

SEQUENCE LISTING

<110> FOUNDATION MEDICINE, INC.

<120> NOVEL KIF5B-RET FUSION MOLECULES AND USES THEREOF

<130> F2036-7025WO

<140> PCT/US2012/051978

<141> 2012-08-23

<150> 61/594,739

<151> 2012-02-03

<150> 61/542,112

<151> 2011-09-30

<150> 61/537,024

<151> 2011-09-20

<150> 61/526,613

<151> 2011-08-23

<160> 9

<170> PatentIn version 3.5

<210> 1

<211> 2934

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>

<221> CDS

<222> (1)..(2931)

<400> 1

atg gcg gac ctg gcc gag tgc aac atc aaa gtg atg tgt cgc ttc aga	48
Met Ala Asp Leu Ala Glu Cys Asn Ile Lys Val Met Cys Arg Phe Arg	
1 5 10 15	
cct ctg aac gag tct gaa gtg aac cgc ggc gac aag tac atc gcc aag	96
Pro Leu Asn Glu Ser Glu Val Asn Arg Gly Asp Lys Tyr Ile Ala Lys	
20 25 30	
ttt cag gga gaa gac acg gtc gtg atc gcg tcc aag cct tat gca ttt	144
Phe Gln Gly Glu Asp Thr Val Val Ile Ala Ser Lys Pro Tyr Ala Phe	
35 40 45	
gat cgg gtg ttc cag tca agc aca tct caa gag caa gtg tat aat gac	192
Asp Arg Val Phe Gln Ser Ser Thr Ser Gln Glu Gln Val Tyr Asn Asp	
50 55 60	
tgt gca aag aag att gtt aaa gat gta ctt gaa gga tat aat gga aca	240
Cys Ala Lys Lys Ile Val Lys Asp Val Leu Glu Gly Tyr Asn Gly Thr	
65 70 75 80	
ata ttt gca tat gga caa aca tcc tct ggg aag aca cac aca atg gag	288
Ile Phe Ala Tyr Gly Gln Thr Ser Ser Gly Lys Thr His Thr Met Glu	
85 90 95	
ggg aaa ctt cat gat cca gaa ggc atg gga att att cca aga ata gtg	336
Gly Lys Leu His Asp Pro Glu Gly Met Gly Ile Ile Pro Arg Ile Val	

100	105	110	
caa gat att ttt aat tat att tac tcc atg gat gaa aat ttg gaa ttt Gln Asp Ile Phe Asn Tyr Ile Tyr Ser Met Asp Glu Asn Leu Glu Phe 115 120 125			384
cat att aag gtt tca tat ttt gaa ata tat ttg gat aag ata agg gac His Ile Lys Val Ser Tyr Phe Glu Ile Tyr Leu Asp Lys Ile Arg Asp 130 135 140			432
ctg tta gat gtt tca aag acc aac ctt tca gtt cat gaa gac aaa aac Leu Leu Asp Val Ser Lys Thr Asn Leu Ser Val His Glu Asp Lys Asn 145 150 155 160			480
cga gtt ccc tat gta aag ggg tgc aca gag cgt ttt gta tgt agt cca Arg Val Pro Tyr Val Lys Gly Cys Thr Glu Arg Phe Val Cys Ser Pro 165 170 175			528
gat gaa gtt atg gat acc ata gat gaa gga aaa tcc aac aga cat gta Asp Glu Val Met Asp Thr Ile Asp Glu Gly Lys Ser Asn Arg His Val 180 185 190			576
gca gtt aca aat atg aat gaa cat agc tct agg agt cac agt ata ttt Ala Val Thr Asn Met Asn Glu His Ser Ser Arg Ser His Ser Ile Phe 195 200 205			624
ctt att aat gtc aaa caa gag aac aca caa acg gaa caa aag ctg agt Leu Ile Asn Val Lys Gln Glu Asn Thr Gln Thr Glu Gln Lys Leu Ser 210 215 220			672
gga aaa ctt tat ctg gtt gat tta gct ggt agt gaa aag gtt agt aaa Gly Lys Leu Tyr Leu Val Asp Leu Ala Gly Ser Glu Lys Val Ser Lys 225 230 235 240			720
act gga gct gaa ggt gct gtg ctg gat gaa gct aaa aac atc aac aag Thr Gly Ala Glu Gly Ala Val Leu Asp Glu Ala Lys Asn Ile Asn Lys 245 250 255			768
tca ctt tct gct ctt gga aat gtt att tct gct ttg gct gag ggt agt Ser Leu Ser Ala Leu Gly Asn Val Ile Ser Ala Leu Ala Glu Gly Ser 260 265 270			816
aca tat gtt cca tat cga gat agt aaa atg aca aga atc ctt caa gat Thr Tyr Val Pro Tyr Arg Asp Ser Lys Met Thr Arg Ile Leu Gln Asp 275 280 285			864
tca tta ggt ggc aac tgt aga acc act att gta att tgc tgc tct cca Ser Leu Gly Gly Asn Cys Arg Thr Thr Ile Val Ile Cys Cys Ser Pro 290 295 300			912
tca tca tac aat gag tct gaa aca aaa tct aca ctc tta ttt ggc caa Ser Ser Tyr Asn Glu Ser Glu Thr Lys Ser Thr Leu Leu Phe Gly Gln 305 310 315 320			960
agg gcc aaa aca att aag aac aca gtt tgt gtc aat gtg gag tta act Arg Ala Lys Thr Ile Lys Asn Thr Val Cys Val Asn Val Glu Leu Thr 325 330 335			1008
gca gaa cag tgg aaa aag aag tat gaa aaa gaa aaa gaa aaa aat aag Ala Glu Gln Trp Lys Lys Lys Tyr Glu Lys Glu Lys Glu Lys Asn Lys 340 345 350			1056
atc ctg cgg aac act att cag tgg ctt gaa aat gag ctc aac aga tgg Ile Leu Arg Asn Thr Ile Gln Trp Leu Glu Asn Glu Leu Asn Arg Trp 355 360 365			1104
cgt aat ggg gag acg gtg cct att gat gaa cag ttt gac aaa gag aaa Arg Asn Gly Glu Thr Val Pro Ile Asp Gln Phe Asp Lys Glu Lys			1152

370	375	380	
gcc aac ttg gaa gct ttc aca gtg gat aaa gat att act ctt acc aat Ala Asn Leu Glu Ala Phe Thr Val Asp Lys Asp Ile Thr Leu Thr Asn 385 390 395 400			1200
gat aaa cca gca acc gca att gga gtt ata gga aat ttt act gat gct Asp Lys Pro Ala Thr Ala Ile Gly Val Ile Gly Asn Phe Thr Asp Ala 405 410 415			1248
gaa aga aga aag tgt gaa gaa gaa att gct aaa tta tac aaa cag ctt Glu Arg Arg Lys Cys Glu Glu Glu Ile Ala Lys Leu Tyr Lys Gln Leu 420 425 430			1296
gat gac aag gat gaa gaa att aac cag caa agt caa ctg gta gag aaa Asp Asp Lys Asp Glu Glu Ile Asn Gln Gln Ser Gln Leu Val Glu Lys 435 440 445			1344
ctg aag acg caa atg ttg gat cag gag gag ctt ttg gca tct acc aga Leu Lys Thr Gln Met Leu Asp Gln Glu Glu Leu Leu Ala Ser Thr Arg 450 455 460			1392
agg gat caa gac aat atg caa gct gag ctg aat cgc ctt caa gca gaa Arg Asp Gln Asp Asn Met Gln Ala Glu Leu Asn Arg Leu Gln Ala Glu 465 470 475 480			1440
aat gat gcc tct aaa gaa gaa gtg aaa gaa gtt tta cag gcc cta gaa Asn Asp Ala Ser Lys Glu Glu Val Lys Glu Val Leu Gln Ala Leu Glu 485 490 495			1488
gaa ctt gct gtc aat tat gat cag aag tct cag gaa gtt gaa gac aaa Glu Leu Ala Val Asn Tyr Asp Gln Lys Ser Gln Glu Val Glu Asp Lys 500 505 510			1536
act aag gaa tat gaa ttg ctt agt gat gaa ttg aat cag aaa tcg gca Thr Lys Glu Tyr Glu Leu Leu Ser Asp Glu Leu Asn Gln Lys Ser Ala 515 520 525			1584
act tta gcg agt ata gat gct gag ctt cag aaa ctt aag gaa atg acc Thr Leu Ala Ser Ile Asp Ala Glu Leu Gln Lys Leu Lys Glu Met Thr 530 535 540			1632
aac cac cag aaa aaa cga gca gct gag atg atg gca tct tta cta aaa Asn His Gln Lys Lys Arg Ala Ala Glu Met Met Ala Ser Leu Leu Lys 545 550 555 560			1680
gac ctt gca gaa ata gga att gct gtg gga aat aat gat gta aag gag Asp Leu Ala Glu Ile Gly Ile Ala Val Gly Asn Asn Asp Val Lys Glu 565 570 575			1728
gat cca aag tgg gaa ttc cct cgg aag aac ttg gtt ctt gga aaa act Asp Pro Lys Trp Glu Phe Pro Arg Lys Asn Leu Val Leu Gly Lys Thr 580 585 590			1776
cta gga gaa ggc gaa ttt gga aaa gtg gtc aag gca acg gcc ttc cat Leu Gly Glu Gly Glu Phe Gly Lys Val Val Lys Ala Thr Ala Phe His 595 600 605			1824
ctg aaa ggc aga gca ggg tac acc acg gtg gcc gtg aag atg ctg aaa Leu Lys Gly Arg Ala Gly Tyr Thr Thr Val Ala Val Lys Met Leu Lys 610 615 620			1872
gag aac gcc tcc ccg agt gag ctg cga gac ctg ctg tca gag ttc aac Glu Asn Ala Ser Pro Ser Glu Leu Arg Asp Leu Leu Ser Glu Phe Asn 625 630 635 640			1920
gtc ctg aag cag gtc aac cac cca cat gtc atc aaa ttg tat ggg gcc Val Leu Lys Gln Val Asn His Pro His Val Ile Lys Leu Tyr Gly Ala			1968

645	650	655	
tgc agc cag gat ggc ccg ctc ctc ctc atc gtg gag tac gcc aaa tac Cys Ser Gln Asp Gly Pro Leu Leu Leu Ile Val Glu Tyr Ala Lys Tyr 660 665 670			2016
ggc tcc ctg cgg ggc ttc ctc cgc gag agc cgc aaa gtg ggg cct ggc Gly Ser Leu Arg Gly Phe Leu Arg Glu Ser Arg Lys Val Gly Pro Gly 675 680 685			2064
tac ctg ggc agt gga ggc agc cgc aac tcc agc tcc ctg gac cac ccg Tyr Leu Gly Ser Gly Gly Ser Arg Asn Ser Ser Ser Leu Asp His Pro 690 695 700			2112
gat gag cgg gcc ctc acc atg ggc gac ctc atc tca ttt gcc tgg cag Asp Glu Arg Ala Leu Thr Met Gly Asp Leu Ile Ser Phe Ala Trp Gln 705 710 715 720			2160
atc tca cag ggg atg cag tat ctg gcc gag atg aag ctc gtt cat ccg Ile Ser Gln Gly Met Gln Tyr Leu Ala Glu Met Lys Leu Val His Arg 725 730 735			2208
gac ttg gca gcc aga aac atc ctg gta gct gag ggg cgg aag atg aag Asp Leu Ala Ala Arg Asn Ile Leu Val Ala Glu Gly Arg Lys Met Lys 740 745 750			2256
att tcc gat ttc ggc ttg tcc cga gat gtt tat gaa gag gat tcc tac Ile Ser Asp Phe Gly Leu Ser Arg Asp Val Tyr Glu Glu Asp Ser Tyr 755 760 765			2304
gtg aag agg agc cag ggt cgg att cca gtt aaa tgg atg gca att gaa Val Lys Arg Ser Gln Gly Arg Ile Pro Val Lys Trp Met Ala Ile Glu 770 775 780			2352
tcc ctt ttt gat cat atc tac acc acg caa agt gat gta tgg tct ttt Ser Leu Phe Asp His Ile Tyr Thr Thr Gln Ser Asp Val Trp Ser Phe 785 790 795 800			2400
ggt gtc ctg ctg tgg gag atc gtg acc cta ggg gga aac ccc tat cct Gly Val Leu Leu Trp Glu Ile Val Thr Leu Gly Gly Asn Pro Tyr Pro 805 810 815			2448
ggg att cct cct gag cgg ctc ttc aac ctt ctg aag acc ggc cac ccg Gly Ile Pro Pro Glu Arg Leu Phe Asn Leu Leu Lys Thr Gly His Arg 820 825 830			2496
atg gag agg cca gac aac tgc agc gag gag atg tac cgc ctg atg ctg Met Glu Arg Pro Asp Asn Cys Ser Glu Glu Met Tyr Arg Leu Met Leu 835 840 845			2544
caa tgc tgg aag cag gag ccg gac aaa agg ccg gtg ttt gcg gac atc Gln Cys Trp Lys Gln Glu Pro Asp Lys Arg Pro Val Phe Ala Asp Ile 850 855 860			2592
agc aaa gac ctg gag aag atg atg gtt aag agg aga gac tac ttg gac Ser Lys Asp Leu Glu Lys Met Met Val Lys Arg Arg Asp Tyr Leu Asp 865 870 875 880			2640
ctt gcg gcg tcc act cca tct gac tcc ctg att tat gac gac ggc ctc Leu Ala Ala Ser Thr Pro Ser Asp Ser Leu Ile Tyr Asp Asp Gly Leu 885 890 895			2688
tca gag gag gag aca ccg ctg gtg gac tgt aat aat gcc ccc ctc cct Ser Glu Glu Glu Thr Pro Leu Val Asp Cys Asn Asn Ala Pro Leu Pro 900 905 910			2736
cga gcc ctc cct tcc aca tgg att gaa aac aaa ctc tat ggc atg tca Arg Ala Leu Pro Ser Thr Trp Ile Glu Asn Lys Leu Tyr Gly Met Ser			2784

915	920	925	
gac ccg aac tgg cct gga gag agt cct gta cca ctc acg aga gct gat			2832
Asp Pro Asn Trp Pro Gly Glu Ser Pro Val Pro Leu Thr Arg Ala Asp			
930	935	940	
ggc act aac act ggg ttt cca aga tat cca aat gat agt gta tat gct			2880
Gly Thr Asn Thr Gly Phe Pro Arg Tyr Pro Asn Asp Ser Val Tyr Ala			
945	950	955	960
aac tgg atg ctt tca ccc tca gcg gca aaa tta atg gac acg ttt gat			2928
Asn Trp Met Leu Ser Pro Ser Ala Ala Lys Leu Met Asp Thr Phe Asp			
	965	970	975
agt taa			2934
Ser			

<210> 2
 <211> 977
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 2
 Met Ala Asp Leu Ala Glu Cys Asn Ile Lys Val Met Cys Arg Phe Arg
 1 5 10 15

Pro Leu Asn Glu Ser Glu Val Asn Arg Gly Asp Lys Tyr Ile Ala Lys
 20 25 30

Phe Gln Gly Glu Asp Thr Val Val Ile Ala Ser Lys Pro Tyr Ala Phe
 35 40 45

Asp Arg Val Phe Gln Ser Ser Thr Ser Gln Glu Gln Val Tyr Asn Asp
 50 55 60

Cys Ala Lys Lys Ile Val Lys Asp Val Leu Glu Gly Tyr Asn Gly Thr
 65 70 75 80

Ile Phe Ala Tyr Gly Gln Thr Ser Ser Gly Lys Thr His Thr Met Glu
 85 90 95

Gly Lys Leu His Asp Pro Glu Gly Met Gly Ile Ile Pro Arg Ile Val
 100 105 110

Gln Asp Ile Phe Asn Tyr Ile Tyr Ser Met Asp Glu Asn Leu Glu Phe
 115 120 125

His Ile Lys Val Ser Tyr Phe Glu Ile Tyr Leu Asp Lys Ile Arg Asp
 130 135 140

Leu Leu Asp Val Ser Lys Thr Asn Leu Ser Val His Glu Asp Lys Asn
 145 150 155 160

Arg Val Pro Tyr Val Lys Gly Cys Thr Glu Arg Phe Val Cys Ser Pro
 165 170 175

Asp Glu Val Met Asp Thr Ile Asp Glu Gly Lys Ser Asn Arg His Val
 180 185 190

Ala Val Thr Asn Met Asn Glu His Ser Ser Arg Ser His Ser Ile Phe
 195 200 205

Leu Ile Asn Val Lys Gln Glu Asn Thr Gln Thr Glu Gln Lys Leu Ser
 210 215 220

Gly Lys Leu Tyr Leu Val Asp Leu Ala Gly Ser Glu Lys Val Ser Lys
 225 230 235 240

Thr Gly Ala Glu Gly Ala Val Leu Asp Glu Ala Lys Asn Ile Asn Lys
 245 250 255

Ser Leu Ser Ala Leu Gly Asn Val Ile Ser Ala Leu Ala Glu Gly Ser
 260 265 270

Thr Tyr Val Pro Tyr Arg Asp Ser Lys Met Thr Arg Ile Leu Gln Asp
 275 280 285

Ser Leu Gly Gly Asn Cys Arg Thr Thr Ile Val Ile Cys Cys Ser Pro
 290 295 300

Ser Ser Tyr Asn Glu Ser Glu Thr Lys Ser Thr Leu Leu Phe Gly Gln
 305 310 315 320

Arg Ala Lys Thr Ile Lys Asn Thr Val Cys Val Asn Val Glu Leu Thr
 325 330 335

Ala Glu Gln Trp Lys Lys Lys Tyr Glu Lys Glu Lys Glu Lys Asn Lys
 340 345 350

Ile Leu Arg Asn Thr Ile Gln Trp Leu Glu Asn Glu Leu Asn Arg Trp
 355 360 365

Arg Asn Gly Glu Thr Val Pro Ile Asp Glu Gln Phe Asp Lys Glu Lys
 370 375 380

Ala Asn Leu Glu Ala Phe Thr Val Asp Lys Asp Ile Thr Leu Thr Asn
 385 390 395 400

Asp Lys Pro Ala Thr Ala Ile Gly Val Ile Gly Asn Phe Thr Asp Ala
 405 410 415

Glu Arg Arg Lys Cys Glu Glu Glu Ile Ala Lys Leu Tyr Lys Gln Leu
 420 425 430

Asp Asp Lys Asp Glu Glu Ile Asn Gln Gln Ser Gln Leu Val Glu Lys
 435 440 445

Leu Lys Thr Gln Met Leu Asp Gln Glu Glu Leu Leu Ala Ser Thr Arg
 450 455 460

Arg Asp Gln Asp Asn Met Gln Ala Glu Leu Asn Arg Leu Gln Ala Glu
 465 470 475 480

Asn Asp Ala Ser Lys Glu Glu Val Lys Glu Val Leu Gln Ala Leu Glu
 485 490 495

Glu Leu Ala Val Asn Tyr Asp Gln Lys Ser Gln Glu Val Glu Asp Lys
 500 505 510

Thr Lys Glu Tyr Glu Leu Leu Ser Asp Glu Leu Asn Gln Lys Ser Ala
 515 520 525

Thr Leu Ala Ser Ile Asp Ala Glu Leu Gln Lys Leu Lys Glu Met Thr
 530 535 540

Asn His Gln Lys Lys Arg Ala Ala Glu Met Met Ala Ser Leu Leu Lys
 545 550 555 560

Asp Leu Ala Glu Ile Gly Ile Ala Val Gly Asn Asn Asp Val Lys Glu
 565 570 575

Asp Pro Lys Trp Glu Phe Pro Arg Lys Asn Leu Val Leu Gly Lys Thr
 580 585 590

Leu Gly Glu Gly Glu Phe Gly Lys Val Val Lys Ala Thr Ala Phe His
 595 600 605

Leu Lys Gly Arg Ala Gly Tyr Thr Thr Val Ala Val Lys Met Leu Lys
 610 615 620

Glu Asn Ala Ser Pro Ser Glu Leu Arg Asp Leu Leu Ser Glu Phe Asn
 625 630 635 640

Val Leu Lys Gln Val Asn His Pro His Val Ile Lys Leu Tyr Gly Ala
 645 650 655

Cys Ser Gln Asp Gly Pro Leu Leu Leu Ile Val Glu Tyr Ala Lys Tyr
 660 665 670

Gly Ser Leu Arg Gly Phe Leu Arg Glu Ser Arg Lys Val Gly Pro Gly
 675 680 685

Tyr Leu Gly Ser Gly Gly Ser Arg Asn Ser Ser Ser Leu Asp His Pro
 690 695 700

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

Ser

<210> 3
<211> 3303
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<221> CDS
<222> (1)..(3300)

<400> 3
atg gcg aag gcg acg tcc ggt gcc gcg ggg ctg cgt ctg ctg ttg ctg 48
Met Ala Lys Ala Thr Ser Gly Ala Ala Gly Leu Arg Leu Leu Leu Leu
1 5 10 15
ctg ctg ctg ccg ctg cta ggc aaa gtg gca ttg ggc ctc tac ttc tgg 96
Leu Leu Leu Pro Leu Leu Gly Lys Val Ala Leu Gly Leu Tyr Phe Ser
20 25 30
agg gat gct tac tgg gag aag ctg tat gtg gac cag gca gcc ggc acg 144
Arg Asp Ala Tyr Trp Glu Lys Leu Tyr Val Asp Gln Ala Ala Gly Thr
35 40 45
ccc ttg ctg tac gtc cat gcc ctg ccg gac gcc cct gag gag gtg ccc 192
Pro Leu Leu Tyr Val His Ala Leu Arg Asp Ala Pro Glu Glu Val Pro
50 55 60
agc ttc cgc ctg ggc cag cat ctc tac ggc acg tac cgc aca cgg ctg 240
Ser Phe Arg Leu Gly Gln His Leu Tyr Gly Thr Tyr Arg Thr Arg Leu
65 70 75 80
cat gag aac aac tgg atc tgc atc cag gag gac acc ggc ctc ctc tac 288
His Glu Asn Asn Trp Ile Cys Ile Gln Glu Asp Thr Gly Leu Leu Tyr
85 90 95
ctt aac cgg agc ctg gac cat agc tcc tgg gag aag ctc agt gtc cgc 336
Leu Asn Arg Ser Leu Asp His Ser Ser Trp Glu Lys Leu Ser Val Arg
100 105 110
aac cgc ggc ttt ccc ctg ctc acc gtc tac ctc aag gtc ttc ctg tca 384
Asn Arg Gly Phe Pro Leu Leu Thr Val Tyr Leu Lys Val Phe Leu Ser
115 120 125
ccc aca tcc ctt cgt gag ggc gag tgc cag tgg cca ggc tgt gcc cgc 432
Pro Thr Ser Leu Arg Glu Gly Glu Cys Gln Trp Pro Gly Cys Ala Arg
130 135 140
gta tac ttc tcc ttc ttc aac acc tcc ttt cca gcc tgc agc tcc ctc 480
Val Tyr Phe Ser Phe Phe Asn Thr Ser Phe Pro Ala Cys Ser Ser Leu
145 150 155 160
aag ccc cgg gag ctc tgc ttc cca gag aca agg ccc tcc ttc cgc att 528
Lys Pro Arg Glu Leu Cys Phe Pro Glu Thr Arg Pro Ser Phe Arg Ile
165 170 175
cgg gag aac cga ccc cca ggc acc ttc cac cag ttc cgc ctg ctg cct 576
Arg Glu Asn Arg Pro Pro Gly Thr Phe His Gln Phe Arg Leu Leu Pro
180 185 190

gtg cag ttc ttg tgc ccc aac atc agc gtg gcc tac agg ctc ctg gag	624
Val Gln Phe Leu Cys Pro Asn Ile Ser Val Ala Tyr Arg Leu Leu Glu	
195 200 205	
ggg gag ggt ctg ccc ttc cgc tgc gcc ccg gac agc ctg gag gtg agc	672
Gly Glu Gly Leu Pro Phe Arg Cys Ala Pro Asp Ser Leu Glu Val Ser	
210 215 220	
acg cgc tgg gcc ctg gac cgc gag cag cgg gag aag tac gag ctg gtg	720
Thr Arg Trp Ala Leu Asp Arg Glu Gln Arg Glu Lys Tyr Glu Leu Val	
225 230 235 240	
gcc gtg tgc acc gtg cac gcc ggc gcg cgc gag gag gtg gtg atg gtg	768
Ala Val Cys Thr Val His Ala Gly Ala Arg Glu Glu Val Val Met Val	
245 250 255	
ccc ttc ccg gtg acc gtg tac gac gag gac gac tgg gcg ccc acc ttc	816
Pro Phe Pro Val Thr Val Tyr Asp Glu Asp Asp Ser Ala Pro Thr Phe	
260 265 270	
ccc gcg ggc gtc gac acc gcc agc gcc gtg gtg gag ttc aag cgg aag	864
Pro Ala Gly Val Asp Thr Ala Ser Ala Val Val Glu Phe Lys Arg Lys	
275 280 285	
gag gac acc gtg gtg gcc acg ctg cgt gtc ttc gat gca gac gtg gta	912
Glu Asp Thr Val Val Ala Thr Leu Arg Val Phe Asp Ala Asp Val Val	
290 295 300	
cct gca tca ggg gag ctg gtg agg cgg tac aca agc acg ctg ctc ccc	960
Pro Ala Ser Gly Glu Leu Val Arg Arg Tyr Thr Ser Thr Leu Leu Pro	
305 310 315 320	
ggg gac acc tgg gcc cag cag acc ttc cgg gtg gaa cac tgg ccc aac	1008
Gly Asp Thr Trp Ala Gln Gln Thr Phe Arg Val Glu His Trp Pro Asn	
325 330 335	
gag acc tgg gtc cag gcc aac ggc agc ttc gtg cgg gcg acc gta cat	1056
Glu Thr Ser Val Gln Ala Asn Gly Ser Phe Val Arg Ala Thr Val His	
340 345 350	
gac tat agg ctg gtt ctc aac cgg aac ctc tcc atc tgg gag aac cgc	1104
Asp Tyr Arg Leu Val Leu Asn Arg Asn Leu Ser Ile Ser Glu Asn Arg	
355 360 365	
acc atg cag ctg gcg gtg ctg gtc aat gac tca gac ttc cag ggc cca	1152
Thr Met Gln Leu Ala Val Leu Val Asn Asp Ser Asp Phe Gln Gly Pro	
370 375 380	
gga gcg ggc gtc ctc ttg ctc cac ttc aac gtg tgg gtg ctg ccg gtc	1200
Gly Ala Gly Val Leu Leu Leu His Phe Asn Val Ser Val Leu Pro Val	
385 390 395 400	
agc ctg cac ctg ccc agt acc tac tcc ctc tcc gtg agc agg agg gct	1248
Ser Leu His Leu Pro Ser Thr Tyr Ser Leu Ser Val Ser Arg Arg Ala	
405 410 415	
cgc cga ttt gcc cag atc ggg aaa gtc tgt gtg gaa aac tgc cag gca	1296
Arg Arg Phe Ala Gln Ile Gly Lys Val Cys Val Glu Asn Cys Gln Ala	
420 425 430	
ttc agt ggc atc aac gtc cag tac aag ctg cat tcc tct ggt gcc aac	1344
Phe Ser Gly Ile Asn Val Gln Tyr Lys Leu His Ser Ser Gly Ala Asn	
435 440 445	
tgc agc acg cta ggg gtg gtc acc tca gcc gag gac acc tgg ggg atc	1392
Cys Ser Thr Leu Gly Val Val Thr Ser Ala Glu Asp Thr Ser Gly Ile	
450 455 460	

ctg ttt gtg aat gac acc aag gcc ctg cgg cgg ccc aag tgt gcc gaa Leu Phe Val Asn Asp Thr Lys Ala Leu Arg Arg Pro Lys Cys Ala Glu 465 470 475 480	1440
ctt cac tac atg gtg gtg gcc acc gac cag cag acc tct agg cag gcc Leu His Tyr Met Val Val Ala Thr Asp Gln Gln Thr Ser Arg Gln Ala 485 490 495	1488
cag gcc cag ctg ctt gta aca gtg gag ggg tca tat gtg gcc gag gag Gln Ala Gln Leu Val Thr Val Glu Gly Ser Tyr Val Ala Glu Glu 500 505 510	1536
gcg ggc tgc ccc ctg tcc tgt gca gtc agc aag aga cgg ctg gag tgt Ala Gly Cys Pro Leu Ser Cys Ala Val Ser Lys Arg Arg Leu Glu Cys 515 520 525	1584
gag gag tgt ggc ggc ctg ggc tcc cca aca ggc agg tgt gag tgg agg Glu Glu Cys Gly Gly Leu Gly Ser Pro Thr Gly Arg Cys Glu Trp Arg 530 535 540	1632
caa gga gat ggc aaa ggg atc acc agg aac ttc tcc acc tgc tct ccc Gln Gly Asp Gly Lys Gly Ile Thr Arg Asn Phe Ser Thr Cys Ser Pro 545 550 555 560	1680
agc acc aag acc tgc ccc gac ggc cac tgc gat gtt gtg gag acc caa Ser Thr Lys Thr Cys Pro Asp Gly His Cys Asp Val Val Glu Thr Gln 565 570 575	1728
gac atc aac att tgc cct cag gac tgc ctc cgg ggc agc att gtt ggg Asp Ile Asn Ile Cys Pro Gln Asp Cys Leu Arg Gly Ser Ile Val Gly 580 585 590	1776
gga cac gag cct ggg gag ccc cgg ggg att aaa gct ggc tat ggc acc Gly His Glu Pro Gly Glu Pro Arg Gly Ile Lys Ala Gly Tyr Gly Thr 595 600 605	1824
tgc aac tgc ttc cct gag gag gag aag tgc ttc tgc gag ccc gaa gac Cys Asn Cys Phe Pro Glu Glu Glu Lys Cys Phe Cys Glu Pro Glu Asp 610 615 620	1872
atc cag gat cca ctg tgc gac gag ctg tgc cgc acg gtg atc gca gcc Ile Gln Asp Pro Leu Cys Asp Glu Leu Cys Arg Thr Val Ile Ala Ala 625 630 635 640	1920
gct gtc ctc ttc tcc ttc atc gtc tgg gtg ctg ctg tct gcc ttc tgc Ala Val Leu Phe Ser Phe Ile Val Ser Val Leu Leu Ser Ala Phe Cys 645 650 655	1968
atc cac tgc tac cac aag ttt gcc cac aag cca ccc atc tcc tca gct Ile His Cys Tyr His Lys Phe Ala His Lys Pro Pro Ile Ser Ser Ala 660 665 670	2016
gag atg acc ttc cgg agg ccc gcc cag gcc ttc ccg gtc agc tac tcc Glu Met Thr Phe Arg Arg Pro Ala Gln Ala Phe Pro Val Ser Tyr Ser 675 680 685	2064
tct tcc ggt gcc cgc cgg ccc tgg ctg gac tcc atg gag aac cag gtc Ser Ser Gly Ala Arg Arg Pro Ser Leu Asp Ser Met Glu Asn Gln Val 690 695 700	2112
tcc gtg gat gcc ttc aag atc ctg cag cct gag gga act ggc atg ata Ser Val Asp Ala Phe Lys Ile Leu Gln Pro Glu Gly Thr Gly Met Ile 705 710 715 720	2160
gat gaa gag ttc act gtt gca aga ctc tac att agc aaa atg aag tca Asp Glu Glu Phe Thr Val Ala Arg Leu Tyr Ile Ser Lys Met Lys Ser 725 730 735	2208

gaa gta aaa acc atg gtg aaa cgt tgc aag cag tta gaa agc aca caa Glu Val Lys Thr Met Val Lys Arg Cys Lys Gln Leu Glu Ser Thr Gln 740 745 750	2256
act gag agc aac aaa aaa atg gaa gaa aat gaa aag gag tta gca gca Thr Glu Ser Asn Lys Lys Met Glu Glu Asn Glu Lys Glu Leu Ala Ala 755 760 765	2304
tgt cag ctt cgt atc tct caa cat gaa gcc aaa atc aag tca ttg act Cys Gln Leu Arg Ile Ser Gln His Glu Ala Lys Ile Lys Ser Leu Thr 770 775 780	2352
gaa tac ctt caa aat gtg gaa caa aag aaa aga cag ttg gag gaa tct Glu Tyr Leu Gln Asn Val Glu Gln Lys Lys Arg Gln Leu Glu Glu Ser 785 790 795 800	2400
gtc gat gcc ctc agt gaa gaa cta gtc cag ctt cga gca caa gag aaa Val Asp Ala Leu Ser Glu Glu Leu Val Gln Leu Arg Ala Gln Glu Lys 805 810 815	2448
gtc cat gaa atg gaa aag gag cac tta aat aag gtt cag act gca aat Val His Glu Met Glu Lys Glu His Leu Asn Lys Val Gln Thr Ala Asn 820 825 830	2496
gaa gtt aag caa gct gtt gaa cag cag atc cag agc cat aga gaa act Glu Val Lys Gln Ala Val Glu Gln Gln Ile Gln Ser His Arg Glu Thr 835 840 845	2544
cat caa aaa cag atc agt agt ttg aga gat gaa gta gaa gca aaa gca His Gln Lys Gln Ile Ser Ser Leu Arg Asp Glu Val Glu Ala Lys Ala 850 855 860	2592
aaa ctt att act gat ctt caa gac caa aac cag aaa atg atg tta gag Lys Leu Ile Thr Asp Leu Gln Asp Gln Asn Gln Lys Met Met Leu Glu 865 870 875 880	2640
cag gaa cgt cta aga gta gaa cat gag aag ttg aaa gcc aca gat cag Gln Glu Arg Leu Arg Val Glu His Glu Lys Leu Lys Ala Thr Asp Gln 885 890 895	2688
gaa aag agc aga aaa cta cat gaa ctt acg gtt atg caa gat aga cga Glu Lys Ser Arg Lys Leu His Glu Leu Thr Val Met Gln Asp Arg Arg 900 905 910	2736
gaa caa gca aga caa gac ttg aag ggt ttg gaa gag aca gtg gca aaa Glu Gln Ala Arg Gln Asp Leu Lys Gly Leu Glu Glu Thr Val Ala Lys 915 920 925	2784
gaa ctt cag act tta cac aac ctg cgc aaa ctc ttt gtt cag gac ctg Glu Leu Gln Thr Leu His Asn Leu Arg Lys Leu Phe Val Gln Asp Leu 930 935 940	2832
gct aca aga gtt aaa aag agt gct gag att gat tct gat gac acc gga Ala Thr Arg Val Lys Lys Ser Ala Glu Ile Asp Ser Asp Asp Thr Gly 945 950 955 960	2880
ggc agc gct gct cag aag caa aaa atc tcc ttt ctt gaa aat aat ctt Gly Ser Ala Ala Gln Lys Gln Lys Ile Ser Phe Leu Glu Asn Asn Leu 965 970 975	2928
gaa cag ctc act aaa gtg cac aaa cag ttg gta cgt gat aat gca gat Glu Gln Leu Thr Lys Val His Lys Gln Leu Val Arg Asp Asn Ala Asp 980 985 990	2976
ctc cgc tgt gaa ctt cct aag ttg gaa aag cga ctt cga gct aca gct Leu Arg Cys Glu Leu Pro Lys Leu Glu Lys Arg Leu Arg Ala Thr Ala 995 1000 1005	3024

gag aga	gtg aaa gct ttg gaa	tca gca ctg aaa gaa	gct aaa gaa	3069
Glu Arg	Val Lys Ala Leu Glu	Ser Ala Leu Lys Glu	Ala Lys Glu	
1010	1015	1020		
aat gca	tct cgt gat cgc aaa	cgc tat cag caa gaa	gta gat cgc	3114
Asn Ala	Ser Arg Asp Arg Lys	Arg Tyr Gln Gln Glu	Val Asp Arg	
1025	1030	1035		
ata aag	gaa gca gtc agg tca	aag aat atg gcc aga	aga ggg cat	3159
Ile Lys	Glu Ala Val Arg Ser	Lys Asn Met Ala Arg	Arg Gly His	
1040	1045	1050		
tct gca	cag att gct aaa cct	att cgt ccc ggg caa	cat cca gca	3204
Ser Ala	Gln Ile Ala Lys Pro	Ile Arg Pro Gly Gln	His Pro Ala	
1055	1060	1065		
gct tct	cca act cac cca agt	gca att cgt gga gga	ggt gca ttt	3249
Ala Ser	Pro Thr His Pro Ser	Ala Ile Arg Gly Gly	Gly Ala Phe	
1070	1075	1080		
gtt cag	aac agc cag cca gtg	gca gtg cga ggt gga	gga ggc aaa	3294
Val Gln	Asn Ser Gln Pro Val	Ala Val Arg Gly Gly	Gly Gly Lys	
1085	1090	1095		
caa gtg	taa			3303
Gln Val				
1100				

<210> 4
 <211> 1100
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 4
 Met Ala Lys Ala Thr Ser Gly Ala Ala Gly Leu Arg Leu Leu Leu Leu
 1 5 10 15

Leu Leu Leu Pro Leu Leu Gly Lys Val Ala Leu Gly Leu Tyr Phe Ser
 20 25 30

Arg Asp Ala Tyr Trp Glu Lys Leu Tyr Val Asp Gln Ala Ala Gly Thr
 35 40 45

Pro Leu Leu Tyr Val His Ala Leu Arg Asp Ala Pro Glu Glu Val Pro
 50 55 60

Ser Phe Arg Leu Gly Gln His Leu Tyr Gly Thr Tyr Arg Thr Arg Leu
 65 70 75 80

His Glu Asn Asn Trp Ile Cys Ile Gln Glu Asp Thr Gly Leu Leu Tyr
 85 90 95

Leu Asn Arg Ser Leu Asp His Ser Ser Trp Glu Lys Leu Ser Val Arg
 100 105 110

Asn Arg Gly Phe Pro Leu Leu Thr Val Tyr Leu Lys Val Phe Leu Ser

115

120

125

Pro Thr Ser Leu Arg Glu Gly Glu Cys Gln Trp Pro Gly Cys Ala Arg
130 135 140

Val Tyr Phe Ser Phe Phe Asn Thr Ser Phe Pro Ala Cys Ser Ser Leu
145 150 155 160

Lys Pro Arg Glu Leu Cys Phe Pro Glu Thr Arg Pro Ser Phe Arg Ile
165 170 175

Arg Glu Asn Arg Pro Pro Gly Thr Phe His Gln Phe Arg Leu Leu Pro
180 185 190

Val Gln Phe Leu Cys Pro Asn Ile Ser Val Ala Tyr Arg Leu Leu Glu
195 200 205

Gly Glu Gly Leu Pro Phe Arg Cys Ala Pro Asp Ser Leu Glu Val Ser
210 215 220

Thr Arg Trp Ala Leu Asp Arg Glu Gln Arg Glu Lys Tyr Glu Leu Val
225 230 235 240

Ala Val Cys Thr Val His Ala Gly Ala Arg Glu Glu Val Val Met Val
245 250 255

Pro Phe Pro Val Thr Val Tyr Asp Glu Asp Asp Ser Ala Pro Thr Phe
260 265 270

Pro Ala Gly Val Asp Thr Ala Ser Ala Val Val Glu Phe Lys Arg Lys
275 280 285

Glu Asp Thr Val Val Ala Thr Leu Arg Val Phe Asp Ala Asp Val Val
290 295 300

Pro Ala Ser Gly Glu Leu Val Arg Arg Tyr Thr Ser Thr Leu Leu Pro
305 310 315 320

Gly Asp Thr Trp Ala Gln Gln Thr Phe Arg Val Glu His Trp Pro Asn
325 330 335

Glu Thr Ser Val Gln Ala Asn Gly Ser Phe Val Arg Ala Thr Val His
340 345 350

Asp Tyr Arg Leu Val Leu Asn Arg Asn Leu Ser Ile Ser Glu Asn Arg
355 360 365

Thr Met Gln Leu Ala Val Leu Val Asn Asp Ser Asp Phe Gln Gly Pro
370 375 380

Gly Ala Gly Val Leu Leu Leu His Phe Asn Val Ser Val Leu Pro Val
Page 14

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

660

665

670

Glu Met Thr Phe Arg Arg Pro Ala Gln Ala Phe Pro Val Ser Tyr Ser
675 680 685

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

Ser Val Asp Ala Phe Lys Ile Leu Gln Pro Glu Gly Thr Gly Met Ile
705 710 715 720

Asp Glu Glu Phe Thr Val Ala Arg Leu Tyr Ile Ser Lys Met Lys Ser
725 730 735

Glu Val Lys Thr Met Val Lys Arg Cys Lys Gln Leu Glu Ser Thr Gln
740 745 750

Thr Glu Ser Asn Lys Lys Met Glu Glu Asn Glu Lys Glu Leu Ala Ala
755 760 765

Cys Gln Leu Arg Ile Ser Gln His Glu Ala Lys Ile Lys Ser Leu Thr
770 775 780

Glu Tyr Leu Gln Asn Val Glu Gln Lys Lys Arg Gln Leu Glu Glu Ser
785 790 795 800

Val Asp Ala Leu Ser Glu Glu Leu Val Gln Leu Arg Ala Gln Glu Lys
805 810 815

Val His Glu Met Glu Lys Glu His Leu Asn Lys Val Gln Thr Ala Asn
820 825 830

Glu Val Lys Gln Ala Val Glu Gln Gln Ile Gln Ser His Arg Glu Thr
835 840 845

His Gln Lys Gln Ile Ser Ser Leu Arg Asp Glu Val Glu Ala Lys Ala
850 855 860

Lys Leu Ile Thr Asp Leu Gln Asp Gln Asn Gln Lys Met Met Leu Glu
865 870 875 880

Gln Glu Arg Leu Arg Val Glu His Glu Lys Leu Lys Ala Thr Asp Gln
885 890 895

Glu Lys Ser Arg Lys Leu His Glu Leu Thr Val Met Gln Asp Arg Arg
900 905 910

Glu Gln Ala Arg Gln Asp Leu Lys Gly Leu Glu Glu Thr Val Ala Lys
915 920 925

Glu Leu Gln Thr Leu His Asn Leu Arg Lys Leu Phe Val Gln Asp Leu

930 935 940
 Ala Thr Arg Val Lys Lys Ser Ala Glu Ile Asp Ser Asp Asp Thr Gly
 945 950 955 960
 Gly Ser Ala Ala Gln Lys Gln Lys Ile Ser Phe Leu Glu Asn Asn Leu
 965 970 975
 Glu Gln Leu Thr Lys Val His Lys Gln Leu Val Arg Asp Asn Ala Asp
 980 985 990
 Leu Arg Cys Glu Leu Pro Lys Leu Glu Lys Arg Leu Arg Ala Thr Ala
 995 1000 1005
 Glu Arg Val Lys Ala Leu Glu Ser Ala Leu Lys Glu Ala Lys Glu
 1010 1015 1020
 Asn Ala Ser Arg Asp Arg Lys Arg Tyr Gln Gln Glu Val Asp Arg
 1025 1030 1035
 Ile Lys Glu Ala Val Arg Ser Lys Asn Met Ala Arg Arg Gly His
 1040 1045 1050
 Ser Ala Gln Ile Ala Lys Pro Ile Arg Pro Gly Gln His Pro Ala
 1055 1060 1065
 Ala Ser Pro Thr His Pro Ser Ala Ile Arg Gly Gly Gly Ala Phe
 1070 1075 1080
 Val Gln Asn Ser Gln Pro Val Ala Val Arg Gly Gly Gly Gly Lys
 1085 1090 1095
 Gln Val
 1100

<210> 5
 <211> 200
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<220>
 <221> modified_base
 <222> (16)..(185)
 <223> a, c, t, g, unknown or other

<400> 5
 atcgccaccag cgtgtannnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 60
 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 120
 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 180

nnnnncactg cggctcctca

200

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

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 6
Lys Val Asp Asn Asn Gly Val Ala Ile Gly Ile Glu Ala Leu Asp Lys
1 5 10 15

<210> 7
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 7
Glu Asp Pro Lys Trp Glu Phe Pro Arg Lys Asn Leu Val Leu Gly Lys
1 5 10 15

Thr

<210> 8
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 8
tgtaaaggag gatc

14

<210> 9
<211> 976
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 9
Met Ala Asp Leu Ala Glu Cys Asn Ile Lys Val Met Cys Arg Phe Arg
1 5 10 15

Pro Leu Asn Glu Ser Glu Val Asn Arg Gly Asp Lys Tyr Ile Ala Lys
20 25 30

Phe Gln Gly Glu Asp Thr Val Val Ile Ala Ser Lys Pro Tyr Ala Phe
Page 18

305 310 315 320
 Ala Lys Thr Ile Lys Asn Thr Val Cys Val Asn Val Glu Leu Thr Ala
 325 330 335
 Glu Gln Trp Lys Lys Lys Tyr Glu Lys Glu Lys Glu Lys Asn Lys Ile
 340 345 350
 Leu Arg Asn Thr Ile Gln Trp Leu Glu Asn Glu Leu Asn Arg Trp Arg
 355 360 365
 Asn Gly Glu Thr Val Pro Ile Asp Glu Gln Phe Asp Lys Glu Lys Ala
 370 375 380
 Asn Leu Glu Ala Phe Thr Val Asp Lys Asp Ile Thr Leu Thr Asn Asp
 385 390 395 400
 Lys Pro Ala Thr Ala Ile Gly Val Ile Gly Asn Phe Thr Asp Ala Glu
 405 410 415
 Arg Arg Lys Cys Glu Glu Glu Ile Ala Lys Leu Tyr Lys Gln Leu Asp
 420 425 430
 Asp Lys Asp Glu Glu Ile Asn Gln Gln Ser Gln Leu Val Glu Lys Leu
 435 440 445
 Lys Thr Gln Met Leu Asp Gln Glu Glu Leu Leu Ala Ser Thr Arg Arg
 450 455 460
 Asp Gln Asp Asn Met Gln Ala Glu Leu Asn Arg Leu Gln Ala Glu Asn
 465 470 475 480
 Asp Ala Ser Lys Glu Glu Val Lys Glu Val Leu Gln Ala Leu Glu Glu
 485 490 495
 Leu Ala Val Asn Tyr Asp Gln Lys Ser Gln Glu Val Glu Asp Lys Thr
 500 505 510
 Lys Glu Tyr Glu Leu Leu Ser Asp Glu Leu Asn Gln Lys Ser Ala Thr
 515 520 525
 Leu Ala Ser Ile Asp Ala Glu Leu Gln Lys Leu Lys Glu Met Thr Asn
 530 535 540
 His Gln Lys Lys Arg Ala Ala Glu Met Met Ala Ser Leu Leu Lys Asp
 545 550 555 560
 Leu Ala Glu Ile Gly Ile Ala Val Gly Asn Asn Asp Val Lys Glu Asp
 565 570 575
 Pro Lys Trp Glu Phe Pro Arg Lys Asn Leu Val Leu Gly Lys Thr Leu

580

585

590

Gly Glu Gly Glu Phe Gly Lys Val Val Lys Ala Thr Ala Phe His Leu
595 600 605

Lys Gly Arg Ala Gly Tyr Thr Thr Val Ala Val Lys Met Leu Lys Glu
610 615 620

Asn Ala Ser Pro Ser Glu Leu Arg Asp Leu Leu Ser Glu Phe Asn Val
625 630 635 640

Leu Lys Gln Val Asn His Pro His Val Ile Lys Leu Tyr Gly Ala Cys
645 650 655

Ser Gln Asp Gly Pro Leu Leu Leu Ile Val Glu Tyr Ala Lys Tyr Gly
660 665 670

Ser Leu Arg Gly Phe Leu Arg Glu Ser Arg Lys Val Gly Pro Gly Tyr
675 680 685

Leu Gly Ser Gly Gly Ser Arg Asn Ser Ser Ser Leu Asp His Pro Asp
690 695 700

Glu Arg Ala Leu Thr Met Gly Asp Leu Ile Ser Phe Ala Trp Gln Ile
705 710 715 720

Ser Gln Gly Met Gln Tyr Leu Ala Glu Met Lys Leu Val His Arg Asp
725 730 735

Leu Ala Ala Arg Asn Ile Leu Val Ala Glu Gly Arg Lys Met Lys Ile
740 745 750

Ser Asp Phe Gly Leu Ser Arg Asp Val Tyr Glu Glu Asp Ser Tyr Val
755 760 765

Lys Arg Ser Gln Gly Arg Ile Pro Val Lys Trp Met Ala Ile Glu Ser
770 775 780

Leu Phe Asp His Ile Tyr Thr Thr Gln Ser Asp Val Trp Ser Phe Gly
785 790 795 800

Val Leu Leu Trp Glu Ile Val Thr Leu Gly Gly Asn Pro Tyr Pro Gly
805 810 815

Ile Pro Pro Glu Arg Leu Phe Asn Leu Leu Lys Thr Gly His Arg Met
820 825 830

Glu Arg Pro Asp Asn Cys Ser Glu Glu Met Tyr Arg Leu Met Leu Gln
835 840 845

Cys Trp Lys Gln Glu Pro Asp Lys Arg Pro Val Phe Ala Asp Ile Ser
Page 21

850		855		860
Lys Asp Leu Glu Lys Met Met Val Lys Arg Arg Asp Tyr Leu Asp Leu				
865		870		875
Ala Ala Ser Thr Pro Ser Asp Ser Leu Ile Tyr Asp Asp Gly Leu Ser				
	885		890	895
Glu Glu Glu Thr Pro Leu Val Asp Cys Asn Asn Ala Pro Leu Pro Arg				
	900		905	910
Ala Leu Pro Ser Thr Trp Ile Glu Asn Lys Leu Tyr Gly Met Ser Asp				
	915		920	925
Pro Asn Trp Pro Gly Glu Ser Pro Val Pro Leu Thr Arg Ala Asp Gly				
	930		935	940
Thr Asn Thr Gly Phe Pro Arg Tyr Pro Asn Asp Ser Val Tyr Ala Asn				
	945		950	955
Trp Met Leu Ser Pro Ser Ala Ala Lys Leu Met Asp Thr Phe Asp Ser				
	965		970	975