

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25
SEQUENCE LISTING

<110> iCell Gene Therapeutics LLC
<120> Chimeric Antigen Receptors (CARs), Compositions and
Methods of Use
<130> 2541-3 PCT
<140> 00000000
<141> 2016-06-24
<150> 62/184,321
<151> 2015-06-25
<160> 36
<170> PatentIn version 3.5
<210> 1
<211> 830
<212> PRT
<213> Artificial Sequence
<220>
<223> synthetic sequence
<400> 1

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20 25 30

Ala Val Ser Leu Gly Glu Arg Val Thr Met Asn Cys Lys Ser Ser Gln
35 40 45

Ser Leu Leu Tyr Ser Thr Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln
50 55 60

Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr
65 70 75 80

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Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
85 90 95

Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Val Ala Val
100 105 110

Tyr Tyr Cys Gln Gln Tyr Tyr Ser Tyr Arg Thr Phe Gly Gly Gly Thr
115 120 125

Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Val Val
145 150 155 160

Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr
165 170 175

Phe Thr Ser Tyr Val Ile His Trp Val Arg Gln Lys Pro Gly Gln Gly
180 185 190

Leu Asp Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Asp Tyr
195 200 205

Asp Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Thr Ser Thr
210 215 220

Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
225 230 235 240

Val Tyr Tyr Cys Ala Arg Glu Lys Asp Asn Tyr Ala Thr Gly Ala Trp
245 250 255

Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Thr
260 265 270

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Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
275 280 285

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
290 295 300

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
305 310 315 320

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
325 330 335

Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
340 345 350

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
355 360 365

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg
370 375 380

Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln
385 390 395 400

Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu
405 410 415

Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
420 425 430

Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
435 440 445

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
450 455 460

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Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly
465 470 475 480

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
485 490 495

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
500 505 510

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
515 520 525

Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu
530 535 540

Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Tyr Arg
545 550 555 560

Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr Asn
565 570 575

Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro
580 585 590

Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile
595 600 605

Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu
610 615 620

Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu
625 630 635 640

Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His
645 650 655

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Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser
660 665 670

Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu
675 680 685

Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln
690 695 700

Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
705 710 715 720

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln
725 730 735

Ala Pro Arg Arg Ala Arg Gly Cys Arg Thr Leu Gly Leu Pro Ala Leu
740 745 750

Leu Leu Leu Leu Leu Leu Arg Pro Pro Ala Thr Arg Gly Ile Thr Cys
755 760 765

Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr
770 775 780

Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg
785 790 795 800

Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys Ala Thr
805 810 815

Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg
820 825 830

<210> 2
<211> 2509
<212> DNA

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 2

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agagggtg	ac	catgaact	gc	aaaagc	agcc	agtcct	ctgct	gtactcc	acc	aaccaga	aaga	180
actacctg	gc	ttggtat	caa	cagaag	ccccg	gacagag	ccc	caagct	gctg	atctattg	ggg	240
ccagcact	tag	ggaaag	cggc	gtgccc	gata	ggttcag	cgg	cagcggg	agc	ggcacag	act	300
tcactctg	ac	cattagc	agc	gtgcagg	ctg	aggatgt	ggc	cgtctact	ac	tgccagc	agt	360
actacagc	tac	caggacct	ttt	gggggc	ggaa	ctaagct	gga	gatcaagg	ga	gggggggg	gat	420
ccgggggg	agg	aggctcc	ggc	ggaggc	ggaa	gccaa	agtgc	actgcag	cag	agcggccc	ag	480
aggtgg	tcaa	acctggg	gca	agcgtg	aaga	tgagctg	caa	ggctagc	ggc	tataacct	tca	540
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acatcaac	ccc	ctacaat	gac	ggcacc	gatt	atgacg	aaaa	attcaagg	ggg	aaggcc	accc	660
tgaccagc	ga	caccagc	aca	agcacc	gcct	acatgg	agct	gtccagc	cctg	aggtcc	gagg	720
acaccgcc	gt	gtattact	gt	gccagg	gaga	aggaca	atta	cgccacc	ggc	gcttggtt	ctg	780
cctactgg	ggg	ccagggc	aca	ctgg	tgacag	tgagcag	cac	cacgac	gcca	gcgccg	cgc	840
caccaac	acc	ggcgccc	acc	atcg	ctgc	agcccc	tgtc	cctgcg	ccca	gaggcgt	gcc	900
ggccagc	ggc	ggggggc	gca	gtgcac	acga	ggggg	ctgga	cttcgc	cctgt	gatatct	taca	960
tctgggc	gcc	cttggcc	ggg	acttgt	gggg	tccttct	cct	gtcact	gggt	atcacc	cttt	1020
actgcagg	ag	taagagg	agc	aggctc	ctgc	acagtga	cta	catgaac	atg	actcccc	gcc	1080
gccccggg	cc	caccgc	aag	cattacc	agc	cctatg	cccc	accacg	cgc	ttcgca	cct	1140
atcgctcc	aa	acggggc	aga	aagaaa	actcc	tgtatat	att	caaaca	acca	tttatg	agac	1200
cagtacaa	ac	tactca	agag	gaagat	ggct	gtagct	gccg	atttcc	agaa	gaagaag	aag	1260

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gaggatgtga actgagagtg aagttcagca ggagcgcaga cgccccgcg taccagcagg	1320
gccagaacca gctctataac gagctcaatc taggacgaag agaggagtag gatgttttgg	1380
acaagagacg tggccgggac cctgagatgg ggggaaagcc gcagagaagg aagaaccctc	1440
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cagccaccaa ggacacctac gacgcccttc acatgcaggc cctgccccct cgcggaagcg	1620
gagccaccaa cttcagcctg ctgaagcagg ccggcgacgt ggaggagaac cccggcccca	1680
tgtacagaat gcagctgctg agctgcatcg ccctgagcct ggccctgggtg accaacagcg	1740
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ccgtggagaa cctgatcatc ctggccaaca acagcctgag cagcaacggc aacgtgaccg	2040
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gcttcgtgca catcgtgcag atgttcatca acaccagctc cggcggcggc tccggcggcg	2160
gcggctccgg cggcggcggc tccggcggcg gcggctccgg cggcggctcc ctgcaggccc	2220
ccagaagagc cagaggctgc agaaccctgg gcctgcccgc cctgctgctg ctgctgctgc	2280
tgagaccccc cgccaccaga ggcatcacct gcccccccc catgagcgtg gagcacgccg	2340
acatctgggt gaagagctac agcctgtaca gcagagagag atacatctgc aacagcggct	2400
tcaagagaaa ggccggcacc agcagcctga ccgagtgcgt gctgaacaag gccaccaacg	2460
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<210> 3

<211> 995

<212> PRT

<213> Artificial Sequence

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

<220>

<223> synthetic sequence

<400> 3

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu
20 25 30

Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln
35 40 45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
50 55 60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
85 90 95

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
130 135 140

Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser
145 150 155 160

Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly
165 170 175

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Val Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly
180 185 190

Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser
195 200 205

Arg Leu Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys
210 215 220

Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys
225 230 235 240

His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly
245 250 255

Thr Ser Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro
260 265 270

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
275 280 285

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
290 295 300

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
305 310 315 320

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg
325 330 335

Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln
340 345 350

Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu
355 360 365

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
370 375 380

Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
385 390 395 400

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
405 410 415

Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly
420 425 430

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
435 440 445

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
450 455 460

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
465 470 475 480

Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu
485 490 495

Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu
500 505 510

Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala
515 520 525

Arg Pro Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser
530 535 540

Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser
545 550 555 560

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp
565 570 575

Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Val Arg Phe Ser
580 585 590

Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu
595 600 605

Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser Asn Pro
610 615 620

Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly
625 630 635 640

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
645 650 655

Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser
660 665 670

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val
675 680 685

Lys Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro
690 695 700

Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr
705 710 715 720

Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser
725 730 735

Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ser Thr Tyr
740 745 750

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly Ala Gly Thr Thr Val
755 760 765

Thr Val Ser Ala Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
770 775 780

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
785 790 795 800

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
805 810 815

Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
820 825 830

Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu
835 840 845

Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr
850 855 860

Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr
865 870 875 880

Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
885 890 895

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
900 905 910

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
915 920 925

Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
930 935 940

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Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
945 950 955 960

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
965 970 975

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
980 985 990

Pro Pro Arg
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<210> 4
<211> 3004
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

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acagagtcac catcagttgc agggcaagtc aggacattag taaatattta aattggtatc 180
agcagaaacc agatggaact gttaaactcc tgatctacca tacatcaaga ttacactcag 240
gagtcccatc aaggttcagt ggcagtgggt ctggaacaga ttattctctc accattagca 300
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cacagagcct gtccgtcaca tgcactgtct caggggtctc attacccgac tatggtgtaa 540
gctggattcg ccagcctcca cgaaagggtc tggagtggct gggagtaata tggggtagtg 600
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2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

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cagtcaccgt ctcctcaacc acgacgccag cgccgcgacc accaacaccg gcgccccacca	840
tcgcgtcgca gcccctgtcc ctgcgcccag aggcgtgccg gccagcggcg gggggcgag	900
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gcggagggtc cggaggcggc ggaagcgggg gagggggaag ccagggtcaa ctgcaacagc	1980
ccggagcaga actgggtcaaa ccaggcgcca gcgtgaagat gagctgcaag gccagcgggt	2040
acaccttcac ttcctataac atgcactggg tgaagcagac cccaggaagg ggccctggagt	2100

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

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ccagcgagga cagcgccgtg tactattgcg ccagaagcac ttattacgga ggggactggt	2280
acttcaacgt gtggggggca gggaccaccg tgaccgtgtc cgccaccacg acgccagcgc	2340
cgcgaccacc aacaccggcg cccaccatcg cgtcgcagcc cctgtccctg cgcccagagg	2400
cgtgccggcc agcggcgggg ggcgcagtg acacgagggg gctggacttc gcctgtgata	2460
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acaagagacg tggccgggac cctgagatgg ggggaaaagcc gcagagaagg aagaaccctc	2820
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aaac	3004

<210> 5
 <211> 1001
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 5

Asp	Arg	Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu
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Leu Leu His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Thr Thr Ser

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20

25

30

Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala
35 40 45

Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp
50 55 60

Gly Thr Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly
65 70 75 80

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
85 90 95

Thr Ile Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln
100 105 110

Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu
115 120 125

Ile Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

Ser Glu Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser
145 150 155 160

Gln Ser Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp
165 170 175

Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp
180 185 190

Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu
195 200 205

Lys Ser Arg Leu Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe

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210

215

220

Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys
225 230 235 240

Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly
245 250 255

Gln Gly Thr Ser Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg
260 265 270

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
275 280 285

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
290 295 300

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
305 310 315 320

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg
325 330 335

Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro
340 345 350

Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu
355 360 365

Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala
370 375 380

Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
385 390 395 400

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25
405 410 415

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
420 425 430

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
435 440 445

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
450 455 460

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
465 470 475 480

His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser
485 490 495

Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala
500 505 510

Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala
515 520 525

Ala Arg Pro Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
530 535 540

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Ile
545 550 555 560

Val His Ser Val Gly Asn Thr Phe Leu Glu Trp Tyr Gln Gln Lys Pro
565 570 575

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
580 585 590

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

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595

600

605

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
610 615 620

Phe Gln Gly Ser Gln Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val
625 630 635 640

Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
645 650 655

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
660 665 670

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Glu Phe Ser
675 680 685

Arg Ser Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
690 695 700

Trp Val Gly Arg Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Ser Gly
705 710 715 720

Lys Phe Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr
725 730 735

Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
740 745 750

Tyr Cys Ala Arg Asp Gly Ser Ser Trp Asp Trp Tyr Phe Asp Val Trp
755 760 765

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro
770 775 780

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu

785 790 795 800

785 790 795 800

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
805 810 815

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
820 825 830

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys
835 840 845

Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg
850 855 860

Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro
865 870 875 880

Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser
885 890 895

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
900 905 910

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
915 920 925

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
930 935 940

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
945 950 955 960

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
965 970 975

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

980

985

990

Leu His Met Gln Ala Leu Pro Pro Arg
 995 1000

<210> 6
 <211> 3016
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 6
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 acagagtcac catcagttgc agggcaagtc aggacattag taaatattta aattggtatc 180
 agcagaaaacc agatggaact gttaaaactcc tgatctacca tacatcaaga ttacactcag 240
 gagtcccatc aaggttcagt ggcagtgggt ctggaacaga ttattctctc accattagca 300
 acctggagca agaagatatt gccacttact ttgccaaca gggtaatacg cttccgtaca 360
 cgttcggagg ggggaccaag ctggagatca cagggtggcg tggctcgggc ggtgggtgggt 420
 cgggtggcg cggatctgag gtgaaactgc aggagtcagg acctggcctg gtggcgccct 480
 cacagagcct gtccgtcaca tgactgtct caggggtctc attacccgac tatggtgtaa 540
 gctggattcg ccagcctcca cgaaagggtc tggagtggct gggagtaata tggggtagtg 600
 aaaccacata ctataattca gctctcaaact ccagactgac catcatcaag gacaactcca 660
 agagccaagt tttcttaaaa atgaacagtc tgcaaaactga tgacacagcc atttactact 720
 gtgccaacaa ttattactac ggtggtagct atgctatgga ctactggggc caaggaacct 780
 cagtcaccgt ctctcaacc acgacgccag cgccgcgacc accaacaccg gcgcccacca 840
 tcgcgtcgca gcccctgtcc ctgcgcccag aggcgtgccg gccagcggcg gggggcgag 900
 tgcacacgag ggggctggac ttgcctgtg atatctacat ctgggcgccc ttggccggga 960

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

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aactcctgta tatattcaaa caaccattta tgagaccagt acaaactact caagaggaag	1080
atggctgtag ctgccgattt ccagaagaag aagaaggagg atgtgaactg agagtgaagt	1140
tcagcaggag cgcagacgcc cccgcgtacc agcagggccca gaaccagctc tataacgagc	1200
tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc cgggacctg	1260
agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat gaactgcaga	1320
aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc cggaggggca	1380
aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc tacgacgcc	1440
ttcacatgca ggccctgccc cctcgcgga gcgagccac caacttcagc ctgctgaagc	1500
aggccggcga cgtggaggag aaccccgcc ccatggcctt accagtgacc gccttgctcc	1560
tgccgctggc cttgctgctc cacgcccca ggccggatat ccagatgacc cagagcccca	1620
gctccctgtc cgcattccgtg ggcgacagag tgacaattac ctgtagaagc agccaaagca	1680
tcgtgcatag cgtcggcaac acttttctgg agtggatatca acagaagccc gggaaggccc	1740
ccaaactgct gatctacaag gtgagcaaca gattcagcgg ggtcccaagc agattctccg	1800
gcagcggctc cgggactgac ttcacctga ccattagcag cctgcagcca gaggacttcg	1860
ccacatacta ctgcttcaa gggagccagt tcccctacac cttcgcccaa ggcactaagg	1920
tggagatcaa agggggggga ggaagcggcg gaggaggag cggaggcggg ggatccgaag	1980
tgcaactggc cgaatccgga ggggggctgg tccagcctgg agggtcctg agactgagct	2040
gcgccgcaag cggctacgag ttctccaggc cctggatgaa ctgggtgagg caggccccag	2100
gaaaagggct ggaatgggtg ggcaggatct accctggcga cggcgatacc aactactccg	2160
gaaagttaa gggcagggtt actatcagcg ccgacactag caagaatacc gcctacctgc	2220
agatgaatag cctgagggcc gaggacaccg ccgtgtatta ctgcgctaga gacggcagca	2280
gctgggattg gtacttcgac gtgtggggcc agggcactct ggtgactgtg agcagacca	2340
cgacgccagc gccgcgacca ccaacaccgg cgcccaccat cgcgtcgag cccctgtccc	2400

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

tcgccccaga ggcgtgccgg ccagcggcgg ggggcgcagt gcacacgagg gggctggact	2460
tcgcctgtga tatctacatc tgggcgccct tggccgggac ttgtgggggtc cttctcctgt	2520
cactggttat caccctttac tgcaaacggg gcagaaagaa actcctgtat atattcaaac	2580
aaccatttat gagaccagta caaactactc aagaggaaga tggctgtagc tgccgatttc	2640
cagaagaaga agaaggagga tgtgaactga gagtgaagtt cagcaggagc gcagacgccc	2700
ccgcgtacca gcagggccag aaccagctct ataacgagct caatctagga cgaagagagg	2760
agtacgatgt tttggacaag agacgtggcc gggaccctga gatgggggga aagccgagaa	2820
ggaagaaccc tcaggaaggc ctgtacaatg aactgcagaa agataagatg gcggaggcct	2880
acagtgagat tgggatgaaa ggcgagcgcc ggaggggcaa ggggcacgat ggcctttacc	2940
agggtctcag tacagccacc aaggacacct acgacgccct tcacatgcag gccctgcccc	3000
ctcgctaagt ttaaac	3016

<210> 7
 <211> 990
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 7

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10					15		

His	Ala	Ala	Arg	Pro	Asp	Ile	Gln	Met	Thr	Gln	Thr	Thr	Ser	Ser	Leu
			20					25					30		

Ser	Ala	Ser	Leu	Gly	Asp	Arg	Val	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Gln
		35					40					45			

Asp	Ile	Ser	Lys	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Asp	Gly	Thr
	50					55					60				

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
85 90 95

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
130 135 140

Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser
145 150 155 160

Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly
165 170 175

Val Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly
180 185 190

Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser
195 200 205

Arg Leu Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys
210 215 220

Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys
225 230 235 240

His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly
245 250 255

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Thr Ser Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro
260 265 270

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
275 280 285

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
290 295 300

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
305 310 315 320

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg
325 330 335

Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln
340 345 350

Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu
355 360 365

Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
370 375 380

Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
385 390 395 400

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
405 410 415

Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly
420 425 430

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
435 440 445

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
450 455 460

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
465 470 475 480

Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu
485 490 495

Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu
500 505 510

Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala
515 520 525

Arg Pro Asp Val Gln Ile Thr Gln Ser Pro Ser Tyr Leu Ala Ala Ser
530 535 540

Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala Ser Lys Ser Ile Ser
545 550 555 560

Lys Asp Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Thr Asn Lys Leu
565 570 575

Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly Ile Pro Ser Arg Phe
580 585 590

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
595 600 605

Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln Gln His Asn Lys Tyr
610 615 620

Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly
625 630 635 640

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
645 650 655

Gln Gln Pro Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Lys Leu
660 665 670

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Trp Met Asn Trp
675 680 685

Val Lys Gln Arg Pro Asp Gln Gly Leu Glu Trp Ile Gly Arg Ile Asp
690 695 700

Pro Tyr Asp Ser Glu Thr His Tyr Asn Gln Lys Phe Lys Asp Lys Ala
705 710 715 720

Ile Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser
725 730 735

Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Asn
740 745 750

Trp Asp Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Thr
755 760 765

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
770 775 780

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
785 790 795 800

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
805 810 815

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
820 825 830

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr
835 840 845

Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln
850 855 860

Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys
865 870 875 880

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
885 890 895

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
900 905 910

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg
915 920 925

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
930 935 940

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
945 950 955 960

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
965 970 975

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
980 985 990

<210> 8

<211> 2989

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic sequence

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

<400> 8

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ccgccaggcc ggacatccag atgacacaga ctacatcctc cctgtctgcc tctctgggag	120
acagagtcac catcagttgc agggcaagtc aggacattag taaatattta aattggtatc	180
agcagaaaacc agatggaact gttaaaactcc tgatctacca tacatcaaga ttacactcag	240
gagtcccatc aaggttcagt ggcagtgggt ctggaacaga ttattctctc accattagca	300
acctggagca agaagatatt gccacttact ttgccaaca gggtaatacg cttccgtaca	360
cgttcggagg ggggaccaag ctggagatca caggtaggcg tggctcgggc ggtggtgggt	420
cgggtggcgg cggatctgag gtgaaactgc aggagtcagg acctggcctg gtggcgccct	480
cacagagcct gtccgtcaca tgcactgtct caggggtctc attacccgac tatggtgtaa	540
gctggattcg ccagcctcca cgaaagggtc tggagtggct gggagtaata tggggtagtg	600
aaaccacata ctataattca gctctcaa at ccagactgac catcatcaag gacaactcca	660
agagccaagt tttcttaaaa atgaacagtc tgcaaactga tgacacagcc atttactact	720
gtgccaacaa ttattactac ggtggtagct atgctatgga ctactggggc caaggaacct	780
cagtcaccgt ctctcaacc acgacgccag cgccgcgacc accaacaccg gcgcccacca	840
tcgcgtcgca gcccctgtcc ctgcgcccag aggcgtgccg gccagcggcg gggggcgag	900
tgcacacgag ggggctggac ttgcctgtg atatctacat ctgggcgccc ttggccggga	960
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tcagcaggag cgcagacgcc cccgcgtacc agcagggccga gaaccagctc tataacgagc	1200
tcaatctagg acgaagagag gactacgatg ttttggacaa gagacgtggc cgggaccctg	1260
agatgggggg aaagccgcag agaaggaaga accctcagga aggcctgtac aatgaactgc	1320
agaaagataa gatggcggag gcctacagtg agattgggat gaaaggcgag cgccggaggg	1380

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

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cccttcacat gcaggccctg cccctcgcg gaagcggagc caccaacttc agcctgctga	1500
agcaggccgg cgacgtggag gagaaccccc gccccatggc cttaccagtg accgccttgc	1560
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ccagctacct ggccgccagc cccggcgaga ccatcaccat caactgcaga gccagcaaga	1680
gcatcagcaa ggacctggcc tggtagcagg agaagcccgg caagaccaac aagctgctga	1740
tctacagcgg cagcaccctg cagagcggca tccccagcag attcagcggc agcggcagcg	1800
gcaccgactt caccctgacc atcagcagcc tggagcccga ggacttcgcc atgtactact	1860
gccagcagca caacaagtac ccctacacct tcggcggcgg caccaagctg gagatcaagg	1920
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agcccggcgc cgagctgggtg agacccggcg ccagcgtgaa gctgagctgc aaggccagcg	2040
gctacacctt caccagctac tggatgaact gggatgaagca gagacccgac cagggcctgg	2100
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cggcgccac catcgcgtcg cagccccctgt ccctgcgcc agaggcgtgc cggccagcgg	2400
cggggggcgc agtgcacacg agggggctgg acttcgcctg tgatatctac atctgggcgc	2460
ccttggccgg gacttgtggg gtccttctcc tgtcactggc tatcaccctt tactgcagga	2520
gtaagaggag caggctcctg cacagtgact acatgaacat gactccccgc cgccccgggc	2580
ccaccgcaa gcattaccag ccctatgccc caccacgcga cttcgagcc tatcgctcca	2640
gagtgaagtt cagcaggagc gcagacgccc ccgcgtacca gcagggccag aaccagctct	2700
ataacgagct caatctagga cgaagagagg agtacgatgt tttggacaag agacgtggcc	2760
gggaccctga gatgggggga aagccgcaga gaaggaagaa ccctcaggaa ggctgtaca	2820

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

atgaactgca gaaagataag atggcggagg cctacagtga gattgggatg aaaggcgagc 2880
gccggagggg caaggggcac gatggccttt accagggtct cagtacagcc accaaggaca 2940
cctacgacgc ccttcacatg caggccctgc cccctcgcta agtttaaac 2989

<210> 9
<211> 1066
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 9

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met
20 25 30

Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser
35 40 45

Ser Ile Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro
50 55 60

Lys Leu Trp Ile Tyr Thr Thr Ser Asn Leu Ala Ser Gly Val Pro Ala
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser
85 90 95

Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Ser
100 105 110

Thr Tyr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Leu Lys Gly
115 120 125

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
130 135 140

Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Lys Pro Gly Ala Ser Val
145 150 155 160

Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Arg Met
165 170 175

His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
180 185 190

Ile Asn Pro Ser Thr Gly Tyr Thr Glu Tyr Asn Gln Lys Phe Lys Asp
195 200 205

Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln
210 215 220

Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg
225 230 235 240

Gly Gly Gly Val Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
245 250 255

Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
260 265 270

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
275 280 285

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
290 295 300

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
305 310 315 320

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His
325 330 335

Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys
340 345 350

His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
355 360 365

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
370 375 380

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
385 390 395 400

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
405 410 415

Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
420 425 430

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
435 440 445

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
450 455 460

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
465 470 475 480

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
485 490 495

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
500 505 510

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn
515 520 525

Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro
530 535 540

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
545 550 555 560

His Ala Ala Arg Pro Asp Val Gln Ile Thr Gln Ser Pro Ser Tyr Leu
565 570 575

Ala Ala Ser Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala Ser Lys
580 585 590

Ser Ile Ser Lys Asp Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Thr
595 600 605

Asn Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly Ile Pro
610 615 620

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
625 630 635 640

Ser Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln Gln His
645 650 655

Asn Lys Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
660 665 670

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
675 680 685

Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Arg Pro Gly Ala Ser
690 695 700

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Trp
705 710 715 720

Met Asn Trp Val Lys Gln Arg Pro Asp Gln Gly Leu Glu Trp Ile Gly
725 730 735

Arg Ile Asp Pro Tyr Asp Ser Glu Thr His Tyr Asn Gln Lys Phe Lys
740 745 750

Asp Lys Ala Ile Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met
755 760 765

Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
770 775 780

Arg Gly Asn Trp Asp Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
785 790 795 800

Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
805 810 815

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
820 825 830

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
835 840 845

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
850 855 860

Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His
865 870 875 880

Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys
885 890 895

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His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
900 905 910

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
915 920 925

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
930 935 940

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
945 950 955 960

Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
965 970 975

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
980 985 990

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
995 1000 1005

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
1010 1015 1020

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
1025 1030 1035

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
1040 1045 1050

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
1055 1060 1065

<210> 10
<211> 3217
<212> DNA

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 10

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tgcccc	gccag	attcag	cg	gc	aggg	cag	cg	gcacc	ag	cta	cagc	ctg	acc	atcag	ca	gaa	300
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2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

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2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

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<210> 11
 <211> 985
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 11

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His Ala Ala Arg Pro Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met
 20 25 30

Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser
 35 40 45

Ser Ile Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro
 50 55 60

Lys Leu Trp Ile Tyr Thr Thr Ser Asn Leu Ala Ser Gly Val Pro Ala
 65 70 75 80

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser
85 90 95

Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Ser
100 105 110

Thr Tyr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Leu Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
130 135 140

Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Lys Pro Gly Ala Ser Val
145 150 155 160

Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Arg Met
165 170 175

His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
180 185 190

Ile Asn Pro Ser Thr Gly Tyr Thr Glu Tyr Asn Gln Lys Phe Lys Asp
195 200 205

Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln
210 215 220

Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg
225 230 235 240

Gly Gly Gly Val Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
245 250 255

Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
260 265 270

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
275 280 285

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
290 295 300

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
305 310 315 320

Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr
325 330 335

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
340 345 350

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
355 360 365

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
370 375 380

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
385 390 395 400

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
405 410 415

Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
420 425 430

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
435 440 445

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
450 455 460

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
465 470 475 480

Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly
485 490 495

Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu
500 505 510

Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asp Val Gln
515 520 525

Ile Thr Gln Ser Pro Ser Tyr Leu Ala Ala Ser Pro Gly Glu Thr Ile
530 535 540

Thr Ile Asn Cys Arg Ala Ser Lys Ser Ile Ser Lys Asp Leu Ala Trp
545 550 555 560

Tyr Gln Glu Lys Pro Gly Lys Thr Asn Lys Leu Leu Ile Tyr Ser Gly
565 570 575

Ser Thr Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser
580 585 590

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
595 600 605

Ala Met Tyr Tyr Cys Gln Gln His Asn Lys Tyr Pro Tyr Thr Phe Gly
610 615 620

Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly
625 630 635 640

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Pro Gly Ala
645 650 655

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Glu Leu Val Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser
660 665 670

Gly Tyr Thr Phe Thr Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro
675 680 685

Asp Gln Gly Leu Glu Trp Ile Gly Arg Ile Asp Pro Tyr Asp Ser Glu
690 695 700

Thr His Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Leu Thr Val Asp
705 710 715 720

Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu
725 730 735

Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Asn Trp Asp Asp Tyr Trp
740 745 750

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Thr Thr Thr Pro Ala Pro
755 760 765

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
770 775 780

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
785 790 795 800

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
805 810 815

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg
820 825 830

Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro
835 840 845

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
850 855 860

Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala
865 870 875 880

Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
885 890 895

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
900 905 910

Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln
915 920 925

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
930 935 940

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
945 950 955 960

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
965 970 975

Leu His Met Gln Ala Leu Pro Pro Arg
980 985

<210> 12
<211> 2974
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 12
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2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

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2974

<210> 13
 <211> 546
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 13

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Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser
 35 40 45

Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr Leu His Trp Tyr Gln Gln
 50 55 60

Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu
 65 70 75 80

Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 85 90 95

Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr
 100 105 110

Tyr Cys Gln His Ser Arg Glu Leu Pro Phe Thr Phe Gly Ser Gly Thr
 115 120 125

Lys Leu Glu Ile Lys Lys Ile Ser Gly Gly Gly Gly Ser Gly Gly Gly
 130 135 140

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
145 150 155 160

Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
165 170 175

Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser Arg
180 185 190

Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
195 200 205

Ile Gly Glu Ile Asn Pro Thr Ser Ser Thr Ile Asn Phe Thr Pro Ser
210 215 220

Leu Lys Asp Lys Val Phe Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu
225 230 235 240

Tyr Leu Gln Met Ser Lys Val Arg Ser Glu Asp Thr Ala Leu Tyr Tyr
245 250 255

Cys Ala Arg Gly Asn Tyr Tyr Arg Tyr Gly Asp Ala Met Asp Tyr Trp
260 265 270

Gly Gln Gly Thr Ser Val Thr Val Ser Thr Thr Thr Pro Ala Pro Arg
275 280 285

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
290 295 300

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
305 310 315 320

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
325 330 335

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Ser
340 345 350

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
355 360 365

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
370 375 380

Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr
385 390 395 400

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
405 410 415

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
420 425 430

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
435 440 445

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
450 455 460

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
465 470 475 480

Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
485 490 495

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
500 505 510

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
515 520 525

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

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Pro Arg
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<210> 14
<211> 1657
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 14
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ccgccaggcc gagcgacatc gtgctgaccc agagccccgc cagcctggcc gtgagcctgg 120
gccagagagc caccatcagc tgcagagcca gcaagagcgt gagcaccagc ggctacagct 180
acctgcactg gtaccagcag aagcccggcc agccccccaa gctgctgatc tacctggcca 240
gcaacctgga gagcggcggtg cccgccagat tcagcggcag cggcagcggc accgacttca 300
ccctgaacat ccaccccggtg gaggaggagg acgccgccac ctactactgc cagcacagca 360
gagagctgcc cttcaccttc ggcagcggca ccaagctgga gatcaagaag atcagcggcg 420
gcggcggcag cggcggcggc ggcagcggcg gcggcggcag cggcggcggc ggcagcggcg 480
gcggcggcag ccaggtgcag ctggtggaga gcggcggcgg cctggtgcag cccggcggca 540
gcctgaagct gagctgcgcc gccagcggct tcgacttcag cagatactgg atgagctggg 600
tgagacaggc ccccggaag ggcctggagt ggatcggcga gatcaacccc accagcagca 660
ccatcaactt cccccagc ctgaaggaca aggtgttcat cagcagagac aacgccaaga 720
acaccctgta cctgcagatg agcaaggatga gaagcgagga caccgccctg tactactgcg 780
ccagaggcaa ctactacaga tacggcgacg ccatggacta ctggggccag ggcaccagcg 840
tgaccgtgag caccacgacg ccagcggcg gaccaccaac accggcgccc accatcgcgt 900

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

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cgagccccct gtccctgcgc ccagaggcgt gccggccagc ggcggggggc gcagtgcaca      960
cgaggggggct ggacttcgcc tgtgatattct acatctgggc gcccttggcc gggacttgtg      1020
gggtcctttct cctgtcactg gttatcaccc ttctactgcag gagtaagagg agcaggctcc      1080
tgcacagtga ctacatgaac atgactcccc gccgccccgg gccacccgc aagcattacc      1140
agccctatgc cccaccacgc gacttcgcag cctatcgctc caaacggggc agaaagaaac      1200
tcctgtatat attcaaaca ccattttatga gaccagtaca aactactcaa gaggaagatg      1260
gctgtagctg ccgattttcca gaagaagaag aaggaggatg tgaactgaga gtgaagttca      1320
gcaggagcgc agacgcccc gcgtaccagc agggccagaa ccagctctat aacgagctca      1380
atctaggacg aagagaggag tacgatgttt tggacaagag acgtggccgg gaccctgaga      1440
tgggggggaaa gccgcagaga aggaagaacc ctcaggaagg cctgtacaat gaactgcaga      1500
aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc cggaggggca      1560
aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc tacgacgccc      1620
ttcacatgca ggccctgccc cctcgctaag tttaaac                                1657

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<210> 15
 <211> 490
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 15

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Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1           5           10          15

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His Ala Ala Arg Pro Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu
20           25          30

```

```

Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys
35           40          45

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2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

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

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Tyr Tyr Cys Ala Arg Gly Asn Tyr Tyr Arg Tyr Gly Asp Ala Met Asp
245 250 255

Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Thr Thr Thr Pro Ala
260 265 270

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
275 280 285

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
290 295 300

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
305 310 315 320

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
325 330 335

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
340 345 350

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
355 360 365

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser
370 375 380

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
385 390 395 400

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
405 410 415

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro
420 425 430

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
435 440 445

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
450 455 460

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
465 470 475 480

Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 16
<211> 1489
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 16
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agagggccac catcagctgc agggccagca agagcgtgag caccagcggc tacagctacc 180
tgacttggtta ccagcagaag cccggccagc cccccaagct gctgatctac ctggccagca 240
acctggagag cggcgtgccc gccaggttca gcggcagcgg cagcggcacc gacttcaccc 300
tgaacatcca ccccgaggag gaggaggacg ccgccaccta ctactgccag cacagcaggg 360
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ggggaggagg ctccggcgga ggcggaagcc aggtgcagct ggtggagagc ggcggcggcc 480
tggtgcagcc cggcggcagc ctgaagctga gctgcgccgc cagcggcttc gacttcagca 540
ggtactggat gagctgggtg aggcaggccc ccggcaaggg cctggagtgg atcggcgaga 600
tcaacccac cagcagcacc atcaacttca cccccagcct gaaggacaag gtgttcatca 660

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

gcagggacaa cgccaagaac accctgtacc tgcagatgag caaggtgagg agcgaggaca	720
ccgccctgta ctactgcgcc aggggcaact actacaggta cggcgacgcc atggactact	780
ggggccaggg caccagcgtg accgtgagca ccacgacgcc agcgccgcga ccaccaacac	840
cggcgcccac catcgcgtcg cagcccctgt ccctgcgccc agaggcgtgc cggccagcgg	900
cggggggcgc agtgcacacg agggggctgg acttcgcctg tgatatctac atctgggcgc	960
ccttggccgg gacttgtggg gtccttctcc tgtcactggt tatcaccctt tactgcagga	1020
gtaagaggag caggctcctg cacagtgact acatgaacat gactccccgc cgccccgggc	1080
ccacccgcaa gcattaccag ccctatgccc caccacgcga cttcgagcc tatcgctcca	1140
gagtgaagtt cagcaggagc gcagacgccc ccgcgtacca gcagggccag aaccagctct	1200
ataacgagct caatctagga cgaagagagg agtacgatgt tttggacaag agacgtggcc	1260
gggaccctga gatgggggga aagccgcaga gaaggaagaa ccctcaggaa ggctgtaca	1320
atgaactgca gaaagataag atggcggagg cctacagtga gattgggatg aaaggcgagc	1380
gccggagggg caaggggcac gatggccttt accagggtct cagtacagcc accaaggaca	1440
cctacgacgc ccttcacatg caggccctgc cccctcgcta agtttaaac	1489

<210> 17
 <211> 491
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 17

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5						10					15

His	Ala	Ala	Arg	Pro	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Ser	Leu
			20							25				30	

Ala	Val	Ser	Leu	Gly	Gln	Arg	Ala	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

35

40

45

Ser Val Ser Thr Ser Gly Tyr Ser Tyr Leu His Trp Tyr Gln Gln Lys
50 55 60

Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu
65 70 75 80

Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
85 90 95

Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr
100 105 110

Cys Gln His Ser Arg Glu Leu Pro Phe Thr Phe Gly Ser Gly Thr Lys
115 120 125

Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
145 150 155 160

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe
165 170 175

Ser Arg Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
180 185 190

Glu Trp Ile Gly Glu Ile Asn Pro Thr Ser Ser Thr Ile Asn Phe Thr
195 200 205

Pro Ser Leu Lys Asp Lys Val Phe Ile Ser Arg Asp Asn Ala Lys Asn
210 215 220

Thr Leu Tyr Leu Gln Met Ser Lys Val Arg Ser Glu Asp Thr Ala Leu

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

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

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

420 425 430

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
435 440 445

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
450 455 460

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
465 470 475 480

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 18
<211> 1492
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 18
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agagggccac catcagctgc agggccagca agagcgtgag caccagcggc tacagctacc 180
tgactggta ccagcagaag cccggccagc cccccaagct gctgatctac ctggccagca 240
acctggagag cggcgtgccc gccaggttca gcggcagcgg cagcggcacc gacttcaccc 300
tgaacatcca ccccgctggag gaggaggacg ccgccaccta ctactgccag cacagcaggg 360
agctgccctt caccttcggc agcggcacca agctggagat caagggaggg gggggatccg 420
ggggaggagg ctccggcgga ggcggaagcc aggtgcagct ggtggagagc ggcggcggcc 480
tggtgcagcc cggcggcagc ctgaagctga gctgcgccgc cagcggcttc gacttcagca 540
ggtactggat gagctgggtg aggcaggccc ccggcaaggg cctggagtgg atcggcgaga 600

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

tcaacccac cagcagcacc atcaacttca cccccagcct gaaggacaag gtgttcatca	660
gcagggacaa cgccaagaac accctgtacc tgcagatgag caaggtgagg agcgaggaca	720
ccgccctgta ctactgcgcc aggggcaact actacaggta cggcgacgcc atggactact	780
ggggccaggg caccagcgtg accgtgagca ccacgacgcc agcgccgcga ccaccaacac	840
cggcgccac catcgcgtcg cagcccctgt ccctgcgccc agaggcgtgc cggccagcgg	900
cggggggcgc agtgcacacg agggggctgg acttcgcctg tgatatctac atctgggcgc	960
ccttgccgg gacttgtggg gtccttctcc tgtcactggt tatcaccctt tactgcaaac	1020
ggggcagaaa gaaactcctg tatatatcca aacaaccatt tatgagacca gtacaaacta	1080
ctcaagagga agatggctgt agctgccgat ttccagaaga agaagaagga ggatgtgaac	1140
tgagagtga gttcagcagg agcgacagc ccccgcgta ccagcagggc cagaaccagc	1200
tctataacga gctcaatcta ggacgaagag aggagtacga tgttttggac aagagacgtg	1260
gccgggaccc tgagatgggg ggaaagccgc agagaaggaa gaaccctcag gaaggcctgt	1320
acaatgaact gcagaaagat aagatggcgg aggcctacag tgagattggg atgaaaggcg	1380
agcgccggag gggcaagggg cacgatggcc tttaccaggg tctcagtaca gccaccaagg	1440
acacctacga cgcccttcac atgcaggccc tgccccctcg ctaagtttaa ac	1492

<210> 19
 <211> 997
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 19

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5					10					15	

His	Ala	Ala	Arg	Pro	Asp	Val	Val	Met	Thr	Gln	Ser	His	Arg	Phe	Met
			20					25					30		

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Arg Ala Ser Gln
35 40 45

Asp Val Asn Thr Ala Val Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser
50 55 60

Pro Lys Leu Leu Ile Phe Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro
65 70 75 80

Asp Arg Phe Thr Gly Ser Gly Ser Gly Ala Asp Phe Thr Leu Thr Ile
85 90 95

Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His
100 105 110

Tyr Ser Thr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
130 135 140

Ile Gln Leu Val Gln Ser Gly Pro Asp Leu Lys Lys Pro Gly Glu Thr
145 150 155 160

Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Phe Gly
165 170 175

Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Phe Lys Trp Met Ala
180 185 190

Trp Ile Asn Thr Thr Arg Tyr Thr Gly Glu Ser Tyr Phe Ala Asp Asp
195 200 205

Phe Lys Gly Arg Phe Ala Phe Ser Val Glu Thr Ser Ala Thr Thr Ala
210 215 220

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Tyr Leu Gln Ile Asn Asn Leu Lys Thr Glu Asp Thr Ala Thr Tyr Phe
225 230 235 240

Cys Ala Arg Gly Glu Ile Tyr Tyr Gly Tyr Asp Gly Gly Phe Ala Tyr
245 250 255

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Thr Thr Thr Pro Ala
260 265 270

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
275 280 285

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
290 295 300

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
305 310 315 320

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
325 330 335

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
340 345 350

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
355 360 365

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
370 375 380

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
385 390 395 400

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
405 410 415

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn
420 425 430

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
435 440 445

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
450 455 460

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
465 470 475 480

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr
485 490 495

Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly
500 505 510

Pro Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
515 520 525

His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
530 535 540

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln
545 550 555 560

Asp Val Gly Ile Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val
565 570 575

Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro
580 585 590

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
595 600 605

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr
610 615 620

Ser Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
625 630 635 640

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
645 650 655

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
660 665 670

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser Arg Tyr Trp
675 680 685

Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly
690 695 700

Glu Ile Asn Pro Asp Ser Ser Thr Ile Asn Tyr Ala Pro Ser Leu Lys
705 710 715 720

Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
725 730 735

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
740 745 750

Arg Pro Asp Gly Asn Tyr Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr
755 760 765

Leu Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
770 775 780

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
785 790 795 800

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
805 810 815

Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val
820 825 830

Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser
835 840 845

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
850 855 860

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
865 870 875 880

Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
885 890 895

Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
900 905 910

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
915 920 925

Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
930 935 940

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
945 950 955 960

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
965 970 975

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
980 985 990

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Ala Leu Pro Pro Arg
995

<210> 20
<211> 2994
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 20
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ccgggccaga gcccgaact gctgattttt agcgcgagct atcgtatac cggcgtgccg 240
gatcgcttta ccggcagcgg cagcggcgcg gattttacct tgaccattag cagcgtgcag 300
gcggaagatc tggcgggtgta ttattgccag cagcattata gcaccccggtg gacctttggc 360
ggcggcacca aactggaaat taaaggaggg gggggatccg ggggaggagg ctccggcgga 420
ggcggaagcc agattcagct ggtgcagagc ggcccggatc tgaaaaaacc gggcgaaacc 480
gtgaaactga gctgcaaagc gagcggctat acctttacca actttggcat gaactgggtg 540
aaacaggcgc cgggcaaagg ctttaaattg atggcgtgga ttaacaccac ccgctatacc 600
ggcgaaagct attttgcgga tgattttaaa ggccgctttg cgttttagcgt ggaaaccagc 660
gcgaccaccg cgtatctgca gattaacaac ctgaaaaccg aagataccgc gacctatatt 720
tgcgcgcgcg gcgaaattta ttatggctat gatggcggct ttgcgtattg gggccagggc 780
accctggtga ccgtgagcgc gaccacgacg ccagcgcgcg gaccaccaac accggcgccc 840
accatcgcgt cgcagcccct gtccctgcgc ccagaggcgt gccggccagc ggcggggggc 900
gcagtgcaca cgagggggct ggacttcgcc tgtgatatct acatctgggc gcccttggcc 960
gggacttgtg gggtccttct cctgtcactg gttatcacc tttactgcaa acggggcaga 1020

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

aagaaactcc tgtatatatt caaacaacca tttatgagac cagtacaaac tactcaagag	1080
gaagatggct gtagctgccg atttccagaa gaagaagaag gaggatgtga actgagagtg	1140
aagttcagca ggagcgcaga cgtcccccgcg taccagcagg gccagaacca gctctataac	1200
gagctcaatc taggacgaag agaggagtac gatgttttgg acaagagacg tggccggggac	1260
cctgagatgg ggggaaaagcc gcagagaagg aagaaccctc aggaaggcct gtacaatgaa	1320
ctgcagaaaag ataagatggc ggaggcctac agtgagattg ggatgaaagg cgagcgccgg	1380
aggggcaagg ggcacgatgg cctttaccag ggtctcagta cagccaccaa ggacacctac	1440
gacgcccttc acatgcaggc cctgccccct cgcggaagcg gagccaccaa cttcagcctg	1500
ctgaagcagg ccggcgacgt ggaggagaac cccggccccg ctttaccagt gaccgccttg	1560
ctcctgccgc tggccttgct gctccacgcc gccaggccgg atattcagat gacccagagc	1620
ccgagcagcc tgagcgcgag cgtggggcgat cgcgtgacca ttacctgcaa agcgagccag	1680
gatgtgggca ttgcggtggc gtggtatcag cagaaaccgg gcaaagtgcc gaaactgctg	1740
atttattggg cgagcacccg ccataccggc gtgccggatc gctttagcgg cagcggcagc	1800
ggcaccgatt ttaccctgac cattagcagc ctgcagccgg aagatgtggc gacctattat	1860
tgccagcagt atagcagcta tccgtatacc tttggccagg gcaccaaagt ggaaattaaa	1920
ggaggggggg gatccggggg aggaggctcc ggcgaggcg gaagcgaagt gcagctgggtg	1980
gaaagcggcg gcggcctggt gcagccgggc ggagcctgc gcctgagctg cgcggcgagc	2040
ggctttgatt ttagccgcta ttggatgagc tgggtgcgcc aggcgccggg caaaggcctg	2100
gaatggattg gcgaaattaa cccggatagc agcaccatta actatgcgcc gagcctgaaa	2160
gataaattta ttattagccg cgataacgcg aaaaacagcc tgtatctgca gatgaacagc	2220
ctgcgcgcgg aagataccgc ggtgtattat tgcgcgcgcc cgcatggcaa ctattggtat	2280
tttgatgtgt ggggcccagg caccctgggt accgtgagca gcaccacgac gccagcgccg	2340
cgaccaccaa caccggcgcc caccatcgcg tcgcagcccc tgtccctgcg cccagaggcg	2400
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2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

tacatctggg cgcccttggc cgggacttgt ggggtccttc tcctgtcact ggttatcacc	2520
ctttactgca ggagtaagag gagcaggctc ctgcacagtg actacatgaa catgactccc	2580
cgccgccccg ggcccacccg caagcattac cagccctatg ccccaccacg cgacttcgca	2640
gcctatcgct ccagagtga gttcagcagg agcgcagacg cccccgcgta ccagcagggc	2700
cagaaccagc tctataacga gctcaatcta ggacgaagag aggagtacga tgttttggac	2760
aagagacgtg gccgggaccc tgagatgggg ggaaagccgc agagaaggaa gaaccctcag	2820
gaaggcctgt acaatgaact gcagaaagat aagatggcgg aggcctacag tgagattggg	2880
atgaaaggcg agcgccggag gggcaagggg cacgatggcc tttaccaggg tctcagtaca	2940
gccaccaagg acacctacga cgcccttcac atgcaggccc tgccccctcg ctaa	2994

<210> 21
 <211> 997
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 21

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5						10					15

His	Ala	Ala	Arg	Pro	Asp	Val	Val	Met	Thr	Gln	Ser	His	Arg	Phe	Met
			20					25					30		

Ser	Thr	Ser	Val	Gly	Asp	Arg	Val	Ser	Ile	Thr	Cys	Arg	Ala	Ser	Gln
		35					40					45			

Asp	Val	Asn	Thr	Ala	Val	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser
	50					55					60				

Pro	Lys	Leu	Leu	Ile	Phe	Ser	Ala	Ser	Tyr	Arg	Tyr	Thr	Gly	Val	Pro
65					70					75					80

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Asp Arg Phe Thr Gly Ser Gly Ser Gly Ala Asp Phe Thr Leu Thr Ile
85 90 95

Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His
100 105 110

Tyr Ser Thr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Asp Ile Lys
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
130 135 140

Ile Gln Leu Val Gln Ser Gly Pro Asp Leu Lys Lys Pro Gly Glu Thr
145 150 155 160

Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Phe Gly
165 170 175

Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Phe Lys Trp Met Ala
180 185 190

Trp Ile Asn Thr Tyr Thr Gly Glu Ser Tyr Phe Ala Asp Asp Phe Lys
195 200 205

Gly Arg Phe Ala Phe Ser Val Glu Thr Ser Ala Thr Thr Ala Tyr Leu
210 215 220

Gln Ile Asn Asn Leu Lys Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala
225 230 235 240

Arg Gly Glu Ile Tyr Tyr Gly Tyr Asp Gly Gly Phe Ala Tyr Trp Gly
245 250 255

Gln Gly Thr Leu Val Thr Val Ser Ala Thr Thr Thr Pro Ala Pro Arg
260 265 270

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
275 280 285

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
290 295 300

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
305 310 315 320

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg
325 330 335

Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro
340 345 350

Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu
355 360 365

Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala
370 375 380

Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
385 390 395 400

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
405 410 415

Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln
420 425 430

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
435 440 445

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
450 455 460

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
465 470 475 480

Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn Phe
485 490 495

Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met
500 505 510

Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His
515 520 525

Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
530 535 540

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
545 550 555 560

Val Gly Ile Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro
565 570 575

Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp
580 585 590

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
595 600 605

Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser
610 615 620

Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
625 630 635 640

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val
645 650 655

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
660 665 670

Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser Arg Tyr Trp Met
675 680 685

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu
690 695 700

Ile Asn Pro Asp Ser Ser Thr Ile Asn Tyr Ala Pro Ser Leu Lys Asp
705 710 715 720

Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
725 730 735

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
740 745 750

Pro Asp Gly Asn Tyr Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu
755 760 765

Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
770 775 780

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
785 790 795 800

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
805 810 815

Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
820 825 830

Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys
835 840 845

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr
850 855 860

Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly
865 870 875 880

Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
885 890 895

Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
900 905 910

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
915 920 925

Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
930 935 940

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
945 950 955 960

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
965 970 975

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
980 985 990

Ala Leu Pro Pro Arg
995

<210> 22
<211> 3009
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

<400> 22

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tcgagtgagc attacctgcc gcgcgagcca ggatgtgaac accgcggtga gctggtatca	180
gcagaaaccg ggccagagcc cgaaactgct gatttttagc gcgagctatc gctataccgg	240
cgtgccggat cgctttaccg gcagcggcag cggcgcggat tttaccctga ccattagcag	300
cgtgcaggcg gaagatctgg cgggtgtatta ttgccagcag cattatagca ccccgtaggac	360
ctttggcggc ggcaccaaac tggatattaa aggagggggg ggatccgggg gaggaggctc	420
cggcggaggc ggaagccaga ttcagctggt gcagagcggc ccggatctga aaaaaccggg	480
cgaaaccgtg aaactgagct gcaaagcgag cggctatacc tttaccaact ttggcatgaa	540
ctgggtgaaa caggcgccgg gcaaaggctt taaatggatg gcgtggatta acacctatac	600
cggcgaaaagc tattttgcgg atgattttta aggccgcttt gcgttttagcg tggaaccag	660
cgcgaccacc gcgtatctgc agattaacaa cctgaaaacc gaagataccg cgacctat	720
ttgcgcgcgc ggcgaaat	780
cacctggtg accgtgagcg cgaccacgac gccagcgccg cgaccaccaa caccggcgcc	840
caccatcgcg tcgcagcccc tgtccctgcg cccagaggcg tgccggccag cggcgggggg	900
cgcagtgcac acgagggggc tggacttcgc ctgtgatatc tacatctggg cgcccttggc	960
cgggacttgt ggggtccttc tcctgtcact ggttatcacc ctttactgca aacggggcag	1020
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ggaagatggc tgtagctgcc gatttccaga agaagaagaa ggaggatgtg aactgagagt	1140
gaagttcagc aggagcgcag acgccccgc gtaccagcag ggccagaacc agctctataa	1200
cgagctcaat ctaggacgaa gagaggagta cgatgttttg gacaagagac gtggccggga	1260
ccctgagatg gggggaaaagc cgagagaaag gaagaaccct caggaaaggcc tgtacaatga	1320
actgcagaaa gataagatgg cggaggccta cagtgaagatt gggatgaaag gcgagcgccg	1380

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

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gagcccagc agcctgagcg cgagcgtggg cgaccgcgtg accattacct gcaaagcgag	1680
ccaggatgtg ggcattgcgg tggcgtggta tcagcagaaa ccgggcaaag tgccgaaact	1740
gctgatttat tgggcgagca cccgccatac cggcgtgccg gatcgcttta gcggcagcgg	1800
cagcggcacc gattttaccc tgaccattag cagcctgcag ccggaagatg tggcgaccta	1860
ttattgccag cagtatagca gctatccgta tacctttggc cagggcacca aagtggaaat	1920
taaaggaggg gggggatccg ggggaggagg ctccggcggg ggcggaagcg aagtgcagct	1980
ggtggaaagc ggcggcggcc tgggtgcagc gggcggcagc ctgcgcctga gctgcgcggc	2040
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gaaagataaa tttattatta gccgcgataa cgcgaaaaac agcctgtatc tgcagatgaa	2220
cagcctgcgc gcggaagata ccgcggtgta ttattgcgcg cgcccggatg gcaactattg	2280
gtattttgat gtgtggggcc agggcacccct ggtgaccgtg agcagcacca cgacgccagc	2340
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ggcgtgccgg ccagcggcgg ggggcgcagt gcacacgagg gggctggact tcgcctgtga	2460
tatctacatc tgggcgccct tggccgggac ttgtggggtc cttctcctgt cactggttat	2520
caccctttac tgcaaacggg gcagaaagaa actcctgtat atattcaagc aaccatttat	2580
gagaccagta caaactactc aagaggaaga tggctgtagc tgccgatttc cagaagaaga	2640
agaaggagga tgtgaactga gagtgaagtt cagcaggagc gcagacgccc ccgcgtacca	2700
gcagggccag aaccagctct ataacgagct caatctagga cgaagagagg agtacgatgt	2760
tttgacaag agacgtggcc gggaccctga gatgggggga aagccgcaga gaaggaagaa	2820

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

ccctcaggaa ggcctgtaca atgaactgca gaaagataag atggcggagg cctacagtga	2880
gattgggatg aaaggcgagc gccggagggg caaggggcac gatggccttt accagggtct	2940
cagtacagcc accaaggaca cctacgacgc ccttcacatg caggccctgc cccctcgcta	3000
agtttaaac	3009

<210> 23
 <211> 423
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 23 agctagctgc agtaacgcca ttttgcaagg catggaaaaa taccaaacca agaatagaga	60
agttcagatc aagggcgggt acatgaaaat agctaacgtt gggccaaaca ggatatctgc	120
ggtgagcagt ttcggccccg gcccggggcc aagaacagat ggtcaccgca gtttcggccc	180
cggcccgagg ccaagaacag atgggtcccca gatatggccc aaccctcagc agtttcttaa	240
gacccatcag atgtttccag gctcccccaa ggacctgaaa tgaccctgcg ccttatttga	300
attaaccaat cagcctgctt ctcgcttctg ttcgcgcgct tctgcttccc gagctctata	360
aaagagctca caaccctca ctcggcgcgc cagtcctccg acagactgag tcgcccgggt	420
acc	423

<210> 24
 <211> 165
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 24

Met	Ser	Gly	Leu	Gly	Arg	Ser	Arg	Arg	Gly	Gly	Arg	Ser	Arg	Val	Asp
1				5					10					15	

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg
20 25 30

Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met
35 40 45

Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
50 55 60

Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
65 70 75 80

His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His
85 90 95

Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
100 105 110

Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn
115 120 125

Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
130 135 140

Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
145 150 155 160

Ala Leu Val Tyr Ser
165

<210> 25
<211> 54
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

<400> 25

Met Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser
1 5 10 15

Leu Leu His Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr
20 25 30

Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser
35 40 45

Val Lys Gly Thr Asn Ala
50

<210> 26

<211> 204

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 26

Ser Gly Pro Val Lys Glu Leu Val Gly Ser Val Gly Gly Ala Val Thr
1 5 10 15

Phe Pro Leu Lys Ser Lys Val Lys Gln Val Asp Ser Ile Val Trp Thr
20 25 30

Phe Asn Thr Thr Pro Leu Val Thr Ile Gln Pro Glu Gly Gly Thr Ile
35 40 45

Ile Val Thr Gln Asn Arg Asn Arg Glu Arg Val Asp Phe Pro Asp Gly
50 55 60

Gly Tyr Ser Leu Lys Leu Ser Lys Leu Lys Lys Asn Asp Ser Gly Ile
65 70 75 80

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Tyr Tyr Val Gly Ile Tyr Ser Ser Ser Leu Gln Gln Pro Ser Thr Gln
85 90 95

Glu Tyr Val Leu His Val Tyr Glu His Leu Ser Lys Pro Lys Val Thr
100 105 110

Met Gly Leu Gln Ser Asn Lys Asn Gly Thr Cys Val Thr Asn Leu Thr
115 120 125

Cys Cys Met Glu His Gly Glu Glu Asp Val Ile Tyr Thr Trp Lys Ala
130 135 140

Leu Gly Gln Ala Ala Asn Glu Ser His Asn Gly Ser Ile Leu Pro Ile
145 150 155 160

Ser Trp Arg Trp Gly Glu Ser Asp Met Thr Phe Ile Cys Val Ala Arg
165 170 175

Asn Pro Val Ser Arg Asn Phe Ser Ser Pro Ile Leu Ala Arg Lys Leu
180 185 190

Cys Glu Gly Ala Ala Asp Asp Pro Asp Ser Ser Met
195 200

<210> 27
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 27

Met Asp Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu
1 5 10 15

Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

20 25 30

Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys
35 40 45

<210> 28
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 28

Asp Pro Asn Phe Trp Leu Gln Val Gln Glu Ser Val Thr Val Gln Glu
1 5 10 15

Gly Leu Cys Val Leu Val Pro Cys Thr Phe Phe His Pro Ile Pro Tyr
20 25 30

Tyr Asp Lys Asn Ser Pro Val His Gly Tyr Trp Phe Arg Glu Gly Ala
35 40 45

Ile Ile Ser Arg Asp Ser Pro Val Ala Thr Asn Lys Leu Asp Gln Glu
50 55 60

Val Gln Glu Glu Thr Gln Gly Arg Phe Arg Leu Leu Gly Asp Pro Ser
65 70 75 80

Arg Asn Asn Cys Ser Leu Ser Ile Val Asp Ala Arg Arg Arg Asp Asn
85 90 95

Gly Ser Tyr Phe Phe Arg Met Glu Arg Gly Ser Thr Lys Tyr Ser Tyr
100 105 110

Lys Ser Pro Gln Leu Ser Val His Val Thr Asp Leu Thr His Arg Pro
115 120 125

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Lys Ile Leu Ile Pro Gly Thr Leu Glu Pro Gly His Ser Lys Asn Leu
130 135 140

Thr Cys Ser Val Ser Trp Ala Cys Glu Gln Gly Thr Pro Pro Ile Phe
145 150 155 160

Ser Trp Leu Ser Ala Ala Pro Thr Ser Leu Gly Pro Arg Thr Thr His
165 170 175

Ser Ser Val Leu Ile Ile Thr Pro Arg Pro Gln Asp His Gly Thr Asn
180 185 190

Leu Thr Cys Gln Val Lys Phe Ala Gly Ala Gly Val Thr Thr Glu Arg
195 200 205

Thr Ile Gln Leu Asn Val Thr Tyr Val Pro Gln Asn Pro Thr Thr Gly
210 215 220

Ile Phe Pro Gly Asp Gly Ser Gly Lys Gln Glu Thr Arg Ala Gly Val
225 230 235 240

Val His

<210> 29
<211> 287
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 29

Thr Lys Glu Asp Pro Asn Pro Pro Ile Thr Asn Leu Arg Met Lys Ala
1 5 10 15

Lys Ala Gln Gln Leu Thr Trp Asp Leu Asn Arg Asn Val Thr Asp Ile

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

20

25

30

Glu Cys Val Lys Asp Ala Asp Tyr Ser Met Pro Ala Val Asn Asn Ser
35 40 45

Tyr Cys Gln Phe Gly Ala Ile Ser Leu Cys Glu Val Thr Asn Tyr Thr
50 55 60

Val Arg Val Ala Asn Pro Pro Phe Ser Thr Trp Ile Leu Phe Pro Glu
65 70 75 80

Asn Ser Gly Lys Pro Trp Ala Gly Ala Glu Asn Leu Thr Cys Trp Ile
85 90 95

His Asp Val Asp Phe Leu Ser Cys Ser Trp Ala Val Gly Pro Gly Ala
100 105 110

Pro Ala Asp Val Gln Tyr Asp Leu Tyr Leu Asn Val Ala Asn Arg Arg
115 120 125

Gln Gln Tyr Glu Cys Leu His Tyr Lys Thr Asp Ala Gln Gly Thr Arg
130 135 140

Ile Gly Cys Arg Phe Asp Asp Ile Ser Arg Leu Ser Ser Gly Ser Gln
145 150 155 160

Ser Ser His Ile Leu Val Arg Gly Arg Ser Ala Ala Phe Gly Ile Pro
165 170 175

Cys Thr Asp Lys Phe Val Val Phe Ser Gln Ile Glu Ile Leu Thr Pro
180 185 190

Pro Asn Met Thr Ala Lys Cys Asn Lys Thr His Ser Phe Met His Trp
195 200 205

Lys Met Arg Ser His Phe Asn Arg Lys Phe Arg Tyr Glu Leu Gln Ile

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

210

215

220

Gln Lys Arg Met Gln Pro Val Ile Thr Glu Gln Val Arg Asp Arg Thr
225 230 235 240

Ser Phe Gln Leu Leu Asn Pro Gly Thr Tyr Thr Val Gln Ile Arg Ala
245 250 255

Arg Glu Arg Val Tyr Glu Phe Leu Ser Ala Trp Ser Thr Pro Gln Arg
260 265 270

Phe Glu Cys Asp Gln Glu Glu Gly Ala Asn Thr Arg Ala Trp Arg
275 280 285

<210> 30
<211> 272
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 30

Pro Glu Glu Pro Leu Val Val Lys Val Glu Glu Gly Asp Asn Ala Val
1 5 10 15

Leu Gln Cys Leu Lys Gly Thr Ser Asp Gly Pro Thr Gln Gln Leu Thr
20 25 30

Trp Ser Arg Glu Ser Pro Leu Lys Pro Phe Leu Lys Leu Ser Leu Gly
35 40 45

Leu Pro Gly Leu Gly Ile His Met Arg Pro Leu Ala Ile Trp Leu Phe
50 55 60

Ile Phe Asn Val Ser Gln Gln Met Gly Gly Phe Tyr Leu Cys Gln Pro
65 70 75 80

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Gly Pro Pro Ser Glu Lys Ala Trp Gln Pro Gly Trp Thr Val Asn Val
85 90 95

Glu Gly Ser Gly Glu Leu Phe Arg Trp Asn Val Ser Asp Leu Gly Gly
100 105 110

Leu Gly Cys Gly Leu Lys Asn Arg Ser Ser Glu Gly Pro Ser Ser Pro
115 120 125

Ser Gly Lys Leu Met Ser Pro Lys Leu Tyr Val Trp Ala Lys Asp Arg
130 135 140

Pro Glu Ile Trp Glu Gly Glu Pro Pro Cys Leu Pro Pro Arg Asp Ser
145 150 155 160

Leu Asn Gln Ser Leu Ser Gln Asp Leu Thr Met Ala Pro Gly Ser Thr
165 170 175

Leu Trp Leu Ser Cys Gly Val Pro Pro Asp Ser Val Ser Arg Gly Pro
180 185 190

Leu Ser Trp Thr His Val His Pro Lys Gly Pro Lys Ser Leu Leu Ser
195 200 205

Leu Glu Leu Lys Asp Asp Arg Pro Ala Arg Asp Met Trp Val Met Glu
210 215 220

Thr Gly Leu Leu Leu Pro Arg Ala Thr Ala Gln Asp Ala Gly Lys Tyr
225 230 235 240

Tyr Cys His Arg Gly Asn Leu Thr Met Ser Phe His Leu Glu Ile Thr
245 250 255

Ala Arg Pro Val Leu Trp His Trp Leu Leu Arg Thr Gly Gly Trp Lys
260 265 270

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

<210> 31
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 31

Pro Ile Cys Val Thr Val
 1 5

<210> 32
 <211> 47
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 32

Lys Ile Ser His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala
 1 5 10 15

His Thr Pro Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser
 20 25 30

Glu Lys Asn Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser
 35 40 45

<210> 33
 <211> 480
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 33

Asp Ser Ser Lys Trp Val Phe Glu His Pro Glu Thr Leu Tyr Ala Trp

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

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195

200

205

Phe Leu Ser Asn Asp Thr Val Gln Leu Asn Val Lys His Thr Pro Lys
210 215 220

Leu Glu Ile Lys Val Thr Pro Ser Asp Ala Ile Val Arg Glu Gly Asp
225 230 235 240

Ser Val Thr Met Thr Cys Glu Val Ser Ser Ser Asn Pro Glu Tyr Thr
245 250 255

Thr Val Ser Trp Leu Lys Asp Gly Thr Ser Leu Lys Lys Gln Asn Thr
260 265 270

Phe Thr Leu Asn Leu Arg Glu Val Thr Lys Asp Gln Ser Gly Lys Tyr
275 280 285

Cys Cys Gln Val Ser Asn Asp Val Gly Pro Gly Arg Ser Glu Glu Val
290 295 300

Phe Leu Gln Val Gln Tyr Ala Pro Glu Pro Ser Thr Val Gln Ile Leu
305 310 315 320

His Ser Pro Ala Val Glu Gly Ser Gln Val Glu Phe Leu Cys Met Ser
325 330 335

Leu Ala Asn Pro Leu Pro Thr Asn Tyr Thr Trp Tyr His Asn Gly Lys
340 345 350

Glu Met Gln Gly Arg Thr Glu Glu Lys Val His Ile Pro Lys Ile Leu
355 360 365

Pro Trp His Ala Gly Thr Tyr Ser Cys Val Ala Glu Asn Ile Leu Gly
370 375 380

Thr Gly Gln Arg Gly Pro Gly Ala Glu Leu Asp Val Gln Tyr Pro Pro

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385 390 395 400

Lys Lys Val Thr Thr Val Ile Gln Asn Pro Met Pro Ile Arg Glu Gly
405 410 415

Asp Thr Val Thr Leu Ser Cys Asn Tyr Asn Ser Ser Asn Pro Ser Val
420 425 430

Thr Arg Tyr Glu Trp Lys Pro His Gly Ala Trp Glu Glu Pro Ser Leu
435 440 445

Gly Val Leu Lys Ile Gln Asn Val Gly Trp Asp Asn Thr Thr Ile Ala
450 455 460

Cys Ala Ala Cys Asn Ser Trp Cys Ser Trp Ala Ser Pro Val Ala Leu
465 470 475 480

<210> 34
<211> 480
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 34

Gln Ser Pro Thr Pro Ser Pro Thr Gly Leu Thr Thr Ala Lys Met Pro
1 5 10 15

Ser Val Pro Leu Ser Ser Asp Pro Leu Pro Thr His Thr Thr Ala Phe
20 25 30

Ser Pro Ala Ser Thr Phe Glu Arg Glu Asn Asp Phe Ser Glu Thr Thr
35 40 45

Thr Ser Leu Ser Pro Asp Asn Thr Ser Thr Gln Val Ser Pro Asp Ser
50 55 60

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Leu Asp Asn Ala Ser Ala Phe Asn Thr Thr Gly Val Ser Ser Val Gln
65 70 75 80

Thr Pro His Leu Pro Thr His Ala Asp Ser Gln Thr Pro Ser Ala Gly
85 90 95

Thr Asp Thr Gln Thr Phe Ser Gly Ser Ala Ala Asn Ala Lys Leu Asn
100 105 110

Pro Thr Pro Gly Ser Asn Ala Ile Ser Asp Val Pro Gly Glu Arg Ser
115 120 125

Thr Ala Ser Thr Phe Pro Thr Asp Pro Val Ser Pro Leu Thr Thr Thr
130 135 140

Leu Ser Leu Ala His His Ser Ser Ala Ala Leu Pro Ala Arg Thr Ser
145 150 155 160

Asn Thr Thr Ile Thr Ala Asn Thr Ser Asp Ala Tyr Leu Asn Ala Ser
165 170 175

Glu Thr Thr Thr Leu Ser Pro Ser Gly Ser Ala Val Ile Ser Thr Thr
180 185 190

Thr Ile Ala Thr Thr Pro Ser Lys Pro Thr Cys Asp Glu Lys Tyr Ala
195 200 205

Asn Ile Thr Val Asp Tyr Leu Tyr Asn Lys Glu Thr Lys Leu Phe Thr
210 215 220

Ala Lys Leu Asn Val Asn Glu Asn Val Glu Cys Gly Asn Asn Thr Cys
225 230 235 240

Thr Asn Asn Glu Val His Asn Leu Thr Glu Cys Lys Asn Ala Ser Val
245 250 255

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Ser Ile Ser His Asn Ser Cys Thr Ala Pro Asp Lys Thr Leu Ile Leu
260 265 270

Asp Val Pro Pro Gly Val Glu Lys Phe Gln Leu His Asp Cys Thr Gln
275 280 285

Val Glu Lys Ala Asp Thr Thr Ile Cys Leu Lys Trp Lys Asn Ile Glu
290 295 300

Thr Phe Thr Cys Asp Thr Gln Asn Ile Thr Tyr Arg Phe Gln Cys Gly
305 310 315 320

Asn Met Ile Phe Asp Asn Lys Glu Ile Lys Leu Glu Asn Leu Glu Pro
325 330 335

Glu His Glu Tyr Lys Cys Asp Ser Glu Ile Leu Tyr Asn Asn His Lys
340 345 350

Phe Thr Asn Ala Ser Lys Ile Ile Lys Thr Asp Phe Gly Ser Pro Gly
355 360 365

Glu Pro Gln Ile Ile Phe Cys Arg Ser Glu Ala Ala His Gln Gly Val
370 375 380

Ile Thr Trp Asn Pro Pro Gln Arg Ser Phe His Asn Phe Thr Leu Cys
385 390 395 400

Tyr Ile Lys Glu Thr Glu Lys Asp Cys Leu Asn Leu Asp Lys Asn Leu
405 410 415

Ile Lys Tyr Asp Leu Gln Asn Leu Lys Pro Tyr Thr Lys Tyr Val Leu
420 425 430

Ser Leu His Ala Tyr Ile Ile Ala Lys Val Gln Arg Asn Gly Ser Ala
435 440 445

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Ala Met Cys His Phe Thr Thr Lys Ser Ala Pro Pro Ser Gln Val Trp
 450 455 460

Asn Met Thr Val Ser Met Thr Ser Asp Asn Ser Met His Val Lys Cys
 465 470 475 480

<210> 35
 <211> 65
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 35

Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val
 1 5 10 15

Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly
 20 25 30

Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn
 35 40 45

Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile
 50 55 60

Arg
 65

<210> 36
 <211> 153
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 36

2541_3_PCT_Text_Sequence_Listing_6_24_16_ST25

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
1 5 10 15

Val Thr Asn Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala
20 25 30

Gly Leu Pro Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu
35 40 45

Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu
50 55 60

Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys
65 70 75 80

Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala
85 90 95

Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser
100 105 110

Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu
115 120 125

Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His
130 135 140

Ile Val Gln Met Phe Ile Asn Thr Ser
145 150