

SEQUENCE LISTING

<110> GLAXOSMITHKLINE INTELLECTUAL PROPERTY DEVELOPMENT LIMITED

<120> BIOPHARMACEUTICAL COMPOSITIONS AND
RELATED METHODS

<130> PU66209

<160> 21

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence identified using molecular
biology techniques.

<400> 1

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

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Tyr Ile Thr
 245 250 255
 Arg Glu Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 260 265 270
 Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 275 280 285
 Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 290 295 300
 Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 305 310 315 320
 Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 325 330 335
 Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 340 345 350
 Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
 355 360 365
 Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 370 375 380
 Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 385 390 395 400
 Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 405 410 415
 Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 420 425 430
 Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 435 440 445
 Lys

<210> 2

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence identified using molecular biology techniques.

<400> 2

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

Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp
		115					120					125			
Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn
	130					135					140				
Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu
145					150					155					160
Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp
			165						170					175	
Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr
			180					185					190		
Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser
		195					200					205			
Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys				
	210					215					220				

<210> 3

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence identified using molecular biology techniques.

<400> 3

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

<210> 4

<211> 114

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence identified using molecular biology techniques.

<400> 4

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

<210> 5
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence identified using molecular
 biology techniques.

<400> 5
 Gly Ser Ser Val His
 1 5

<210> 6
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence identified using molecular
 biology techniques.

<400> 6
 Val Ile Trp Ala Ser Gly Gly Thr Asp Tyr Asn Ser Ala Leu Met Ser
 1 5 10 15

<210> 7
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence identified using molecular
 biology techniques.

<400> 7
Asp Pro Pro Ser Gly Leu Leu Arg Leu Asp Tyr
1 5 10

<210> 8
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence identified using molecular
biology techniques.

<400> 8
Lys Ser Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu
1 5 10 15
Ala

<210> 9
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence identified using molecular
biology techniques.

<400> 9
Gly Ala Ser Thr Arg Glu Ser
1 5

<210> 10
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence identified using molecular
biology techniques.

<400> 10
Gln Asn Val His Ser Phe Pro Phe Thr
1 5

<210> 11
<211> 115
<212> PRT
<213> Homo sapien

<400> 11

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

<210> 12

<211> 400

<212> PRT

<213> Homo sapien

<400> 12

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

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

<210> 13

<211> 1404

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence identified using molecular biology techniques.

<400> 13

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gtgaccctga	gggagagcgg	ccccgccctg	gtgaagccca	cacagaccct	cactctgacc	120
tgcaccgtga	gcggcttcag	cctgaccggc	tctagcgtcc	actgggtgag	gcagcccccc	180
ggcaagggcc	tggagtggct	gggcgtgatc	tgggcaagcg	gggggacgga	ctacaactcg	240
gccctgatga	gcaggctctc	catcagcaag	gacaccagcc	ggaaccaggt	ggtgctgacc	300
atgaccaaca	tggaccccg	ggacaccgcc	acctattact	gcgccaggga	ccctccctcc	360
ggcctgctga	ggctggacta	ctggggcgagg	ggaacactag	tgaccgtgtc	cagcgccagc	420
accaagggcc	ccagcgtggt	ccccctggcc	cccagcagca	agagcaccag	cggcggcaca	480
gccgccctgg	gctgcctggt	gaaggactac	ttccccgagc	ccgtgaccgt	gtcctggaac	540
agcggagccc	tgaccagcgg	cgtgcacacc	ttccccgccg	tgctgcagag	cagcggcctg	600
tacagcctga	gcagcgtggt	gaccgtgccc	agcagcagcc	tgggcaccca	gacctacatc	660
tgtaacgtga	accacaagcc	cagcaacacc	aaggtggaca	agcgggtgga	gccaagagc	720
tgtgacaaga	cccacacctg	ccccccctgc	cctgcccccg	agctgctggg	aggccccagc	780
gtgttcctgt	ttcccccaaa	gcctaaggac	accctgtaca	tcaccagaga	acccgaggtg	840
acctgtgtgg	tgggtggatgt	gagccacgag	gaccctgagg	tgaagttcaa	ctggtacgtg	900
gacggcgtgg	aggtgcacaa	tgccaagacc	aagcccaggg	aggagcagta	caacagcacc	960
taccgggtgg	tgtccgtgct	gaccgtgctg	caccaggatt	ggctgaacgg	caaggagtac	1020
aagtgtaaag	tgtccaacaa	ggccctgcct	gcccctatcg	agaaaaccat	cagcaaggcc	1080
aagggccagc	ccagagagcc	ccaggtgtac	accctgcccc	ctagcagaga	ggagatgacc	1140
aagaaccagg	tgtccctgac	ctgcctggtg	aagggtctct	accccagcga	catcgccgtg	1200

gagtgggaga	gcaacggcca	gcccgagaac	aactacaaga	ccaccccccc	tgtgctggac	1260
agcgatggca	gcttcttctt	gtacagcaag	ctgaccgtgg	acaagagcag	atggcagcag	1320
ggcaacgtgt	tcagctgctc	cgtgatgcac	gaggccctgc	acaatcacta	caccagaag	1380
agcctgagcc	tgtcccctgg	caag				1404

<210> 14

<211> 717

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence identified using molecular biology techniques.

<400> 14

atgggctggg	cctgcatcat	cctgtttctg	gtggccaccg	ccaccggtgt	gcacagcgac	60
atcgtgatga	cccagtctcc	cgattcactg	gccgtgagcc	tgggcgagag	ggccaccatc	120
aactgcaaga	gcagccagag	cctcctgaac	agcggcaacc	agaagaacta	cctggcctgg	180
taccagcaga	aacccggcca	gcccccaag	ctgctgatct	atggcgcttc	caccagggag	240
agcggcgtgc	cagacagggt	tagcggcagc	ggcagcggca	ccgacttcac	cctgacaatc	300
agcagcctgc	aggccgagga	cgtggccgtg	tactactgcc	agaacgtcca	cagcttcccc	360
ttcaccttcg	gcgggggaac	caagctggag	atcaagcgta	cggtggccgc	ccccagcgtg	420
ttcatcttcc	ccccagcga	tgagcagctg	aagagcggca	ccgccagcgt	ggtgtgtctg	480
ctgaacaact	tctacccccg	ggaggccaag	gtgcagtgga	aggtggacaa	tgccctgcag	540
agcggcaaca	gccaggagag	cgtgaccgag	caggacagca	aggactccac	ctacagcctg	600
agcagcacc	tgaccctgag	caaggccgac	tacgagaagc	acaaggtgta	cgctgtgtag	660
gtgaccacc	agggcctgtc	cagccccgtg	accaagagct	tcaaccgggg	cgagtgc	717

<210> 15

<211> 356

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence identified using molecular biology techniques.

<400> 15

aggtgaccct	gagggagagc	ggccccgccc	tggtgaagcc	cacacagacc	ctcactctga	60
cctgcaccgt	gagcggcttc	agcctgaccg	gctctagcgt	ccactgggtg	aggcagcccc	120
ccggcaaggg	cctggagtgg	ctgggcgtga	tctgggcaag	cgggggggacg	gactacaact	180
cggccctgat	gagcaggctc	tccatcagca	aggacaccag	ccggaaccag	gtggtgctga	240
ccatgaccaa	catggacccc	gtggacaccg	ccacctatta	ctgcgccagg	gaccctccct	300
ccggcctgct	gaggctggac	tactggggca	ggggaacact	agtgaccgtg	tccagc	356

<210> 16

<211> 342

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence identified using molecular biology techniques.

<400> 16
gacatcgtga tgaccagtc tcccgattca ctggccgtga gcctgggcga gagggccacc 60
atcaactgca agagcagcca gagcctcctg aacagcggca accagaagaa ctacctggcc 120
tggtaccagc agaaacccgg ccagcccccc aagctgctga tctatggcgc ctccaccagg 180
gagagcggcg tgccagacag gtttagcggc agcggcagcg gcaccgactt caccctgaca 240
atcagcagcc tgcaggccga ggacgtggcc gtgtactact gccagaacgt ccacagcttc 300
cccttcacct tcggcggggg aaccaagctg gagatcaagc gt 342

<210> 17

<211> 1347

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence identified using molecular biology techniques.

<400> 17

caggtgaccc tgaggagag cggccccgcc ctggtgaagc ccacacagac ctcactctg 60
acctgcaccg tgagcggcct cagcctgacc ggctctagcg tccactgggt gaggcagccc 120
ccgggcaagg gcctggagt gctgggcgtg atctgggcaa gcggggggac ggactacaac 180
tcggccctga tgagcaggct ctccatcagc aaggacacca gccggaacca ggtggtgctg 240
accatgacca acatggaccc cgtggacacc gccacctatt actgcgccag ggacctctcc 300
tccggcctgc tgaggctgga ctactggggc aggggaacac tagtgaccgt gtccagcgcc 360
agcaccaagg gcccagcgt gttccccctg gcccagca gcaagagcac cagcggcggc 420
acagccgccc tgggctgcct ggtgaaggac tacttccccg agcccgtgac cgtgtcctgg 480
aacagcggag ccctgaccag cggcgtgcac accttccccg ccgtgctgca gagcagcggc 540
ctgtacagcc tgagcagcgt ggtgaccgtg cccagcagca gcctgggcac ccagacctac 600
atctgtaacg tgaaccacaa gcccagcaac accaaggtgg acaagcgggt ggagcccaag 660
agctgtgaca agaccacac ctgccccccc tgccctgccc ccgagctgct gggaggcccc 720
agcgtgttcc tgttcccccc caagcctaag gacaccctgt acatcaccag agaaccgag 780
gtgacctgtg tgggtggtgga tgtgagccac gaggaccctg aggtgaagtt caactggtac 840
gtggacggcg tggaggtgca caatgccaag accaagccca gggaggagca gtacaacagc 900
acctaccggg tgggtgtccgt gctgaccgtg ctgcaccagg attggctgaa cggcaaggag 960
tacaagtgtg aggtgtccaa caaggccctg cctgccccta tcgagaaaac catcagcaag 1020
gccaagggcc agcccagaga gcccaggtg tacaccctgc cccctagcag agaggagatg 1080
accaagaacc aggtgtccct gacctgcctg gtgaagggt tctaccccag cgacatcgcc 1140
gtggagtggg agagcaacgg ccagcccag aacaactaca agaccacccc ccctgtgctg 1200
gacagcgatg gcagcttctt cctgtacagc aagctgaccg tggacaagag cagatggcag 1260
cagggcaacg tgttcagctg ctccgtgatg cacgaggccc tgcacaatca ctacaccag 1320
aagagcctga gcctgtcccc tggcaag 1347

<210> 18

<211> 660

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence identified using molecular biology techniques.

<400> 18

gacatcgtga tgaccagtc tcccgattca ctggccgtga gcctgggcga gagggccacc 60
atcaactgca agagcagcca gagcctcctg aacagcggca accagaagaa ctacctggcc 120

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tggtaccagc agaaacccgg ccagcccccc aagctgctga tctatggcgc ctccaccagg 180
gagagcggcg tgccagacag gtttagcggc agcggcagcg gcaccgactt caccctgaca 240
atcagcagcc tgcaggccga ggacgtggcc gtgtactact gccagaacgt ccacagcttc 300
cccttcacct tcggcggggg aaccaagctg gagatcaagc gtacgggtggc cgcccccagc 360
gtgttcatct tccccccag cgatgagcag ctgaagagcg gcaccgccag cgtggtgtgt 420
ctgctgaaca acttctaccc ccgggaggcc aaggtgcagt ggaaggtgga caatgccctg 480
cagagcggca acagccagga gagcgtgacc gagcaggaca gcaaggactc cacctacagc 540
ctgagcagca ccctgaccct gagcaaggcc gactacgaga agcacaaggt gtacgcctgt 600
gaggtgaccc accagggcct gtccagcccc gtgaccaaga gcttcaaccg gggcgagtgc 660

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<210> 19

<211> 19

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biology techniques.

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Val His Ser

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