

US1251978
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

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic polynucleotide

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<221> CDS

<222> (1)..(2931)

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cct	ctc	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	
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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	
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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	
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ata	ttt	gca	tat	gga	caa	aca	tcc	tct	ggg	aag	aca	cac	aca	atg	gag	288
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US1251978																
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caa Gln	gat Asp	att Ile 115	ttt Phe	aat Asn	tat Tyr	att Ile	tac Tyr 120	tcc Ser	atg Met	gat Asp	gaa Glu	aat Asn 125	ttg Leu	gaa Glu	ttt Phe	384
cat His 130	att Ile	aag Lys	gtt Val	tca Ser	tat Tyr	ttt Phe 135	gaa Glu	ata Ile	tat Tyr	ttg Leu	gat Asp 140	aag Lys	ata Ile	agg Arg	gac Asp	432
ctg Leu 145	tta Leu	gat Asp	gtt Val	tca Ser	aag Lys 150	acc Thr	aac Asn	ctt Leu	tca Ser	gtt Val 155	cat His	gaa Glu	gac Asp	aaa Lys	aac Asn 160	480
cga Arg	gtt Val	ccc Pro	tat Tyr	gta Val 165	aag Lys	ggg Gly	tgc Cys	aca Thr	gag Glu 170	cgt Arg	ttt Phe	gta Val	tgt Cys	agt Ser 175	cca Pro	528
gat Asp	gaa Glu	gtt Val	atg Met 180	gat Asp	acc Thr	ata Ile	gat Asp	gaa Glu 185	gga Gly	aaa Lys	tcc Ser	aac Asn	aga Arg 190	cat His	gta Val	576
gca Ala	gtt Val	aca Thr 195	aat Asn	atg Met	aat Asn	gaa Glu	cat His 200	agc Ser	tct Ser	agg Arg	agt Ser	cac His 205	agt Ser	ata Ile	ttt Phe	624
ctt Leu 210	att Ile	aat Asn	gtc Val	aaa Lys	caa Gln	gag Glu 215	aac Asn	aca Thr	caa Gln	acg Thr	gaa Glu 220	caa Gln	aag Lys	ctg Leu	agt Ser	672
gga Gly 225	aaa Lys	ctt Leu	tat Tyr	ctg Leu	gtt Val 230	gat Asp	tta Leu	gct Ala	ggt Gly	agt Ser 235	gaa Glu	aag Lys	gtt Val	agt Ser	aaa Lys 240	720
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tca Ser 305	tca Ser	tac Tyr	aat Asn	gag Glu	tct Ser 310	gaa Glu	aca Thr	aaa Lys	tct Ser	aca Thr 315	ctc Leu	tta Leu	ttt Phe	ggc Gly	caa Gln 320	960
agg Arg	gcc Ala	aaa Lys	aca Thr	att Ile 325	aag Lys	aac Asn	aca Thr	gtt Val	tgt Cys 330	gtc Val	aat Asn	gtg Val	gag Glu	tta Leu 335	act Thr	1008

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gat Asp	aaa Lys	cca Pro	gca Ala	acc Thr 405	gca Ala	att Ile	gga Gly	gtt Val	ata Ile 410	gga Gly	aat Asn	ttt Phe	act Thr	gat Asp 415	gct Ala	1248
gaa Glu	aga Arg	aga Arg	aag Lys 420	tgt Cys	gaa Glu	gaa Glu	gaa Glu	att Ile 425	gct Ala	aaa Lys	tta Leu	tac Tyr	aaa Lys 430	cag Gln	ctt Leu	1296
gat Asp	gac Asp	aag Lys 435	gat Asp	gaa Glu	gaa Glu	att Ile	aac Asn 440	cag Gln	caa Gln	agt Ser	caa Gln	ctg Leu 445	gta Val	gag Glu	aaa Lys	1344
ctg Leu	aag Lys 450	acg Thr	caa Gln	atg Met	ttg Leu	gat Asp 455	cag Gln	gag Glu	gag Glu	ctt Leu	ttg Leu 460	gca Ala	tct Ser	acc Thr	aga Arg	1392
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gac Asp	ctt Leu	gca Ala	gaa Glu	ata Ile 565	gga Gly	att Ile	gct Ala	gtg Val	gga Gly 570	aat Asn	aat Asn	gat Asp	gta Val	aag Lys 575	gag Glu	1728
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ctg Leu	aaa Lys 610	ggc Gly	aga Arg	gca Ala	ggg Gly	tac Tyr 615	acc Thr	acg Thr	gtg Val	gcc Ala	gtg Val 620	aag Lys	atg Met	ctg Leu	aaa Lys	1872
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gtc Val	ctg Leu	aag Lys	cag Gln	gtc Val 645	aac Asn	cac His	cca Pro	cat His	gtc Val 650	atc Ile	aaa Lys	ttg Leu	tat Tyr	ggg Gly 655	gcc Ala	1968
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tac Tyr	ctg Leu 690	ggc Gly	agt Ser	gga Gly	ggc Gly	agc Ser 695	cgc Arg	aac Asn	tcc Ser	agc Ser	tcc Ser 700	ctg Leu	gac Asp	cac His	ccg Pro	2112
gat Asp 705	gag Glu	cgg Arg	gcc Ala	ctc Leu	acc Thr 710	atg Met	ggc Gly	gac Asp	ctc Leu	atc Ile 715	tca Ser	ttt Phe	gcc Ala	tgg Trp	cag Gln 720	2160
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gtg Val 770	aag Lys	agg Arg	agc Ser	cag Gln	ggt Gly	cgg Arg 775	att Ile	cca Pro	gtt Val	aaa Lys	tgg Trp 780	atg Met	gca Ala	att Ile	gaa Glu	2352
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ggg Gly	att Ile	cct Pro	cct Pro 820	gag Glu	cgg Arg	ctc Leu	ttc Phe	aac Asn 825	ctt Leu	ctg Leu	aag Lys	acc Thr	ggc Gly 830	cac His	cgg Arg	2496
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Gln Cys Trp Lys Gln Glu Pro Asp Lys Arg Pro Val Phe Ala Asp Ile			
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agc aaa gac ctg gag aag atg atg gtt aag agg aga gac tac ttg gac			2640
Ser Lys Asp Leu Glu Lys Met Met Val Lys Arg Arg Asp Tyr Leu Asp			
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ctt gcg gcg tcc act cca tct gac tcc ctg att tat gac gac ggc ctc			2688
Leu Ala Ala Ser Thr Pro Ser Asp Ser Leu Ile Tyr Asp Asp Gly Leu			
885	890	895	
tca gag gag gag aca ccg ctg gtg gac tgt aat aat gcc ccc ctc cct			2736
Ser Glu Glu Glu Thr Pro Leu Val Asp Cys Asn Asn Ala Pro Leu Pro			
900	905	910	
cga gcc ctc cct tcc aca tgg att gaa aac aaa ctc tat ggc atg tca			2784
Arg Ala Leu Pro Ser Thr Trp Ile Glu Asn Lys Leu Tyr Gly Met Ser			
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			
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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			
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<213> Artificial Sequence

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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

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Cys Ala Lys Lys Ile Val Lys Asp Val Leu Glu Gly Tyr Asn Gly Thr
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 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

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

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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 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

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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
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Asn Trp Met Leu Ser Pro Ser Ala Ala Lys Leu Met Asp Thr Phe Asp
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Ser

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic polynucleotide

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<221> CDS

<222> (1)..(3300)

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1 5 10 15

48

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agg Arg	gat Asp	gct Ala 35	tac Tyr	tgg Trp	gag Glu	aag Lys	ctg Leu 40	tat Tyr	gtg Val	gac Asp	cag Gln	gca Ala 45	gcc Ala	ggc Gly	acg Thr	144
ccc Pro	ttg Leu 50	ctg Leu	tac Tyr	gtc Val	cat His	gcc Ala 55	ctg Leu	cgg Arg	gac Asp	gcc Ala	cct Pro 60	gag Glu	gag Glu	gtg Val	ccc Pro	192
agc Ser 65	ttc Phe	cgc Arg	ctg Leu	ggc Gly	cag Gln 70	cat His	ctc Leu	tac Tyr	ggc Gly	acg Thr 75	tac Tyr	cgc Arg	aca Thr	cgg Arg	ctg Leu 80	240
cat His	gag Glu	aac Asn	aac Asn	tgg Trp 85	atc Ile	tgc Cys	atc Ile	cag Gln	gag Glu 90	gac Asp	acc Thr	ggc Gly	ctc Leu 95	ctc Leu 95	tac Tyr	288
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aac Asn	cgc Arg	ggc Gly 115	ttt Phe	ccc Pro	ctg Leu	ctc Leu	acc Thr 120	gtc Val	tac Tyr	ctc Leu	aag Lys	gtc Val 125	ttc Phe	ctg Leu	tca Ser	384
ccc Pro	aca Thr 130	tcc Ser	ctt Leu	cgt Arg	gag Glu	ggc Gly 135	gag Glu	tgc Cys	cag Gln	tgg Trp	cca Pro 140	ggc Gly	tgt Cys	gcc Ala	cgc Arg	432
gta Val 145	tac Tyr	ttc Phe	tcc Ser	ttc Phe	ttc Phe 150	aac Asn	acc Thr	tcc Ser	ttt Phe	cca Pro 155	gcc Ala	tgc Cys	agc Ser	tcc Ser	ctc Leu 160	480
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cgg Arg	gag Glu	aac Asn	cga Arg 180	ccc Pro	cca Pro	ggc Gly	acc Thr	ttc Phe 185	cac His	cag Gln	ttc Phe	cgc Arg	ctg Leu 190	ctg Leu	cct Pro	576
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ccc Pro	ttc Phe	ccg Pro	gtg Val	acc Thr	gtg Val	tac Tyr	gac Asp	gag Glu	gac Asp	gac Asp	tcg Ser	gcg Ala	ccc Pro	acc Thr	ttc Phe	816

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		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	tcg	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	tcg	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	tcg	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	tcg	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	1440
Leu	Phe	Val	Asn	Asp	Thr	Lys	Ala	Leu	Arg	Arg	Pro	Lys	Cys	Ala	Glu	
465					470					475					480	
ctt	cac	tac	atg	gtg	gtg	gcc	acc	gac	cag	cag	acc	tct	agg	cag	gcc	1488
Leu	His	Tyr	Met	Val	Val	Ala	Thr	Asp	Gln	Gln	Thr	Ser	Arg	Gln	Ala	
				485					490					495		
cag	gcc	cag	ctg	ctt	gta	aca	gtg	gag	ggg	tca	tat	gtg	gcc	gag	gag	1536
Gln	Ala	Gln	Leu	Leu	Val	Thr	Val	Glu	Gly	Ser	Tyr	Val	Ala	Glu	Glu	
			500					505					510			
gcg	ggc	tgc	ccc	ctg	tcc	tgt	gca	gtc	agc	aag	aga	cgg	ctg	gag	tgt	1584

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Ala	Gly	Cys	Pro	Leu	Ser	Cys	Ala	Val	Ser	Lys	Arg	Arg	Leu	Glu	Cys	
		515					520					525				
gag	gag	tgt	ggc	ggc	ctg	ggc	tcc	cca	aca	ggc	agg	tgt	gag	tgg	agg	1632
Glu	Glu	Cys	Gly	Gly	Leu	Gly	Ser	Pro	Thr	Gly	Arg	Cys	Glu	Trp	Arg	
	530					535					540					
caa	gga	gat	ggc	aaa	ggg	atc	acc	agg	aac	ttc	tcc	acc	tgc	tct	ccc	1680
Gln	Gly	Asp	Gly	Lys	Gly	Ile	Thr	Arg	Asn	Phe	Ser	Thr	Cys	Ser	Pro	
545					550					555					560	
agc	acc	aag	acc	tgc	ccc	gac	ggc	cac	tgc	gat	gtt	gtg	gag	acc	caa	1728
Ser	Thr	Lys	Thr	Cys	Pro	Asp	Gly	His	Cys	Asp	Val	Val	Glu	Thr	Gln	
				565					570				575			
gac	atc	aac	att	tgc	cct	cag	gac	tgc	ctc	cgg	ggc	agc	att	gtt	ggg	1776
Asp	Ile	Asn	Ile	Cys	Pro	Gln	Asp	Cys	Leu	Arg	Gly	Ser	Ile	Val	Gly	
			580					585					590			
gga	cac	gag	cct	ggg	gag	ccc	cgg	ggg	att	aaa	gct	ggc	tat	ggc	acc	1824
Gly	His	Glu	Pro	Gly	Glu	Pro	Arg	Gly	Ile	Lys	Ala	Gly	Tyr	Gly	Thr	
		595					600					605				
tgc	aac	tgc	ttc	cct	gag	gag	gag	aag	tgc	ttc	tgc	gag	ccc	gaa	gac	1872
Cys	Asn	Cys	Phe	Pro	Glu	Glu	Glu	Lys	Cys	Phe	Cys	Glu	Pro	Glu	Asp	
	610					615					620					
atc	cag	gat	cca	ctg	tgc	gac	gag	ctg	tgc	cgc	acg	gtg	atc	gca	gcc	1920
Ile	Gln	Asp	Pro	Leu	Cys	Asp	Glu	Leu	Cys	Arg	Thr	Val	Ile	Ala	Ala	
625					630					635					640	
gct	gtc	ctc	ttc	tcc	ttc	atc	gtc	tcg	gtg	ctg	ctg	tct	gcc	ttc	tgc	1968
Ala	Val	Leu	Phe	Ser	Phe	Ile	Val	Ser	Val	Leu	Leu	Ser	Ala	Phe	Cys	
				645					650					655		
atc	cac	tgc	tac	cac	aag	ttt	gcc	cac	aag	cca	ccc	atc	tcc	tca	gct	2016
Ile	His	Cys	Tyr	His	Lys	Phe	Ala	His	Lys	Pro	Pro	Ile	Ser	Ser	Ala	
			660					665					670			
gag	atg	acc	ttc	cgg	agg	ccc	gcc	cag	gcc	ttc	ccg	gtc	agc	tac	tcc	2064
Glu	Met	Thr	Phe	Arg	Arg	Pro	Ala	Gln	Ala	Phe	Pro	Val	Ser	Tyr	Ser	
		675					680					685				
tct	tcc	ggt	gcc	cgc	cgg	ccc	tcg	ctg	gac	tcc	atg	gag	aac	cag	gtc	2112
Ser	Ser	Gly	Ala	Arg	Arg	Pro	Ser	Leu	Asp	Ser	Met	Glu	Asn	Gln	Val	
	690					695					700					
tcc	gtg	gat	gcc	ttc	aag	atc	ctg	cag	cct	gag	gga	act	ggc	atg	ata	2160
Ser	Val	Asp	Ala	Phe	Lys	Ile	Leu	Gln	Pro	Glu	Gly	Thr	Gly	Met	Ile	
705					710					715					720	
gat	gaa	gag	ttc	act	gtt	gca	aga	ctc	tac	att	agc	aaa	atg	aag	tca	2208
Asp	Glu	Glu	Phe	Thr	Val	Ala	Arg	Leu	Tyr	Ile	Ser	Lys	Met	Lys	Ser	
				725					730					735		
gaa	gta	aaa	acc	atg	gtg	aaa	cgt	tgc	aag	cag	tta	gaa	agc	aca	caa	2256
Glu	Val	Lys	Thr	Met	Val	Lys	Arg	Cys	Lys	Gln	Leu	Glu	Ser	Thr	Gln	
			740					745					750			
act	gag	agc	aac	aaa	aaa	atg	gaa	gaa	aat	gaa	aag	gag	tta	gca	gca	2304
Thr	Glu	Ser	Asn	Lys	Lys	Met	Glu	Glu	Asn	Glu	Lys	Glu	Leu	Ala	Ala	
		755					760					765				

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tgt Cys	cag Gln 770	ctt Leu	cgt Arg	atc Ile	tct Ser	caa Gln 775	cat His	gaa Glu	gcc Ala	aaa Lys	atc Ile 780	aag Lys	tca Ser	ttg Leu	act Thr	2352
gaa Glu 785	tac Tyr	ctt Leu	caa Gln	aat Asn	gtg Val 790	gaa Glu	caa Gln	aag Lys	aaa Lys	aga Arg 795	cag Gln	ttg Leu	gag Glu	gaa Glu	tct Ser 800	2400
gtc Val	gat Asp	gcc Ala	ctc Leu	agt Ser 805	gaa Glu	gaa Glu	cta Leu	gtc Val	cag Gln 810	ctt Leu	cga Arg	gca Ala	caa Gln	gag Glu 815	aaa Lys	2448
gtc Val	cat His	gaa Glu	atg Met 820	gaa Glu	aag Lys	gag Glu	cac His	tta Leu 825	aat Asn	aag Lys	gtt Val	cag Gln	act Thr 830	gca Ala	aat Asn	2496
gaa Glu	gtt Val	aag Lys 835	caa Gln	gct Ala	gtt Val	gaa Glu	cag Gln 840	cag Gln	atc Ile	cag Gln	agc Ser	cat His 845	aga Arg	gaa Glu	act Thr	2544
cat His	caa Gln 850	aaa Lys	cag Gln	atc Ile	agt Ser	agt Ser 855	ttg Leu	aga Arg	gat Asp	gaa Glu	gta Val 860	gaa Glu	gca Ala	aaa Lys	gca Ala	2592
aaa Lys 865	ctt Leu	att Ile	act Thr	gat Asp	ctt Leu 870	caa Gln	gac Asp	caa Gln	aac Asn	cag Gln 875	aaa Lys	atg Met	atg Met	tta Leu	gag Glu 880	2640
cag Gln	gaa Glu	cgt Arg	cta Leu	aga Arg 885	gta Val	gaa Glu	cat His	gag Glu	aag Lys 890	ttg Leu	aaa Lys	gcc Ala	aca Thr	gat Asp 895	cag Gln	2688
gaa Glu	aag Lys	agc Ser	aga Arg 900	aaa Lys	cta Leu	cat His	gaa Glu	ctt Leu 905	acg Thr	gtt Val	atg Met	caa Gln	gat Asp 910	aga Arg	cga Arg	2736
gaa Glu	caa Gln 915	gca Ala	aga Arg	caa Gln	gac Asp	ttg Leu	aag Lys 920	ggt Gly	ttg Leu	gaa Glu	gag Glu	aca Thr 925	gtg Val	gca Ala	aaa Lys	2784
gaa Glu 930	ctt Leu	cag Gln	act Thr	tta Leu	cac His	aac Asn 935	ctg Leu	cgc Arg	aaa Lys	ctc Leu	ttt Phe 940	gtt Val	cag Gln	gac Asp	ctg Leu	2832
gct Ala 945	aca Thr	aga Arg	gtt Val	aaa Lys	aag Lys 950	agt Ser	gct Ala	gag Glu	att Ile	gat Asp 955	tct Ser	gat Asp	gac Asp	acc Thr	gga Gly 960	2880
ggc Gly	agc Ser	gct Ala	gct Ala	cag Gln 965	aag Lys	caa Gln	aaa Lys	atc Ile	tcc Ser 970	ttt Phe	ctt Leu	gaa Glu	aat Asn	aat Asn 975	ctt Leu	2928
gaa Glu	cag Gln	ctc Leu	act Thr 980	aaa Lys	gtg Val	cac His	aaa Lys	cag Gln 985	ttg Leu	gta Val	cgt Arg	gat Asp	aat Asn 990	gca Ala	gat Asp	2976
ctc Leu	cgc Arg	tgt Cys 995	gaa Glu	ctt Leu	cct Pro	aag Lys	ttg Leu	gaa Glu 1000	aag Lys	cga Arg	ctt Leu	cga Arg	gct Ala	aca Thr	gct Ala	3024
gag Glu 1010	aga Arg	gtg Val	aaa Lys	gct Ala	ttg Leu	gaa Glu 1015	tca Ser	gca Ala	ctg Leu	aaa Lys	gaa Glu 1020	gct Ala	aaa Lys	gaa Glu		3069

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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

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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

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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
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

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610		615		620
Ile 625	Gln	Asp	Pro	Leu 630
	Cys	Asp	Glu	Leu 635
	Arg	Thr	Val	Ile 640
	Ala			
Ala 645	Val	Leu	Phe	Ser 650
	Phe	Ile	Val	Ser 655
	Leu	Leu	Ser	Ala 660
	Phe			
Ile 665	His	Lys	Pro	Pro 670
	Ser			
	Ser			
	Ala			
Glu 675	Met	Thr	Phe	Arg 680
	Arg	Pro	Ala	Gln 685
	Phe	Pro	Val	Ser 690
	Tyr			
Ser 695	Ser	Gly	Ala	Arg 700
	Arg	Pro	Ser	Leu 705
	Asp	Ser	Met	Glu 710
	Asn	Gln	Val	
Ser 715	Val	Asp	Ala	Phe 720
	Lys	Ile	Leu	Gln 725
	Pro	Glu	Gly	Thr 730
	Gly	Met	Ile	
Asp 735	Glu	Glu	Phe	Thr 740
	Val	Ala	Arg	Leu 745
	Tyr	Ile	Ser	Lys 750
	Met	Lys	Ser	
Glu 755	Val	Lys	Thr	Met 760
	Val	Lys	Arg	Cys 765
	Met	Val	Lys	Arg 770
	Val	Lys	Arg	Cys 775
	Val	Lys	Arg	Cys 780
Glu 785	Tyr	Leu	Gln	Asn 790
	Val	Glu	Gln	Lys 795
	Lys	Lys	Arg	Gln 800
	Leu	Glu	Glu	Ser 805
Val 810	Asp	Ala	Leu	Ser 815
	Glu	Glu	Leu	Val 820
	Gln	Leu	Arg	Ala 825
	Gln	Leu	Arg	Ala 830
Val 835	His	Glu	Met	Glu 840
	Lys	Glu	Lys	Glu 845
	Val	Gln	Thr	Ala 850
	Ala	Val	Glu	Gln 855
	Gln	Ile	Gln	Ser 860
	Ser	His	Arg	Glu 865
His 870	Gln	Lys	Gln	Ile 875
	Ser	Ser	Leu	Arg 880
	Asp	Glu	Val	Glu 885
	Ala	Lys	Ala	

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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
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 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

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<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
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	Ile	Cys	Cys	Ser	Pro	Ser
	290					295					300				
Ser	Tyr	Asn	Glu	Ser	Glu	Thr	Lys	Ser	Thr	Leu	Leu	Phe	Gly	Gln	Arg
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		

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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

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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
 850 855 860
 Lys Asp Leu Glu Lys Met Met Val Lys Arg Arg Asp Tyr Leu Asp Leu
 865 870 875 880
 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

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Thr	Asn	Thr	Gly	Phe	Pro	Arg	Tyr	Pro	Asn	Asp	Ser	Val	Tyr	Ala	Asn
945					950					955					960

Trp	Met	Leu	Ser	Pro	Ser	Ala	Ala	Lys	Leu	Met	Asp	Thr	Phe	Asp	Ser
				965					970					975	