gln	Asn	Val	Thr	Asp	Thr	Lys	Ala	Pro	Ile	Asp	Thr			
1490						1495					1500						
Pro	Thr	Gln	Gln	Leu	Ile	Gln	Asp	Ile	Lys	Glu	Asn	Cys	Leu	Asn			
1505						1510					1515						
Ser	Asp	Val	Val	Glu	Gln	Ile	Tyr	Lys	Arg	Asn	Pro	Ile	Leu	Arg			
1520						1525					1530						
Tyr	Thr	His	His	Pro	Leu	His	Ser	Pro	Leu	Leu	Pro	Leu	Pro	Tyr			
1535						1540					1545						
Gly	Asp	Ile	Asn	Leu	Asn	Leu	Leu	Lys	Asp	Lys	Gly	Tyr	Thr	Thr			
1550						1555					1560						
Leu	Gln	Asp	Glu	Ala	Ile	Lys	Ile	Phe	Asn	Ser	Leu	Gln	Gln	Leu			
1565						1570					1575						
Glu	Ser	Met	Ser	Asp	Pro	Ile	Pro	Ile	Ile	Gln	Gly	Ile	Leu	Gln			
1580						1585					1590						
Thr	Gly	His	Asp	Leu	Arg	Pro	Leu	Arg	Asp	Glu	Leu	Tyr	Cys	Gln			
1595						1600					1605						
Leu	Ile	Lys	Gln	Thr	Asn	Lys	Val	Pro	His	Pro	Gly	Ser	Val	Gly			
1610						1615					1620						
Asn	Leu	Tyr	Ser	Trp	Gln	Ile	Leu	Thr	Cys	Leu	Ser	Cys	Thr	Phe			
1625						1630					1635						

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Leu	Pro	Ser	Arg	Gly	Ile	Leu	Lys	Tyr	Leu	Lys	Phe	His	Leu	Lys
1640						1645					1650			
Arg	Ile	Arg	Glu	Gln	Phe	Pro	Gly	Thr	Glu	Met	Glu	Lys	Tyr	Ala
1655						1660					1665			
Leu	Phe	Thr	Tyr	Glu	Ser	Leu	Lys	Lys	Thr	Lys	Cys	Arg	Glu	Phe
1670						1675					1680			
Val	Pro	Ser	Arg	Asp	Glu	Ile	Glu	Ala	Leu	Ile	His	Arg	Gln	Glu
1685						1690					1695			
Met	Thr	Ser	Thr	Val	Tyr	Cys	His	Gly	Gly	Gly	Ser	Cys	Lys	Ile
1700						1705					1710			
Thr	Ile	Asn	Ser	His	Thr	Thr	Ala	Gly	Glu	Val	Val	Glu	Lys	Leu
1715						1720					1725			
Ile	Arg	Gly	Leu	Ala	Met	Glu	Asp	Ser	Arg	Asn	Met	Phe	Ala	Leu
1730						1735					1740			
Phe	Glu	Tyr	Asn	Gly	His	Val	Asp	Lys	Ala	Ile	Glu	Ser	Arg	Thr
1745						1750					1755			
Val	Val	Ala	Asp	Val	Leu	Ala	Lys	Phe	Glu	Lys	Leu	Ala	Ala	Thr
1760						1765					1770			
Ser	Glu	Val	Gly	Asp	Leu	Pro	Trp	Lys	Phe	Tyr	Phe	Lys	Leu	Tyr
1775						1780					1785			
Cys	Phe	Leu	Asp	Thr	Asp	Asn	Val	Pro	Lys	Asp	Ser	Val	Glu	Phe
1790						1795					1800			
Ala	Phe	Met	Phe	Glu	Gln	Ala	His	Glu	Ala	Val	Ile	His	Gly	His
1805						1810					1815			
His	Pro	Ala	Pro	Glu	Glu	Asn	Leu	Gln	Val	Leu	Ala	Ala	Leu	Arg
1820						1825					1830			
Leu	Gln	Tyr	Leu	Gln	Gly	Asp	Tyr	Thr	Leu	His	Ala	Ala	Ile	Pro
1835						1840					1845			
Pro	Leu	Glu	Glu	Val	Tyr	Ser	Leu	Gln	Arg	Leu	Lys	Ala	Arg	Ile
1850						1855					1860			
Ser	Gln	Ser	Thr	Lys	Thr	Phe	Thr	Pro	Cys	Glu	Arg	Leu	Glu	Lys
1865						1870					1875			
Arg	Arg	Thr	Ser	Phe	Leu	Glu	Gly	Thr	Leu	Arg	Arg	Ser	Phe	Arg
1880						1885					1890			
Thr	Gly	Ser	Val	Val	Arg	Gln	Lys	Val	Glu	Glu	Glu	Gln	Met	Leu
1895						1900					1905			
Asp	Met	Trp	Ile	Lys	Glu	Glu	Val	Ser	Ser	Ala	Arg	Ala	Ser	Ile
1910						1915					1920			

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Ile	Asp	Lys	Trp	Arg	Lys	Phe	Gln	Gly	Met	Asn	Gln	Glu	Gln	Ala
1925						1930					1935			
Met	Ala	Lys	Tyr	Met	Ala	Leu	Ile	Lys	Glu	Trp	Pro	Gly	Tyr	Gly
1940						1945					1950			
Ser	Thr	Leu	Phe	Asp	Val	Glu	Cys	Lys	Glu	Gly	Gly	Phe	Pro	Gln
1955						1960					1965			
Glu	Leu	Trp	Leu	Gly	Val	Ser	Ala	Asp	Ala	Val	Ser	Val	Tyr	Lys
1970						1975					1980			
Arg	Gly	Glu	Gly	Arg	Pro	Leu	Glu	Val	Phe	Gln	Tyr	Glu	His	Ile
1985						1990					1995			
Leu	Ser	Phe	Gly	Ala	Pro	Leu	Ala	Asn	Thr	Tyr	Lys	Ile	Val	Val
2000						2005					2010			
Asp	Glu	Arg	Glu	Leu	Leu	Phe	Glu	Thr	Ser	Glu	Val	Val	Asp	Val
2015						2020					2025			
Ala	Lys	Leu	Met	Lys	Ala	Tyr	Ile	Ser	Met	Ile	Val	Lys	Lys	Arg
2030						2035					2040			
Tyr	Ser	Thr	Thr	Arg	Ser	Ala	Ser	Ser	Gln	Gly	Ser	Ser	Arg	
2045						2050					2055			

Table 11 hMX2 nucleotide sequence (SEQ ID NO:11)

agctagtatc	ttttattgtc	agaacttctg	tgagccaaca	aacagttttg	catggttgta	60
cacaaaggga	caaggcaaat	ttcttttttc	gtgtgggtag	acttagttgg	cccaagtcct	120
taaaactttt	ccatataaaa	ataaaaagtc	caagaccaga	ttatttttct	tctggtcata	180
aatgctgatt	tatttacagg	tgccttggtc	agaccaccat	tataaacttg	ggataaaaata	240
tgtgtgtatt	aaagcctcag	catttaatgt	cagggtcctt	tgaagattca	ctcaagtgtt	300
aagacgtttc	tggaatgcag	cgtctctccc	ccatagtcaa	catggttatt	atatctgtaa	360
tctatccaga	atgatagaag	ctaaccttcc	aagtaacact	ttgtttttta	cttaaactctt	420
ttagacatga	aagactccaa	aatgacttca	ttcttggttct	aaaaccagca	ctggagccag	480
ctggttgaaga	gtggtttata	aatacagtta	tcttgtaggc	tgcttatctg	tttataatac	540
agcagacaca	gatggcagac	tttgctacat	gtaaaacaat	ggagtcaaca	cgtgtttttc	600
aaaatacagc	aaagacagga	aatccagga	tttggggttg	ttaataaaac	caccttataa	660
agtaacaatt	gagactatag	ctctgcatta	ttaaaatata	cagactgtgt	acaccattac	720
acatcctttt	tccctttgct	ttttaatgct	catgaaacca	tgattaaggt	gttgagttta	780
tgaacacatg	cacgaacagg	caagcacgta	cacttaaaag	atgaaacaaa	gaaaaaagtt	840
gattcatgtc	attccatgag	aaaggctgcc	cgcagcactc	cagctcaaac	acactgtccc	900
ctcgagctct	ccatccccct	tcccactccc	tcaccttccc	tcagattcgg	ggaaatcagg	960
ttgggagggt	agtgcacat	tgacagagaa	tgccccctt	ccacgctctg	ttaagtctcc	1020
cccagaaggg	ggaaaggcag	ttcccttcag	tagcacagtt	acggtcgatt	agtgttggtt	1080

ccacaagtta	aggcacttcc	ggctgctttg	gtggcagcgt	ggttcctccc	ctcctttttt	1140
aaggcatgtg	tcctctaaga	gtagtaaagc	tttggaaact	gtgcagactg	ttaaagttga	1200
cagcttaata	caggatcaat	gaaggcggca	ggcaaaagga	tcctcggaga	cacctccctc	1260
agaccagaag	cttccagaaa	gcctgggcag	ctctgtgttt	gttttggctg	ggcatggcac	1320
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tcaaagagca	gctccctctc	atcgaccacg	atcttatacg	tattcgccag	gggtgccccca	1560
aaagagagga	tgtgttcata	ctggaagact	tccagtggtc	ttccctctcc	acgcttgtag	1620
acggagacgg	cgtccgcgct	gacacccaac	cagagttcct	gaggggaagcc	accttccttg	1680
cactgggtggg	caagagtcaa	cagaagagtt	aagtcatgaa	gtgggttgga	acagaaagca	1740
tctaaaccat	aagacaggct	ttgagtgaag	tcctctgtgc	agaagattaa	atatattcga	1800
tgtgcatgca	tgcatggagg	ggcctgaaat	atgaaaaatg	gcacctctct	ggctatcttg	1860
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aagccaagtc	tactcttgta	ttaatatctc	cagttctgcc	tccaatcctc	tttgcggatg	2100
gttagtcttc	aaatacaaaa	tctaggatca	cagaggaaaa	ttctccaaat	cacgcatgct	2160
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tgagttcaag	cgattctcct	gtctcagcct	ctcgagtagc	tgggattaca	ggtgcatgcc	2580
accacgcccc	gctaattttt	tgcagagatg	gggtttcacc	gtgttagcca	ggatggtctc	2640
gatctcctga	cctcatgatc	cgcccgctt	ggcctcccaa	agcgctggga	ttacaggcat	2700
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ccaatcaaaa	acatcaccta	atgaaaagcc	accacggat	tctagaattt	ataatattta	2940
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aagattttta	gactttgtgg	atcacatggc	ctctgtcaca	actactcaac	tctgtacaaa	3120
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tgggttgatg	ccaatggcta	aattccatta	cgagatagac	attcttcctt	tcaaacagat	3360

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ggctgtaaag	aaaaaaca	gtaaaatgca	agtatatcca	aagtttctaa	tttgtatata	3420
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gccatggcaa	tagaccgtgg	atgtcatctt	ctgcctgtgg	atcagagctt	ctatttcac	4560
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gcagtacagc	tcgtcccgc	gaggtcgcag	gtcatgccct	gtctgtagga	tgccctggat	4860
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cgtgtcggcg	ttgcagtgca	gcacccggtt	ggccgtgatg	atcaciaaacg	agttgggtct	5580
atcagggtctg	tcagaggcac	acacagaatc	aatcagcccc	acatccaagg	tgcccacagc	5640

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attctgtggg	tttgccctgct	catcatgcat	ctcctggatc	tcctgggtccg	tggacgcgtg	5700
gacctgactc	agcacgctga	accactggct	ggcatcttct	ggggactctg	caatcaggtg	5760
gaaagtccta	tcggccataa	tgatgtcgat	cccattctcc	ttggtggtgt	tatctatgat	5820
ctcttttgcc	gttcgcactt	ctacgggtgcc	cttgagcttc	tcctcgctgt	cgttttcaaa	5880
gtacatcagc	ttggactggc	ggaggacaaa	ccagcgcttc	ttccaatttc	tcctggacag	5940
cgtggaggag	ccccccctt	ttttgtggag	ccagccttgc	ttgagggcct	cctgcttggg	6000
gcggaaccac	aagaaggttt	catccttgag	gacgcaccag	cggcgtttcc	aagagttcat	6060
caggccacct	ttcatgtaca	gaaagctgtg	gaaatacggc	agagtgcac	agctgtacac	6120
agagtcacgc	cggtatgaaa	gctcatcatc	tgtatcaaac	ctggaatcaa	agtcctcttc	6180
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gtaggtcccc	acagagcagc	ggtagtcggg	ggaccactgg	ctgccgtagg	agttggagaa	6300
ggtcacgctg	ctgccggaag	tgatggcacc	gtcctcatag	tcatcctggg	cgtagtcgta	6360
gtcgccgtct	ggggagggca	agtccccagc	gttctggggc	atgcagtagg	tggactcgcc	6420
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gagctcggtc	tctcttcgct	ctctctctct	ttctctttct	tcttctctcc	gtttcttctt	7140
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cagggtgcaaa	aatctcctcc	tcagaaggaa	tgctctgtaa	ttcttctgta	ttatcaccac	7320
acaataaagg	acctttctgt	attgtttccg	tgctaagaag	ccaagacat	gggcccgaat	7380
caccatggcc	gcgtggctca	cttcctcttc	cctccgcttc	tccagtttct	gttccaagga	7440
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ctgcagcagg	ctcgtgcact	tccctcggac	gtcctcaggc	agagccagat	tcctcatcag	7560
cactttatac	cttttgtaaa	agtcctgaaa	gggtcttcgg	accgcatacc	cagctttgcg	7620
gattctcaca	gtctccagca	tccctgagta	ccgcagctgg	ttcagcacia	ccgcctggtc	7680
aaactgggtc	ggcatcttct	gcatgtttgg	cttgatacag	cgaacaaaga	aaggattaga	7740
ggagcttagc	gttgccatta	aggaatgcag	tgagtcaacc	ttgaactgtg	agctgactgt	7800
aggccgccga	tgtttgcttc	cacatttcaa	ggatatcctg	ttgttgccgc	ttgaaacatg	7860
ttcaaaaaga	tcgtagataa	agtcaaaccg	gctttctctt	agcaaattga	gaaggtcac	7920

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tcgaaatgta tctctgttct tctccaagat acctcggaca tcatattgca cctctccagc	7980
atagtgttcc actccaaaat tgttaactgc aactctgggc ttcacataaa agtgggttatt	8040
cgcattgctga ctgtgtagct tctccaataa ggtgctgtct gtggcttgag gaaaatggct	8100
ttcttcattg ataagggcta ggaggccaag tttcttctca atcaagtcca ggcattctcc	8160
attgtctatc cagtcaatat cttcccacac taatccttcc ctgctatatt ctagttgttc	8220
taaagaaaaa atatgcttgt tgaagtactc ctgaagtttc tcgtttgcat agtttatatt	8280
gaactgttca aagtgattaa cctcaaagtt ttcaaatacca aagatgtcga ggatgccaat	8340
agacttgaag tcctcattgc ctttgatcct gctgttgatc ttcttgatta cccactcaaa	8400
gcagcacgca tacagagcca tggccaggga gtccctgctg tctactgcct gttgaacatt	8460
gagaggcgtg aggatctctt ctcccctgag gaacattgat ctctgggtca aagcatctgt	8520
gagctgtgtt ggggccagcc caagtaactc cgcagatctg cccaaagctg ttttgaagga	8580
aacctgtgcc ccaccagcag tgataaatc tatgttccca agatgcagta taccagcaag	8640
cagcctcgac acttcccga cttcctcctt gctgaactgc atcacgtcca ttgccgtaat	8700
aacttccta aaggattcct ggtcactgat tgtcttgtct tctacacatc cagactgatt	8760
caagtagtgg tagttttctg gcgtagataa ataaaattct tctctttctt catgttccag	8820
ccctgccagc agtgcataaa atatgtgata attcctttcc ccgggatttt gccttactac	8880
tcggttctgg gaagagagga tacaatctac aattctcccg ccctgaatat ttctttctg	8940
acagatgttc agctgaacaa acttcccaaa gcgactagag ttgttggtgt acacggctctt	9000
cgcattgccg aaagcttcca tgatggggct gctttcaaga atagctcgtt caacacagga	9060
tgtcttctcc tttaaggaca attccaaaga ctgttgactg atgactgaca gaaacttgag	9120
gatcaattta gtgctttcgg ttttacctgc cccactttca cccttgatga ggatgcactg	9180
gttgctcgtg cgcttccaca ggcagcggta gcactcgttg gcgatggcga agatgtgcgg	9240
gggcagctcg cccaggtggc gccggctgta ctgctccatg gtggcaggct cgtacagccc	9300
ggcgatgggc tggtaggggt tcacagaggc caggatggag ccgatgtagg tccatatttg	9360
atttctctta taccgctgga ataagttata catgatggag ccgccatgga gctctgtcaa	9420
ggacgccatg tcatccacgc cctcctcgtt cgtgggggtgc atagcagtca ccttctggtg	9480
ggtaattgtg ctctgcttgt aagtgaatac ctgaccatag tctgtccgga agacgacgat	9540
gccttctgca caggaattta cagtacttgg aaaatgctgg ccattttctc tcagccagac	9600
ccgtgttccc tgtaaacaaa a	9621

Table 12 hMX2 polypeptide sequence (SEQ ID NO:12)

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

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Met	Ala	Ser	Leu	Thr	Glu	Leu	His	Gly	Gly	Ser	Ile	Met	Tyr	Asn	Leu	65	70	75	80
Phe	Gln	Arg	Tyr	Lys	Arg	Asn	Gln	Ile	Trp	Thr	Tyr	Ile	Gly	Ser	Ile	85	90	95	
Leu	Ala	Ser	Val	Asn	Pro	Tyr	Gln	Pro	Ile	Ala	Gly	Leu	Tyr	Glu	Pro	100	105	110	
Ala	Thr	Met	Glu	Gln	Tyr	Ser	Arg	Arg	His	Leu	Gly	Glu	Leu	Pro	Pro	115	120	125	
His	Ile	Phe	Ala	Ile	Ala	Asn	Glu	Cys	Tyr	Arg	Cys	Leu	Trp	Lys	Arg	130	135	140	
His	Asp	Asn	Gln	Cys	Ile	Leu	Ile	Lys	Gly	Glu	Ser	Gly	Ala	Gly	Lys	145	150	155	160
Thr	Glu	Ser	Thr	Lys	Leu	Ile	Leu	Lys	Phe	Leu	Ser	Val	Ile	Ser	Gln	165	170	175	
Gln	Ser	Leu	Glu	Leu	Ser	Leu	Lys	Glu	Lys	Thr	Ser	Cys	Val	Glu	Arg	180	185	190	
Ala	Ile	Leu	Glu	Ser	Ser	Pro	Ile	Met	Glu	Ala	Phe	Gly	Asn	Ala	Lys	195	200	205	
Thr	Val	Tyr	Asn	Asn	Asn	Ser	Ser	Arg	Phe	Gly	Lys	Phe	Val	Gln	Leu	210	215	220	
Asn	Ile	Cys	Gln	Lys	Gly	Asn	Ile	Gln	Gly	Gly	Arg	Ile	Val	Asp	Cys	225	230	235	240
Ile	Leu	Ser	Ser	Gln	Asn	Arg	Val	Val	Arg	Gln	Asn	Pro	Gly	Glu	Arg	245	250	255	
Asn	Tyr	His	Ile	Phe	Tyr	Ala	Leu	Leu	Ala	Gly	Leu	Glu	His	Glu	Glu	260	265	270	
Arg	Glu	Glu	Phe	Tyr	Leu	Ser	Thr	Pro	Glu	Asn	Tyr	His	Tyr	Leu	Asn	275	280	285	
Gln	Ser	Gly	Cys	Val	Glu	Asp	Lys	Thr	Ile	Ser	Asp	Gln	Glu	Ser	Phe	290	295	300	
Arg	Glu	Val	Ile	Thr	Ala	Met	Asp	Val	Met	Gln	Phe	Ser	Lys	Glu	Glu	305	310	315	320
Val	Arg	Glu	Val	Ser	Arg	Leu	Leu	Ala	Gly	Ile	Leu	His	Leu	Gly	Asn	325	330	335	
Ile	Glu	Phe	Ile	Thr	Ala	Gly	Gly	Ala	Gln	Val	Ser	Phe	Lys	Thr	Ala	340	345	350	
Leu	Gly	Arg	Ser	Ala	Glu	Leu	Leu	Gly	Leu	Asp	Pro	Thr	Gln	Leu	Thr	355	360	365	

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Asp	Ala	Leu	Thr	Gln	Arg	Ser	Met	Phe	Leu	Arg	Gly	Glu	Glu	Ile	Leu	
370						375					380					
Thr	Pro	Leu	Asn	Val	Gln	Gln	Ala	Val	Asp	Ser	Arg	Asp	Ser	Leu	Ala	
385					390				395						400	
Met	Ala	Leu	Tyr	Ala	Cys	Cys	Phe	Glu	Trp	Val	Ile	Lys	Lys	Ile	Asn	
				405					410					415		
Ser	Arg	Ile	Lys	Gly	Asn	Glu	Asp	Phe	Lys	Ser	Ile	Gly	Ile	Leu	Asp	
			420					425					430			
Ile	Phe	Gly	Phe	Glu	Asn	Phe	Glu	Val	Asn	His	Phe	Glu	Gln	Phe	Asn	
		435					440					445				
Ile	Asn	Tyr	Ala	Asn	Glu	Lys	Leu	Gln	Glu	Tyr	Phe	Asn	Lys	His	Ile	
	450					455					460					
Phe	Ser	Leu	Glu	Gln	Leu	Glu	Tyr	Ser	Arg	Glu	Gly	Leu	Val	Trp	Glu	
465					470					475					480	
Asp	Ile	Asp	Trp	Ile	Asp	Asn	Gly	Glu	Cys	Leu	Asp	Leu	Ile	Glu	Lys	
				485					490					495		
Lys	Leu	Gly	Leu	Leu	Ala	Leu	Ile	Asn	Glu	Glu	Ser	His	Phe	Pro	Gln	
			500					505					510			
Ala	Thr	Asp	Ser	Thr	Leu	Leu	Glu	Lys	Leu	His	Ser	Gln	His	Ala	Asn	
		515					520					525				
Asn	His	Phe	Tyr	Val	Lys	Pro	Arg	Val	Ala	Val	Asn	Asn	Phe	Gly	Val	
	530					535					540					
Lys	His	Tyr	Ala	Gly	Glu	Val	Gln	Tyr	Asp	Val	Arg	Gly	Ile	Leu	Glu	
545					550					555					560	
Lys	Asn	Arg	Asp	Thr	Phe	Arg	Asp	Asp	Leu	Leu	Asn	Leu	Leu	Arg	Glu	
				565					570					575		
Ser	Arg	Phe	Asp	Phe	Ile	Tyr	Asp	Leu	Phe	Glu	His	Val	Ser	Ser	Arg	
			580					585					590			
Asn	Asn	Gln	Asp	Thr	Leu	Lys	Cys	Gly	Ser	Lys	His	Arg	Arg	Pro	Thr	
		595					600					605				
Val	Ser	Ser	Gln	Phe	Lys	Val	Asp	Ser	Leu	His	Ser	Leu	Met	Ala	Thr	
	610					615					620					
Leu	Ser	Ser	Ser	Asn	Pro	Phe	Phe	Val	Arg	Cys	Ile	Lys	Pro	Asn	Met	
625					630					635					640	
Gln	Lys	Met	Pro	Asp	Gln	Phe	Asp	Gln	Ala	Val	Val	Leu	Asn	Gln	Leu	
				645					650					655		
Arg	Tyr	Ser	Gly	Met	Leu	Glu	Thr	Val	Arg	Ile	Arg	Lys	Ala	Gly	Tyr	
			660					665					670			
Ala	Val	Arg	Arg	Pro	Phe	Gln	Asp	Phe	Tyr	Lys	Arg	Tyr	Lys	Val	Leu	

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675					680					685					
Met	Arg	Asn	Leu	Ala	Leu	Pro	Glu	Asp	Val	Arg	Gly	Lys	Cys	Thr	Ser
	690					695					700				
Leu	Leu	Gln	Leu	Tyr	Asp	Ala	Ser	Asn	Ser	Glu	Trp	Gln	Leu	Gly	Lys
705					710					715					720
Thr	Lys	Val	Phe	Leu	Arg	Glu	Ser	Leu	Glu	Gln	Lys	Leu	Glu	Lys	Arg
				725					730					735	
Arg	Glu	Glu	Glu	Val	Ser	His	Ala	Ala	Met	Val	Ile	Arg	Ala	His	Val
			740					745					750		
Leu	Gly	Phe	Leu	Ala	Arg	Lys	Gln	Tyr	Arg	Lys	Val	Leu	Tyr	Cys	Val
		755					760					765			
Val	Ile	Ile	Gln	Lys	Asn	Tyr	Arg	Ala	Phe	Leu	Leu	Arg	Arg	Arg	Phe
	770					775					780				
Leu	His	Leu	Lys	Lys	Ala	Ala	Ile	Val	Phe	Gln	Lys	Gln	Leu	Arg	Gly
785					790					795					800
Gln	Ile	Ala	Arg	Arg	Val	Tyr	Arg	Gln	Leu	Leu	Ala	Glu	Lys	Arg	Glu
				805					810					815	
Gln	Glu	Glu	Lys	Lys	Lys	Gln	Glu	Glu	Glu	Glu	Lys	Lys	Lys	Arg	Glu
			820					825					830		
Glu	Glu	Glu	Arg	Glu	Arg	Glu	Arg	Glu	Arg	Arg	Glu	Ala	Glu	Leu	Arg
			835				840					845			
Ala	Gln	Gln	Glu	Glu	Glu	Thr	Arg	Lys	Gln	Gln	Glu	Leu	Glu	Ala	Leu
	850					855					860				
Gln	Lys	Ser	Gln	Lys	Glu	Ala	Glu	Leu	Thr	Arg	Glu	Leu	Glu	Lys	Gln
865					870					875					880
Lys	Glu	Asn	Lys	Gln	Val	Glu	Glu	Ile	Leu	Arg	Leu	Glu	Lys	Glu	Ile
				885					890					895	
Glu	Asp	Leu	Gln	Arg	Met	Lys	Glu	Gln	Gln	Glu	Leu	Ser	Leu	Thr	Glu
			900					905					910		
Ala	Ser	Leu	Gln	Lys	Leu	Gln	Glu	Arg	Arg	Asp	Gln	Glu	Leu	Arg	Arg
		915					920					925			
Leu	Glu	Glu	Glu	Ala	Cys	Arg	Ala	Ala	Gln	Glu	Phe	Leu	Glu	Ser	Leu
	930					935					940				
Asn	Phe	Asp	Glu	Ile	Asp	Glu	Cys	Val	Arg	Asn	Ile	Glu	Arg	Ser	Leu
945					950					955					960
Ser	Gly	Gly	Ser	Glu	Phe	Ser	Ser	Glu	Leu	Ala	Glu	Ser	Ala	Cys	Glu
				965					970					975	
Glu	Lys	Pro	Asn	Phe	Asn	Phe	Ser	Gln	Pro	Tyr	Pro	Glu	Glu	Glu	Val
			980					985					990		

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Asp	Glu	Gly	Phe	Glu	Ala	Asp	Asp	Asp	Ala	Phe	Lys	Asp	Ser	Pro	Asn
		995						1000							1005
Pro	Ser	Glu	His	Gly	His	Ser	Asp	Gln	Arg	Thr	Ser	Gly	Ile	Arg	
	1010					1015					1020				
Thr	Ser	Asp	Asp	Ser	Ser	Glu	Glu	Asp	Pro	Tyr	Met	Asn	Asp	Thr	
	1025					1030					1035				
Val	Val	Pro	Thr	Ser	Pro	Ser	Ala	Asp	Ser	Thr	Val	Leu	Leu	Ala	
	1040					1045					1050				
Pro	Ser	Val	Gln	Asp	Ser	Gly	Ser	Leu	His	Asn	Ser	Ser	Ser	Gly	
	1055					1060					1065				
Glu	Ser	Thr	Tyr	Cys	Met	Pro	Gln	Asn	Ala	Gly	Asp	Leu	Pro	Ser	
	1070					1075					1080				
Pro	Asp	Gly	Asp	Tyr	Asp	Tyr	Asp	Gln	Asp	Asp	Tyr	Glu	Asp	Gly	
	1085					1090					1095				
Ala	Ile	Thr	Ser	Gly	Ser	Ser	Val	Thr	Phe	Ser	Asn	Ser	Tyr	Gly	
	1100					1105					1110				
Ser	Gln	Trp	Ser	Pro	Asp	Tyr	Arg	Cys	Ser	Val	Gly	Thr	Tyr	Asn	
	1115					1120					1125				
Ser	Ser	Gly	Ala	Tyr	Arg	Phe	Ser	Ser	Glu	Gly	Ala	Gln	Ser	Ser	
	1130					1135					1140				
Phe	Glu	Asp	Ser	Glu	Glu	Asp	Phe	Asp	Ser	Arg	Phe	Asp	Thr	Asp	
	1145					1150					1155				
Asp	Glu	Leu	Ser	Tyr	Arg	Arg	Asp	Ser	Val	Tyr	Ser	Cys	Val	Thr	
	1160					1165					1170				
Leu	Pro	Tyr	Phe	His	Ser	Phe	Leu	Tyr	Met	Lys	Gly	Gly	Leu	Met	
	1175					1180					1185				
Asn	Ser	Trp	Lys	Arg	Arg	Trp	Cys	Val	Leu	Lys	Asp	Glu	Thr	Phe	
	1190					1195					1200				
Leu	Trp	Phe	Arg	Ser	Lys	Gln	Glu	Ala	Leu	Lys	Gln	Gly	Trp	Leu	
	1205					1210					1215				
His	Lys	Lys	Gly	Gly	Gly	Ser	Ser	Thr	Leu	Ser	Arg	Arg	Asn	Trp	
	1220					1225					1230				
Lys	Lys	Arg	Trp	Phe	Val	Leu	Arg	Gln	Ser	Lys	Leu	Met	Tyr	Phe	
	1235					1240					1245				
Glu	Asn	Asp	Ser	Glu	Glu	Lys	Leu	Lys	Gly	Thr	Val	Glu	Val	Arg	
	1250					1255					1260				
Thr	Ala	Lys	Glu	Ile	Ile	Asp	Asn	Thr	Thr	Lys	Glu	Asn	Gly	Ile	
	1265					1270					1275				

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Asp	Ile	Ile	Met	Ala	Asp	Arg	Thr	Phe	His	Leu	Ile	Ala	Glu	Ser
1280						1285					1290			
Pro	Glu	Asp	Ala	Ser	Gln	Trp	Phe	Ser	Val	Leu	Ser	Gln	Val	His
1295						1300					1305			
Ala	Ser	Thr	Asp	Gln	Glu	Ile	Gln	Glu	Met	His	Asp	Glu	Gln	Ala
1310						1315					1320			
Asn	Pro	Gln	Asn	Ala	Val	Gly	Thr	Leu	Asp	Val	Gly	Leu	Ile	Asp
1325						1330					1335			
Ser	Val	Cys	Ala	Ser	Asp	Ser	Pro	Asp	Arg	Pro	Asn	Ser	Phe	Val
1340						1345					1350			
Ile	Ile	Thr	Ala	Asn	Arg	Val	Leu	His	Cys	Asn	Ala	Asp	Thr	Pro
1355						1360					1365			
Glu	Glu	Met	His	His	Trp	Ile	Thr	Leu	Leu	Gln	Arg	Ser	Lys	Gly
1370						1375					1380			
Asp	Thr	Arg	Val	Glu	Gly	Gln	Glu	Phe	Ile	Val	Arg	Gly	Trp	Leu
1385						1390					1395			
His	Lys	Glu	Val	Lys	Asn	Ser	Pro	Lys	Met	Ser	Ser	Leu	Lys	Leu
1400						1405					1410			
Lys	Lys	Arg	Trp	Phe	Val	Leu	Thr	His	Asn	Ser	Leu	Asp	Tyr	Tyr
1415						1420					1425			
Lys	Ser	Ser	Glu	Lys	Asn	Ala	Leu	Lys	Leu	Gly	Thr	Leu	Val	Leu
1430						1435					1440			
Asn	Ser	Leu	Cys	Ser	Val	Val	Pro	Pro	Asp	Glu	Lys	Ile	Phe	Lys
1445						1450					1455			
Glu	Thr	Gly	Tyr	Trp	Asn	Val	Thr	Val	Tyr	Gly	Arg	Lys	His	Cys
1460						1465					1470			
Tyr	Arg	Leu	Tyr	Thr	Lys	Leu	Leu	Asn	Glu	Ala	Thr	Arg	Trp	Ser
1475						1480					1485			
Ser	Val	Ile	Gln	Asn	Val	Thr	Asp	Thr	Lys	Ala	Pro	Ile	Asp	Thr
1490						1495					1500			
Pro	Thr	Gln	Gln	Leu	Ile	Gln	Asp	Ile	Lys	Glu	Asn	Cys	Leu	Asn
1505						1510					1515			
Ser	Asp	Val	Val	Glu	Gln	Ile	Tyr	Lys	Arg	Asn	Pro	Ile	Leu	Arg
1520						1525					1530			
Tyr	Thr	His	His	Pro	Leu	His	Ser	Pro	Leu	Leu	Pro	Leu	Pro	Tyr
1535						1540					1545			
Gly	Asp	Ile	Asn	Leu	Asn	Leu	Leu	Lys	Asp	Lys	Gly	Tyr	Thr	Thr
1550						1555					1560			
Leu	Gln	Asp	Glu	Ala	Ile	Lys	Ile	Phe	Asn	Ser	Leu	Gln	Gln	Leu

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1565						1570					1575			
Glu Ser Met Ser Asp Pro Ile	Pro Ile Ile Gln Gly	Ile Leu Gln												
1580						1585					1590			
Thr Gly His Asp Leu Arg Pro	Leu Arg Asp Glu Leu	Tyr Cys Gln												
1595						1600					1605			
Leu Ile Lys Gln Thr Asn Lys	Val Pro His Pro Gly	Ser Val Gly												
1610						1615					1620			
Asn Leu Tyr Ser Trp Gln Ile	Leu Thr Cys Leu Ser	Cys Thr Phe												
1625						1630					1635			
Leu Pro Ser Arg Gly Ile Leu	Lys Tyr Leu Lys Phe	His Leu Lys												
1640						1645					1650			
Arg Ile Arg Glu Gln Phe Pro	Gly Thr Glu Met Glu	Lys Tyr Ala												
1655						1660					1665			
Leu Phe Thr Tyr Glu Ser Leu	Lys Lys Thr Lys Cys	Arg Glu Phe												
1670						1675					1680			
Val Pro Ser Arg Asp Glu Ile	Glu Ala Leu Ile His	Arg Gln Glu												
1685						1690					1695			
Met Thr Ser Thr Val Tyr Cys	His Gly Gly Gly Ser	Cys Lys Ile												
1700						1705					1710			
Thr Ile Asn Ser His Thr Thr	Ala Gly Glu Val Val	Glu Lys Leu												
1715						1720					1725			
Ile Arg Gly Leu Ala Met Glu	Asp Ser Arg Asn Met	Phe Ala Leu												
1730						1735					1740			
Phe Glu Tyr Asn Gly His Val	Asp Lys Ala Ile Glu	Ser Arg Thr												
1745						1750					1755			
Val Val Ala Asp Val Leu Ala	Lys Phe Glu Lys Leu	Ala Ala Thr												
1760						1765					1770			
Ser Glu Val Gly Asp Leu Pro	Trp Lys Phe Tyr Phe	Lys Leu Tyr												
1775						1780					1785			
Cys Phe Leu Asp Thr Asp Asn	Val Pro Lys Asp Ser	Val Glu Phe												
1790						1795					1800			
Ala Phe Met Phe Glu Gln Ala	His Glu Ala Val Ile	His Gly His												
1805						1810					1815			
His Pro Ala Pro Glu Glu Asn	Leu Gln Val Leu Ala	Ala Leu Arg												
1820						1825					1830			
Leu Gln Tyr Leu Gln Gly Asp	Tyr Thr Leu His Ala	Ala Ile Pro												
1835						1840					1845			
Pro Leu Glu Glu Val Tyr Ser	Leu Gln Arg Leu Lys	Ala Arg Ile												
1850						1855					1860			

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Ser	Gln	Ser	Thr	Lys	Thr	Phe	Thr	Pro	Cys	Glu	Arg	Leu	Glu	Lys
1865						1870					1875			
Arg	Arg	Thr	Ser	Phe	Leu	Glu	Gly	Thr	Leu	Arg	Arg	Ser	Phe	Arg
1880						1885					1890			
Thr	Gly	Ser	Val	Val	Arg	Gln	Lys	Val	Glu	Glu	Glu	Gln	Met	Leu
1895						1900					1905			
Asp	Met	Trp	Ile	Lys	Glu	Glu	Val	Ser	Ser	Ala	Arg	Ala	Ser	Ile
1910						1915					1920			
Ile	Asp	Lys	Trp	Arg	Lys	Phe	Gln	Gly	Met	Asn	Gln	Glu	Gln	Ala
1925						1930					1935			
Met	Ala	Lys	Tyr	Met	Ala	Leu	Ile	Lys	Glu	Trp	Pro	Gly	Tyr	Gly
1940						1945					1950			
Ser	Thr	Leu	Phe	Asp	Val	Glu	Val	Arg	Thr	Gly	Cys	His	Val	Leu
1955						1960					1965			
Gly	Trp	Ala	Gly	Cys	Trp	His	Leu	Arg	Thr	Trp	Ile	Thr	Ala	Lys
1970						1975					1980			
Phe	Met	Trp	Arg	Glu	Asp	Lys	Met	Glu	His	Phe	Ala	Leu	Ser	Thr
1985						1990					1995			
Ser	Phe	Phe	Arg	Ala	Pro	Lys	Ile	Val	Pro	Leu	Thr	Pro	Pro	Phe
2000						2005					2010			
Ser	Ser	Gln	Phe	Leu	Phe	Ser	Cys	Val	Val	Asn	Ala	Ser	Val	Ile
2015						2020					2025			
Leu	Gly	Met	Asn	Ala	Lys	Leu	Arg	Cys	His	Leu	Phe	Phe	Tyr	Pro
2030						2035					2040			
Ser	Leu	Gly	Lys	Leu										
2045														

Table 13 hMP nucleotide sequence (SEQ ID NO:13)

ccaacttttg	cagctccacc	caggatgtgg	cctcgctcca	ccccagctgt	gcgcctctct	60
ccacccttag	gcgaaggcac	tagaatttcc	caaattaaga	acgaagagga	agtttggacc	120
ttttcggcca	ccgctcgctt	caatatggct	gccccaggg	agagacgagg	ctaccatgaa	180
ggagccgagc	gcagaccctg	agtccgtcac	ccatggatcg	cagcgcggag	ttcaggaaat	240
ggaaggcgca	atgtttgagc	aaagcggacc	tcagccggaa	gggcagtgtt	gacgaggatg	300
tggtagagct	tgtgcagttt	ctgaacatgc	gagatcagtt	tttcaccacc	agctccttcg	360
ctggccgcat	cctactcctt	gaccggggta	taaatggttt	tgaggttcag	aaacaaaact	420
gttgctggct	actggttaca	cacaaacttt	gtgtaaaaga	tgatgtgatt	gtagctctga	480
agaaagcaaa	tggtgatgcc	actttgaaat	ttgaaccatt	tgttcttcat	gtgcagtgtc	540
gacaattgca	ggatgcacag	attctgcatt	ccatggcaat	agattctggt	ttcagggaact	600

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ctggcataac ggtgggaaag agaggaaaaa ctatgttggc tgtccggagt acacatggct	660
tagaagttcc attaagccat aagggaaaac tgatggtgac agaggaatat attgacttcc	720
tggttaaagt ggcaaataca aaaatggagg aaaacaagaa aagaattgag aggttttaca	780
actgcctaca gcatgctttg gaaagggaaa cgatgactaa cttacatccc aagatcaaag	840
agaaaaataa ctcatacatat attcataaga aaaaaagaaa cccagaaaaa acacgtgccc	900
agtgtattac taaagaaagt gatgaagaac ttgaaaatga tgatgatgat gatctaggaa	960
tcaatgttac catcttccct gaagattact <u>aagctttggg</u> tctgatgtgt cttggccgta	1020
atgttttctag taggttttat aaagctgctc ttcataagag tattttagtt tgttgagtgt	1080
atcagccatt cataagccag taatgacaag tgcagagctt caaactataa ctttggtgcc	1140
cagaggatgt gcagttgtca tctaagctct cagcagtacc cggcttatcc tacgacttca	1200
cctgaaatgc tatagttatc cctacttttt taccagtttc tcccagaagc acctgcttaa	1260
taaatcaaag atgtttgaaa aaaaaaaaa	1288

Table 14 hMP polypeptide sequence (SEQ ID NO:14)

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

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Gln	His	Ala	Leu	Glu	Arg	Glu	Thr	Met	Thr	Asn	Leu	His	Pro	Lys	Ile
		195					200					205			
Lys	Glu	Lys	Asn	Asn	Ser	Ser	Tyr	Ile	His	Lys	Lys	Lys	Arg	Asn	Pro
	210					215					220				
Glu	Lys	Thr	Arg	Ala	Gln	Cys	Ile	Thr	Lys	Glu	Ser	Asp	Glu	Glu	Leu
225					230					235					240
Glu	Asn	Asp	Asp	Asp	Asp	Asp	Leu	Gly	Ile	Asn	Val	Thr	Ile	Phe	Pro
				245					250					255	
Glu	Asp	Tyr													

Table 15 NHR nucleotide sequence (SEQ ID NO:15)

acgcgtgcag	gtggcgtggc	gccagggatt	tgaaccgcgc	tgacgaagtt	tggtgatcca	60
tcttccgagt	atcgccggga	tttcgaatcg	<u>cgat</u> gatcat	cccctctcta	gaggagctgg	120
actccctcaa	gtacagtgac	ctgcagaact	tagccaagag	tctgggtctc	cgggccaacc	180
tgagggcaac	caagttgtta	aaagccttga	aaggctacat	taaacatgag	gcaagaaaag	240
gaaatgagaa	tcaggatgaa	agtcaaactt	ctgcatcctc	ttgtgatgag	actgagatac	300
agatcagcaa	ccaggaagag	ctgagagaca	gccacttggc	catgtcacca	aaacaaggag	360
aaggtgcaag	actgtccgtg	tggaccctga	ctcacagaga	atcattcaga	gataaaaata	420
<u>agta</u> atccca	ctgaattcca	gaatcatgaa	aagcaggaaa	gccaggatct	cagagcactg	480
caaaagttcc	ttctccacca	gacgagcacc	aagaagctga	gaatgctggt	tcctcaggta	540
acagagattc	aaaggtacct	tcagaaggaa	agaaatctct	ctacacagat	gagtcatcca	600
aacctggaaa	aaataaaaaga	actgcaatca	ctactccaaa	ctttaagaag	cttcatgaag	660
ctcatttttaa	ggaaatggag	tccattgatc	caatatatng	aggagaaaaa	aagaaacatt	720
ttgaagaaca	caattccatg	aatgaactga	agcagccgcc	catcaataag	ggaggggtca	780
ggactccagt	acctccaaga	ggaagactct	ctgtggcttc	tactcccatc	agccaacgac	840
gctcgcaagg	ccggtcttgt	ggccctgcaa	gtcagagtac	cttgggtctg	aaggggtcac	900
tcaagcgctc	tgctatctct	gcagctaaaa	cgggtgtcag	gttttcagct	gctactaaag	960
ataatgagca	taagcgttca	ctgaccaaga	ctccagccag	aaagtctgca	catgtgaccg	1020
tgtctggggg	cacccaaaaa	ggcgaggctg	tgcttggggac	acacaaatta	aagaccatca	1080
cggggaattc	tgctgctggt	attaccccat	tcaagttgac	aactgaggca	acgcagactc	1140
cagtctccaa	taagaaacca	gtgtttgatc	ttaaagcaag	tttgtctcgt	cccctcaact	1200
atgaaccaca	caaaggaaag	ctaaaaccat	gggggcaatc	taaagaaaat	aattatctaa	1260
atcaacatgt	caacaaatta	acttctacaa	gaaaacttac	aaacaacccc	atctccagac	1320
aaaggaagag	caacggaaga	aacgcgagca	agaagaaagg	agaagaaagc	aaaggttttg	1380
ggaatgcgaa	ggggcctcat	tttggctgaa	gattaataat	tttttaacat	cttgtaaata	1440
ttcctgtatt	ctcaactttt	ttccttttgt	aaattttttt	tttttgctgt	catccccact	1500
ttagtcacga	gatctttttc	tgctaactgt	tcatagtctg	tgtagtgtcc	atgggttctt	1560
catgtgctat	gatctctgaa	aagacgttat	caccttaaag	ctcaaattct	ttgggatggt	1620

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ttttacttaa gtccattaac aattcagggt tctaacgaga cccatcctaa aattctcttt	1680
ctagtttttt aatgtcacca tcccaaactc ccgtttctgg attttttaatc cccagctccc	1740
cagttccctc ttatcgtact aatattaaca gaactgcagt cttctgctag ccaatagcat	1800
ttacctgatg gcagctagtt atgcaagctt caggagaatt tgaacaataa caagaatagg	1860
gtaagctggg atagaaaggc cacctcttca ctctctatag aatatagtaa cctttatgaa	1920
acgggggcat atagtttggt tatgacatca atattttacc taggtgaaat tgtttaggct	1980
tatgtacctt cggtcaaata tcctcatgta attgccatct gtcactcact atattcacaa	2040
aaataaaact ctacaactca ttctaactt gcttacttaa aagctacata gccctatcga	2100
aatgcgagga ttaatgcttt aatgctttta gagacagggt ctcactgtgt tgcccaggct	2160
ggctctcaaac tccaccaaata gtacttctta ttcattttat ggaaaagact aggctttgct	2220
tagtatcatg tccatgtttc cttcacctca gtggagcttc tgagttttat actgctcaag	2280
atcgtcataa ataaaatttt ttctcattgt caaaaaaaaa aaaaaaaaaa aaaaaaaaaa	2340
aaaaaaaaaa aa	2352

Table 16 NHR polypeptide sequence (SEQ ID NO:16)

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

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Phe	Lys	Glu	Met	Glu	Ser	Ile	Asp	Pro	Ile	Tyr	Xaa	Gly	Glu	Lys	Lys	
		195					200					205				
Lys	His	Phe	Glu	Glu	His	Asn	Ser	Met	Asn	Glu	Leu	Lys	Gln	Pro	Pro	
	210					215					220					
Ile	Asn	Lys	Gly	Gly	Val	Arg	Thr	Pro	Val	Pro	Pro	Arg	Gly	Arg	Leu	
225					230					235					240	
Ser	Val	Ala	Ser	Thr	Pro	Ile	Ser	Gln	Arg	Arg	Ser	Gln	Gly	Arg	Ser	
				245					250					255		
Cys	Gly	Pro	Ala	Ser	Gln	Ser	Thr	Leu	Gly	Leu	Lys	Gly	Ser	Leu	Lys	
			260					265					270			
Arg	Ser	Ala	Ile	Ser	Ala	Ala	Lys	Thr	Gly	Val	Arg	Phe	Ser	Ala	Ala	
		275					280					285				
Thr	Lys	Asp	Asn	Glu	His	Lys	Arg	Ser	Leu	Thr	Lys	Thr	Pro	Ala	Arg	
	290					295					300					
Lys	Ser	Ala	His	Val	Thr	Val	Ser	Gly	Gly	Thr	Gln	Lys	Gly	Glu	Ala	
305					310					315					320	
Val	Leu	Gly	Thr	His	Lys	Leu	Lys	Thr	Ile	Thr	Gly	Asn	Ser	Ala	Ala	
				325					330					335		
Val	Ile	Thr	Pro	Phe	Lys	Leu	Thr	Thr	Glu	Ala	Thr	Gln	Thr	Pro	Val	
			340					345					350			
Ser	Asn	Lys	Lys	Pro	Val	Phe	Asp	Leu	Lys	Ala	Ser	Leu	Ser	Arg	Pro	
		355					360					365				
Leu	Asn	Tyr	Glu	Pro	His	Lys	Gly	Lys	Leu	Lys	Pro	Trp	Gly	Gln	Ser	
	370					375					380					
Lys	Glu	Asn	Asn	Tyr	Leu	Asn	Gln	His	Val	Asn	Arg	Ile	Asn	Phe	Tyr	
385					390					395					400	
Lys	Lys	Thr	Tyr	Lys	Gln	Pro	His	Leu	Gln	Thr	Lys	Glu	Glu	Gln	Arg	
				405					410					415		
Lys	Lys	Arg	Glu	Gln	Glu	Arg	Lys	Glu	Lys	Lys	Ala	Lys	Val	Leu	Gly	
			420					425					430			
Met	Arg	Arg	Gly	Leu	Ile	Leu	Ala	Glu	Asp							
			435				440									

Table 17 displays alignment of hMX1, hMX2 with human myosin (SEQ ID NO:31; GenBank AF247457) (Berg *et al.*, 2000). As seen from the alignment, hMX1 and hMX2 have a likely N-terminus of M N D residues. One of skill in the art can easily

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verify this observation by probing cDNA or genomic human libraries, or PCR techniques, to acquire the full length polynucleotide sequence.

Table 17 Alignment of hMX1, hMX2 and human myosin X

10	1	---FCLQGTRVWLRENGQHFPSTVNSCAEGIVVFRTDYGQVFTYKQSTIT
12	1	---FCLQGTRVWLRENGQHFPSTVNSCAEGIVVFRTDYGQVFTYKQSTIT
humX	1	MDNFFTEGTRVWLRENGQHFPSTVNSCAEGIVVFRTDYGQVFTYKQSTIT
10	48	HQKVTAMHPTNEEGVDDMASLTEHGGSIMYNLFQRYKRNQIWYIGSIL
12	48	HQKVTAMHPTNEEGVDDMASLTEHGGSIMYNLFQRYKRNQIWYIGSIL
humX	51	HQKVTAMHPTNEEGVDDMASLTEHGGSIMYNLFQRYKRNQIYTYIGSIL
10	98	ASVNPYQPIAGLYEPATMEQYSRRHLGELPPHIFAIANECYRCLWKRHDN
12	98	ASVNPYQPIAGLYEPATMEQYSRRHLGELPPHIFAIANECYRCLWKRHDN
humX	101	ASVNPYQPIAGLYEPATMEQYSRRHLGELPPHIFAIANECYRCLWKRYDN
10	148	QCILIKGESGAGKTESTKLILKFLSVISQQSLELSLKEKTSCVERAILES
12	148	QCILIKGESGAGKTESTKLILKFLSVISQQSLELSLKEKTSCVERAILES
humX	151	QCILISGESGAGKTESTKLILKFLSVISQQSLELSLKEKTSCVERAILES
10	198	SPIMEAFGNAKTVYNNNSSRFGKFVQLNICQKGNIQGGRIVDCILSSQNR
12	198	SPIMEAFGNAKTVYNNNSSRFGKFVQLNICQKGNIQGGRIVDCILSSQNR
humX	201	SPIMEAFGNAKTVYNNNSSRFGKFVQLNICQKGNIQGGRIVDYILLE-KNR
10	248	VVRQNPGERNYHIFYALLAGLEHEEREFEYLSTPENYHYLNQSGCVEDKT
12	248	VVRQNPGERNYHIFYALLAGLEHEEREFEYLSTPENYHYLNQSGCVEDKT
humX	250	VVRQNPGERNYHIFYALLAGLEHEEREFEYLSTPENYHYLNQSGCVEDKT
10	298	ISDQESFREVITAMDVMQFSKEEVREVSRLLAGILHLGNIEFITAGGAQV
12	298	ISDQESFREVITAMDVMQFSKEEVREVSRLLAGILHLGNIEFITAGGAQV
humX	300	ISDQESFREVITAMDVMQFSKEEVREVSRLLAGILHLGNIEFITAGGAQV
10	348	SFKTALGRSAELLGLDPTQLTDALTQSRMFLRGEEILTPLNVQQAVDSRD
12	348	SFKTALGRSAELLGLDPTQLTDALTQSRMFLRGEEILTPLNVQQAVDSRD
humX	350	SFKTALGRSAELLGLDPTQLTDALTQSRMFLRGEEILTPLNVQQAVDSRD
10	398	SLAMALYACCFEWWIKKINSRIKGNEDFKSIGILDIFGFENFEVNHFEQF
12	398	SLAMALYACCFEWWIKKINSRIKGNEDFKSIGILDIFGFENFEVNHFEQF
humX	400	SLAMALYACCFEWWIKKINSRIKGNEDFKSIGILDIFGFENFEVNHFEQF
10	448	NINYANEKLQEYFNKHIFSLEQLEYSREGLVWEDIDWIDNGECLDLIEKK
12	448	NINYANEKLQEYFNKHIFSLEQLEYSREGLVWEDIDWIDNGECLDLIEKK
humX	450	NINYANEKLQEYFNKHIFSLEQLEYSREGLVWEDIDWIDNGECLDLIEKK
10	498	LGLLALINEESHFPQATDSTLLEKLHSQHANNHFYVKPRVAVNNFGVKHY
12	498	LGLLALINEESHFPQATDSTLLEKLHSQHANNHFYVKPRVAVNNFGVKHY
humX	500	LGLLALINEESHFPQATDSTLLEKLHSQHANNHFYVKPRVAVNNFGVKHY
10	548	AGEVQYDVRGILEKNRDTFRDDLNLNLLRESRFDIFIYDLFEHVSSRNNQDT
12	548	AGEVQYDVRGILEKNRDTFRDDLNLNLLRESRFDIFIYDLFEHVSSRNNQDT
humX	550	AGEVQYDVRGILEKNRDTFRDDLNLNLLRESRFDIFIYDLFEHVSSRNNQDT
10	598	LKCGSKHRRPTVSSQFKVDSLHSLMATLSSSNPFFVRCIKPNMQKMPDQF
12	598	LKCGSKHRRPTVSSQFKVDSLHSLMATLSSSNPFFVRCIKPNMQKMPDQF
humX	600	LKCGSKHRRPTVSSQFKDS-LHSLMATLSSSNPFFVRCIKPNMQKMPDQF

10	648	DQAVVLNQLRYSGMLETVRIRKAGYAVRRPFQDFYKRYKVLMRNLALPED
12	648	DQAVVLNQLRYSGMLETVRIRKAGYAVRRPFQDFYKRYKVLMRNLALPED
humX	649	DQAVVLNQLRYSGMLETVRIRKAGYAVRRPFQDFYKRYKVLMRNLALPED
10	698	VRGKCTSLQLYDASNSEWQLGKTKVFLRESLEQKLEKRREEEVSHAAMV
12	698	VRGKCTSLQLYDASNSEWQLGKTKVFLRESLEQKLEKRREEEVSHAAMV
humX	699	VRGKCTSLQLYDASNSEWQLGKTKVFLRESLEQKLEKRREEEVSHAAMV
10	748	IRAHVLGFLARKQYRKVLYCVVIIQKNYRAFLRRRFLHLKKAIVFQKQ
12	748	IRAHVLGFLARKQYRKVLYCVVIIQKNYRAFLRRRFLHLKKAIVFQKQ
humX	749	IRAHVLGFLARKQYRKVLYCVVIIQKNYRAFLRRRFLHLKKAIVFQKQ
10	798	LRGQIARRVYRQLLAEKREQEKKKKQEEEEKKKREEEEREREREREREAEL
12	798	LRGQIARRVYRQLLAEKREQEKKKKQEEEEKKKREEEEREREREREREAEL
humX	799	LRGQIARRVYRQLLAEKREQEKKKKQEEEEKKKREEEEREREREREREAEL
10	848	RAQQEEETRKKQOELEALQKSQKEAELTRELEKQKENKQVEEILRLEKEIE
12	848	RAQQEEETRKKQOELEALQKSQKEAELTRELEKQKENKQVEEILRLEKEIE
humX	849	RAQQEEETRKKQOELEALQKSQKEAELTRELEKQKENKQVEEILRLEKEIE
10	898	DLQRMKEQQELSLTEASLQKLQERRDQELRRLEEEACRAAQEFLES LNFD
12	898	DLQRMKEQQELSLTEASLQKLQERRDQELRRLEEEACRAAQEFLES LNFD
humX	899	DLQRMKEQQELSLTEASLQKLQERRDQELRRLEEEACRAAQEFLES LNFD
10	948	EIDECVRNIERSLSGGSEFSSELAESACEEKPNFNFSQPYPEEEVDEGFE
12	948	EIDECVRNIERSLSGGSEFSSELAESACEEKPNFNFSQPYPEEEVDEGFE
humX	949	EIDECVRNIERSLSVGSEFSSELAESACEEKPNFNFSQPYPEEEVDEGFE
10	998	ADDDAFKDSPNPSEHGHS DQRTSGIRTSDDSSEEDPYMNDTVVPTSPSAD
12	998	ADDDAFKDSPNPSEHGHS DQRTSGIRTSDDSSEEDPYMNDTVVPTSPSAD
humX	999	ADDDAFKDSPNPSEHGHS DQRTSGIRTSDDSSEEDPYMNDTVVPTSPSAD
10	1048	STVLLAPSVQDSGSLHNSSSGESTYCMPQNAGDLPSPDGDYDYDQDDYED
12	1048	STVLLAPSVQDSGSLHNSSSGESTYCMPQNAGDLPSPDGDYDYDQDDYED
humX	1049	STVLLAPSVQDSGSLHNSSSGESTYCMPQNAGDLPSPDGDYDYDQDDYED
10	1098	GAITSGSSVTFSNSYGSQWSPDYRCSVGTYNSSGAYRFSSEGAQSSFEDS
12	1098	GAITSGSSVTFSNSYGSQWSPDYRCSVGTYNSSGAYRFSSEGAQSSFEDS
humX	1099	GAITSGSSVTFSNSYGSQWSPDYRCSVGTYNSSGAYRFSSEGAQSSFEDS
10	1148	EEDFDSRFDTDDELSYRRDSVYSCVTLPYFHSFLYMKGGLMNSWKRRWCV
12	1148	EEDFDSRFDTDDELSYRRDSVYSCVTLPYFHSFLYMKGGLMNSWKRRWCV
humX	1149	EEDFDSRFDTDDELSYRRDSVYSCVTLPYFHSFLYMKGGLMNSWKRRWCV
10	1198	LKDETFLWFRSKQEALKQGWLHKKGGGSSTLSRRNWKKRWFVLRQSKLMY
12	1198	LKDETFLWFRSKQEALKQGWLHKKGGGSSTLSRRNWKKRWFVLRQSKLMY
humX	1199	LKDETFLWFRSKQEALKQGWLHKKGGGSSTLSRRNWKKRWFVLRQSKLMY
10	1248	FENDSEEKLKGTVEVRTAKEIIDNTTKENGIDIIMADRTFHLIAESPEDA
12	1248	FENDSEEKLKGTVEVRTAKEIIDNTTKENGIDIIMADRTFHLIAESPEDA
humX	1249	FENDSEEKLKGTVEVRTAKEIIDNTTKENGIDIIMADRTFHLIAESPEDA
10	1298	SQWFSVLSQVHASTDQEIQEMHDEQANPQNAVGTLDVGLIDSVCASDSPD
12	1298	SQWFSVLSQVHASTDQEIQEMHDEQANPQNAVGTLDVGLIDSVCASDSPD
humX	1299	SQWFSVLSQVHASTDQEIQEMHDEQANPQNAVGTLDVGLIDSVCASDSPD
10	1348	RPNSFVIITANRVLHCNADTPEEMHHWITLLQRSKGDTRVEGQEFIVRGW

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12	1348	RPNSFVIITANRVLHCNADTPEEMHHWITLLQRSKGDTRVEGQEFIVRGW
humX	1349	RPNSFVIITANRVLHCNADTPEEMHHWITLLQRSKGDTRVEGQEFIVRGW
10	1398	LHKEVKNSPKMSSLKLLKKRWFVLTHNSLDYYKSSEKNALKLGTLLVLSLC
12	1398	LHKEVKNSPKMSSLKLLKKRWFVLTHNSLDYYKSSEKNALKLGTLLVLSLC
humX	1399	LHKEVKNSPKMSSLKLLKKRWFVLTHNSLDYYKSSEKNALKLGTLLVLSLC
10	1448	SVVPPDEKIFKETGYWNVTVYGRKHCYRLYTKLLNEATRWSSVIQNVTDT
12	1448	SVVPPDEKIFKETGYWNVTVYGRKHCYRLYTKLLNEATRWSSVIQNVTDT
humX	1449	SVVPPDEKIFKETGYWNVTVYGRKHCYRLYTKLLNEATRWSSAIQNVTDT
10	1498	KAPIDTPTQQLIQDIKENCLNSDVVEQIYKRNPIILRYTHHPLHSPLLPLP
12	1498	KAPIDTPTQQLIQDIKENCLNSDVVEQIYKRNPIILRYTHHPLHSPLLPLP
humX	1499	KAPIDTPTQQLIQDIKENCLNSDVVEQIYKRNPIILRYTHHPLHSPLLPLP
10	1548	YGDINLNLLKDKGYTTLQDEAIKIFNSLQQLESMSDPIPIIQGILQTGHD
12	1548	YGDINLNLLKDKGYTTLQDEAIKIFNSLQQLESMSDPIPIIQGILQTGHD
humX	1549	YGDINLNLLKDKGYTTLQDEAIKIFNSLQQLESMSDPIPIIQGILQTGHD
10	1598	LRPLRDELYCQLIKQTNKVPHPGSGVGNLYSWQILTCLSCFTLPSRGILKY
12	1598	LRPLRDELYCQLIKQTNKVPHPGSGVGNLYSWQILTCLSCFTLPSRGILKY
humX	1599	LRPLRDELYCQLIKQTNKVPHPGSGVGNLYSWQILTCLSCFTLPSRGILKY
10	1648	LKFHLKRIREQFPGTEMEKYALFTYESLKKTKCREFVPSRDEIEALHRQ
12	1648	LKFHLKRIREQFPGTEMEKYALFTYESLKKTKCREFVPSRDEIEALHRQ
humX	1649	LKFHLKRIREQFPGTEMEKYALFTYESLKKTKCREFVPSRDEIEALHRQ
10	1698	EMTSTVYCHGGGSCKITINSHTTAGEVVEKLIIRGLAMEDSRNMFALFEYN
12	1698	EMTSTVYCHGGGSCKITINSHTTAGEVVEKLIIRGLAMEDSRNMFALFEYN
humX	1699	EMTSTVYCHGGGSCKITINSHTTAGEVVEKLIIRGLAMEDSRNMFALFEYN
10	1748	GHVDKAIESRTVVADVLAKEKLAATSEVGDLPWKFYFKLYCFLDTDNVP
12	1748	GHVDKAIESRTVVADVLAKEKLAATSEVGDLPWKFYFKLYCFLDTDNVP
humX	1749	GHVDKAIESRTVVADVLAKEKLAATSEVGDLPWKFYFKLYCFLDTDNVP
10	1798	KDSVEFAFMFEQAHEAVIHGHHPAPEENLQVLAALRLQYLQGDYTLHAAI
12	1798	KDSVEFAFMFEQAHEAVIHGHHPAPEENLQVLAALRLQYLQGDYTLHAAI
humX	1799	KDSVEFAFMFEQAHEAVIHGHHPAPEENLQVLAALRLQYLQGDYTLHAAI
10	1848	PPLVEVYSLQRLKARISQSTKTFTPCERLEKRRTSFLEGTLLRRSFRTGSV
12	1848	PPLVEVYSLQRLKARISQSTKTFTPCERLEKRRTSFLEGTLLRRSFRTGSV
humX	1849	PPLVEVYSLQRLKARISQSTKTFTPCERLEKRRTSFLEGTLLRRSFRTGSV
10	1898	VRQKVEEEQMLDMWIKKEEVSSARASIIDKWRKFQGMNQEQAAMAKYMALIK
12	1898	VRQKVEEEQMLDMWIKKEEVSSARASIIDKWRKFQGMNQEQAAMAKYMALIK
humX	1899	VRQKVEEEQMLDMWIKKEEVSSARASIIDKWRKFQGMNQEQAAMAKYMALIK
10	1948	EWPGYGSTLFDVECKEGGFPQELWLGVSAVASVYKRGEGRPLEVFQYEH
12	1948	EWPGYGSTLFDVEVRTG-CHVLGWAGCWHLRTWITAKFMWREDKMEHFAL
humX	1949	EWPGYGSTLFDVECKEGGFPQELWLGVSAVASVYKRGEGRPLEVFQYEH
10	1998	ILSFGAPLANTYKIVVDERELLFETSEVVDVAKLMKAYISMIVKKRYSTT
12	1997	STSFFRAPKIVPLTPPFSSQFLFSCVNASVILGMNAKLRCHLFFYPPLG
humX	1999	ILSFGAPLANTYKIVVDERELLFETSEVVDVAKLMKAYISMIVKKRYSTT
10	2048	RSASSQGSSR
12	2047	KL-----
humX	2049	RSASSQGSSR



The invention also includes polypeptides and nucleotides having 80-100%, including 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98 and 99%, sequence identity to SEQ ID NOS:1-16, as well as nucleotides encoding any of these polypeptides, and compliments of any of these nucleotides. In an alternative embodiment, polypeptides and/or nucleotides (and compliments thereof) identical to any one of, or more than one of, SEQ ID NOS:1-16 are excluded. In yet another embodiment, polypeptides and/or nucleotides (and compliments thereof) having 81-100% identical, including 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98 and 99%, sequence identity to SEQ ID NOS:1-16 are excluded.

The nucleic acids and proteins of the invention are potentially useful in promoting wound healing, for example after organ transplantation, or in the treatment of myocardial infarction, but also in treating tumors, and in cancers, diabetic retinopathy, macular degeneration, psoriasis, and rheumatoid arthritis. For example, a cDNA encoding AAP may be useful in gene therapy, and AAP proteins may be useful when administered to a subject in need thereof. The novel nucleic acid encoding AAP, and the AAP proteins of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These materials are further useful in the generation of Abs that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods.

Kelch-like protein (KLP)

The putative protein encoded by *KLP* contains 1 putative BTB domain and 4 putative Kelch motifs. The BTB (broad complex, tramtrack, bric-a-brac)/POZ (poxvirus, zinc finger) domain is involved in protein protein interactions. The kelch motif is sixfold tandem element in the sequence of the *Drosophila* kelch ORF1 protein that also contains BTB. Kelch ORF1 localizes to the ring canals in the egg chamber and helps to organize the F-actin cytoskeleton (Adams *et al.*, 2000). The repeated kelch motifs predict a conserved tertiary structure, a β -propeller. This module appears in many different polypeptide contexts and contains multiple potential protein-protein interaction sites. Members of this growing superfamily are present throughout the cell and extracellularly

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and have diverse activities (Adams *et al.*, 2000). Such activities include cytoskeleton organization, as well as other morphological processes, gene expression, interactions with viruses, and various extracellular events, such as cell spreading.

Alignment with *Drosophila* kelch and other kelch-like proteins, human kelch-like protein (GenBank AAF20938 (SEQ ID NO:17)), hypothetical *C. elegans* (GenBank O61795 (SEQ ID NO:18) and the skeletal muscle-specific sarcosin (GenBank O60662 (SEQ ID NO:19); (Taylor *et al.*, 1998)) reveals that the disclosed protein (SEQ ID NO:2) is a member of a new subfamily

KLP is associated with tube formation and angiogenesis because it is upregulated in the *in vitro* model of angiogenesis of Example 1. Kelch mediates cytoskeletal associations, it is involved in morphogenetic processes, such as tube formation, that depend on cytoskeletal arrangements and signaling. KLP represents an attractive target for small molecule drug therapy.

Human ortholog of mouse BAZF (hBAZF)

hBAZF (SEQ ID NO:4) is the human ortholog of mouse BAZF (GenBank AB011665; SEQ ID NO:20), BAZF is a Bcl-6 (LAZ3) homolog, a transcription repressor that controls germinal center formation and the T cell-dependent immune response. Expression of Bcl-6 negatively correlates with cellular proliferation: Bcl-6 suppresses growth associated with impaired mitotic S phase progression and apoptosis (Albagli *et al.*, 1999).

BAZF contains a BTB/POZ domain and five repeats of the Kruppel-like zinc finger motifs, instead of 6 in Bcl-6 (Okabe *et al.*, 1998). Expression of *BAZF* mRNA is relegated to heart and lung, unlike *Bcl-6* mRNA, but is induced in activated lymphocytes as an immediate-early gene, like *Bcl-6* (Okabe *et al.*, 1998).

The hBAZF sequence was derived by using tblastn (protein query –translated database) (Altschul *et al.*, 1997), with the mouse protein sequence (GenBank O88282; SEQ ID NO:21) that has homology to GenBank AC015918 (SEQ ID NO:22), a clone of *Homo sapiens* chromosome 17. Human BAZF contains five Kruppel-like zinc finger motif repeats and a BTB/POZ domain.

The peptide sequence, “RSQ...PQV” that is present in the human sequence, might represent an alternative spliced form of the gene. Alignment with mouse BAZF, and

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alignment with mouse and human Bcl-6 demonstrates that the four proteins are almost identical in this region, but only human BAZF has this inserted sequence.

hBAZF is upregulated in HUVE cells grown embedded in collagen gels but not as a monolayer grown on collagen. When HUVE cells are suspended in collagen, they do not proliferate. Analogous to the role of mBAZF plays a role in regulating cell proliferation (Okabe *et al.*, 1998), hBAZF plays a roll in cell proliferation in HUVE suspended in collagen. Because of its high expression during vessel morphogenesis, hBAZF represents an excellent molecular marker, as well as an attractive target for various therapies to inhibit angiogenesis.

hmt-Elongation Factor G (hEF-G)

The original isolation of hEF-G (SEQ ID NO:6) is 84% identical and colinear with *Rattus norvegicus* nuclear encoded mitochondrial elongation factor G (GenBank L14684 (SEQ ID NO:23); (Barker *et al.*, 1993). No human gene is described in GenBank. However, searching EST databases, the human gene is contained inside GenBank AC010936 (SEQ ID NO:24), a chromosome 3 clone. Alignment of hEF-G with rat mtEF-G and yeast EF-G1 demonstrates that the novel sequence is the ortholog of rat nuclear-encoded mitochondrial elongation factor G.

Bacterial elongation factor G (EF-G) physically associates with translocation-competent ribosomes and facilitates transition to the subsequent codon through the coordinate binding and hydrolysis of GTP. The deduced amino acid sequence of hmt-EF-G reveals characteristic motifs shared by all GTP binding proteins. Therefore, similarly to other elongation factors, the enzymatic function of hmt-EF-G is predicted to depend on GTP binding and hydrolysis.

Hmt-EF-G is strongly induced (30-fold) in an *in vitro* model of angiogenesis (Example 1), and as such, hmt-EF-G represents an excellent molecular marker for vessel formation. Because of its putative localization to the mitochondrion, hmt-EF-G is also an attractive therapeutic target to treat disease states associated with mitochondrial dysfunction.

Human thyroid regulated transcript (hTRG)

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hTRG (SEQ ID NO:8) is the human ortholog of rat TRG, a novel thyroid transcript negatively regulated by TSH (GenBank KIAA1058 (SEQ ID NO:25); (Bonapace *et al.*, 1990).

SEQ ID NO:25 appears to be a partial peptide since there are *C. elegans* homologous proteins of 2000 residues. Using tblastn (Altschul *et al.*, 1997) against genomic sequences, the hTRG sequence (SEQ ID NO:8) was assembled.

In *C. elegans*, homologous proteins localize either to the plasma membrane or to the mitochondrial inner membrane. A partial sequence, KIAA0694 (SEQ ID NO:26) also localizes to the mitochondrial matrix. hTRG has a PH domain, and has weak homology to an extracellular fibronectin-binding protein precursor. SEQ ID NO:26 has homology to *Drosophila* DOS and mouse Gab-2 proteins; both of which are involved in signal transduction, acting as adapter proteins between receptors and kinases like Ras1 (Hibi and Hirano, 2000).

Because of hTRG is upregulated during the *in vitro* model of angiogenesis (Example 1), and because of its homologies with adapter proteins, hTRG is likely to be involved in signal transduction between receptors and kinases. As such, hTRG represent an excellent candidate for small molecule drug therapy to modulate angiogenesis and treat angiogenesis-related diseases. In addition, because of its putative ability to respond to thyroid stimulating hormone (TSH), modulation of hTRG is useful to treat diseases related to TSH imbalance.

Human myosin X (hMX1(SEQ ID NO:10) and hMX2 (SEQ ID NO:12)

The hMX proteins represent the human ortholog of bovine myosin X, (GenBank AAB39486; SEQ ID NO:27). Using tblastn (Altschul *et al.*, 1997) and the bovine sequence, a series of genomic clones from human chromosome 5 were identified; GenBank AC010310 (SEQ ID NO:28) appears to contain the entire sequence. Interestingly, a partial cDNA sequence from mouse (GenBank AF184153; SEQ ID NO:29) localizes to a 0.8 cM interval on the short arm of chromosome 5, between the polymorphic microsatellite markers D5S416 and D5S2114. In this region lies the gene for familial chondrocalcinosis (*CCAL2*) (Rojas *et al.*, 1999).

Another GenBank entry, AB018342 (SEQ ID NO:30) that represents the 3' region of *hMX*, appears to encode an alternative splice form. Noteworthy, this variant (hMX2)

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has a very hydrophobic carboxy terminus, while the more prevalent form (hMX1) is hydrophilic and potentially interacts with DNA/RNA since it has homology to high mobility group box (HMG) and ribosomal proteins. Additionally, a myosin head domain was found in the NH terminus, as well as a myosin talin domain, two calmodulin binding domains, four pleckstrin domains and a band 4.1 domain.

The band 4.1 domain represents a crossroads between cytoskeletal organization and signal transduction. The domain was first described in the red blood cell protein band 4.1. The ERM proteins ezrin, radixin, and moesin and the unconventional myosins VIIa and X all possess the band 4.1 domain (Louvet-Vallee, 2000). The band 4.1 domain binds single transmembrane protein at the membrane-proximal region in the C-terminal cytoplasmic tail.

HMX is upregulated during angiogenesis in an *in vitro* model (Example 1). Because hMX contains the protein-protein interaction domains PH and band 4.1 domain, hMX1 and hMX2 are involved in angiogenesis, likely transducing signals from angiogenic factors, perhaps modulating the cytoskeleton.

Human mitochondrial protein (hMP)

Analysis of hMP (SEQ ID NO:14) reveals several subdomain that are homologous to proteins involved in transport across membranes, K⁺ATPase α and γ chains. Further analysis indicates that hMP may bind DNA and or RNA, since hMP is homologous to histones and transcription factors, especially those possessing basic region plus leucine zipper domains.

Although PSORT analysis (Nakai and Horton, 1999) predicts nuclear localization (P=.6), hMP may in fact be a nuclear-encoded mitochondrial protein. Homologies with mostly bacterial proteins and a PSORT prediction of mitochondrial matrix space localization (P=0.4478) strongly support this contention.

Because hMP is upregulated in an *in vitro* model of angiogenesis (Example 1), and because of its homologies with mitochondrial and nuclear-localized polypeptides, hMP is important in vascular morphogenesis, most likely through either powering the cellular differentiation-redifferentiation process, and/or affecting changes in the nuclear matrix that change global gene expression. Alternatively, hMP may be a transcription factor for either the nuclear or mitochondrial genomes.

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Nuclear hormone receptor (NHR)

NHR (SEQ ID NO:16) has two domains: (1) the NH region is similar to Swi3 (yeast SWI/SNF complexes regulate transcription by chromatin remodeling), indicating a role in transcriptional regulation, and (2) the COOH region is similar to parathyroid hormone-related proteins that bind parathyroid hormones. PSORT (Nakai and Horton, 1999) predicts the protein to localize in the nucleus $P=0.9600$.

The identification of this new putative hormone receptor-transcriptional regulator and hBAZF suggest a novel human transcriptional pathway that resembles, to some extent, that of Bcl-6.

Bcl-6 suppresses transcription via the BTB domain, which recruits a complex containing SMRT, retinoid thyroid hormone receptor, nuclear receptor corepressor (N-CoR), mammalian Sin3A, and histone deacetylase (HDAC). hBAZF, which also possesses a BTB domain, might recruit a similar complex containing deacetylase. Expression data indicate that *hBAZF* is up-regulated while *NHR* is down-regulated. These data agree with other evidence related to tube formation. Testosterone (a steroid) and dexamethasone (a steroid-like molecule) strongly inhibit vessel formation, and all-trans retinoic acid (at-RA) and 9-cis retinoic acid (9-cis RA) stimulate capillary-like tubular structures (Lansink *et al.*, 1998).

Upon angiogenic stimulation, endothelial cells may become incompetent to respond to anti-angiogenic responses mediated by hormones using a dual mechanism, sequestering hormones and suppressing transcription. Because nHR is down-regulated during *in vitro* angiogenesis (Example 1), this polypeptide is likely to be involved in non-angiogenesis-specific gene transcription. nHR is an attractive therapeutic target, especially in therapies that are directed at preventing vascularization.

AAP polynucleotides

One aspect of the invention pertains to isolated nucleic acid molecules that encode AAP or biologically-active portions thereof. Also included in the invention are nucleic acid fragments sufficient for use as hybridization probes to identify AAP-encoding nucleic acids (*e.g.*, *AAP* mRNAs) and fragments for use as polymerase chain reaction (PCR) primers for the amplification and/or mutation of *AAP* molecules. A "nucleic acid

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molecule" includes DNA molecules (*e.g.*, cDNA or genomic DNA), RNA molecules (*e.g.*, mRNA), analogs of the DNA or RNA generated using nucleotide analogs, and derivatives, fragments and homologs. The nucleic acid molecule may be single-stranded or double-stranded, but preferably comprises double-stranded DNA.

1. *probes*

Probes are nucleic acid sequences of variable length, preferably between at least about 10 nucleotides (nt), 100 nt, or many (*e.g.*, 6,000 nt) depending on the specific use. Probes are used to detect identical, similar, or complementary nucleic acid sequences. Longer length probes can be obtained from a natural or recombinant source, are highly specific, and much slower to hybridize than shorter-length oligomer probes. Probes may be single- or double-stranded and designed to have specificity in PCR, membrane-based hybridization technologies, or ELISA-like technologies. Probes are substantially purified oligonucleotides that will hybridize under stringent conditions to at least optimally 12, 25, 50, 100, 150, 200, 250, 300, 350 or 400 consecutive sense strand nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, or 15; or an anti-sense strand nucleotide sequence of these sequences; or of a naturally occurring mutant of these sequences.

The full- or partial length native sequence *AAP* may be used to "pull out" similar (homologous) sequences (Ausubel *et al.*, 1987; Sambrook, 1989), such as: (1) full-length or fragments of *AAP* cDNA from a cDNA library from any species (*e.g.* human, murine, feline, canine, bacterial, viral, retroviral, yeast), (2) from cells or tissues, (3) variants within a species, and (4) homologues and variants from other species. To find related sequences that may encode related genes, the probe may be designed to encode unique sequences or degenerate sequences. Sequences may also be genomic sequences including promoters, enhancer elements and introns of native sequence *AAP*.

For example, an *AAP* coding region in another species may be isolated using such probes. A probe of about 40 bases is designed, based on an *AAP*, and made. To detect hybridizations, probes are labeled using, for example, radionuclides such as ³²P or ³⁵S, or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin-biotin systems. Labeled probes are used to detect nucleic acids having a complementary sequence to that of an *AAP* in libraries of cDNA, genomic DNA or mRNA of a desired species.

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Such probes can be used as a part of a diagnostic test kit for identifying cells or tissues which mis-express an AAP, such as by measuring a level of an *AAP* in a sample of cells from a subject *e.g.*, detecting *AAP* mRNA levels or determining whether a genomic *AAP* has been mutated or deleted.

2. *isolated nucleic acid*

An isolated nucleic acid molecule is separated from other nucleic acid molecules that are present in the natural source of the nucleic acid. Preferably, an isolated nucleic acid is free of sequences that naturally flank the nucleic acid (*i.e.*, sequences located at the 5'- and 3'-termini of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, isolated *AAP* molecules can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell/tissue from which the nucleic acid is derived (*e.g.*, brain, heart, liver, spleen, *etc.*). Moreover, an isolated nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material or culture medium when produced by recombinant techniques, or of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the invention, *e.g.*, a nucleic acid molecule having the nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15, or a complement of this aforementioned nucleotide sequence, can be isolated using standard molecular biology techniques and the provided sequence information. Using all or a portion of the nucleic acid sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15 as a hybridization probe, *AAP* molecules can be isolated using standard hybridization and cloning techniques (Ausubel *et al.*, 1987; Sambrook, 1989).

PCR amplification techniques can be used to amplify *AAP* using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers. Such nucleic acids can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to *AAP* sequences can be prepared by standard synthetic techniques, *e.g.*, an automated DNA synthesizer.

3. *oligonucleotide*

An oligonucleotide comprises a series of linked nucleotide residues, which oligonucleotide has a sufficient number of nucleotide bases to be used in a PCR reaction

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or other application. A short oligonucleotide sequence may be based on, or designed from, a genomic or cDNA sequence and is used to amplify, confirm, or reveal the presence of an identical, similar or complementary DNA or RNA in a particular cell or tissue. Oligonucleotides comprise portions of a nucleic acid sequence having about 10 nt, 50 nt, or 100 nt in length, preferably about 15 nt to 30 nt in length. In one embodiment of the invention, an oligonucleotide comprising a nucleic acid molecule less than 100 nt in length would further comprise at least 6 contiguous nucleotides of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15, or a complement thereof. Oligonucleotides may be chemically synthesized and may also be used as probes.

4. *complementary nucleic acid sequences; binding*

In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13 or 15, or a portion of this nucleotide sequence (*e.g.*, a fragment that can be used as a probe or primer or a fragment encoding a biologically-active portion of an AAP). A nucleic acid molecule that is complementary to the nucleotide sequence shown in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15, is one that is sufficiently complementary to the nucleotide sequence shown in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15, that it can hydrogen bond with little or no mismatches to the nucleotide sequence shown in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15, thereby forming a stable duplex.

“Complementary” refers to Watson-Crick or Hoogsteen base pairing between nucleotides units of a nucleic acid molecule, and the term “binding” means the physical or chemical interaction between two polypeptides or compounds or associated polypeptides or compounds or combinations thereof. Binding includes ionic, non-ionic, van der Waals, hydrophobic interactions, and the like. A physical interaction can be either direct or indirect. Indirect interactions may be through or due to the effects of another polypeptide or compound. Direct binding refers to interactions that do not take place through, or due to, the effect of another polypeptide or compound, but instead are without other substantial chemical intermediates.

Nucleic acid fragments are at least 6 (contiguous) nucleic acids or at least 4 (contiguous) amino acids, a length sufficient to allow for specific hybridization in the case of nucleic acids or for specific recognition of an epitope in the case of amino acids,

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respectively, and are at most some portion less than a full-length sequence. Fragments may be derived from any contiguous portion of a nucleic acid or amino acid sequence of choice.

5. *derivatives, and analogs*

Derivatives are nucleic acid sequences or amino acid sequences formed from the native compounds either directly or by modification or partial substitution. Analogs are nucleic acid sequences or amino acid sequences that have a structure similar to, but not identical to, the native compound but differ from it in respect to certain components or side chains. Analogs may be synthetic or from a different evolutionary origin and may have a similar or opposite metabolic activity compared to wild type. Homologs are nucleic acid sequences or amino acid sequences of a particular gene that are derived from different species.

Derivatives and analogs may be full length or other than full length, if the derivative or analog contains a modified nucleic acid or amino acid, as described below. Derivatives or analogs of the nucleic acids or proteins of the invention include, but are not limited to, molecules comprising regions that are substantially homologous to the nucleic acids or proteins of the invention, in various embodiments, by at least about 70%, 80%, or 95% identity (with a preferred identity of 80-95%) over a nucleic acid or amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to the complement of a sequence encoding the aforementioned proteins under stringent, moderately stringent, or low stringent conditions (Ausubel *et al.*, 1987).

6. *homology*

A "homologous nucleic acid sequence" or "homologous amino acid sequence," or variations thereof, refer to sequences characterized by homology at the nucleotide level or amino acid level as discussed above. Homologous nucleotide sequences encode those sequences coding for isoforms of AAP. Isoforms can be expressed in different tissues of the same organism as a result of, for example, alternative splicing of RNA. Alternatively, different genes can encode isoforms. In the invention, homologous nucleotide sequences include nucleotide sequences encoding for an AAP of species other than humans, including, but not limited to: vertebrates, and thus can include, *e.g.*, frog, mouse, rat,

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rabbit, dog, cat cow, horse, and other organisms. Homologous nucleotide sequences also include, but are not limited to, naturally occurring allelic variations and mutations of the nucleotide sequences set forth herein. A homologous nucleotide sequence does not, however, include the exact nucleotide sequence encoding human AAP. Homologous nucleic acid sequences include those nucleic acid sequences that encode conservative amino acid substitutions (see below) in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14 or 16, as well as a polypeptide possessing AAP biological activity. Various biological activities of the AAP are described below.

7. *open reading frames*

The open reading frame (ORF) of an *AAP* gene encodes an AAP. An ORF is a nucleotide sequence that has a start codon (ATG) and terminates with one of the three "stop" codons (TAA, TAG, or TGA). In this invention, however, an ORF may be any part of a coding sequence that may or may not comprise a start codon and a stop codon. To achieve a unique sequence, preferable *AAP* ORFs encode at least 50 amino acids.

AAP polypeptides

1. *mature*

An *AAP* can encode a mature AAP. A "mature" form of a polypeptide or protein disclosed in the present invention is the product of a naturally occurring polypeptide or precursor form or proprotein. The naturally occurring polypeptide, precursor or proprotein includes, by way of nonlimiting example, the full-length gene product, encoded by the corresponding gene. Alternatively, it may be defined as the polypeptide, precursor or proprotein encoded by an open reading frame described herein. The product "mature" form arises, again by way of nonlimiting example, as a result of one or more naturally occurring processing steps as they may take place within the cell, or host cell, in which the gene product arises. Examples of such processing steps leading to a "mature" form of a polypeptide or protein include the cleavage of the N-terminal methionine residue encoded by the initiation codon of an open reading frame, or the proteolytic cleavage of a signal peptide or leader sequence. Thus a mature form arising from a precursor polypeptide or protein that has residues 1 to N, where residue 1 is the N-terminal methionine, would have residues 2 through N remaining after removal of the N-terminal methionine. Alternatively, a mature form arising from a precursor polypeptide

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or protein having residues 1 to N, in which an N-terminal signal sequence from residue 1 to residue M is cleaved, would have the residues from residue M+1 to residue N remaining. Further as used herein, a "mature" form of a polypeptide or protein may arise from a step of post-translational modification other than a proteolytic cleavage event. Such additional processes include, by way of non-limiting example, glycosylation, myristoylation or phosphorylation. In general, a mature polypeptide or protein may result from the operation of only one of these processes, or a combination of any of them.

2. *active*

An active AAP polypeptide or AAP polypeptide fragment retains a biological and/or an immunological activity similar, but not necessarily identical, to an activity of a naturally-occurring (wild-type) AAP polypeptide of the invention, including mature forms. A particular biological assay, with or without dose dependency, can be used to determine AAP activity. A nucleic acid fragment encoding a biologically-active portion of AAP can be prepared by isolating a portion of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15 that encodes a polypeptide having an AAP biological activity (the biological activities of the AAP are described below), expressing the encoded portion of AAP (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of AAP. Immunological activity refers to the ability to induce the production of an antibody against an antigenic epitope possessed by a native AAP; biological activity refers to a function, either inhibitory or stimulatory, caused by a native AAP that excludes immunological activity.

AAP nucleic acid variants and hybridization

1. *variant polynucleotides, genes and recombinant genes* The invention further encompasses nucleic acid molecules that differ from the nucleotide sequences shown in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15 due to degeneracy of the genetic code and thus encode the same AAP as that encoded by the nucleotide sequences shown in SEQ ID NO NOS:1, 3, 5, 7, 9, 11, 13 or 15. An isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14 or 16.

In addition to the AAP sequences shown in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15, DNA sequence polymorphisms that change the amino acid sequences of the AAP may

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exist within a population. For example, allelic variation among individuals will exhibit genetic polymorphism in an *AAP*. The terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame (ORF) encoding an *AAP*, preferably a vertebrate *AAP*. Such natural allelic variations can typically result in 1-5% variance in an *AAP*. Any and all such nucleotide variations and resulting amino acid polymorphisms in an *AAP*, which are the result of natural allelic variation and that do not alter the functional activity of an *AAP* are within the scope of the invention.

Moreover, *AAP* from other species that have a nucleotide sequence that differs from the human sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15, are contemplated. Nucleic acid molecules corresponding to natural allelic variants and homologues of an *AAP* cDNAs of the invention can be isolated based on their homology to an *AAP* of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15 using cDNA-derived probes to hybridize to homologous *AAP* sequences under stringent conditions.

"AAP variant polynucleotide" or "AAP variant nucleic acid sequence" means a nucleic acid molecule which encodes an active *AAP* that (1) has at least about 80% nucleic acid sequence identity with a nucleotide acid sequence encoding a full-length native *AAP*, (2) a full-length native *AAP* lacking the signal peptide, (3) an extracellular domain of an *AAP*, with or without the signal peptide, or (4) any other fragment of a full-length *AAP*. Ordinarily, an *AAP* variant polynucleotide will have at least about 80% nucleic acid sequence identity, more preferably at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% nucleic acid sequence identity and yet more preferably at least about 99% nucleic acid sequence identity with the nucleic acid sequence encoding a full-length native *AAP*. An *AAP* variant polynucleotide may encode a full-length native *AAP* lacking the signal peptide, an extracellular domain of an *AAP*, with or without the signal sequence, or any other fragment of a full-length *AAP*. Variants do not encompass the native nucleotide sequence.

Ordinarily, *AAP* variant polynucleotides are at least about 30 nucleotides in length, often at least about 60, 90, 120, 150, 180, 210, 240, 270, 300, 450, 600 nucleotides in length, more often at least about 900 nucleotides in length, or more.

"Percent (%) nucleic acid sequence identity" with respect to *AAP*-encoding nucleic acid sequences identified herein is defined as the percentage of nucleotides in a

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candidate sequence that are identical with the nucleotides in the *AAP* sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining % nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared.

When nucleotide sequences are aligned, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) can be calculated as follows:

$$\% \text{nucleic acid sequence identity} = W/Z \cdot 100$$

where

W is the number of nucleotides cored as identical matches by the sequence alignment program's or algorithm's alignment of C and D

and

Z is the total number of nucleotides in D.

When the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C.

2. *Stringency*

Homologs (*i.e.*, nucleic acids encoding an AAP derived from species other than human) or other related sequences (*e.g.*, paralogs) can be obtained by low, moderate or high stringency hybridization with all or a portion of the particular human sequence as a probe using methods well known in the art for nucleic acid hybridization and cloning.

The specificity of single stranded DNA to hybridize complementary fragments is determined by the "stringency" of the reaction conditions. Hybridization stringency increases as the propensity to form DNA duplexes decreases. In nucleic acid hybridization reactions, the stringency can be chosen to either favor specific hybridizations (high stringency), which can be used to identify, for example, full-length

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clones from a library. Less-specific hybridizations (low stringency) can be used to identify related, but not exact, DNA molecules (homologous, but not identical) or segments.

DNA duplexes are stabilized by: (1) the number of complementary base pairs, (2) the type of base pairs, (3) salt concentration (ionic strength) of the reaction mixture, (4) the temperature of the reaction, and (5) the presence of certain organic solvents, such as formamide which decreases DNA duplex stability. In general, the longer the probe, the higher the temperature required for proper annealing. A common approach is to vary the temperature: higher relative temperatures result in more stringent reaction conditions. (Ausubel *et al.*, 1987) provide an excellent explanation of stringency of hybridization reactions.

To hybridize under "stringent conditions" describes hybridization protocols in which nucleotide sequences at least 60% homologous to each other remain hybridized. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH . The T_m is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target sequence hybridize to the target sequence at equilibrium. Since the target sequences are generally present at excess, at T_m , 50% of the probes are occupied at equilibrium.

(a) *high stringency*

"Stringent hybridization conditions" conditions enable a probe, primer or oligonucleotide to hybridize only to its target sequence. Stringent conditions are sequence-dependent and will differ. Stringent conditions comprise: (1) low ionic strength and high temperature washes (*e.g.* 15 mM sodium chloride, 1.5 mM sodium citrate, 0.1 % sodium dodecyl sulfate at 50°C); (2) a denaturing agent during hybridization (*e.g.* 50% (v/v) formamide, 0.1% bovine serum albumin, 0.1% Ficoll, 0.1% polyvinylpyrrolidone, 50mM sodium phosphate buffer (pH 6.5; 750 mM sodium chloride, 75 mM sodium citrate at 42°C); or (3) 50% formamide. Washes typically also comprise 5X SSC (0.75 M NaCl, 75 mM sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash

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consisting of 0.1 x SSC containing EDTA at 55°C. Preferably, the conditions are such that sequences at least about 65%, 70%, 75%, 85%, 90%, 95%, 98%, or 99% homologous to each other typically remain hybridized to each other. These conditions are presented as examples and are not meant to be limiting.

(b) *moderate stringency*

"Moderately stringent conditions" use washing solutions and hybridization conditions that are less stringent (Sambrook, 1989), such that a polynucleotide will hybridize to the entire, fragments, derivatives or analogs of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15. One example comprises hybridization in 6X SSC, 5X Denhardt's solution, 0.5% SDS and 100 mg/ml denatured salmon sperm DNA at 55°C, followed by one or more washes in 1X SSC, 0.1% SDS at 37°C. The temperature, ionic strength, *etc.*, can be adjusted to accommodate experimental factors such as probe length. Other moderate stringency conditions are described in (Ausubel *et al.*, 1987; Kriegler, 1990).

(c) *low stringency*

"Low stringent conditions" use washing solutions and hybridization conditions that are less stringent than those for moderate stringency (Sambrook, 1989), such that a polynucleotide will hybridize to the entire, fragments, derivatives or analogs of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15. A non-limiting example of low stringency hybridization conditions are hybridization in 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml denatured salmon sperm DNA, 10% (wt/vol) dextran sulfate at 40°C, followed by one or more washes in 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS at 50°C. Other conditions of low stringency, such as those for cross-species hybridizations are described in (Ausubel *et al.*, 1987; Kriegler, 1990; Shilo and Weinberg, 1981).

3. *Conservative mutations*

In addition to naturally-occurring allelic variants of AAP, changes can be introduced by mutation into SEQ ID NO NOS:1, 3, 5, 7, 9, 11, 13 or 15 sequences that incur alterations in the amino acid sequences of the encoded AAP that do not alter the AAP function. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in the sequence of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14 or 16. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequences of the AAP without altering their biological activity,

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whereas an "essential" amino acid residue is required for such biological activity. For example, amino acid residues that are conserved among the AAP of the invention are predicted to be particularly non-amenable to alteration. Amino acids for which conservative substitutions can be made are well-known in the art.

Useful conservative substitutions are shown in Table A, "Preferred substitutions." Conservative substitutions whereby an amino acid of one class is replaced with another amino acid of the same type fall within the scope of the subject invention so long as the substitution does not materially alter the biological activity of the compound. If such substitutions result in a change in biological activity, then more substantial changes, indicated in Table B as exemplary are introduced and the products screened for an AAP polypeptide's biological activity.

Table A Preferred substitutions

Original residue	Exemplary substitutions	Preferred substitutions
Ala (A)	Val, Leu, Ile	Val
Arg (R)	Lys, Gln, Asn	Lys
Asn (N)	Gln, His, Lys, Arg	Gln
Asp (D)	Glu	Glu
Cys (C)	Ser	Ser
Gln (Q)	Asn	Asn
Glu (E)	Asp	Asp
Gly (G)	Pro, Ala	Ala
His (H)	Asn, Gln, Lys, Arg	Arg
Ile (I)	Leu, Val, Met, Ala, Phe, Norleucine	Leu
Leu (L)	Norleucine, Ile, Val, Met, Ala, Phe	Ile
Lys (K)	Arg, Gln, Asn	Arg
Met (M)	Leu, Phe, Ile	Leu
Phe (F)	Leu, Val, Ile, Ala, Tyr	Leu
Pro (P)	Ala	Ala
Ser (S)	Thr	Thr
Thr (T)	Ser	Ser
Trp (W)	Tyr, Phe	Tyr
Tyr (Y)	Trp, Phe, Thr, Ser	Phe
Val (V)	Ile, Leu, Met, Phe, Ala, Norleucine	Leu

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Non-conservative substitutions that effect (1) the structure of the polypeptide backbone, such as a β -sheet or α -helical conformation, (2) the charge or (3) hydrophobicity, or (4) the bulk of the side chain of the target site can modify an AAP polypeptide's function or immunological identity. Residues are divided into groups based on common side-chain properties as denoted in Table B. Non-conservative substitutions entail exchanging a member of one of these classes for another class. Substitutions may be introduced into conservative substitution sites or more preferably into non-conserved sites.

Table B Amino acid classes

Class	Amino acids
hydrophobic	Norleucine, Met, Ala, Val, Leu, Ile
neutral hydrophilic	Cys, Ser, Thr
acidic	Asp, Glu
basic	Asn, Gln, His, Lys, Arg
disrupt chain conformation	Gly, Pro
aromatic	Trp, Tyr, Phe

The variant polypeptides can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis (Carter, 1986; Zoller and Smith, 1987), cassette mutagenesis, restriction selection mutagenesis (Wells *et al.*, 1985) or other known techniques can be performed on the cloned DNA to produce the AAP variant DNA (Ausubel *et al.*, 1987; Sambrook, 1989).

In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 45%, preferably 60%, more preferably 70%, 80%, 90%, and most preferably about 95% homologous to SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, or 15.

A mutant AAP can be assayed for blocking angiogenesis *in vitro*.

4. *Anti-sense nucleic acids*

Using antisense and sense AAP oligonucleotides can prevent AAP polypeptide expression. These oligonucleotides bind to target nucleic acid sequences, forming duplexes that block transcription or translation of the target sequence by enhancing

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degradation of the duplexes, terminating prematurely transcription or translation, or by other means.

Antisense or sense oligonucleotides are single-stranded nucleic acids, either RNA or DNA, which can bind a target *AAP* mRNA (sense) or an *AAP* DNA (antisense) sequences. Anti-sense nucleic acids can be designed according to Watson and Crick or Hoogsteen base pairing rules. The anti-sense nucleic acid molecule can be complementary to the entire coding region of an *AAP* mRNA, but more preferably, to only a portion of the coding or noncoding region of an *AAP* mRNA. For example, the anti-sense oligonucleotide can be complementary to the region surrounding the translation start site of an *AAP* mRNA. Antisense or sense oligonucleotides may comprise a fragment of the *AAP* DNA coding region of at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. In general, antisense RNA or DNA molecules can comprise at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100 bases in length or more. Among others, (Stein and Cohen, 1988; van der Krol *et al.*, 1988a) describe methods to derive antisense or a sense oligonucleotides from a given cDNA sequence.

Examples of modified nucleotides that can be used to generate the anti-sense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the anti-sense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been sub-cloned in an anti-sense orientation such that the transcribed RNA will be complementary to a target nucleic acid of interest.

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To introduce antisense or sense oligonucleotides into target cells (cells containing the target nucleic acid sequence), any gene transfer method may be used. Examples of gene transfer methods include (1) biological, such as gene transfer vectors like Epstein-Barr virus or conjugating the exogenous DNA to a ligand-binding molecule, (2) physical, such as electroporation and injection, and (3) chemical, such as CaPO_4 precipitation and oligonucleotide-lipid complexes.

An antisense or sense oligonucleotide is inserted into a suitable gene transfer retroviral vector. A cell containing the target nucleic acid sequence is contacted with the recombinant retroviral vector, either *in vivo* or *ex vivo*. Examples of suitable retroviral vectors include those derived from the murine retrovirus M-MuLV, N2 (a retrovirus derived from M-MuLV), or the double copy vectors designated DCT5A, DCT5B and DCT5C (WO 90/13641, 1990). To achieve sufficient nucleic acid molecule transcription, vector constructs in which the transcription of the anti-sense nucleic acid molecule is controlled by a strong pol II or pol III promoter are preferred.

To specify target cells in a mixed population of cells cell surface receptors that are specific to the target cells can be exploited. Antisense and sense oligonucleotides are conjugated to a ligand-binding molecule, as described in (WO 91/04753, 1991). Ligands are chosen for receptors that are specific to the target cells. Examples of suitable ligand-binding molecules include cell surface receptors, growth factors, cytokines, or other ligands that bind to cell surface receptors or molecules. Preferably, conjugation of the ligand-binding molecule does not substantially interfere with the ability of the receptors or molecule to bind the ligand-binding molecule conjugate, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell.

Liposomes efficiently transfer sense or an antisense oligonucleotide to cells (WO 90/10448, 1990). The sense or antisense oligonucleotide-lipid complex is preferably dissociated within the cell by an endogenous lipase.

The anti-sense nucleic acid molecule of the invention may be an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual α -units, the strands run parallel to each other (Gautier *et al.*, 1987). The anti-sense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.*, 1987a) or a chimeric RNA-DNA analogue (Inoue *et al.*, 1987b).

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In one embodiment, an anti-sense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes, such as hammerhead ribozymes (Haseloff and Gerlach, 1988) can be used to catalytically cleave *AAP* mRNA transcripts and thus inhibit translation. A ribozyme specific for an *AAP*-encoding nucleic acid can be designed based on the nucleotide sequence of an *AAP* cDNA (*i.e.*, SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an *AAP*-encoding mRNA (Cech *et al.*, U.S. Patent No. 5,116,742, 1992; Cech *et al.*, U.S. Patent No. 4,987,071, 1991). An *AAP* mRNA can also be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules (Bartel and Szostak, 1993).

Alternatively, *AAP* expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an *AAP* (*e.g.*, an *AAP* promoter and/or enhancers) to form triple helical structures that prevent transcription of an *AAP* in target cells (Helene, 1991; Helene *et al.*, 1992; Maher, 1992).

Modifications of antisense and sense oligonucleotides can augment their effectiveness. Modified sugar-phosphodiester bonds or other sugar linkages (WO 91/06629, 1991), increase *in vivo* stability by conferring resistance to endogenous nucleases without disrupting binding specificity to target sequences. Other modifications can increase the affinities of the oligonucleotides for their targets, such as covalently linked organic moieties (WO 90/10448, 1990) or poly-(L)-lysine. Other attachments modify binding specificities of the oligonucleotides for their targets, including metal complexes or intercalating (*e.g.* ellipticine) and alkylating agents.

For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (Hyrup and Nielsen, 1996). "Peptide nucleic acids" or "PNAs" refer to nucleic acid mimics (*e.g.*, DNA mimics) in that the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs allows for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of

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PNA oligomers can be performed using standard solid phase peptide synthesis protocols (Hyrup and Nielsen, 1996; Perry-O'Keefe *et al.*, 1996).

PNAs of an AAP can be used in therapeutic and diagnostic applications. For example, PNAs can be used as anti-sense or antigene agents for sequence-specific modulation of gene expression by inducing transcription or translation arrest or inhibiting replication. AAP PNAs may also be used in the analysis of single base pair mutations (*e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S₁ nucleases (Hyrup and Nielsen, 1996); or as probes or primers for DNA sequence and hybridization (Hyrup and Nielsen, 1996; Perry-O'Keefe *et al.*, 1996).

PNAs of an AAP can be modified to enhance their stability or cellular uptake. Lipophilic or other helper groups may be attached to PNAs, PNA-DNA dimmers formed, or the use of liposomes or other drug delivery techniques. For example, PNA-DNA chimeras can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes (*e.g.*, RNase H and DNA polymerases) to interact with the DNA portion while the PNA portion provides high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup and Nielsen, 1996). The synthesis of PNA-DNA chimeras can be performed (Finn *et al.*, 1996; Hyrup and Nielsen, 1996). For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Finn *et al.*, 1996; Hyrup and Nielsen, 1996). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.*, 1996). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment (Petersen *et al.*, 1976).

The oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (Lemaitre *et al.*, 1987; Letsinger *et al.*, 1989) or PCT Publication No. WO88/09810) or the blood-brain barrier (*e.g.*, PCT Publication No. WO 89/10134). In addition, oligonucleotides can be modified with hybridization-triggered cleavage agents

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(van der Krol *et al.*, 1988b) or intercalating agents (Zon, 1988). The oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, and the like.

AAP polypeptides

One aspect of the invention pertains to isolated AAP, and biologically-active portions derivatives, fragments, analogs or homologs thereof. Also provided are polypeptide fragments suitable for use as immunogens to raise anti-AAP Abs. In one embodiment, a native AAP can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, AAP are produced by recombinant DNA techniques. Alternative to recombinant expression, an AAP can be synthesized chemically using standard peptide synthesis techniques.

1. *Polypeptides*

An AAP polypeptide includes the amino acid sequence of an AAP whose sequences are provided in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14 or 16. The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residues shown in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14 or 16, while still encoding a protein that maintains its AAP activities and physiological functions, or a functional fragment thereof.

2. *Variant AAP polypeptides*

In general, an AAP variant that preserves an AAP-like function and includes any variant in which residues at a particular position in the sequence have been substituted by other amino acids, and further includes the possibility of inserting an additional residue or residues between two residues of the parent protein as well as the possibility of deleting one or more residues from the parent sequence. Any amino acid substitution, insertion, or deletion is encompassed by the invention. In favorable circumstances, the substitution is a conservative substitution as defined above.

“AAP polypeptide variant” means an active AAP polypeptide having at least: (1) about 80% amino acid sequence identity with a full-length native sequence AAP polypeptide sequence, (2) an AAP polypeptide sequence lacking the signal peptide, (3) an extracellular domain of an AAP polypeptide, with or without the signal peptide, or (4)

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any other fragment of a full-length AAP polypeptide sequence. For example, AAP polypeptide variants include AAP polypeptides wherein one or more amino acid residues are added or deleted at the N- or C- terminus of the full-length native amino acid sequence. An AAP polypeptide variant will have at least about 80% amino acid sequence identity, preferably at least about 81% amino acid sequence identity, more preferably at least about 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% amino acid sequence identity and most preferably at least about 99% amino acid sequence identity with a full-length native sequence AAP polypeptide sequence. An AAP polypeptide variant may have a sequence lacking the signal peptide, an extracellular domain of an AAP polypeptide, with or without the signal peptide, or any other fragment of a full-length AAP polypeptide sequence. Ordinarily, AAP variant polypeptides are at least about 10 amino acids in length, often at least about 20 amino acids in length, more often at least about 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, or 300 amino acids in length, or more.

“Percent (%) amino acid sequence identity” is defined as the percentage of amino acid residues that are identical with amino acid residues in a disclosed AAP polypeptide sequence in a candidate sequence when the two sequences are aligned. To determine % amino acid identity, sequences are aligned and if necessary, gaps are introduced to achieve the maximum % sequence identity; conservative substitutions are not considered as part of the sequence identity. Amino acid sequence alignment procedures to determine percent identity are well known to those of skill in the art. Often publicly available computer software such as BLAST, BLAST2, ALIGN2 or Megalign (DNASTAR) software is used to align peptide sequences. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared.

When amino acid sequences are aligned, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) can be calculated as:

$$\% \text{amino acid sequence identity} = X/Y \cdot 100$$

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where

X is the number of amino acid residues scored as identical matches by the sequence alignment program's or algorithm's alignment of A and B

and

Y is the total number of amino acid residues in B.

If the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A.

3. *Isolated/purified polypeptides*

An "isolated" or "purified" polypeptide, protein or biologically active fragment is separated and/or recovered from a component of its natural environment. Contaminant components include materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous materials. Preferably, the polypeptide is purified to a sufficient degree to obtain at least 15 residues of N-terminal or internal amino acid sequence. To be substantially isolated, preparations having less than 30% by dry weight of non-AAP contaminating material (contaminants), more preferably less than 20%, 10% and most preferably less than 5% contaminants. An isolated, recombinantly-produced AAP or biologically active portion is preferably substantially free of culture medium, *i.e.*, culture medium represents less than 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the AAP preparation. Examples of contaminants include cell debris, culture media, and substances used and produced during *in vitro* synthesis of an AAP.

4. *Biologically active*

Biologically active portions of an AAP include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequences of an AAP (SEQ ID NOS:2, 4, 6, 8, 10, 12, 14 or 16) that include fewer amino acids than a full-length AAP, and exhibit at least one activity of an AAP. Biologically active portions comprise a domain or motif with at least one activity of a native AAP. A biologically active portion of an AAP can be a polypeptide that is, for example, 10, 25, 50, 100 or more amino acid residues in length. Other biologically active portions, in which other

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regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native AAP.

Biologically active portions of an AAP may have an amino acid sequence shown in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14 or 16, or substantially homologous to SEQ ID NOS:2, 4, 6, 8, 10, 12, 14 or 16, and retains the functional activity of the protein of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14 or 16, yet differs in amino acid sequence due to natural allelic variation or mutagenesis. Other biologically active AAP may comprise an amino acid sequence at least 45% homologous to the amino acid sequence of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14 or 16, and retains the functional activity of native AAP.

5. *Determining homology between two or more sequences*

“AAP variant” means an active AAP having at least: (1) about 80% amino acid sequence identity with a full-length native sequence AAP sequence, (2) an AAP sequence lacking the signal peptide, (3) an extracellular domain of an AAP, with or without the signal peptide, or (4) any other fragment of a full-length AAP sequence. For example, AAP variants include an AAP wherein one or more amino acid residues are added or deleted at the N- or C- terminus of the full-length native amino acid sequence. An AAP variant will have at least about 80% amino acid sequence identity, preferably at least about 81% amino acid sequence identity, more preferably at least about 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% amino acid sequence identity and most preferably at least about 99% amino acid sequence identity with a full-length native sequence AAP sequence. An AAP variant may have a sequence lacking the signal peptide, an extracellular domain of an AAP, with or without the signal peptide, or any other fragment of a full-length AAP sequence. Ordinarily, AAP variant polypeptides are at least about 10 amino acids in length, often at least about 20 amino acids in length, more often at least about 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, or 300 amino acids in length, or more.

“Percent (%) amino acid sequence identity” is defined as the percentage of amino acid residues that are identical with amino acid residues in a disclosed AAP sequence in a candidate sequence when the two sequences are aligned. To determine % amino acid identity, sequences are aligned and if necessary, gaps are introduced to achieve the maximum % sequence identity; conservative substitutions are not considered as part of the sequence identity. Amino acid sequence alignment procedures to determine percent

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identity are well known to those of skill in the art. Often publicly available computer software such as BLAST, BLAST2, ALIGN2 or Megalign (DNASTAR) software is used to align peptide sequences. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared.

When amino acid sequences are aligned, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) can be calculated as:

$$\% \text{amino acid sequence identity} = X/Y \cdot 100$$

where

X is the number of amino acid residues scored as identical matches by the sequence alignment program's or algorithm's alignment of A and B
and

Y is the total number of amino acid residues in B.

If the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A.

6. *Chimeric and fusion proteins*

Fusion polypeptides are useful in expression studies, cell-localization, bioassays, and AAP purification. An AAP "chimeric protein" or "fusion protein" comprises an AAP fused to a non-AAP polypeptide. A non-AAP polypeptide is not substantially homologous to an AAP (SEQ ID NOS:2, 4, 6, 8, 10, 12, 14 or 16). An AAP fusion protein may include any portion to an entire AAP, including any number of the biologically active portions. An AAP may be fused to the C-terminus of the GST (glutathione S-transferase) sequences. Such fusion proteins facilitate the purification of a recombinant AAP. In certain host cells, (e.g. mammalian), heterologous signal

sequences fusions may ameliorate AAP expression and/or secretion. Additional exemplary fusions are presented in Table C.

Other fusion partners can adapt an AAP therapeutically. Fusions with members of the immunoglobulin (Ig) protein family are useful in therapies that inhibit an AAP ligand or substrate interactions, consequently suppressing an AAP-mediated signal transduction *in vivo*. Such fusions, incorporated into pharmaceutical compositions, may be used to treat proliferative and differentiation disorders, as well as modulating cell survival. An AAP-Ig fusion polypeptides can also be used as immunogens to produce an anti-AAP Abs in a subject, to purify AAP ligands, and to screen for molecules that inhibit interactions of an AAP with other molecules.

Fusion proteins can be easily created using recombinant methods. A nucleic acid encoding an AAP can be fused in-frame with a non-AAP encoding nucleic acid, to an AAP NH₂- or COO- -terminus, or internally. Fusion genes may also be synthesized by conventional techniques, including automated DNA synthesizers. PCR amplification using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (Ausubel *et al.*, 1987) is also useful. Many vectors are commercially available that facilitate sub-cloning an AAP in-frame to a fusion moiety.

Table C Useful non-AAP fusion polypeptides

Reporter	<i>in vitro</i>	<i>in vivo</i>	Notes	Reference
Human growth hormone (hGH)	Radioimmunoassay	none	Expensive, insensitive, narrow linear range.	(Selden <i>et al.</i> , 1986)
β -glucuronidase (GUS)	Colorimetric, fluorescent, or chemiluminescent	colorimetric (histo-chemical staining with X-gluc)	sensitive, broad linear range, non-isotopic.	(Gallagher, 1992)
Green fluorescent protein (GFP) and related molecules (RFP, BFP, AAP, <i>etc.</i>)	Fluorescent	fluorescent	can be used in live cells; resists photo-bleaching	(Chalfie <i>et al.</i> , 1994)

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Luciferase (firefly)	bioluminescent	Bio-luminescent	protein is unstable, difficult to reproduce, signal is brief	(de Wet <i>et al.</i> , 1987)
Chloramphenicol acetyltransferase (CAT)	Chromatography, differential extraction, fluorescent, or immunoassay	none	Expensive radioactive substrates, time-consuming, insensitive, narrow linear range	(Gorman <i>et al.</i> , 1982)
β -galactosidase	colorimetric, fluorescence, chemiluminescence	colorimetric (histochemical staining with X-gal), bioluminescent in live cells	sensitive, broad linear range; some cells have high endogenous activity	(Alam and Cook, 1990)
Secreted alkaline phosphatase (SEAP)	colorimetric, bioluminescent, chemiluminescent	none	Chemiluminescence assay is sensitive and broad linear range; some cells have endogenous alkaline phosphatase activity	(Berger <i>et al.</i> , 1988)

Therapeutic applications of AAP

1. *Agonists and antagonists*

“Antagonist” includes any molecule that partially or fully blocks, inhibits, or neutralizes a biological activity of an endogenous AAP. Similarly, “agonist” includes any molecule that mimics a biological activity of an endogenous AAP. Molecules that can act as agonists or antagonists include Abs or antibody fragments, fragments or variants of an endogenous AAP, peptides, antisense oligonucleotides, small organic molecules, *etc.*

2. *Identifying antagonists and agonists*

To assay for antagonists, an AAP is added to, or expressed in, a cell along with the compound to be screened for a particular activity. If the compound inhibits the

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activity of interest in the presence of an AAP, that compound is an antagonist to the AAP; if an AAP activity is enhanced, the compound is an agonist.

(a) *Specific examples of potential antagonists and agonist*

Any molecule that alters AAP cellular effects is a candidate antagonist or agonist. Screening techniques well known to those skilled in the art can identify these molecules. Examples of antagonists and agonists include: (1) small organic and inorganic compounds, (2) small peptides, (3) Abs and derivatives, (4) polypeptides closely related to an AAP, (5) antisense DNA and RNA, (6) ribozymes, (7) triple DNA helices and (8) nucleic acid aptamers.

Small molecules that bind to an AAP active site or other relevant part of the polypeptide and inhibit the biological activity of the AAP are antagonists. Examples of small molecule antagonists include small peptides, peptide-like molecules, preferably soluble, and synthetic non-peptidyl organic or inorganic compounds. These same molecules, if they enhance an AAP activity, are examples of agonists.

Almost any antibody that affects an AAP's function is a candidate antagonist, and occasionally, agonist. Examples of antibody antagonists include polyclonal, monoclonal, single-chain, anti-idiotypic, chimeric Abs, or humanized versions of such Abs or fragments. Abs may be from any species in which an immune response can be raised. Humanized Abs are also contemplated.

Alternatively, a potential antagonist or agonist may be a closely related protein, for example, a mutated form of an AAP that recognizes an AAP-interacting protein but imparts no effect, thereby competitively inhibiting AAP action. Alternatively, a mutated AAP may be constitutively activated and may act as an agonist.

Antisense RNA or DNA constructs can be effective antagonists. Antisense RNA or DNA molecules block function by inhibiting translation by hybridizing to targeted mRNA. Antisense technology can be used to control gene expression through triple-helix formation or antisense DNA or RNA, both of which depend on polynucleotide binding to DNA or RNA. For example, the 5' coding portion of an AAP sequence 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) (Beal and Dervan, 1991; Cooney *et al.*, 1988; Lee *et al.*, 1979), thereby preventing transcription and the production of the AAP. The antisense RNA

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oligonucleotide hybridizes to the mRNA *in vivo* and blocks translation of the mRNA molecule into the AAP (antisense) (Cohen, 1989; Okano *et al.*, 1991). These oligonucleotides can also be delivered to cells such that the antisense RNA or DNA may be expressed *in vivo* to inhibit production of the AAP. When antisense DNA is used, oligodeoxyribonucleotides derived from the translation-initiation site, *e.g.*, between about -10 and +10 positions of the target gene nucleotide sequence, are preferred.

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. Ribozymes act by sequence-specific hybridization to the complementary target RNA, followed by endonucleolytic cleavage. Specific ribozyme cleavage sites within a potential RNA target can be identified by known techniques (WO 97/33551, 1997; Rossi, 1994).

To inhibit transcription, triple-helix nucleic acids that are single-stranded and comprise deoxynucleotides are useful antagonists. These oligonucleotides are designed such that triple-helix formation via Hoogsteen base-pairing rules is promoted, generally requiring stretches of purines or pyrimidines (WO 97/33551, 1997).

Aptamers are short oligonucleotide sequences that can be used to recognize and specifically bind almost any molecule. The systematic evolution of ligands by exponential enrichment (SELEX) process (Ausubel *et al.*, 1987; Ellington and Szostak, 1990; Tuerk and Gold, 1990) is powerful and can be used to find such aptamers. Aptamers have many diagnostic and clinical uses; almost any use in which an antibody has been used clinically or diagnostically, aptamers too may be used. In addition, they are cheaper to make once they have been identified, and can be easily applied in a variety of formats, including administration in pharmaceutical compositions, in bioassays, and diagnostic tests (Jayasena, 1999).

Anti-AAP Abs

The invention encompasses Abs and antibody fragments, such as F_{ab} or (F_{ab})₂, that bind immunospecifically to any AAP epitopes.

“Antibody” (Ab) comprises single Abs directed against an AAP (anti-AAP Ab; including agonist, antagonist, and neutralizing Abs), anti-AAP Ab compositions with poly-epitope specificity, single chain anti-AAP Abs, and fragments of anti-AAP Abs. A “monoclonal antibody” is obtained from a population of substantially homogeneous Abs,

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i.e., the individual Abs comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts. Exemplary Abs include polyclonal (pAb), monoclonal (mAb), humanized, bi-specific (bsAb), and heteroconjugate Abs.

1. *Polyclonal Abs (pAbs)*

Polyclonal Abs can be raised in a mammalian host, for example, by one or more injections of an immunogen and, if desired, an adjuvant. Typically, the immunogen and/or adjuvant are injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunogen may include an AAP or a fusion protein. Examples of adjuvants include Freund's complete and monophosphoryl Lipid A synthetic-trehalose dicorynomycolate (MPL-TDM). To improve the immune response, an immunogen may be conjugated to a protein that is immunogenic in the host, such as keyhole limpet hemocyanin (KLH), serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Protocols for antibody production are described by (Ausubel *et al.*, 1987; Harlow and Lane, 1988). Alternatively, pAbs may be made in chickens, producing IgY molecules (Schade *et al.*, 1996).

2. *Monoclonal Abs (mAbs)*

Anti-AAP mAbs may be prepared using hybridoma methods (Milstein and Cuello, 1983). Hybridoma methods comprise at least four steps: (1) immunizing a host, or lymphocytes from a host; (2) harvesting the mAb secreting (or potentially secreting) lymphocytes, (3) fusing the lymphocytes to immortalized cells, and (4) selecting those cells that secrete the desired (anti-AAP) mAb.

A mouse, rat, guinea pig, hamster, or other appropriate host is immunized to elicit lymphocytes that produce or are capable of producing Abs that will specifically bind to the immunogen. Alternatively, the lymphocytes may be immunized *in vitro*. If human cells are desired, peripheral blood lymphocytes (PBLs) are generally used; however, spleen cells or lymphocytes from other mammalian sources are preferred. The immunogen typically includes an AAP or a fusion protein.

The lymphocytes are then fused with an immortalized cell line to form hybridoma cells, facilitated by a fusing agent such as polyethylene glycol (Goding, 1996). Rodent, bovine, or human myeloma cells immortalized by transformation may be used, or rat or mouse myeloma cell lines. Because pure populations of hybridoma cells and not unfused

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immortalized cells are preferred, the cells after fusion are grown in a suitable medium that contains one or more substances that inhibit the growth or survival of unfused, immortalized cells. A common technique uses parental cells that lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT). In this case, hypoxanthine, aminopterin and thymidine are added to the medium (HAT medium) to prevent the growth of HGPRT-deficient cells while permitting hybridomas to grow.

Preferred immortalized cells fuse efficiently, can be isolated from mixed populations by selecting in a medium such as HAT, and support stable and high-level expression of antibody after fusion. Preferred immortalized cell lines are murine myeloma lines, available from the American Type Culture Collection (Manassas, VA). Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human mAbs (Kozbor *et al.*, 1984; Schook, 1987).

Because hybridoma cells secrete antibody extracellularly, the culture media can be assayed for the presence of mAbs directed against an AAP (anti-AAP mAbs). Immunoprecipitation or *in vitro* binding assays, such as radio immunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA), measure the binding specificity of mAbs (Harlow and Lane, 1988; Harlow and Lane, 1999), including Scatchard analysis (Munson and Rodbard, 1980).

Anti-AAP mAb secreting hybridoma cells may be isolated as single clones by limiting dilution procedures and sub-cultured (Goding, 1996). Suitable culture media include Dulbecco's Modified Eagle's Medium, RPMI-1640, or if desired, a protein-free or -reduced or serum-free medium (*e.g.*, Ultra DOMA PF or HL-1; Biowhittaker; Walkersville, MD). The hybridoma cells may also be grown *in vivo* as ascites.

The mAbs may be isolated or purified from the culture medium or ascites fluid by conventional Ig purification procedures such as protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, ammonium sulfate precipitation or affinity chromatography (Harlow and Lane, 1988; Harlow and Lane, 1999).

The mAbs may also be made by recombinant methods (U.S. Patent No. 4166452, 1979). DNA encoding anti-AAP mAbs can be readily isolated and sequenced using conventional procedures, *e.g.*, using oligonucleotide probes that specifically bind to murine heavy and light antibody chain genes, to probe preferably DNA isolated from anti-AAP-secreting mAb hybridoma cell lines. Once isolated, the isolated DNA

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fragments are sub-cloned into expression vectors that are then transfected into host cells such as simian COS-7 cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce Ig protein, to express mAbs. The isolated DNA fragments can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4816567, 1989; Morrison *et al.*, 1987), or by fusing the Ig coding sequence to all or part of the coding sequence for a non-Ig polypeptide. Such a non-Ig polypeptide can be substituted for the constant domains of an antibody, or can be substituted for the variable domains of one antigen-combining site to create a chimeric bivalent antibody.

3. *Monovalent Abs*

The Abs may be monovalent Abs that consequently do not cross-link with each other. For example, one method involves recombinant expression of Ig light chain and modified heavy chain. Heavy chain truncations generally at any point in the F_c region will prevent heavy chain cross-linking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted, preventing crosslinking. *In vitro* methods are also suitable for preparing monovalent Abs. Abs can be digested to produce fragments, such as F_{ab} fragments (Harlow and Lane, 1988; Harlow and Lane, 1999).

4. *Humanized and human Abs*

Anti-AAP Abs may further comprise humanized or human Abs. Humanized forms of non-human Abs are chimeric Igs, Ig chains or fragments (such as F_v , F_{ab} , F_{ab}' , $F_{(ab)2}$ or other antigen-binding subsequences of Abs) that contain minimal sequence derived from non-human Ig.

Generally, a humanized antibody has one or more amino acid residues introduced from a non-human source. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization is accomplished by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody (Jones *et al.*, 1986; Riechmann *et al.*, 1988; Verhoeyen *et al.*, 1988). Such "humanized" Abs are chimeric Abs (U.S. Patent No. 4816567, 1989), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized Abs are typically human Abs in which some CDR residues and possibly some

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FR residues are substituted by residues from analogous sites in rodent Abs. Humanized Abs include human Igs (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit, having the desired specificity, affinity and capacity. In some instances, corresponding non-human residues replace F_v framework residues of the human Ig. Humanized Abs may comprise residues that are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody comprises substantially all of at least one, and typically two, variable domains, in which most if not all of the CDR regions correspond to those of a non-human Ig and most if not all of the FR regions are those of a human Ig consensus sequence. The humanized antibody optimally also comprises at least a portion of an Ig constant region (F_c), typically that of a human Ig (Jones *et al.*, 1986; Presta, 1992; Riechmann *et al.*, 1988).

Human Abs can also be produced using various techniques, including phage display libraries (Hoogenboom *et al.*, 1991; Marks *et al.*, 1991) and the preparation of human mAbs (Boerner *et al.*, 1991; Reisfeld and Sell, 1985). Similarly, introducing human Ig genes into transgenic animals in which the endogenous Ig genes have been partially or completely inactivated can be exploited to synthesize human Abs. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire (U.S. Patent No. 5545807, 1996; U.S. Patent No. 5545806, 1996; U.S. Patent No. 5569825, 1996; U.S. Patent No. 5633425, 1997; U.S. Patent No. 5661016, 1997; U.S. Patent No. 5625126, 1997; Fishwild *et al.*, 1996; Lonberg and Huszar, 1995; Lonberg *et al.*, 1994; Marks *et al.*, 1992).

5. *Bi-specific mAbs*

Bi-specific Abs are monoclonal, preferably human or humanized, that have binding specificities for at least two different antigens. For example, a binding specificity is an AAP; the other is for any antigen of choice, preferably a cell-surface protein or receptor or receptor subunit.

Traditionally, the recombinant production of bi-specific Abs is based on the co-expression of two Ig heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, 1983). Because of the random assortment of

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Ig heavy and light chains, the resulting hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the desired bi-specific structure. The desired antibody can be purified using affinity chromatography or other techniques (WO 93/08829, 1993; Traunecker *et al.*, 1991).

To manufacture a bi-specific antibody (Suresh *et al.*, 1986), variable domains with the desired antibody-antigen combining sites are fused to Ig constant domain sequences. The fusion is preferably with an Ig heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. Preferably, the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding is in at least one of the fusions. DNAs encoding the Ig heavy-chain fusions and, if desired, the Ig light chain, are inserted into separate expression vectors and are co-transfected into a suitable host organism.

The interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers that are recovered from recombinant cell culture (WO 96/27011, 1996). The preferred interface comprises at least part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (*e.g.* tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (*e.g.* alanine or threonine). This mechanism increases the yield of the heterodimer over unwanted end products such as homodimers.

Bi-specific Abs can be prepared as full length Abs or antibody fragments (*e.g.* $F_{(ab)2}$ bi-specific Abs). One technique to generate bi-specific Abs exploits chemical linkage. Intact Abs can be proteolytically cleaved to generate $F_{(ab)2}$ fragments (Brennan *et al.*, 1985). Fragments are reduced with a dithiol complexing agent, such as sodium arsenite, to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The generated F_{ab} fragments are then converted to thionitrobenzoate (TNB) derivatives. One of the F_{ab} -TNB derivatives is then reconverted to the F_{ab} -thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other F_{ab} -TNB derivative to form the bi-specific antibody. The produced bi-specific Abs can be used as agents for the selective immobilization of enzymes.

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$F_{ab'}$ fragments may be directly recovered from *E. coli* and chemically coupled to form bi-specific Abs. For example, fully humanized bi-specific $F_{(ab')_2}$ Abs can be produced (Shalaby *et al.*, 1992). Each $F_{ab'}$ fragment is separately secreted from *E. coli* and directly coupled chemically *in vitro*, forming the bi-specific antibody.

Various techniques for making and isolating bi-specific antibody fragments directly from recombinant cell culture have also been described. For example, leucine zipper motifs can be exploited (Kostelny *et al.*, 1992). Peptides from the *Fos* and *Jun* proteins are linked to the $F_{ab'}$ portions of two different Abs by gene fusion. The antibody homodimers are reduced at the hinge region to form monomers and then re-oxidized to form antibody heterodimers. This method can also produce antibody homodimers. The "diabody" technology (Holliger *et al.*, 1993) provides an alternative method to generate bi-specific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker that is too short to allow pairing between the two domains on the same chain. The V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, forming two antigen-binding sites. Another strategy for making bi-specific antibody fragments is the use of single-chain F_v (sF_v) dimers (Gruber *et al.*, 1994). Abs with more than two valencies are also contemplated, such as tri-specific Abs (Tutt *et al.*, 1991).

Exemplary bi-specific Abs may bind to two different epitopes on a given AAP. Alternatively, cellular defense mechanisms can be restricted to a particular cell expressing the particular AAP: an anti-AAP arm may be combined with an arm that binds to a leukocyte triggering molecule, such as a T-cell receptor molecule (*e.g.* CD2, CD3, CD28, or B7), or to F_c receptors for IgG ($F_c\gamma R$), such as $F_c\gamma RI$ (CD64), $F_c\gamma RII$ (CD32) and $F_c\gamma RIII$ (CD16). Bi-specific Abs may also be used to target cytotoxic agents to cells that express a particular AAP. These Abs possess an AAP-binding arm and an arm that binds a cytotoxic agent or a radionuclide chelator.

6. Heteroconjugate Abs

Heteroconjugate Abs, consisting of two covalently joined Abs, have been proposed to target immune system cells to unwanted cells (4,676,980, 1987) and for treatment of human immunodeficiency virus (HIV) infection (WO 91/00360, 1991; WO 92/20373, 1992). Abs prepared *in vitro* using synthetic protein chemistry methods,

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including those involving cross-linking agents, are contemplated. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents include iminothiolate and methyl-4-mercaptopbutyrimidate (4,676,980, 1987).

7. *Immunoconjugates*

Immunoconjugates may comprise an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (*e.g.*, an enzymatically active toxin or fragment of bacterial, fungal, plant, or animal origin), or a radioactive isotope (*i.e.*, a radioconjugate).

Useful enzymatically-active toxins and fragments include Diphtheria A chain, non-binding active fragments of Diphtheria toxin, exotoxin A chain from *Pseudomonas aeruginosa*, ricin A chain, abrin A chain, modeccin A chain, α -sarcin, *Aleurites fordii* proteins, Dianthin proteins, *Phytolaca americana* proteins, *Momordica charantia* inhibitor, curcin, crotin, *Sapaonaria officinalis* inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated Abs, such as ^{212}Bi , ^{131}I , ^{131}In , ^{90}Y , and ^{186}Re .

Conjugates of the antibody and cytotoxic agent are made using a variety of bi-functional protein-coupling agents, such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bi-functional derivatives of imidoesters (such as dimethyl adipimidate HCl), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), *bis*-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), *bis*-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6- diisocyanate), and *bis*-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared (Vitetta *et al.*, 1987). ^{14}C -labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugating radionuclide to antibody (WO 94/11026, 1994).

In another embodiment, the antibody may be conjugated to a "receptor" (such as streptavidin) for utilization in tumor pre-targeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a streptavidin "ligand" (*e.g.*, biotin) that is conjugated to a cytotoxic agent (*e.g.*, a radionuclide).

8. *Effector function engineering*

The antibody can be modified to enhance its effectiveness in treating a disease, such as cancer. For example, cysteine residue(s) may be introduced into the F_c region, thereby allowing interchain disulfide bond formation in this region. Such homodimeric Abs may have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC) (Caron *et al.*, 1992; Shopes, 1992). Homodimeric Abs with enhanced anti-tumor activity can be prepared using hetero-bifunctional cross-linkers (Wolff *et al.*, 1993). Alternatively, an antibody engineered with dual F_c regions may have enhanced complement lysis (Stevenson *et al.*, 1989).

9. *Immunoliposomes*

Liposomes containing the antibody may also be formulated (U.S. Patent No. 4485045, 1984; U.S. Patent No. 4544545, 1985; U.S. Patent No. 5013556, 1991; Eppstein *et al.*, 1985; Hwang *et al.*, 1980). Useful liposomes can be generated by a reverse-phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol, and PEG-derivatized phosphatidylethanolamine (PEG-PE). Such preparations are extruded through filters of defined pore size to yield liposomes with a desired diameter. F_{ab} fragments of the antibody can be conjugated to the liposomes (Martin and Papahadjopoulos, 1982) via a disulfide-interchange reaction. A chemotherapeutic agent, such as Doxorubicin, may also be contained in the liposome (Gabizon *et al.*, 1989). Other useful liposomes with different compositions are contemplated.

10. *Diagnostic applications of Abs directed against an AAP*

Anti-AAP Abs can be used to localize and/or quantitate an AAP (*e.g.*, for use in measuring levels of an AAP within tissue samples or for use in diagnostic methods, *etc.*). Anti-AAP epitope Abs can be utilized as pharmacologically-active compounds.

Anti-AAP Abs can be used to isolate an AAP by standard techniques, such as immunoaffinity chromatography or immunoprecipitation. These approaches facilitate purifying an endogenous AAP antigen-containing polypeptides from cells and tissues. These approaches, as well as others, can be used to detect an AAP in a sample to evaluate the abundance and pattern of expression of the antigenic protein. Anti-AAP Abs can be used to monitor protein levels in tissues as part of a clinical testing procedure; for

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example, to determine the efficacy of a given treatment regimen. Coupling the antibody to a detectable substance (label) allows detection of Ab-antigen complexes. Classes of labels include fluorescent, luminescent, bioluminescent, and radioactive materials, enzymes and prosthetic groups. Useful labels include horseradish peroxidase, alkaline phosphatase, β -galactosidase, acetylcholinesterase, streptavidin/biotin, avidin/biotin, umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride, phycoerythrin, luminol, luciferase, luciferin, aequorin, and ^{125}I , ^{131}I , ^{35}S or ^3H .

11. *Antibody therapeutics*

Abs of the invention, including polyclonal, monoclonal, humanized and fully human Abs, can be used therapeutically. Such agents will generally be employed to treat or prevent a disease or pathology in a subject. An antibody preparation, preferably one having high antigen specificity and affinity generally mediates an effect by binding the target epitope(s). Generally, administration of such Abs may mediate one of two effects: (1) the antibody may prevent ligand binding, eliminating endogenous ligand binding and subsequent signal transduction, or (2) the antibody elicits a physiological result by binding an effector site on the target molecule, initiating signal transduction.

A therapeutically effective amount of an antibody relates generally to the amount needed to achieve a therapeutic objective, epitope binding affinity, administration rate, and depletion rate of the antibody from a subject. Common ranges for therapeutically effective doses may be, as a nonlimiting example, from about 0.1 mg/kg body weight to about 50 mg/kg body weight. Dosing frequencies may range, for example, from twice daily to once a week.

12. *Pharmaceutical compositions of Abs*

Anti-AAP Abs, as well as other AAP interacting molecules (such as aptamers) identified in other assays, can be administered in pharmaceutical compositions to treat various disorders. Principles and considerations involved in preparing such compositions, as well as guidance in the choice of components can be found in (de Boer, 1994; Gennaro, 2000; Lee, 1990).

Since some AAP are intracellular, Abs that are internalized are preferred used when whole Abs are used as inhibitors. Liposomes may also be used as a delivery vehicle for intracellular introduction. Where antibody fragments are used, the smallest

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inhibitory fragment that specifically binds to the epitope is preferred. For example, peptide molecules can be designed that bind a preferred epitope based on the variable-region sequences of a useful antibody. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology (Marasco *et al.*, 1993). Formulations may also contain more than one active compound for a particular treatment, preferably those with activities that do not adversely affect each other. The composition may comprise an agent that enhances function, such as a cytotoxic agent, cytokine, chemotherapeutic agent, or growth-inhibitory agent.

The active ingredients can also be entrapped in microcapsules prepared by coacervation techniques or by interfacial polymerization; for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles, and nanocapsules) or in macroemulsions.

The formulations to be used for *in vivo* administration are highly preferred to be sterile. This is readily accomplished by filtration through sterile filtration membranes or any of a number of techniques.

Sustained-release preparations may also be prepared, such as semi-permeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, *e.g.*, films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (Boswell and Scribner, U.S. Patent No. 3,773,919, 1973), copolymers of L-glutamic acid and γ ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as injectable microspheres composed of lactic acid-glycolic acid copolymer, and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods and may be preferred.

AAP recombinant expression vectors and host cells

Vectors are tools used to shuttle DNA between host cells or as a means to express a nucleotide sequence. Some vectors function only in prokaryotes, while others function

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in both prokaryotes and eukaryotes, enabling large-scale DNA preparation from prokaryotes for expression in eukaryotes. Inserting the DNA of interest, such as an AAP nucleotide sequence or a fragment, is accomplished by ligation techniques and/or mating protocols well-known to the skilled artisan. Such DNA is inserted such that its integration does not disrupt any necessary components of the vector. In the case of vectors that are used to express the inserted DNA protein, the introduced DNA is operably-linked to the vector elements that govern its transcription and translation.

Vectors can be divided into two general classes: Cloning vectors are replicating plasmid or phage with regions that are non-essential for propagation in an appropriate host cell, and into which foreign DNA can be inserted; the foreign DNA is replicated and propagated as if it were a component of the vector. An expression vector (such as a plasmid, yeast, or animal virus genome) is used to introduce foreign genetic material into a host cell or tissue in order to transcribe and translate the foreign DNA. In expression vectors, the introduced DNA is operably-linked to elements, such as promoters, that signal to the host cell to transcribe the inserted DNA. Some promoters are exceptionally useful, such as inducible promoters that control gene transcription in response to specific factors. Operably-linking an *AAP* or anti-sense construct to an inducible promoter can control the expression of an *AAP* or fragments, or anti-sense constructs. Examples of classic inducible promoters include those that are responsive to α -interferon, heat-shock, heavy metal ions, and steroids such as glucocorticoids (Kaufman, 1990) and tetracycline. Other desirable inducible promoters include those that are not endogenous to the cells in which the construct is being introduced, but, however, is responsive in those cells when the induction agent is exogenously supplied.

Vectors have many difference manifestations. A "plasmid" is a circular double stranded DNA molecule into which additional DNA segments can be introduced. Viral vectors can accept additional DNA segments into the viral genome. Certain vectors are capable of autonomous replication in a host cell (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. In general, useful expression vectors are often plasmids. However, other forms of

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expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses) are contemplated.

Recombinant expression vectors that comprise an *AAP* (or fragments) regulate an *AAP* transcription by exploiting one or more host cell-responsive (or that can be manipulated *in vitro*) regulatory sequences that is operably-linked to an *AAP*. "Operably-linked" indicates that a nucleotide sequence of interest is linked to regulatory sequences such that expression of the nucleotide sequence is achieved.

Vectors can be introduced in a variety of organisms and/or cells (Table D). Alternatively, the vectors can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Table D Examples of hosts for cloning or expression

Organisms	Examples	Sources and References*
Prokaryotes		
Enterobacteriaceae	<i>E. coli</i> K 12 strain MM294 X1776 W3110 K5 772	ATCC 31,446 ATCC 31,537 ATCC 27,325 ATCC 53,635
	<i>Enterobacter</i>	
	<i>Erwinia</i>	
	<i>Klebsiella</i>	
	<i>Proteus</i>	
	<i>Salmonella (S. typhimurium)</i>	
	<i>Serratia (S. marcescans)</i>	
	<i>Shigella</i>	
	<i>Bacilli (B. subtilis and B. licheniformis)</i>	
	<i>Pseudomonas (P. aeruginosa)</i>	
	<i>Streptomyces</i>	
Eukaryotes		
Yeasts	<i>Saccharomyces cerevisiae</i>	
	<i>Schizosaccharomyces pombe</i>	
	<i>Kluyveromyces</i>	(Fleer <i>et al.</i> , 1991)
	<i>K. lactis</i> MW98-8C, CBS683, CBS4574	(de Louvencourt <i>et al.</i> , 1983)
	<i>K. fragilis</i> <i>K. bulgaricus</i> <i>K. wickerhamii</i>	ATCC 12,424 ATCC 16,045 ATCC 24,178

Table D Examples of hosts for cloning or expression

Organisms	Examples	Sources and References*
	<i>K. waltii</i>	ATCC 56,500
	<i>K. drosophilum</i>	ATCC 36,906
	<i>K. thermotolerans</i>	
	<i>K. marxianus; yarrowia</i>	(EPO 402226, 1990)
	<i>Pichia pastoris</i>	(Sreekrishna <i>et al.</i> , 1988)
	<i>Candida</i>	
	<i>Trichoderma reesia</i>	
	<i>Neurospora crassa</i>	(Case <i>et al.</i> , 1979)
	<i>Torulopsis</i>	
	<i>Rhodotorula</i>	
	<i>Schwanniomyces (S. occidentalis)</i>	
Filamentous Fungi	<i>Neurospora</i>	
	<i>Penicillium</i>	
	<i>Tolypocladium</i>	(WO 91/00357, 1991)
	<i>Aspergillus (A. nidulans and A. niger)</i>	(Kelly and Hynes, 1985; Tilburn <i>et al.</i> , 1983; Yelton <i>et al.</i> , 1984)
Invertebrate cells	<i>Drosophila</i> S2	
	<i>Spodoptera</i> Sf9	
Vertebrate cells	Chinese Hamster Ovary (CHO)	
	simian COS COS-7	ATCC CRL 1651
	HEK 293	
*Unreferenced cells are generally available from American Type Culture Collection (Manassas, VA).		

Vector choice is dictated by the organism or cells being used and the desired fate of the vector. Vectors may replicate once in the target cells, or may be “suicide” vectors. In general, vectors comprise signal sequences, origins of replication, marker genes, enhancer elements, promoters, and transcription termination sequences. The choice of these elements depends on the organisms in which the vector will be used and are easily determined. Some of these elements may be conditional, such as an inducible or conditional promoter that is turned “on” when conditions are appropriate. Examples of inducible promoters include those that are tissue-specific, which relegate expression to certain cell types, steroid-responsive, or heat-shock reactive. Some bacterial repression systems, such as the *lac* operon, have been exploited in mammalian cells and transgenic animals (Fieck *et al.*, 1992; Wyborski *et al.*, 1996; Wyborski and Short, 1991). Vectors

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often use a selectable marker to facilitate identifying those cells that have incorporated the vector. Many selectable markers are well known in the art for the use with prokaryotes, usually antibiotic-resistance genes or the use of autotrophy and auxotrophy mutants.

Using antisense and sense AAP oligonucleotides can prevent an AAP polypeptide expression. These oligonucleotides bind to target nucleic acid sequences, forming duplexes that block transcription or translation of the target sequence by enhancing degradation of the duplexes, terminating prematurely transcription or translation, or by other means.

Antisense or sense oligonucleotides are single-stranded nucleic acids, either RNA or DNA, which can bind a target AAP mRNA (sense) or an AAP DNA (antisense) sequences. According to the present invention, antisense or sense oligonucleotides comprise a fragment of an AAP DNA coding region of at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. In general, antisense RNA or DNA molecules can comprise at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100 bases in length or more. Among others, (Stein and Cohen, 1988; van der Krol *et al.*, 1988a) describe methods to derive antisense or a sense oligonucleotides from a given cDNA sequence.

Modifications of antisense and sense oligonucleotides can augment their effectiveness. Modified sugar-phosphodiester bonds or other sugar linkages (WO 91/06629, 1991), increase *in vivo* stability by conferring resistance to endogenous nucleases without disrupting binding specificity to target sequences. Other modifications can increase the affinities of the oligonucleotides for their targets, such as covalently linked organic moieties (WO 90/10448, 1990) or poly-(L)-lysine. Other attachments modify binding specificities of the oligonucleotides for their targets, including metal complexes or intercalating (*e.g.* ellipticine) and alkylating agents.

To introduce antisense or sense oligonucleotides into target cells (cells containing the target nucleic acid sequence), any gene transfer method may be used and are well known to those of skill in the art. Examples of gene transfer methods include 1) biological, such as gene transfer vectors like Epstein-Barr virus or conjugating the exogenous DNA to a ligand-binding molecule (WO 91/04753, 1991), 2) physical, such as

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electroporation, and 3) chemical, such as CaPO_4 precipitation and oligonucleotide-lipid complexes (WO 90/10448, 1990).

The terms "host cell" and "recombinant host cell" are used interchangeably. Such terms refer not only to a particular subject cell but also to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term.

Methods of eukaryotic cell transfection and prokaryotic cell transformation are well known in the art. The choice of host cell will dictate the preferred technique for introducing the nucleic acid of interest. Table E, which is not meant to be limiting, summarizes many of the known techniques in the art. Introduction of nucleic acids into an organism may also be done with *ex vivo* techniques that use an *in vitro* method of transfection, as well as established genetic techniques, if any, for that particular organism.

Table E Methods to introduce nucleic acid into cells

Cells	Methods	References	Notes
Prokaryotes (bacteria)	Calcium chloride	(Cohen <i>et al.</i> , 1972; Hanahan, 1983; Mandel and Higa, 1970)	
	Electroporation	(Shigekawa and Dower, 1988)	
Eukaryotes			
Mammalian cells	Calcium phosphate transfection	<i>N</i>-(2-Hydroxyethyl)piperazine-<i>N'</i>-(2-ethanesulfonic acid (HEPES) buffered saline solution (Chen and Okayama, 1988; Graham and van der Eb, 1973; Wigler <i>et al.</i>, 1978) BES (<i>N,N</i>-bis(2-hydroxyethyl)-2-aminoethanesulfonic acid) buffered solution (Ishiura <i>et al.</i>, 1982)	Cells may be "shocked" with glycerol or dimethylsulfoxide (DMSO) to increase transfection efficiency (Ausubel <i>et al.</i> , 1987).

Table E Methods to introduce nucleic acid into cells

Cells	Methods	References	Notes
	Diethylaminoethyl (DEAE)-Dextran transfection	(Fujita <i>et al.</i> , 1986; Lopata <i>et al.</i> , 1984; Selden <i>et al.</i> , 1986)	Most useful for transient, but not stable, transfections. Chloroquine can be used to increase efficiency.
	Electroporation	(Neumann <i>et al.</i> , 1982; Potter, 1988; Potter <i>et al.</i> , 1984; Wong and Neumann, 1982)	Especially useful for hard-to-transfect lymphocytes.
	Cationic lipid reagent transfection	(Elroy-Stein and Moss, 1990; Felgner <i>et al.</i> , 1987; Rose <i>et al.</i> , 1991; Whitt <i>et al.</i> , 1990)	Applicable to both <i>in vivo</i> and <i>in vitro</i> transfection.
	Retroviral	Production exemplified by (Cepko <i>et al.</i> , 1984; Miller and Buttimore, 1986; Pear <i>et al.</i> , 1993) Infection <i>in vitro</i> and <i>in vivo</i> : (Austin and Cepko, 1990; Bodine <i>et al.</i> , 1991; Fekete and Cepko, 1993; Lemischka <i>et al.</i> , 1986; Turner <i>et al.</i> , 1990; Williams <i>et al.</i> , 1984)	Lengthy process, many packaging lines available at ATCC. Applicable to both <i>in vivo</i> and <i>in vitro</i> transfection.
	Polybrene	(Chaney <i>et al.</i> , 1986; Kawai and Nishizawa, 1984)	
	Microinjection	(Capecchi, 1980)	Can be used to establish cell lines carrying integrated copies of AAP DNA sequences.
	Protoplast fusion	(Rassoulzadegan <i>et al.</i> , 1982; Sandri-Goldin <i>et al.</i> , 1981; Schaffner, 1980)	
Insect cells (<i>in vitro</i>)	Baculovirus systems	(Luckow, 1991; Miller, 1988; O'Reilly <i>et al.</i> , 1992)	Useful for <i>in vitro</i> production of proteins with eukaryotic modifications.
Yeast	Electroporation	(Becker and Guarente, 1991)	
	Lithium acetate	(Gietz <i>et al.</i> , 1998; Ito <i>et al.</i> , 1983)	
	Spheroplast fusion	(Beggs, 1978; Hinnen <i>et al.</i> , 1978)	Laborious, can produce aneuploids.

Table E Methods to introduce nucleic acid into cells

Cells	Methods	References	Notes
Plant cells (general reference: (Hansen and Wright, 1999))	Agrobacterium transformation	(Bechtold and Pelletier, 1998; Escudero and Hohn, 1997; Hansen and Chilton, 1999; Touraev and al., 1997)	
	Biolistics (microprojectiles)	(Finer <i>et al.</i> , 1999; Hansen and Chilton, 1999; Shillito, 1999)	
	Electroporation (protoplasts)	(Fromm <i>et al.</i> , 1985; Ou-Lee <i>et al.</i> , 1986; Rhodes <i>et al.</i> , 1988; Saunders <i>et al.</i> , 1989) May be combined with liposomes (Trick and al., 1997)	
	Polyethylene glycol (PEG) treatment	(Shillito, 1999)	
	Liposomes	May be combined with electroporation (Trick and al., 1997)	
	<i>in planta</i> microinjection	(Leduc and al., 1996; Zhou and al., 1983)	
	Seed imbibition	(Trick and al., 1997)	
	Laser beam	(Hoffman, 1996)	
	Silicon carbide whiskers	(Thompson and al., 1995)	

Vectors often use a selectable marker to facilitate identifying those cells that have incorporated the vector. Many selectable markers are well known in the art for the use with prokaryotes, usually antibiotic-resistance genes or the use of autotrophy and auxotrophy mutants. Table F lists often-used selectable markers for mammalian cell transfection.

Table F Useful selectable markers for eukaryote cell transfection

Selectable Marker	Selection	Action	Reference
Adenosine deaminase (ADA)	Media includes 9- β -D- xylofuranosyl adenine (Xyl-A)	Conversion of Xyl-A to Xyl-ATP, which incorporates into nucleic acids, killing	(Kaufman <i>et al.</i> , 1986)

Table F Useful selectable markers for eukaryote cell transfection

Selectable Marker	Selection	Action	Reference
		cells. ADA detoxifies	
Dihydrofolate reductase (DHFR)	Methotrexate (MTX) and dialyzed serum (purine-free media)	MTX competitive inhibitor of DHFR. In absence of exogenous purines, cells require DHFR, a necessary enzyme in purine biosynthesis.	(Simonsen and Levinson, 1983)
Aminoglycoside phosphotransferase ("APH", "neo", "G418")	G418	G418, an aminoglycoside detoxified by APH, interferes with ribosomal function and consequently, translation.	(Southern and Berg, 1982)
Hygromycin-B-phosphotransferase (HPH)	hygromycin-B	Hygromycin-B, an aminocyclitol detoxified by HPH, disrupts protein translocation and promotes mistranslation.	(Palmer <i>et al.</i> , 1987)
Thymidine kinase (TK)	Forward selection (TK+): Media (HAT) incorporates aminopterin. Reverse selection (TK-): Media incorporates 5-bromodeoxyuridine (BrdU).	Forward: Aminopterin forces cells to synthesize dTTP from thymidine, a pathway requiring TK. Reverse: TK phosphorylates BrdU, which incorporates into nucleic acids, killing cells.	(Littlefield, 1964)

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce an AAP. Accordingly, the invention provides methods for producing an AAP using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of the invention (into which a recombinant expression vector encoding an AAP has been introduced) in a suitable medium, such that an AAP is produced. In another embodiment, the method further comprises isolating an AAP from the medium or the host cell.

Transgenic AAP animals

Transgenic animals are useful for studying the function and/or activity of an *AAP* and for identifying and/or evaluating modulators of *AAP* activity. "Transgenic animals" are non-human animals, preferably mammals, more preferably a rodents such as rats or mice, in which one or more of the cells include a transgene. Other transgenic animals include primates, sheep, dogs, cows, goats, chickens, amphibians, *etc.* A "transgene" is exogenous DNA that is integrated into the genome of a cell from which a transgenic animal develops, and that remains in the genome of the mature animal. Transgenes preferably direct the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal with the purpose of preventing expression of a naturally encoded gene product in one or more cell types or tissues (a "knockout" transgenic animal), or serving as a marker or indicator of an integration, chromosomal location, or region of recombination (*e.g. cre/loxP* mice). A "homologous recombinant animal" is a non-human animal, such as a rodent, in which an endogenous *AAP* has been altered by an exogenous DNA molecule that recombines homologously with an endogenous *AAP* in a (*e.g.* embryonic) cell prior to development the animal. Host cells with an exogenous *AAP* can be used to produce non-human transgenic animals, such as fertilized oocytes or embryonic stem cells into which an *AAP*-coding sequences have been introduced. Such host cells can then be used to create non-human transgenic animals or homologous recombinant animals.

1. *Approaches to transgenic animal production*

A transgenic animal can be created by introducing an *AAP* into the male pronuclei of a fertilized oocyte (*e.g.*, by microinjection, retroviral infection) and allowing the oocyte to develop in a pseudopregnant female foster animal (pffa). An *AAP* cDNA sequences (SEQ ID NO:1, 3, 5, 7, 9, 11, 13 or 15) can be introduced as a transgene into the genome of a non-human animal. Alternatively, a homologue of an *AAP*, such as the naturally-occurring variant of an *AAP*, can be used as a transgene. Intronic sequences and polyadenylation signals can also be included in the transgene to increase transgene expression. Tissue-specific regulatory sequences can be operably-linked to the *AAP* transgene to direct expression of the *AAP* to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art, *e.g.* (Evans *et al.*, U.S. Patent No.

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4,870,009, 1989; Hogan, 0879693843, 1994; Leder and Stewart, U.S. Patent No. 4,736,866, 1988; Wagner and Hoppe, US Patent No. 4,873,191, 1989). Other non-mice transgenic animals may be made by similar methods. A transgenic founder animal, which can be used to breed additional transgenic animals, can be identified based upon the presence of the transgene in its genome and/or expression of the transgene mRNA in tissues or cells of the animals. Transgenic animals can be bred to other transgenic animals carrying other transgenes.

2. *Vectors for transgenic animal production*

To create a homologous recombinant animal, a vector containing at least a portion of an *AAP* into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, disrupt or alter the expression of, an *AAP*. An *AAP* can be a murine gene, or other *AAP* homologue, such as a naturally occurring variant. In one approach, a knockout vector functionally disrupts an endogenous *AAP* gene upon homologous recombination, and thus a non-functional AAP protein, if any, is expressed.

Alternatively, the vector can be designed such that, upon homologous recombination, an endogenous *AAP* is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of an endogenous AAP). In this type of homologous recombination vector, the altered portion of the *AAP* is flanked at its 5'- and 3'-termini by additional nucleic acid of the *AAP* to allow for homologous recombination to occur between the exogenous *AAP* carried by the vector and an endogenous *AAP* in an embryonic stem cell. The additional flanking AAP nucleic acid is sufficient to engender homologous recombination with the endogenous *AAP*. Typically, several kilobases of flanking DNA (both at the 5'- and 3'-termini) are included in the vector (Thomas and Capecchi, 1987). The vector is then introduced into an embryonic stem cell line (*e.g.*, by electroporation), and cells in which the introduced *AAP* has homologously-recombined with an endogenous *AAP* are selected (Li *et al.*, 1992).

3. *Introduction of an AAP transgene cells during development*

Selected cells are then injected into a blastocyst of an animal (*e.g.*, a mouse) to form aggregation chimeras (Bradley, 1987). A chimeric embryo can then be implanted into a suitable pffa and the embryo brought to term. Progeny harboring the homologously-recombined DNA in their germ cells can be used to breed animals in

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which all cells of the animal contain the homologously-recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described (Berns *et al.*, WO 93/04169, 1993; Bradley, 1991; Kucherlapati *et al.*, WO 91/01140, 1991; Le Mouellic and Brullet, WO 90/11354, 1990).

Alternatively, transgenic animals that contain selected systems that allow for regulated expression of the transgene can be produced. An example of such a system is the *cre/loxP* recombinase system of bacteriophage P1 (Lakso *et al.*, 1992). Another recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae* (O'Gorman *et al.*, 1991). If a *cre/loxP* recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the *Cre* recombinase and a selected protein are required. Such animals can be produced as "double" transgenic animals, by mating an animal containing a transgene encoding a selected protein to another containing a transgene encoding a recombinase.

Clones of transgenic animals can also be produced (Wilmot *et al.*, 1997). In brief, a cell from a transgenic animal can be isolated and induced to exit the growth cycle and enter G₀ phase. The quiescent cell can then be fused to an enucleated oocyte from an animal of the same species from which the quiescent cell is isolated. The reconstructed oocyte is then cultured to develop to a morula or blastocyte and then transferred to a pffa. The offspring borne of this female foster animal will be a clone of the "parent" transgenic animal.

Pharmaceutical compositions

The *AAP* nucleic acid molecules, *AAP* polypeptides, and anti-*AAP* Abs (active compounds) of the invention, and derivatives, fragments, analogs and homologs thereof, can be incorporated into pharmaceutical compositions. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. A "pharmaceutically acceptable carrier" includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration (Gennaro, 2000). Preferred examples of such carriers or diluents include, but are not limited to, water, saline, finger's solutions, dextrose solution, and 5% human serum albumin. Liposomes and non-aqueous vehicles such as fixed oils may also be used. Except when a

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conventional media or agent is incompatible with an active compound, use of these compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

1. *General considerations*

A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration, including intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (*i.e.*, topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid (EDTA); buffers such as acetates, citrates or phosphates, and agents for the adjustment of tonicity such as sodium chloride or dextrose. The *pH* can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

2. *Injectable formulations*

Pharmaceutical compositions suitable for injection include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, CREMOPHOR EL[™] (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid so as to be administered using a syringe. Such compositions should be stable during manufacture and storage and must be preserved against contamination from microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (such as glycerol, propylene glycol, and liquid polyethylene glycol), and suitable mixtures. Proper fluidity can be maintained, for example, by using a coating such as lecithin, by maintaining the required particle size in the case of dispersion and by using surfactants. Various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, and thimerosal, can contain microorganism

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contamination. Isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, and sodium chloride can be included in the composition. Compositions that can delay absorption include agents such as aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound (*e.g.*, an AAP or anti-AAP antibody) in the required amount in an appropriate solvent with one or a combination of ingredients as required, followed by sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium, and the other required ingredients as discussed. Sterile powders for the preparation of sterile injectable solutions, methods of preparation include vacuum drying and freeze-drying that yield a powder containing the active ingredient and any desired ingredient from a sterile solutions.

3. *Oral compositions*

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash, wherein the compound in the fluid carrier is applied orally. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included. Tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, PRIMOGEL, or corn starch; a lubricant such as magnesium stearate or STEROTES; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

4. *Compositions for inhalation*

For administration by inhalation, the compounds are delivered as an aerosol spray from a nebulizer or a pressurized container that contains a suitable propellant, *e.g.*, a gas such as carbon dioxide.

5. *Systemic administration*

Systemic administration can also be transmucosal or transdermal. For transmucosal or transdermal administration, penetrants that can permeate the target

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barrier(s) are selected. Transmucosal penetrants include, detergents, bile salts, and fusidic acid derivatives. Nasal sprays or suppositories can be used for transmucosal administration. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams.

The compounds can also be prepared in the form of suppositories (*e.g.*, with bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

6. *Carriers*

In one embodiment, the active compounds are prepared with carriers that protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Such materials can be obtained commercially from ALZA Corporation (Mountain View, CA) and NOVA Pharmaceuticals, Inc. (Lake Elsinore, CA), or prepared by one of skill in the art. Liposomal suspensions can also be used as pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, such as in (Eppstein *et al.*, US Patent No. 4,522,811, 1985).

7. *Unit dosage*

Oral formulations or parenteral compositions in unit dosage form can be created to facilitate administration and dosage uniformity. Unit dosage form refers to physically discrete units suited as single dosages for the subject to be treated, containing a therapeutically effective quantity of active compound in association with the required pharmaceutical carrier. The specification for the unit dosage forms of the invention are dictated by, and directly dependent on, the unique characteristics of the active compound and the particular desired therapeutic effect, and the inherent limitations of compounding the active compound.

8. *Gene therapy compositions*

The nucleic acid molecules of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by, for example, intravenous injection, local administration (Nabel and Nabel, US Patent No. 5,328,470, 1994), or by stereotactic injection (Chen *et al.*, 1994). The pharmaceutical preparation of a gene therapy vector can include an acceptable diluent, or can comprise a

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slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, *e.g.*, retroviral vectors, the pharmaceutical preparation can include one or more cells that produce the gene delivery system.

9. *Dosage*

The pharmaceutical composition and method of the present invention may further comprise other therapeutically active compounds as noted herein that are usually applied in the treatment of the above mentioned pathological conditions.

In the treatment or prevention of conditions which require AAP modulation an appropriate dosage level will generally be about 0.01 to 500 mg per kg patient body weight per day which can be administered in single or multiple doses. Preferably, the dosage level will be about 0.1 to about 250 mg/kg per day; more preferably about 0.5 to about 100 mg/kg per day. A suitable dosage level may be about 0.01 to 250 mg/kg per day, about 0.05 to 100 mg/kg per day, or about 0.1 to 50 mg/kg per day. Within this range the dosage may be 0.05 to 0.5, 0.5 to 5 or 5 to 50 mg/kg per day. For oral administration, the compositions are preferably provided in the form of tablets containing 1.0 to 1000 milligrams of the active ingredient, particularly 1.0, 5.0, 10.0, 15.0, 20.0, 25.0, 50.0, 75.0, 100.0, 150.0, 200.0, 250.0, 300.0, 400.0, 500.0, 600.0, 750.0, 800.0, 900.0, and 1000.0 milligrams of the active ingredient for the symptomatic adjustment of the dosage to the patient to be treated. The compounds may be administered on a regimen of 1 to 4 times per day, preferably once or twice per day.

It will be understood, however, that the specific dose level and frequency of dosage for any particular patient may be varied and will depend upon a variety of factors including the activity of the specific compound employed, the metabolic stability and length of action of that compound, the age, body weight, general health, sex, diet, mode and time of administration, rate of excretion, drug combination, the severity of the particular condition, and the host undergoing therapy.

10. *Kits for pharmaceutical compositions*

The pharmaceutical compositions can be included in a kit, container, pack, or dispenser together with instructions for administration. When the invention is supplied as a kit, the different components of the composition may be packaged in separate containers

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and admixed immediately before use. Such packaging of the components separately may permit long-term storage without losing the active components' functions.

Kits may also include reagents in separate containers that facilitate the execution of a specific test, such as diagnostic tests or tissue typing. For example, *AAP* DNA templates and suitable primers may be supplied for internal controls.

(a) *Containers or vessels*

The reagents included in the kits can be supplied in containers of any sort such that the life of the different components are preserved, and are not adsorbed or altered by the materials of the container. For example, sealed glass ampoules may contain lyophilized luciferase or buffer that have been packaged under a neutral, non-reacting gas, such as nitrogen. Ampoules may consist of any suitable material, such as glass, organic polymers, such as polycarbonate, polystyrene, etc., ceramic, metal or any other material typically employed to hold reagents. Other examples of suitable containers include simple bottles that may be fabricated from similar substances as ampoules, and envelopes, that may consist of foil-lined interiors, such as aluminum or an alloy. Other containers include test tubes, vials, flasks, bottles, syringes, or the like. Containers may have a sterile access port, such as a bottle having a stopper that can be pierced by a hypodermic injection needle. Other containers may have two compartments that are separated by a readily removable membrane that upon removal permits the components to mix. Removable membranes may be glass, plastic, rubber, etc.

(b) *Instructional materials*

Kits may also be supplied with instructional materials. Instructions may be printed on paper or other substrate, and/or may be supplied as an electronic-readable medium, such as a floppy disc, CD-ROM, DVD-ROM, Zip disc, videotape, audiotape, etc. Detailed instructions may not be physically associated with the kit; instead, a user may be directed to an internet web site specified by the manufacturer or distributor of the kit, or supplied as electronic mail.

Screening and detection methods

The isolated nucleic acid molecules of the invention can be used to express an *AAP* (e.g., via a recombinant expression vector in a host cell in gene therapy applications), to detect an *AAP* mRNA (e.g., in a biological sample) or a genetic lesion in

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an *AAP*, and to modulate *AAP* activity, as described below. In addition, *AAP* polypeptides can be used to screen drugs or compounds that modulate the *AAP* activity or expression as well as to treat disorders characterized by insufficient or excessive production of an *AAP* or production of *AAP* forms that have decreased or aberrant activity compared to an *AAP* wild-type protein, or modulate biological function that involve an *AAP*. In addition, the anti-*AAP* Abs of the invention can be used to detect and isolate an *AAP* and modulate *AAP* activity.

1. *Screening assays*

The invention provides a method (screening assay) for identifying modalities, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides, peptidomimetics, small molecules or other drugs), foods, combinations thereof, *etc.*, that effect an *AAP*, a stimulatory or inhibitory effect, including translation, transcription, activity or copies of the gene in cells. The invention also includes compounds identified in screening assays.

Testing for compounds that increase or decrease *AAP* activity are desirable. A compound may modulate an *AAP* activity by affecting: (1) the number of copies of the gene in the cell (amplifiers and deamplifiers); (2) increasing or decreasing transcription of an *AAP* (transcription up-regulators and down-regulators); (3) by increasing or decreasing the translation of an *AAP* mRNA into protein (translation up-regulators and down-regulators); or (4) by increasing or decreasing the activity of an *AAP* itself (agonists and antagonists).

(a) *effects of compounds*

To identify compounds that affect an *AAP* at the DNA, RNA and protein levels, cells or organisms are contacted with a candidate compound and the corresponding change in an *AAP* DNA, RNA or protein is assessed (Ausubel *et al.*, 1987). For DNA amplifiers and deamplifiers, the amount of an *AAP* DNA is measured, for those compounds that are transcription up-regulators and down-regulators the amount of an *AAP* mRNA is determined; for translational up- and down-regulators, the amount of an *AAP* polypeptide is measured. Compounds that are agonists or antagonists may be identified by contacting cells or organisms with the compound, and then examining, for example, the model of angiogenesis *in vitro*.

In one embodiment, many assays for screening candidate or test compounds that bind to or modulate the activity of an *AAP* or polypeptide or biologically-active portion

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are available. Test compounds can be obtained using any of the numerous approaches in combinatorial library methods, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptides, while the other four approaches encompass peptide, non-peptide oligomer or small molecule libraries of compounds (Lam, 1997).

(b) *small molecules*

A "small molecule" refers to a composition that has a molecular weight of less than about 5 kD and more preferably less than about 4 kD, most preferably less than 0.6 kD. Small molecules can be, nucleic acids, peptides, polypeptides, peptidomimetics, carbohydrates, lipids or other organic or inorganic molecules. Libraries of chemical and/or biological mixtures, such as fungal, bacterial, or algal extracts, are known in the art and can be screened with any of the assays of the invention. Examples of methods for the synthesis of molecular libraries can be found in: (Carell *et al.*, 1994a; Carell *et al.*, 1994b; Cho *et al.*, 1993; DeWitt *et al.*, 1993; Gallop *et al.*, 1994; Zuckermann *et al.*, 1994).

Libraries of compounds may be presented in solution (Houghten *et al.*, 1992) or on beads (Lam *et al.*, 1991), on chips (Fodor *et al.*, 1993), bacteria, spores (Ladner *et al.*, US Patent No. 5,223,409, 1993), plasmids (Cull *et al.*, 1992) or on phage (Cwirla *et al.*, 1990; Devlin *et al.*, 1990; Felici *et al.*, 1991; Ladner *et al.*, US Patent No. 5,223,409, 1993; Scott and Smith, 1990). A cell-free assay comprises contacting an AAP or biologically-active fragment with a known compound that binds the AAP to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with the AAP, where determining the ability of the test compound to interact with the AAP comprises determining the ability of the AAP to preferentially bind to or modulate the activity of an AAP target molecule.

(c) *cell-free assays*

The cell-free assays of the invention may be used with both soluble or a membrane-bound forms of an AAP. In the case of cell-free assays comprising the membrane-bound form, a solubilizing agent to maintain the AAP in solution. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-

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methylglucamide, TRITON[®] X-100 and others from the TRITON[®] series, THESIT[®], Isotridecypoly(ethylene glycol ether)_n, N-dodecyl--N,N-dimethyl-3-ammonio-1-propane sulfonate, 3-(3-cholamidopropyl) dimethylamminiol-1-propane sulfonate (CHAPS), or 3-(3-cholamidopropyl)dimethylamminiol-2-hydroxy-1-propane sulfonate (CHAPSO).

(d) *immobilization of target molecules to facilitate screening*

In more than one embodiment of the assay methods, immobilizing either an AAP or its partner molecules can facilitate separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate high throughput assays. Binding of a test compound to an AAP, or interaction of an AAP with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants, such as microtiter plates, test tubes, and micro-centrifuge tubes. A fusion protein can be provided that adds a domain that allows one or both of the proteins to be bound to a matrix. For example, GST-AAP fusion proteins or GST-target fusion proteins can be adsorbed onto glutathione sepharose beads (SIGMA Chemical, St. Louis, MO) or glutathione derivatized microtiter plates that are then combined with the test compound or the test compound and either the non-adsorbed target protein or an AAP, and the mixture is incubated under conditions conducive to complex formation (*e.g.*, at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components, the matrix immobilized in the case of beads, complex determined either directly or indirectly, for example, as described. Alternatively, the complexes can be dissociated from the matrix, and the level of AAP binding or activity determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in screening assays. Either an AAP or its target molecule can be immobilized using biotin-avidin or biotin-streptavidin systems. Biotinylation can be accomplished using many reagents, such as biotin-NHS (N-hydroxy-succinimide; PIERCE Chemicals, Rockford, IL), and immobilized in wells of streptavidin-coated 96 well plates (PIERCE Chemical). Alternatively, Abs reactive with an AAP or target molecules, but which do not interfere with binding of the AAP to its target molecule, can be derivatized to the wells of the plate, and unbound target or an AAP trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described for the

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GST-immobilized complexes, include immunodetection of complexes using Abs reactive with an AAP or its target, as well as enzyme-linked assays that rely on detecting an enzymatic activity associated with the AAP or target molecule.

(e) *screens to identify modulators*

Modulators of AAP expression can be identified in a method where a cell is contacted with a candidate compound and the expression of an AAP mRNA or protein in the cell is determined. The expression level of the AAP mRNA or protein in the presence of the candidate compound is compared to the AAP mRNA or protein levels in the absence of the candidate compound. The candidate compound can then be identified as a modulator of the AAP mRNA or protein expression based upon this comparison. For example, when expression of an AAP mRNA or protein is greater (*i.e.*, statistically significant) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of the AAP mRNA or protein expression. Alternatively, when expression of the AAP mRNA or protein is less (statistically significant) in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of the AAP mRNA or protein expression. The level of an AAP mRNA or protein expression in the cells can be determined by methods described for detecting an AAP mRNA or protein.

(i) *hybrid assays*

In yet another aspect of the invention, an AAP can be used as "bait" in two-hybrid or three hybrid assays (Bartel *et al.*, 1993; Brent *et al.*, WO94/10300, 1994; Iwabuchi *et al.*, 1993; Madura *et al.*, 1993; Saifer *et al.*, US Patent No. 5,283,317, 1994; Zervos *et al.*, 1993) to identify other proteins that bind or interact with the AAP and modulate AAP activity. Such AAP-bps are also likely to be involved in the propagation of signals by the AAP as, for example, upstream or downstream elements of an AAP pathway.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for an AAP is fused to a gene encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL4). The other construct, a DNA sequence from a library of DNA sequences that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the

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"prey" proteins are able to interact *in vivo*, forming an AAP-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ) that is operably-linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected, and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene that encodes the AAP-interacting protein.

The invention further pertains to novel agents identified by the aforementioned screening assays and uses thereof for treatments as described herein.

2. *Detection assays*

Portions or fragments of an *AAP* cDNA sequences identified herein (and the complete *AAP* gene sequences) are useful in themselves. By way of non-limiting example, these sequences can be used to: (1) identify an individual from a minute biological sample (tissue typing); and (2) aid in forensic identification of a biological sample.

(a) *Tissue typing*

The *AAP* sequences of the invention can be used to identify individuals from minute biological samples. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes and probed on a Southern blot to yield unique bands. The sequences of the invention are useful as additional DNA markers for "restriction fragment length polymorphisms" (RFLP; (Smulson *et al.*, US Patent No. 5,272,057, 1993)).

Furthermore, the *AAP* sequences can be used to determine the actual base-by-base DNA sequence of targeted portions of an individual's genome. *AAP* sequences can be used to prepare two PCR primers from the 5'- and 3'-termini of the sequences that can then be used to amplify the corresponding sequences from an individual's genome and then sequence the amplified fragment.

Panels of corresponding DNA sequences from individuals can provide unique individual identifications, as each individual will have a unique set of such DNA sequences due to allelic differences. The sequences of the invention can be used to obtain such identification sequences from individuals and from tissue. The *AAP* sequences of

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the invention uniquely represent portions of an individual's genome. Allelic variation occurs to some degree in the coding regions of these sequences, and to a greater degree in the noncoding regions. The allelic variation between individual humans occurs with a frequency of about once every 500 bases. Much of the allelic variation is due to single nucleotide polymorphisms (SNPs), which include RFLPs.

Each of the sequences described herein can, to some degree, be used as a standard against which DNA from an individual can be compared for identification purposes. Because greater numbers of polymorphisms occur in noncoding regions, fewer sequences are necessary to differentiate individuals. Noncoding sequences can positively identify individuals with a panel of 10 to 1,000 primers that each yield a noncoding amplified sequence of 100 bases. If predicted coding sequences, such as those in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, and 15 are used, a more appropriate number of primers for positive individual identification would be 500-2,000.

Predictive medicine

The invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to treat an individual prophylactically. Accordingly, one aspect of the invention relates to diagnostic assays for determining an AAP and/or nucleic acid expression as well as AAP activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant AAP expression or activity, including cancer. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with an AAP, nucleic acid expression or activity. For example, mutations in an *AAP* can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to prophylactically treat an individual prior to the onset of a disorder characterized by or associated with the AAP, nucleic acid expression, or biological activity.

Another aspect of the invention provides methods for determining AAP activity, or nucleic acid expression, in an individual to select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics").

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Pharmacogenomics allows for the selection of modalities (*e.g.*, drugs, foods) for therapeutic or prophylactic treatment of an individual based on the individual's genotype (*e.g.*, the individual's genotype to determine the individual's ability to respond to a particular agent). Another aspect of the invention pertains to monitoring the influence of modalities (*e.g.*, drugs, foods) on the expression or activity of an AAP in clinical trials.

1. *Diagnostic assays*

An exemplary method for detecting the presence or absence of an AAP in a biological sample involves obtaining a biological sample from a subject and contacting the biological sample with a compound or an agent capable of detecting the AAP or the AAP nucleic acid (*e.g.*, mRNA, genomic DNA) such that the presence of the AAP is confirmed in the sample. An agent for detecting the AAP mRNA or genomic DNA is a labeled nucleic acid probe that can hybridize to the AAP mRNA or genomic DNA. The nucleic acid probe can be, for example, a full-length AAP nucleic acid, such as the nucleic acid of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13 or 15, or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to an AAP mRNA or genomic DNA.

An agent for detecting an AAP polypeptide is an antibody capable of binding to the AAP, preferably an antibody with a detectable label. Abs can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment (*e.g.*, F_{ab} or F(ab')₂) can be used. A labeled probe or antibody is coupled (*i.e.*, physically linking) to a detectable substance, as well as indirect detection of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently-labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently-labeled streptavidin. The term "biological sample" includes tissues, cells and biological fluids isolated from a subject, as well as tissues, cells and fluids present within a subject. The detection method of the invention can be used to detect an AAP mRNA, protein, or genomic DNA in a biological sample *in vitro* as well as *in vivo*. For example, *in vitro* techniques for detection of an AAP mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of an AAP polypeptide include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations, and immunofluorescence. *In vitro* techniques for detection of an AAP genomic DNA include

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Southern hybridizations and fluorescence in situ hybridization (FISH). Furthermore, *in vivo* techniques for detecting an AAP include introducing into a subject a labeled anti-AAP antibody. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

In one embodiment, the biological sample from the subject contains protein molecules, and/or mRNA molecules, and/or genomic DNA molecules. A preferred biological sample is blood.

In another embodiment, the methods further involve obtaining a biological sample from a subject to provide a control, contacting the sample with a compound or agent to detect an *AAP*, mRNA, or genomic DNA, and comparing the presence of the *AAP*, mRNA or genomic DNA in the control sample with the presence of the *AAP*, mRNA or genomic DNA in the test sample.

The invention also encompasses kits for detecting an AAP in a biological sample. For example, the kit can comprise: a labeled compound or agent capable of detecting an AAP or an *AAP* mRNA in a sample; reagent and/or equipment for determining the amount of an AAP in the sample; and reagent and/or equipment for comparing the amount of an AAP in the sample with a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect the AAP or nucleic acid.

2. *Prognostic assays*

The diagnostic methods described herein can furthermore be utilized to identify subjects having or at risk of developing a disease or disorder associated with an aberrant AAP expression or activity. For example, the assays described herein, can be used to identify a subject having or at risk of developing a disorder associated with AAP, nucleic acid expression or activity. Alternatively, the prognostic assays can be used to identify a subject having or at risk for developing a disease or disorder. The invention provides a method for identifying a disease or disorder associated with an aberrant AAP expression or activity in which a test sample is obtained from a subject and the AAP or nucleic acid (*e.g.*, mRNA, genomic DNA) is detected. A test sample is a biological sample obtained from a subject. For example, a test sample can be a biological fluid (*e.g.*, serum), cell sample, or tissue.

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Pognotic assays can be used to determine whether a subject can be administered a modality (*e.g.*, an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, food, *etc.*) to treat a disease or disorder associated with an aberrant AAP expression or activity. Such methods can be used to determine whether a subject can be effectively treated with an agent for a disorder. The invention provides methods for determining whether a subject can be effectively treated with an agent for a disorder associated with an aberrant AAP expression or activity in which a test sample is obtained and the AAP or nucleic acid is detected (*e.g.*, where the presence of the AAP or nucleic acid is diagnostic for a subject that can be administered the agent to treat a disorder associated with the aberrant AAP expression or activity).

The methods of the invention can also be used to detect genetic lesions in an *AAP* to determine if a subject with the genetic lesion is at risk for a disorder characterized by aberrant angiogenesis. Methods include detecting, in a sample from the subject, the presence or absence of a genetic lesion characterized by at an alteration affecting the integrity of a gene encoding an AAP polypeptide, or the mis-expression of an *AAP*. Such genetic lesions can be detected by ascertaining: (1) a deletion of one or more nucleotides from an *AAP*; (2) an addition of one or more nucleotides to an *AAP*; (3) a substitution of one or more nucleotides in an *AAP*, (4) a chromosomal rearrangement of an *AAP* gene; (5) an alteration in the level of an *AAP* mRNA transcripts, (6) aberrant modification of an *AAP*, such as a change genomic DNA methylation, (7) the presence of a non-wild-type splicing pattern of an *AAP* mRNA transcript, (8) a non-wild-type level of an *AAP*, (9) allelic loss of an *AAP*, and/or (10) inappropriate post-translational modification of an AAP polypeptide. There are a large number of known assay techniques that can be used to detect lesions in an *AAP*. Any biological sample containing nucleated cells may be used.

In certain embodiments, lesion detection may use a probe/primer in a polymerase chain reaction (PCR) (*e.g.*, (Mullis, US Patent No. 4,683,202, 1987; Mullis *et al.*, US Patent No. 4,683,195, 1987), such as anchor PCR or rapid amplification of cDNA ends (RACE) PCR, or, alternatively, in a ligation chain reaction (LCR) (*e.g.*, (Landegren *et al.*, 1988; Nakazawa *et al.*, 1994), the latter is particularly useful for detecting point mutations in *AAP*-genes (Abravaya *et al.*, 1995). This method may include collecting a sample from a patient, isolating nucleic acids from the sample, contacting the nucleic acids with

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one or more primers that specifically hybridize to an *AAP* under conditions such that hybridization and amplification of the *AAP* (if present) occurs, and detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

Alternative amplification methods include: self sustained sequence replication (Guatelli *et al.*, 1990), transcriptional amplification system (Kwoh *et al.*, 1989); Q β Replicase (Lizardi *et al.*, 1988), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules present in low abundance.

Mutations in an *AAP* from a sample can be identified by alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis and compared. Differences in fragment length sizes between sample and control DNA indicates mutations in the sample DNA. Moreover, the use of sequence specific ribozymes can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

Hybridizing a sample and control nucleic acids, *e.g.*, DNA or RNA, to high-density arrays containing hundreds or thousands of oligonucleotides probes, can identify genetic mutations in an *AAP* (Cronin *et al.*, 1996; Kozal *et al.*, 1996). For example, genetic mutations in an *AAP* can be identified in two-dimensional arrays containing light-generated DNA probes as described in Cronin, *et al.*, *supra*. Briefly, a first hybridization array of probes can be used to scan through long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This is followed by a second hybridization array that allows the characterization of specific mutations by using smaller, specialized probe arrays complementary to all variants or mutations detected. Each mutation array is composed of parallel probe sets, one complementary to the wild-type gene and the other complementary to the mutant gene.

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In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence an *AAP* and detect mutations by comparing the sequence of the sample *AAP*-with the corresponding wild-type (control) sequence. Examples of sequencing reactions include those based on classic techniques (Maxam and Gilbert, 1977; Sanger *et al.*, 1977). Any of a variety of automated sequencing procedures can be used when performing diagnostic assays (Naeve *et al.*, 1995) including sequencing by mass spectrometry (Cohen *et al.*, 1996; Griffin and Griffin, 1993; Koster, WO94/16101, 1994).

Other methods for detecting mutations in an *AAP* include those in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA heteroduplexes (Myers *et al.*, 1985). In general, the technique of "mismatch cleavage" starts by providing heteroduplexes formed by hybridizing (labeled) RNA or DNA containing a wild-type *AAP* sequence with potentially mutant RNA or DNA obtained from a sample. The double-stranded duplexes are treated with an agent that cleaves single-stranded regions of the duplex such as those that arise from base pair mismatches between the control and sample strands. For instance, RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids treated with S₁ nuclease to enzymatically digest the mismatched regions. In other embodiments, either DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide and with piperidine in order to digest mismatched regions. The digested material is then separated by size on denaturing polyacrylamide gels to determine the mutation site (Grompe *et al.*, 1989; Saleeba and Cotton, 1993). The control DNA or RNA can be labeled for detection.

Mismatch cleavage reactions may employ one or more proteins that recognize mismatched base pairs in double-stranded DNA (DNA mismatch repair) in defined systems for detecting and mapping point mutations in an *AAP* cDNAs obtained from samples of cells. For example, the mutY enzyme of *E. coli* cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T at G/T mismatches (Hsu *et al.*, 1994). According to an exemplary embodiment, a probe based on a wild-type *AAP* sequence is hybridized to a cDNA or other DNA product from a test cell(s). The duplex is treated with a DNA mismatch repair enzyme, and the cleavage products, if any, can be detected from electrophoresis protocols or the like (Modrich *et al.*, US Patent No. 5,459,039, 1995).

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Electrophoretic mobility alterations can be used to identify mutations in an *AAP*. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids (Cotton, 1993; Hayashi, 1992; Orita *et al.*, 1989). Single-stranded DNA fragments of sample and control *AAP* nucleic acids are denatured and then renatured. The secondary structure of single-stranded nucleic acids varies according to sequence; the resulting alteration in electrophoretic mobility allows detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA (rather than DNA), in which the secondary structure is more sensitive to a sequence changes. The subject method may use heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility (Keen *et al.*, 1991).

The migration of mutant or wild-type fragments can be assayed using denaturing gradient gel electrophoresis (DGGE; (Myers *et al.*, 1985). In DGGE, DNA is modified to prevent complete denaturation, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. A temperature gradient may also be used in place of a denaturing gradient to identify differences in the mobility of control and sample DNA (Rossiter and Caskey, 1990).

Examples of other techniques for detecting point mutations include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer extension. For example, oligonucleotide primers may be prepared in which the known mutation is placed centrally and then hybridized to target DNA under conditions that permit hybridization only if a perfect match is found (Saiki *et al.*, 1986; Saiki *et al.*, 1989). Such allele-specific oligonucleotides are hybridized to PCR-amplified target DNA or a number of different mutations when the oligonucleotides are attached to the hybridizing membrane and hybridized with labeled target DNA.

Alternatively, allele specific amplification technology that depends on selective PCR amplification may be used. Oligonucleotide primers for specific amplifications may carry the mutation of interest in the center of the molecule (so that amplification depends on differential hybridization (Gibbs *et al.*, 1989)) or at the extreme 3'-terminus of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (Prosser, 1993). Novel restriction site in the region of the mutation may be

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introduced to create cleavage-based detection (Gasparini *et al.*, 1992). Certain amplification may also be performed using *Taq* ligase for amplification (Barany, 1991). In such cases, ligation occurs only if there is a perfect match at the 3'-terminus of the 5' sequence, allowing detection of a known mutation by scoring for amplification.

The described methods may be performed, for example, by using pre-packaged kits comprising at least one probe (nucleic acid or antibody) that may be conveniently used, for example, in clinical settings to diagnose patients exhibiting symptoms or family history of a disease or illness involving an AAP.

Furthermore, any cell type or tissue in which an AAP is expressed may be utilized in the prognostic assays described herein.

3. *Pharmacogenomics*

Agents, or modulators that have a stimulatory or inhibitory effect on AAP activity or expression, as identified by a screening assay can be administered to individuals to treat, prophylactically or therapeutically, disorders, including those associated with angiogenesis. In conjunction with such treatment, the pharmacogenomics (*i.e.*, the study of the relationship between a subject's genotype and the subject's response to a foreign modality, such as a food, compound or drug) may be considered. Metabolic differences of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the selection of effective agents (*e.g.*, drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Pharmacogenomics can further be used to determine appropriate dosages and therapeutic regimens. Accordingly, the activity of an AAP, expression of an *AAP* nucleic acid, or an *AAP* mutation(s) in an individual can be determined to guide the selection of appropriate agent(s) for therapeutic or prophylactic treatment.

Pharmacogenomics deals with clinically significant hereditary variations in the response to modalities due to altered modality disposition and abnormal action in affected persons (Eichelbaum and Evert, 1996; Linder *et al.*, 1997). In general, two pharmacogenetic conditions can be differentiated: (1) genetic conditions transmitted as a single factor altering the interaction of a modality with the body (altered drug action) or (2) genetic conditions transmitted as single factors altering the way the body acts on a modality (altered drug metabolism). These pharmacogenetic conditions can occur either

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as rare defects or as nucleic acid polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a common inherited enzymopathy in which the main clinical complication is hemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (*e.g.*, N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) explains the phenomena of some patients who show exaggerated drug response and/or serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the *CYP2D6* gene is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers due to mutant *CYP2D6* and *CYP2C19* frequently experience exaggerated drug responses and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, PM shows no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. At the other extreme are the so-called ultra-rapid metabolizers who are unresponsive to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

The activity of an AAP, expression of an *AAP* nucleic acid, or mutation content of an *AAP* in an individual can be determined to select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with an AAP modulator, such as a modulator identified by one of the described exemplary screening assays.

4. *Monitoring effects during clinical trials*

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Monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of an AAP (*e.g.*, the ability to modulate angiogenesis) can be applied not only in basic drug screening, but also in clinical trials. For example, the effectiveness of an agent determined by a screening assay to increase an *AAP* expression, protein levels, or up-regulate an AAP's activity can be monitored in clinical trials of subjects exhibiting decreased *AAP* expression, protein levels, or down-regulated AAP activity. Alternatively, the effectiveness of an agent determined to decrease an *AAP* expression, protein levels, or down-regulate an AAP's activity, can be monitored in clinical trials of subjects exhibiting increased the *AAP* expression, protein levels, or up-regulated AAP activity. In such clinical trials, the expression or activity of the AAP and, preferably, other genes that have been implicated in, for example, angiogenesis can be used as a "read out" or markers for a particular cell's responsiveness.

For example, genes, including an *AAP*, that are modulated in cells by treatment with a modality (*e.g.*, food, compound, drug or small molecule) can be identified. To study the effect of agents on angiogenesis, for example, in a clinical trial, cells can be isolated and RNA prepared and analyzed for the levels of expression of an *AAP* and other genes implicated in the disorder. The gene expression pattern can be quantified by Northern blot analysis, nuclear run-on or RT-PCR experiments, or by measuring the amount of protein, or by measuring the activity level of the AAP or other gene products. In this manner, the gene expression pattern itself can serve as a marker, indicative of the cellular physiological response to the agent. Accordingly, this response state may be determined before, and at various points during, treatment of the individual with the agent.

The invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (*e.g.*, an agonist, antagonist, protein, peptide, peptidomimetic, nucleic acid, small molecule, food or other drug candidate identified by the screening assays described herein) comprising the steps of (1) obtaining a pre-administration sample from a subject; (2) detecting the level of expression of an AAP, mRNA, or genomic DNA in the preadministration sample; (3) obtaining one or more post-administration samples from the subject; (4) detecting the level of expression or activity of the AAP, mRNA, or genomic DNA in the post-administration samples; (5) comparing the level of expression or activity of the AAP, mRNA, or genomic DNA in the pre-

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administration sample with the AAP, mRNA, or genomic DNA in the post administration sample or samples; and (6) altering the administration of the agent to the subject accordingly. For example, increased administration of the agent may be desirable to increase the expression or activity of the AAP to higher levels than detected, *i.e.*, to increase the effectiveness of the agent. Alternatively, decreased administration of the agent may be desirable to decrease expression or activity of the AAP to lower levels than detected, *i.e.*, to decrease the effectiveness of the agent.

5. *Methods of treatment*

The invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a disorder associated with aberrant AAP expression or activity. Furthermore, these same methods of treatment may be used to induce or inhibit angiogenesis, by changing the level of expression or activity of an AAP.

6. *Disease and disorders*

Diseases and disorders that are characterized by increased AAP levels or biological activity may be treated with therapeutics that antagonize (*i.e.*, reduce or inhibit) activity. Antagonists may be administered in a therapeutic or prophylactic manner. Therapeutics that may be used include: (1) AAP peptides, or analogs, derivatives, fragments or homologs thereof; (2) Abs to an AAP peptide; (3) AAP nucleic acids; (4) administration of antisense nucleic acid and nucleic acids that are "dysfunctional" (*i.e.*, due to a heterologous insertion within the coding sequences) that are used to eliminate endogenous function of by homologous recombination (Capecchi, 1989); or (5) modulators (*i.e.*, inhibitors, agonists and antagonists, including additional peptide mimetic of the invention or Abs specific to an AAP) that alter the interaction between an AAP and its binding partner.

Diseases and disorders that are characterized by decreased AAP levels or biological activity may be treated with therapeutics that increase (*i.e.*, are agonists to) activity. Therapeutics that upregulate activity may be administered therapeutically or prophylactically. Therapeutics that may be used include peptides, or analogs, derivatives, fragments or homologs thereof; or an agonist that increases bioavailability.

Increased or decreased levels can be readily detected by quantifying peptide and/or RNA, by obtaining a patient tissue sample (*e.g.*, from biopsy tissue) and assaying

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in vitro for RNA or peptide levels, structure and/or activity of the expressed peptides (or *AAP* mRNAs). Methods include, but are not limited to, immunoassays (*e.g.*, by Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate (SDS) polyacrylamide gel electrophoresis, immunocytochemistry, *etc.*) and/or hybridization assays to detect expression of mRNAs (*e.g.*, Northern assays, dot blots, *in situ* hybridization, and the like).

7. *Prophylactic methods*

The invention provides a method for preventing, in a subject, a disease or condition associated with an aberrant AAP expression or activity, by administering an agent that modulates an AAP expression or at least one AAP activity. Subjects at risk for a disease that is caused or contributed to by an aberrant AAP expression or activity can be identified by, for example, any or a combination of diagnostic or prognostic assays. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the AAP aberrancy, such that a disease or disorder is prevented or, alternatively, delayed in its progression. Depending on the type of AAP aberrancy, for example, an AAP agonist or AAP antagonist can be used to treat the subject. The appropriate agent can be determined based on screening assays.

8. *Therapeutic methods*

Another aspect of the invention pertains to methods of modulating an AAP expression or activity for therapeutic purposes. The modulatory method of the invention involves contacting a cell with an agent that modulates one or more of the activities of AAP activity associated with the cell. An agent that modulates AAP activity can be a nucleic acid or a protein, a naturally occurring cognate ligand of an AAP, a peptide, an AAP peptidomimetic, or other small molecule. The agent may stimulate AAP activity. Examples of such stimulatory agents include an active AAP and an *AAP* nucleic acid molecule that has been introduced into the cell. In another embodiment, the agent inhibits AAP activity. Examples of inhibitory agents include antisense *AAP* nucleic acids and anti-AAP Abs. Modulatory methods can be performed *in vitro* (*e.g.*, by culturing the cell with the agent) or, alternatively, *in vivo* (*e.g.*, by administering the agent to a subject). As such, the invention provides methods of treating an individual afflicted with a disease or disorder characterized by aberrant expression or activity of an AAP or nucleic acid molecule. In one embodiment, the method involves administering an agent (*e.g.*, an agent

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identified by a screening assay), or combination of agents that modulates (*e.g.*, up-regulates or down-regulates) AAP expression or activity. In another embodiment, the method involves administering an AAP or nucleic acid molecule as therapy to compensate for reduced or aberrant AAP expression or activity.

Stimulation of AAP activity is desirable in situations in which AAP is abnormally down-regulated and/or in which increased AAP activity is likely to have a beneficial effect. One example of such a situation is where a subject has a disorder characterized by aberrant angiogenesis (*e.g.*, cancer).

9. *Determination of the biological effect of the therapeutic*

Suitable *in vitro* or *in vivo* assays can be performed to determine the effect of a specific therapeutic and whether its administration is indicated for treatment of the affected tissue.

In various specific embodiments, *in vitro* assays may be performed with representative cells of the type(s) involved in the patient's disorder, to determine if a given therapeutic exerts the desired effect upon the cell type(s). Modalities for use in therapy may be tested in suitable animal model systems including, but not limited to rats, mice, chicken, cows, monkeys, rabbits, and the like, prior to testing in human subjects. Similarly, for *in vivo* testing, any of the animal model system known in the art may be used prior to administration to human subjects.

10. *Prophylactic and therapeutic uses of the compositions of the invention*

AAP nucleic acids and proteins are useful in potential prophylactic and therapeutic applications implicated in a variety of disorders including, but not limited to those related to angiogenesis.

As an example, a cDNA encoding an AAP may be useful in gene therapy, and the protein may be useful when administered to a subject in need thereof.

AAP nucleic acids, or fragments thereof, may also be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein is to be assessed. A further use could be as an anti-bacterial molecule (*i.e.*, some peptides have been found to possess anti-bacterial properties). These materials are further useful in the generation of Abs that immunospecifically bind to the novel substances of the invention for use in therapeutic or diagnostic methods.

The following example is meant to not be limiting.

EXAMPLE*Identification of genes differentially-regulated*

A comprehensive mRNA profiling technique (GeneCalling) was used to determine differential gene expression profiles of human endothelial cells undergoing differentiation into tube-like structures (Kahn *et al.*, 2000). To confirm the expression data from GeneCalling, independent experiments were undertaken that used gene-specific PCR oligonucleotide primer pairs and an oligonucleotide probe labeled with a fluorescent dye at the 5' end and quencher fluorescent dye at the 3' end.. Total RNA (50 ng) was added to a 50 µl RT-PCR mixture and run.

The following data were collected:

hEF G	collagen gel 24 hr versus 4h	4.5 fold upregulated
hTRG	collagen gel 24 hr versus 4h	3.5 fold upregulated
KLP	collagen gel 24 hr versus 4h	3.5 fold upregulated
myosin X	collagen gel 24 hr versus 4h	3.5 fold upregulated
NHR	collagen gel 24 hr versus 4h	7.3 fold downregulated
HBAZF	collagen gel 24 hr versus 4h	2.1 fold upregulated

EQUIVALENTS

Although particular embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims that follow. In particular, it is contemplated by the inventors that various substitutions, alterations, and modifications may be made to the invention without departing from the spirit and scope of the invention as defined by the claims. The choice of nucleic acid starting material, clone of interest, or library type is believed to be a matter of routine for a person of ordinary skill in the art with knowledge of the embodiments described herein. Other aspects, advantages, and modifications considered within the scope of the following claims.

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CLAIMS

1. An isolated polypeptide comprising an amino acid sequence having at least 80% sequence identity to the sequence of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14 or 16.
2. The polypeptide of claim 1, wherein said polypeptide is an active AAP polypeptide.
3. The polypeptide of claim 2, wherein said amino acid sequence has at least 90% sequence identity to the sequence of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14 or 16.
4. The polypeptide of claim 2, wherein said amino acid sequence has at least 98% sequence identity to the sequence of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14 or 16.
5. An isolated polynucleotide encoding the polypeptide of any one of claims 1-4, or a complement of said polynucleotide.
6. An isolated polynucleotide comprising a nucleotide sequence having at least 80% sequence identity to the sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15, or a complement of said polynucleotide.
7. The polynucleotide of claim 6, wherein said nucleotide sequence has at least 90% sequence identity to the sequence of NOS:1, 3, 5, 7, 9, 11, 13 or 15, or a complement of said polynucleotide.
8. The polynucleotide of claim 6, wherein said nucleotide sequence has at least 98% sequence identity to the sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15, or a complement of said polynucleotide.
9. An antibody that specifically binds to the polypeptide of any one of claims 1-4.

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10. A method of modulating angiogenesis comprising modulating the activity of at least one AAP.

11. The method of claim 10 wherein said modulating angiogenesis is increasing angiogenesis, and said modulating the activity comprises increasing the activity of at least one polypeptide selected from the group consisting of KLP, hBAZF, hTRG, hMX1, hMX2, hEF-G, and hMP.

12. The method of claim 10 wherein said modulating angiogenesis is decreasing angiogenesis, and said modulating the activity comprises increasing the activity of at least one polypeptide, wherein said at least one polypeptide comprises NHR.

13. The method of claim 10 wherein said modulating angiogenesis is decreasing angiogenesis, and said modulating the activity comprises decreasing the activity of at least one polypeptide selected from the group consisting of KLP, hBAZF, hTRG, hMX1, hMX2, hEF-G, and hMP.

14. The method of claim 10 wherein said modulating angiogenesis is increasing angiogenesis, and said modulating the activity comprises decreasing the activity of at least one polypeptide, wherein said at least one polypeptide comprises NHR.

15. The method of claim 11 or 12 wherein said increasing activity comprises increasing the expression of said at least one polypeptide.

16. The method of claim 13 or 14 wherein said decreasing activity comprises decreasing the expression of said at least one polypeptide.

17. The method of claim 15 wherein said increasing expression comprises transforming a cell to increase expression of a polynucleotide encoding said at least one polypeptide.

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18. The method of claim 16 wherein said decreasing expression comprises transforming a cell to express a polynucleotide anti-sense to at least a portion of an endogenous polynucleotide encoding said at least one polypeptide.

19. The method of claim 13 or 14 wherein said decreasing activity comprises transforming a cell to express an aptamer to said at least one polypeptide.

20. The method of claim 13 or 14 wherein said decreasing activity comprises introducing into a cell an aptamer to said at least one polypeptide.

21. The method claim 13 or 14 wherein said decreasing activity comprises administering to a cell an antibody that selectively binds to said at least one polypeptide.

22. A method of treating tumors comprising decreasing angiogenesis by the method of claim 12 or 13.

23. A method of treating cancer comprising treating a cancerous tumor by the method of claim 22.

24. A method of treating myocardial infarction comprising increasing angiogenesis by the method of claim 11 or 14.

25. A method of promoting healing comprising increasing angiogenesis by the method of claim 11 or 14.

26. A method for determining whether a compound up-regulates or down-regulates the transcription of an AAP gene, comprising:

contacting said compound with a composition comprising a RNA polymerase and said gene and measuring the amount of said AAP gene transcription.

27. The method of claim 26, wherein said composition is in a cell.

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28. A method for determining whether a compound up-regulates or down-regulates the translation of an AAP gene, comprising:

contacting said compound with a composition comprising a ribosome and a polynucleotide corresponding to a mRNA of said gene and measuring the amount of said AAP gene translation.

29. The method of claim 28, wherein said composition is in a cell.

30. A vector, comprising the polynucleotide of any one of claims 5-8.

31. A cell, comprising the vector of claim 30.

32. A method of screening a tissue sample for tumorigenic potential, comprising:

measuring expression of at least one AAP gene in said tissue sample.

33. The method of claim 32, wherein said measuring is measuring an amount of a polypeptide encoded by said at least one AAP gene.

34. The method of claim 32, wherein said measuring expression is measuring an amount of mRNA corresponding to said at least one AAP gene.

35. A transgenic non-human animal, having at least one disrupted AAP gene.

36. The transgenic non-human animal of claim 35, wherein the non-human animal is a mouse.

37. A transgenic non-human animal, comprising an exogenous polynucleotide having at least 80% sequence identity to the sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15, or a complement of said polynucleotide.

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38. The transgenic non-human animal of claim 37, wherein said exogenous polynucleotide has at least 90% sequence identity to the sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15 , or a complement of said polynucleotide.

39. The transgenic non-human animal of claim 37, wherein said exogenous polynucleotide has at least 98% sequence identity to the sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15 , or a complement of said polynucleotide.

40. A method of screening a sample for an AAP gene mutation, comprising:
comparing an AAP nucleotide sequence in the sample with SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15 .

41. A method of determining the clinical stage of tumor comprising comparing expression of at least one AAP gene in a sample with expression of said at least one gene in control samples.