

SEQUENCE LISTING

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<120> Methods for Inhibiting Fibrosis in a Subject in Need Thereof

<130> MP.1.0250.PCT

<150> 62/275,025

<151> 2016-01-05

<150> 62/407,979

<151> 2016-10-13

<160> 85

<170> PatentIn version 3.5

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<213> Homo sapiens

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<221> CDS

<222> (27)..(584)

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Leu Cys Gly Ser Val Ala Thr Pro Leu Gly Pro Lys Trp Pro Glu Pro	
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Val Phe Gly Arg Leu Ala Ser Pro Gly Phe Pro Gly Glu Tyr Ala Asn	
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gac cag gag cgg cgc tgg acc ctg act gca ccc ccc ggc tac cgc ctg	197
Asp Gln Glu Arg Arg Trp Thr Leu Thr Ala Pro Pro Gly Tyr Arg Leu	
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cgc ctc tac ttc acc cac ttc gac ctg gag ctc tcc cac ctc tgc gag	245
Arg Leu Tyr Phe Thr His Phe Asp Leu Glu Leu Ser His Leu Cys Glu	
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tac gac ttc gtc aag ctg agc tcg ggg gcc aag gtg ctg gcc acg ctg	293
Tyr Asp Phe Val Lys Leu Ser Ser Gly Ala Lys Val Leu Ala Thr Leu	
75 80 85	
tgc ggg cag gag agc aca gac acg gag cgg gcc cct ggc aag gac act	341
Cys Gly Gln Glu Ser Thr Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr	
90 95 100 105	
ttc tac tcg ctg ggc tcc agc ctg gac att acc ttc cgc tcc gac tac	389
Phe Tyr Ser Leu Gly Ser Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr	
110 115 120	
tcc aac gag aag ccg ttc acg ggg ttc gag gcc ttc tat gca gcc gag	437
Ser Asn Glu Lys Pro Phe Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu	
125 130 135	
gac att gac gag tgc cag gtg gcc ccg gga gag gcg ccc acc tgc gac	485
Asp Ile Asp Glu Cys Gln Val Ala Pro Gly Glu Ala Pro Thr Cys Asp	
140 145 150	
cac cac tgc cac aac cac ctg ggc ggt ttc tac tgc tcc tgc cgc gca	533
His His Cys His Asn His Leu Gly Gly Phe Tyr Cys Ser Cys Arg Ala	
155 160 165	
ggc tac gtc ctg cac cgt aac aag cgc acc tgc tca gag cag agc ctc	581
Gly Tyr Val Leu His Arg Asn Lys Arg Thr Cys Ser Glu Gln Ser Leu	
170 175 180 185	
tag cctccccctgg agctccggcc tgcccagcag gtcagaagcc agagccagcc	634
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Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp Thr
35 40 45

Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
50 55 60

Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser
65 70 75 80

Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr Asp
85 90 95

Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser
100 105 110

Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
115 120 125

Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln Val
130 135 140

Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His Leu
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Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg Asn
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Lys Arg Thr Cys Ser Glu Gln Ser Leu
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Thr Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His
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Phe Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu
50 55 60

Ser Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr
65 70 75 80

Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser
85 90 95

Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe
100 105 110

Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln
115 120 125

Val Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His
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Asn Lys Arg Thr Cys Ser Glu Gln Ser Leu
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<222> (22)..(2082)

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tgt	ggc	tcg	gtg	gcc	acc	ccc	ttg	ggc	ccg	aag	tgg	cct	gaa	cct	gtg		99
Cys	Gly	Ser	Val	Ala	Thr	Pro	Leu	Gly	Pro	Lys	Trp	Pro	Glu	Pro	Val		
			15					20					25				

ttc	ggg	cgc	ctg	gca	tcc	ccc	ggc	ttt	cca	ggg	gag	tat	gcc	aat	gac		147
Phe	Gly	Arg	Leu	Ala	Ser	Pro	Gly	Phe	Pro	Gly	Glu	Tyr	Ala	Asn	Asp		
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cag	gag	cgg	cgc	tgg	acc	ctg	act	gca	ccc	ccc	ggc	tac	cgc	ctg	cgc		195
Gln	Glu	Arg	Arg	Trp	Thr	Leu	Thr	Ala	Pro	Pro	Gly	Tyr	Arg	Leu	Arg		
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ctc	tac	ttc	acc	cac	ttc	gac	ctg	gag	ctc	tcc	cac	ctc	tgc	gag	tac		243
Leu	Tyr	Phe	Thr	His	Phe	Asp	Leu	Glu	Leu	Ser	His	Leu	Cys	Glu	Tyr		
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gac	ttc	gtc	aag	ctg	agc	tcg	ggg	gcc	aag	gtg	ctg	gcc	acg	ctg	tgc		291
Asp	Phe	Val	Lys	Leu	Ser	Ser	Gly	Ala	Lys	Val	Leu	Ala	Thr	Leu	Cys		
75				80					85					90			

ggg	cag	gag	agc	aca	gac	acg	gag	cgg	gcc	cct	ggc	aag	gac	act	ttc		339
Gly	Gln	Glu	Ser	Thr	Asp	Thr	Glu	Arg	Ala	Pro	Gly	Lys	Asp	Thr	Phe		
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tac	tcg	ctg	ggc	tcc	agc	ctg	gac	att	acc	ttc	cgc	tcc	gac	tac	tcc		387
Tyr	Ser	Leu	Gly	Ser	Ser	Leu	Asp	Ile	Thr	Phe	Arg	Ser	Asp	Tyr	Ser		
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att	gac	gag	tgc	cag	gtg	gcc	ccg	gga	gag	gcg	ccc	acc	tgc	gac	cac		483
Ile	Asp	Glu	Cys	Gln	Val	Ala	Pro	Gly	Glu	Ala	Pro	Thr	Cys	Asp	His		
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cac	tgc	cac	aac	cac	ctg	ggc	ggt	ttc	tac	tgc	tcc	tgc	cgc	gca	ggc		531
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cag gtc ttc acc cag agg tct ggg gag ctc agc agc cct gaa tac cca Gln Val Phe Thr Gln Arg Ser Gly Glu Leu Ser Ser Pro Glu Tyr Pro 190 195 200	627
cgg ccg tat ccc aaa ctc tcc agt tgc act tac agc atc agc ctg gag Arg Pro Tyr Pro Lys Leu Ser Ser Cys Thr Tyr Ser Ile Ser Leu Glu 205 210 215	675
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cct tgc cct tat ccg atg gcg cca cct aat ggc cac gtt tca cct gtg Pro Cys Pro Tyr Pro Met Ala Pro Pro Asn Gly His Val Ser Pro Val 300 305 310	963
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tat act cat gat gct ggc ttt gac aat gac ata gca ctg att aaa ttg Tyr Thr His Asp Ala Gly Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu 525 530 535			1635
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tat gtc gac ata ccg att gtt gac cat caa aaa tgt act gct gca tat Tyr Val Asp Ile Pro Ile Val Asp His Gln Lys Cys Thr Ala Ala Tyr 590 595 600	1827
gaa aag cca ccc tat cca agg gga agt gta act gct aac atg ctt tgt Glu Lys Pro Pro Tyr Pro Arg Gly Ser Val Thr Ala Asn Met Leu Cys 605 610 615	1875
gct ggc tta gaa agt ggg ggc aag gac agc tgc aga ggt gac agc gga Ala Gly Leu Glu Ser Gly Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly 620 625 630	1923
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gga ata gtg tcc tgg ggt tcc atg aat tgt ggg gaa gca ggt cag tat Gly Ile Val Ser Trp Gly Ser Met Asn Cys Gly Glu Ala Gly Gln Tyr 655 660 665	2019
gga gtc tac aca aaa gtt att aac tat att ccc tgg atc gag aac ata Gly Val Tyr Thr Lys Val Ile Asn Tyr Ile Pro Trp Ile Glu Asn Ile 670 675 680	2067
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Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser
65 70 75 80

Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr Asp
85 90 95

Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser
100 105 110

Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
115 120 125

Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln Val
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Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His Leu
145 150 155 160

Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg Asn
165 170 175

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

Ser Ser Cys Thr Tyr Ser Ile Ser Leu Glu Glu Gly Phe Ser Val Ile
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Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Thr Leu
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Cys Pro Tyr Asp Phe Leu Lys Ile Gln Thr Asp Arg Glu Glu His Gly
245 250 255

Pro Phe Cys Gly Lys Thr Leu Pro His Arg Ile Glu Thr Lys Ser Asn
260 265 270

Thr Val Thr Ile Thr Phe Val Thr Asp Glu Ser Gly Asp His Thr Gly
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Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Tyr Pro Met
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Ala Pro Pro Asn Gly His Val Ser Pro Val Gln Ala Lys Tyr Ile Leu
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Lys Asp Ser Phe Ser Ile Phe Cys Glu Thr Gly Tyr Glu Leu Leu Gln
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Gly His Leu Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp Gly
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Ser Trp Asp Arg Pro Met Pro Ala Cys Ser Ile Val Asp Cys Gly Pro
355 360 365

Pro Asp Asp Leu Pro Ser Gly Arg Val Glu Tyr Ile Thr Gly Pro Gly
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Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr Phe
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Tyr Thr Met Lys Val Asn Asp Gly Lys Tyr Val Cys Glu Ala Asp Gly
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Phe Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Glu Pro
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Val Cys Gly Leu Ser Ala Arg Thr Thr Gly Gly Arg Ile Tyr Gly Gly
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Gln Lys Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Ile Leu Gly
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Gly Thr Thr Ala Ala Gly Ala Leu Leu Tyr Asp Asn Trp Val Leu Thr
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Ala Ala His Ala Val Tyr Glu Gln Lys His Asp Ala Ser Ala Leu Asp
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Ile Arg Met Gly Thr Leu Lys Arg Leu Ser Pro His Tyr Thr Gln Ala
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Trp Ser Glu Ala Val Phe Ile His Glu Gly Tyr Thr His Asp Ala Gly
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Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Asn Asn Lys Val Val Ile
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Asn Ser Asn Ile Thr Pro Ile Cys Leu Pro Arg Lys Glu Ala Glu Ser
545 550 555 560

Phe Met Arg Thr Asp Asp Ile Gly Thr Ala Ser Gly Trp Gly Leu Thr
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Gln Arg Gly Phe Leu Ala Arg Asn Leu Met Tyr Val Asp Ile Pro Ile
580 585 590

Val Asp His Gln Lys Cys Thr Ala Ala Tyr Glu Lys Pro Pro Tyr Pro
595 600 605

Arg Gly Ser Val Thr Ala Asn Met Leu Cys Ala Gly Leu Glu Ser Gly
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Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe Leu
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Asp Ser Glu Thr Glu Arg Trp Phe Val Gly Gly Ile Val Ser Trp Gly
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Phe Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu
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Ser Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr
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Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser
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Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe
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Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln
115 120 125

Val Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His
130 135 140

Leu Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg
145 150 155 160

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

Arg Ser Gly Glu Leu Ser Ser Pro Glu Tyr Pro Arg Pro Tyr Pro Lys
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Leu Ser Ser Cys Thr Tyr Ser Ile Ser Leu Glu Glu Gly Phe Ser Val
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Ile Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Thr
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Leu Cys Pro Tyr Asp Phe Leu Lys Ile Gln Thr Asp Arg Glu Glu His
225 230 235 240

Gly Pro Phe Cys Gly Lys Thr Leu Pro His Arg Ile Glu Thr Lys Ser
245 250 255

Asn Thr Val Thr Ile Thr Phe Val Thr Asp Glu Ser Gly Asp His Thr
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Gly Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Tyr Pro

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280

285

Met Ala Pro Pro Asn Gly His Val Ser Pro Val Gln Ala Lys Tyr Ile
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Leu Lys Asp Ser Phe Ser Ile Phe Cys Glu Thr Gly Tyr Glu Leu Leu
 305 310 315 320

Gln Gly His Leu Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp
 325 330 335

Gly Ser Trp Asp Arg Pro Met Pro Ala Cys Ser Ile Val Asp Cys Gly
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Pro Pro Asp Asp Leu Pro Ser Gly Arg Val Glu Tyr Ile Thr Gly Pro
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Gly Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr
 370 375 380

Phe Tyr Thr Met Lys Val Asn Asp Gly Lys Tyr Val Cys Glu Ala Asp
 385 390 395 400

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

Pro Val Cys Gly Leu Ser Ala Arg Thr Thr Gly Gly Arg Ile Tyr Gly
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Gly Gln Lys Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Ile Leu
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Gly Gly Thr Thr Ala Ala Gly Ala Leu Leu Tyr Asp Asn Trp Val Leu
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Thr Ala Ala His Ala Val Tyr Glu Gln Lys His Asp Ala Ser Ala Leu
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Asp Ile Arg Met Gly Thr Leu Lys Arg Leu Ser Pro His Tyr Thr Gln
485 490 495

Ala Trp Ser Glu Ala Val Phe Ile His Glu Gly Tyr Thr His Asp Ala
500 505 510

Gly Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Asn Asn Lys Val Val
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Ile Asn Ser Asn Ile Thr Pro Ile Cys Leu Pro Arg Lys Glu Ala Glu
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Ser Phe Met Arg Thr Asp Asp Ile Gly Thr Ala Ser Gly Trp Gly Leu
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Thr Gln Arg Gly Phe Leu Ala Arg Asn Leu Met Tyr Val Asp Ile Pro
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Pro Arg Gly Ser Val Thr Ala Asn Met Leu Cys Ala Gly Leu Glu Ser
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Leu Asp Ser Glu Thr Glu Arg Trp Phe Val Gly Gly Ile Val Ser Trp
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ccaccattc ttctacctac ccacccatc catccatcct tctatcagca tccttctacc	4860
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<210> 8
 <211> 136
 <212> PRT
 <213> Homo sapiens

<400> 8

Met	Arg	Leu	Leu	Thr	Leu	Leu	Gly	Leu	Leu	Cys	Gly	Ser	Val	Ala	Thr
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Pro	Leu	Gly	Pro	Lys	Trp	Pro	Glu	Pro	Val	Phe	Gly	Arg	Leu	Ala	Ser
			20					25					30		

Pro	Gly	Phe	Pro	Gly	Glu	Tyr	Ala	Asn	Asp	Gln	Glu	Arg	Arg	Trp	Thr
		35					40					45			

Leu	Thr	Ala	Pro	Pro	Gly	Tyr	Arg	Leu	Arg	Leu	Tyr	Phe	Thr	His	Phe
	50					55					60				

Asp	Leu	Glu	Leu	Ser	His	Leu	Cys	Glu	Tyr	Asp	Phe	Val	Lys	Leu	Ser
65					70					75				80	

Ser	Gly	Ala	Lys	Val	Leu	Ala	Thr	Leu	Cys	Gly	Gln	Glu	Ser	Thr	Asp
				85					90					95	

Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser
100 105 110

Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
115 120 125

Gly Phe Glu Ala Phe Tyr Ala Ala
130 135

<210> 9

<211> 181

<212> PRT

<213> Homo sapiens

<400> 9

Met Arg Leu Leu Thr Leu Leu Gly Leu Leu Cys Gly Ser Val Ala Thr
1 5 10 15

Pro Leu Gly Pro Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Ala Ser
20 25 30

Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp Thr
35 40 45

Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
50 55 60

Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser
65 70 75 80

Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr Asp
85 90 95

Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser
100 105 110

Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
115 120 125

Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln Val
130 135 140

Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His Leu
145 150 155 160

Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg Asn
165 170 175

Lys Arg Thr Cys Ser
180

<210> 10
<211> 293
<212> PRT
<213> Homo sapiens

<400> 10

Met Arg Leu Leu Thr Leu Leu Gly Leu Leu Cys Gly Ser Val Ala Thr
1 5 10 15

Pro Leu Gly Pro Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Ala Ser
20 25 30

Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp Thr
35 40 45

Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
50 55 60

Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser
65 70 75 80

Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr Asp
85 90 95

Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser

100

105

110

Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
 115 120 125

Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln Val
 130 135 140

Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His Leu
 145 150 155 160

Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg Asn
 165 170 175

Lys Arg Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gln Arg
 180 185 190

Ser Gly Glu Leu Ser Ser Pro Glu Tyr Pro Arg Pro Tyr Pro Lys Leu
 195 200 205

Ser Ser Cys Thr Tyr Ser Ile Ser Leu Glu Glu Gly Phe Ser Val Ile
 210 215 220

Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Thr Leu
 225 230 235 240

Cys Pro Tyr Asp Phe Leu Lys Ile Gln Thr Asp Arg Glu Glu His Gly
 245 250 255

Pro Phe Cys Gly Lys Thr Leu Pro His Arg Ile Glu Thr Lys Ser Asn
 260 265 270

Thr Val Thr Ile Thr Phe Val Thr Asp Glu Ser Gly Asp His Thr Gly
 275 280 285

Trp Lys Ile His Tyr
 290

<210> 11
<211> 41
<212> PRT
<213> Homo sapiens

<400> 11

Glu Asp Ile Asp Glu Cys Gln Val Ala Pro Gly Glu Ala Pro Thr Cys
1 5 10 15

Asp His His Cys His Asn His Leu Gly Gly Phe Tyr Cys Ser Cys Arg
20 25 30

Ala Gly Tyr Val Leu His Arg Asn Lys
35 40

<210> 12
<211> 242
<212> PRT
<213> Homo sapiens

<400> 12

Ile Tyr Gly Gly Gln Lys Ala Lys Pro Gly Asp Phe Pro Trp Gln Val
1 5 10 15

Leu Ile Leu Gly Gly Thr Thr Ala Ala Gly Ala Leu Leu Tyr Asp Asn
20 25 30

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

Ser Ala Leu Asp Ile Arg Met Gly Thr Leu Lys Arg Leu Ser Pro His
50 55 60

Tyr Thr Gln Ala Trp Ser Glu Ala Val Phe Ile His Glu Gly Tyr Thr
65 70 75 80

His Asp Ala Gly Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Asn Asn
85 90 95

Lys Val Val Ile Asn Ser Asn Ile Thr Pro Ile Cys Leu Pro Arg Lys
100 105 110

Glu Ala Glu Ser Phe Met Arg Thr Asp Asp Ile Gly Thr Ala Ser Gly
115 120 125

Trp Gly Leu Thr Gln Arg Gly Phe Leu Ala Arg Asn Leu Met Tyr Val
130 135 140

Asp Ile Pro Ile Val Asp His Gln Lys Cys Thr Ala Ala Tyr Glu Lys
145 150 155 160

Pro Pro Tyr Pro Arg Gly Ser Val Thr Ala Asn Met Leu Cys Ala Gly
165 170 175

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

Leu Val Phe Leu Asp Ser Glu Thr Glu Arg Trp Phe Val Gly Gly Ile
195 200 205

Val Ser Trp Gly Ser Met Asn Cys Gly Glu Ala Gly Gln Tyr Gly Val
210 215 220

Tyr Thr Lys Val Ile Asn Tyr Ile Pro Trp Ile Glu Asn Ile Ile Ser
225 230 235 240

Asp Phe

<210> 13
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 13

Gly Lys Asp Ser Cys Arg Gly Asp Ala Gly Gly Ala Leu Val Phe Leu
1 5 10 15

<210> 14
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 14

Thr Pro Leu Gly Pro Lys Trp Pro Glu Pro Val Phe Gly Arg Leu
1 5 10 15

<210> 15
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 15

Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe Asp
1 5 10 15

Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser Ser
20 25 30

Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln
35 40

<210> 16
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 16

Thr Phe Arg Ser Asp Tyr Ser Asn
1 5

<210> 17
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 17

Phe Tyr Ser Leu Gly Ser Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr
1 5 10 15

Ser Asn Glu Lys Pro Phe Thr Gly Phe
20 25

<210> 18
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 18

Ile Asp Glu Cys Gln Val Ala Pro Gly
1 5

<210> 19
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 19

Ala Asn Met Leu Cys Ala Gly Leu Glu Ser Gly Gly Lys Asp Ser Cys
1 5 10 15

Arg Gly Asp Ser Gly Gly Ala Leu Val
 20 25

<210> 20
 <211> 960
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (51)..(797)

<400> 20
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 Met Ser
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ctg ttt cca tca ctc cct ctc ctt ctc ctg agt atg gtg gca gcg tct 104
 Leu Phe Pro Ser Leu Pro Leu Leu Leu Ser Met Val Ala Ala Ser
 5 10 15

tac tca gaa act gtg acc tgt gag gat gcc caa aag acc tgc cct gca 152
 Tyr Ser Glu Thr Val Thr Cys Glu Asp Ala Gln Lys Thr Cys Pro Ala
 20 25 30

gtg att gcc tgt agc tct cca ggc atc aac ggc ttc cca ggc aaa gat 200
 Val Ile Ala Cys Ser Ser Pro Gly Ile Asn Gly Phe Pro Gly Lys Asp
 35 40 45 50

ggg cgt gat ggc acc aag gga gaa aag ggg gaa cca ggc caa ggg ctc 248
 Gly Arg Asp Gly Thr Lys Gly Glu Lys Gly Glu Pro Gly Gln Gly Leu
 55 60 65

aga ggc tta cag ggc ccc cct gga aag ttg ggg cct cca gga aat cca 296
 Arg Gly Leu Gln Gly Pro Pro Gly Lys Leu Gly Pro Pro Gly Asn Pro
 70 75 80

ggg cct tct ggg tca cca gga cca aag ggc caa aaa gga gac cct gga 344
 Gly Pro Ser Gly Ser Pro Gly Pro Lys Gly Gln Lys Gly Asp Pro Gly
 85 90 95

aaa agt ccg gat ggt gat agt agc ctg gct gcc tca gaa aga aaa gct 392
 Lys Ser Pro Asp Gly Asp Ser Ser Leu Ala Ala Ser Glu Arg Lys Ala
 100 105 110

ctg caa aca gaa atg gca cgt atc aaa aag tgg ctc acc ttc tct ctg 440
 Leu Gln Thr Glu Met Ala Arg Ile Lys Lys Trp Leu Thr Phe Ser Leu

115	120	125	130	
ggc aaa caa gtt	ggg aac aag ttc ttc	ctg acc aat ggt gaa ata atg		488
Gly Lys Gln Val	Gly Asn Lys Phe Phe	Leu Thr Asn Gly Glu Ile Met		
	135	140	145	
acc ttt gaa aaa gtg aag gcc ttg tgt gtc aag ttc cag gcc tct gtg				536
Thr Phe Glu Lys Val Lys Ala Leu Cys Val Lys Phe Gln Ala Ser Val				
	150	155	160	
gcc acc ccc agg aat gct gca gag aat gga gcc att cag aat ctc atc				584
Ala Thr Pro Arg Asn Ala Ala Glu Asn Gly Ala Ile Gln Asn Leu Ile				
	165	170	175	
aag gag gaa gcc ttc ctg ggc atc act gat gag aag aca gaa ggg cag				632
Lys Glu Glu Ala Phe Leu Gly Ile Thr Asp Glu Lys Thr Glu Gly Gln				
	180	185	190	
ttt gtg gat ctg aca gga aat aga ctg acc tac aca aac tgg aac gag				680
Phe Val Asp Leu Thr Gly Asn Arg Leu Thr Tyr Thr Asn Trp Asn Glu				
	195	200	205	210
ggg gaa ccc aac aat gct ggt tct gat gaa gat tgt gta ttg cta ctg				728
Gly Glu Pro Asn Asn Ala Gly Ser Asp Glu Asp Cys Val Leu Leu Leu				
	215	220	225	
aaa aat ggc cag tgg aat gac gtc ccc tgc tcc acc tcc cat ctg gcc				776
Lys Asn Gly Gln Trp Asn Asp Val Pro Cys Ser Thr Ser His Leu Ala				
	230	235	240	
gtc tgt gag ttc cct atc tga agggatcatat cactcaggcc ctccttgtct				827
Val Cys Glu Phe Pro Ile				
	245			
ttttactgca acccacaggc ccacagtatg cttgaaaaga taaattatat caatttcctc				887
atatccagta ttgttccttt tgtgggcaat cactaaaaat gatcactaac agcaccaaca				947
aagcaataat agt				960

<210> 21
 <211> 248
 <212> PRT
 <213> Homo sapiens

<400> 21

Met Ser Leu Phe Pro Ser Leu Pro Leu Leu Leu Ser Met Val Ala
1 5 10 15

Ala Ser Tyr Ser Glu Thr Val Thr Cys Glu Asp Ala Gln Lys Thr Cys
20 25 30

Pro Ala Val Ile Ala Cys Ser Ser Pro Gly Ile Asn Gly Phe Pro Gly
35 40 45

Lys Asp Gly Arg Asp Gly Thr Lys Gly Glu Lys Gly Glu Pro Gly Gln
50 55 60

Gly Leu Arg Gly Leu Gln Gly Pro Pro Gly Lys Leu Gly Pro Pro Gly
65 70 75 80

Asn Pro Gly Pro Ser Gly Ser Pro Gly Pro Lys Gly Gln Lys Gly Asp
85 90 95

Pro Gly Lys Ser Pro Asp Gly Asp Ser Ser Leu Ala Ala Ser Glu Arg
100 105 110

Lys Ala Leu Gln Thr Glu Met Ala Arg Ile Lys Lys Trp Leu Thr Phe
115 120 125

Ser Leu Gly Lys Gln Val Gly Asn Lys Phe Phe Leu Thr Asn Gly Glu
130 135 140

Ile Met Thr Phe Glu Lys Val Lys Ala Leu Cys Val Lys Phe Gln Ala
145 150 155 160

Ser Val Ala Thr Pro Arg Asn Ala Ala Glu Asn Gly Ala Ile Gln Asn
165 170 175

Leu Ile Lys Glu Glu Ala Phe Leu Gly Ile Thr Asp Glu Lys Thr Glu
180 185 190

Gly Gln Phe Val Asp Leu Thr Gly Asn Arg Leu Thr Tyr Thr Asn Trp
195 200 205

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

Leu Leu Lys Asn Gly Gln Trp Asn Asp Val Pro Cys Ser Thr Ser His
225 230 235 240

Leu Ala Val Cys Glu Phe Pro Ile
245

<210> 22
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Wherein X at position 1 represents hydroxyproline

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Wherein X at position 4 represents hydrophobic residue

<400> 22

Xaa Gly Lys Xaa Gly Pro
1 5

<210> 23
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Wherein X represents hydroxyproline

<400> 23

Xaa Gly Lys Leu Gly
1 5

<210> 24

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> MISC_FEATURE

<222> (9)..(15)

<223> Wherein X at positions 9 and 15 represents hydroxyproline

<400> 24

Gly Leu Arg Gly Leu Gln Gly Pro Xaa Gly Lys Leu Gly Pro Xaa Gly
1 5 10 15

<210> 25

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> MISC_FEATURE

<222> (3)..(27)

<223> Wherein X at positions 3, 6, 15, 21, 24, 27 represents
hydroxyproline

<400> 25

Gly Pro Xaa Gly Pro Xaa Gly Leu Arg Gly Leu Gln Gly Pro Xaa Gly
1 5 10 15

Lys Leu Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa
20 25

<210> 26
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<222> (26)..(26)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (32)..(32)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (35)..(35)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (41)..(41)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (50)..(50)
<223> Xaa can be any naturally occurring amino acid

<400> 26

Gly Lys Asp Gly Arg Asp Gly Thr Lys Gly Glu Lys Gly Glu Pro Gly
1 5 10 15

Gln Gly Leu Arg Gly Leu Gln Gly Pro Xaa Gly Lys Leu Gly Pro Xaa
20 25 30

Gly Asn Xaa Gly Pro Ser Gly Ser Xaa Gly Pro Lys Gly Gln Lys Gly
35 40 45

Asp Xaa Gly Lys Ser
50

<210> 27
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (3)..(33)
<223> Wherein X at positions 3, 6, 12, 18, 21, 30, 33 represents
hydroxyproline

<400> 27

Gly	Ala	Xaa	Gly	Ser	Xaa	Gly	Glu	Lys	Gly	Ala	Xaa	Gly	Pro	Gln	Gly
1				5					10					15	

Pro	Xaa	Gly	Pro	Xaa	Gly	Lys	Met	Gly	Pro	Lys	Gly	Glu	Xaa	Gly	Asp
			20					25					30		

Xaa

<210> 28
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (3)..(45)
<223> Wherein X at positions 3, 6, 9, 27, 30, 36, 42, 45 represents
hydroxyproline

<400> 28

Gly Cys Xaa Gly Leu Xaa Gly Ala Xaa Gly Asp Lys Gly Glu Ala Gly
1 5 10 15

Thr Asn Gly Lys Arg Gly Glu Arg Gly Pro Xaa Gly Pro Xaa Gly Lys
20 25 30

Ala Gly Pro Xaa Gly Pro Asn Gly Ala Xaa Gly Glu Xaa
35 40 45

<210> 29
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 29

Leu Gln Arg Ala Leu Glu Ile Leu Pro Asn Arg Val Thr Ile Lys Ala
1 5 10 15

Asn Arg Pro Phe Leu Val Phe Ile
20

<210> 30
<211> 559
<212> DNA
<213> Homo sapiens

<400> 30
atgaggctgc tgaccctcct gggccttctg tgtggctcgg tggccacccc cttgggcccg 60
aagtggcctg aacctgtgtt cgggcgcctg gcatcccccg gctttccagg ggagtatgcc 120
aatgaccagg agcggcgctg gaccctgact gcaccccccg gctaccgcct gcgcctctac 180
ttcaccact tcgacctgga gctctccac ctctgcgagt acgacttcgt caagctgagc 240
tcgggggcca aggtgctggc cacgctgtgc gggcaggaga gcacagacac ggagcgggcc 300
cctggcaagg acactttcta ctcgtgggc tccagcctgg acattacctt ccgctccgac 360
tactccaacg agaagccgtt cacgggggtt gaggccttct atgcagccga ggacattgac 420

gagtgccagg tggccccggg agaggcgccc acctgcgacc accactgcca caaccacctg 480
ggcggtttct actgctcctg ccgcgcaggc tacgtcctgc accgtaacaa gcgcacctgc 540
tcagccctgt gctccggcc 559

<210> 31
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 31
cgggcacacc atgaggctgc tgaccctcct gggc 34

<210> 32
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 32
gacattacct tccgctccga ctccaacgag aag 33

<210> 33
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Gly Leu Leu Trp Ser Leu Val Ala Thr Leu Leu Gly Ser Lys Trp Pro
10 15 20

gaa cct gta ttc ggg cgc ctg gtg tcc cct ggc ttc cca gag aag tat 149
Glu Pro Val Phe Gly Arg Leu Val Ser Pro Gly Phe Pro Glu Lys Tyr
25 30 35

gct gac cat caa gat cga tcc tgg aca ctg act gca ccc cct ggc tac 197
Ala Asp His Gln Asp Arg Ser Trp Thr Leu Thr Ala Pro Pro Gly Tyr
40 45 50 55

cgc ctg cgc ctc tac ttc acc cac ttt gac ctg gaa ctc tct tac cgc 245
Arg Leu Arg Leu Tyr Phe Thr His Phe Asp Leu Glu Leu Ser Tyr Arg
60 65 70

tgc gag tat gac ttt gtc aag ttg agc tca ggg acc aag gtg ctg gcc 293
Cys Glu Tyr Asp Phe Val Lys Leu Ser Ser Gly Thr Lys Val Leu Ala
75 80 85

aca ctg tgt ggg cag gag agt aca gac act gag cag gca cct ggc aat 341
Thr Leu Cys Gly Gln Glu Ser Thr Asp Thr Glu Gln Ala Pro Gly Asn
90 95 100

gac acc ttc tac tca ctg ggt ccc agc cta aag gtc acc ttc cac tcc 389
Asp Thr Phe Tyr Ser Leu Gly Pro Ser Leu Lys Val Thr Phe His Ser
105 110 115

gac tac tcc aat gag aag ccg ttc aca ggg ttt gag gcc ttc tat gca 437
Asp Tyr Ser Asn Glu Lys Pro Phe Thr Gly Phe Glu Ala Phe Tyr Ala
120 125 130 135

gcg gag gat gtg gat gaa tgc aga gtg tct ctg gga gac tca gtc cct 485
Ala Glu Asp Val Asp Glu Cys Arg Val Ser Leu Gly Asp Ser Val Pro
140 145 150

tgt gac cat tat tgc cac aac tac ttg ggc ggc tac tat tgc tcc tgc 533

Cys	Asp	His	Tyr	Cys	His	Asn	Tyr	Leu	Gly	Gly	Tyr	Tyr	Cys	Ser	Cys		
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aga	gcg	ggc	tac	att	ctc	cac	cag	aac	aag	cac	acg	tgc	tca	gcc	ctt		581
Arg	Ala	Gly	Tyr	Ile	Leu	His	Gln	Asn	Lys	His	Thr	Cys	Ser	Ala	Leu		
		170					175					180					
tgt	tca	ggc	cag	gtg	ttc	aca	gga	aga	tct	ggg	tat	ctc	agt	agc	cct		629
Cys	Ser	Gly	Gln	Val	Phe	Thr	Gly	Arg	Ser	Gly	Tyr	Leu	Ser	Ser	Pro		
	185					190					195						
gag	tac	ccg	cag	cca	tac	ccc	aag	ctc	tcc	agc	tgc	acc	tac	agc	atc		677
Glu	Tyr	Pro	Gln	Pro	Tyr	Pro	Lys	Leu	Ser	Ser	Cys	Thr	Tyr	Ser	Ile		
200					205					210					215		
cgc	ctg	gag	gac	ggc	ttc	agt	gtc	atc	ctg	gac	ttc	gtg	gag	tcc	ttc		725
Arg	Leu	Glu	Asp	Gly	Phe	Ser	Val	Ile	Leu	Asp	Phe	Val	Glu	Ser	Phe		
			220						225					230			
gat	gtg	gag	acg	cac	cct	gaa	gcc	cag	tgc	ccc	tat	gac	tcc	ctc	aag		773
Asp	Val	Glu	Thr	His	Pro	Glu	Ala	Gln	Cys	Pro	Tyr	Asp	Ser	Leu	Lys		
			235					240					245				
att	caa	aca	gac	aag	ggg	gaa	cac	ggc	cca	ttt	tgt	ggg	aag	acg	ctg		821
Ile	Gln	Thr	Asp	Lys	Gly	Glu	His	Gly	Pro	Phe	Cys	Gly	Lys	Thr	Leu		
		250					255					260					
cct	ccc	agg	att	gaa	act	gac	agc	cac	aag	gtg	acc	atc	acc	ttt	gcc		869
Pro	Pro	Arg	Ile	Glu	Thr	Asp	Ser	His	Lys	Val	Thr	Ile	Thr	Phe	Ala		
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act	gac	gag	tcg	ggg	aac	cac	aca	ggc	tgg	aag	ata	cac	tac	aca	agc		917
Thr	Asp	Glu	Ser	Gly	Asn	His	Thr	Gly	Trp	Lys	Ile	His	Tyr	Thr	Ser		
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aca	gca	cgg	ccc	tgc	cct	gat	cca	acg	gcg	cca	cct	aat	ggc	agc	att		965
Thr	Ala	Arg	Pro	Cys	Pro	Asp	Pro	Thr	Ala	Pro	Pro	Asn	Gly	Ser	Ile		
			300					305					310				
tca	cct	gtg	caa	gcc	acg	tat	gtc	ctg	aag	gac	agg	ttt	tct	gtc	ttc		1013
Ser	Pro	Val	Gln	Ala	Thr	Tyr	Val	Leu	Lys	Asp	Arg	Phe	Ser	Val	Phe		
		315					320					325					
tgc	aag	aca	ggc	ttc	gag	ctt	ctg	caa	ggg	tct	gtc	ccc	ctg	aaa	tca		1061
Cys	Lys	Thr	Gly	Phe	Glu	Leu	Leu	Gln	Gly	Ser	Val	Pro	Leu	Lys	Ser		
	330					335						340					
ttc	act	gct	gtc	tgt	cag	aaa	gat	gga	tct	tgg	gac	cgg	ccg	atg	cca		1109
Phe	Thr	Ala	Val	Cys	Gln	Lys	Asp	Gly	Ser	Trp	Asp	Arg	Pro	Met	Pro		
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Glu Cys Ser Ile Ile Asp Cys Gly Pro Pro Asp Asp Leu Pro Asn Gly	
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His Val Asp Tyr Ile Thr Gly Pro Gln Val Thr Thr Tyr Lys Ala Val	
380 385 390	
att cag tac agc tgt gaa gag act ttc tac aca atg agc agc aat ggt	1253
Ile Gln Tyr Ser Cys Glu Glu Thr Phe Tyr Thr Met Ser Ser Asn Gly	
395 400 405	
aaa tat gtg tgt gag gct gat gga ttc tgg acg agc tcc aaa gga gaa	1301
Lys Tyr Val Cys Glu Ala Asp Gly Phe Trp Thr Ser Ser Lys Gly Glu	
410 415 420	
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Ile Gly Gly Arg Ile Val Gly Gly Gln Pro Ala Lys Pro Gly Asp Phe	
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Pro Trp Gln Val Leu Leu Leu Gly Gln Thr Thr Ala Ala Ala Gly Ala	
460 465 470	
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Leu Ile His Asp Asn Trp Val Leu Thr Ala Ala His Ala Val Tyr Glu	
475 480 485	
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Lys Arg Met Ala Ala Ser Ser Leu Asn Ile Arg Met Gly Ile Leu Lys	
490 495 500	
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Arg Leu Ser Pro His Tyr Thr Gln Ala Trp Pro Glu Glu Ile Phe Ile	
505 510 515	
cat gaa ggc tac act cac ggt gct ggt ttt gac aat gat ata gca ttg	1637
His Glu Gly Tyr Thr His Gly Ala Gly Phe Asp Asn Asp Ile Ala Leu	
520 525 530 535	
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Ile Lys Leu Lys Asn Lys Val Thr Ile Asn Gly Ser Ile Met Pro Val	
540 545 550	
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Asn	Leu	Met	Phe	Val	Asp	Ile	Pro	Ile	Ala	Asp	His	Gln	Lys	Cys	Thr		
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Ser	Gly	Gly	Ala	Leu	Val	Phe	Leu	Asp	Asn	Glu	Thr	Gln	Arg	Trp	Phe		
			635					640					645				
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Gln	Tyr	Gly	Val	Tyr	Thr	Lys	Val	Ile	Asn	Tyr	Ile	Pro	Trp	Asn	Glu		
	665					670					675						
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680					685												

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Pro Gly Phe Pro Glu Lys Tyr Ala Asp His Gln Asp Arg Ser Trp Thr
35 40 45

Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
50 55 60

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

Ser Gly Thr Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr Asp
85 90 95

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

Leu Lys Val Thr Phe His Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
115 120 125

Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Val Asp Glu Cys Arg Val
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Ser Leu Gly Asp Ser Val Pro Cys Asp His Tyr Cys His Asn Tyr Leu
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Gly Gly Tyr Tyr Cys Ser Cys Arg Ala Gly Tyr Ile Leu His Gln Asn
165 170 175

Lys His Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gly Arg
180 185 190

Ser Gly Tyr Leu Ser Ser Pro Glu Tyr Pro Gln Pro Tyr Pro Lys Leu
195 200 205

Ser Ser Cys Thr Tyr Ser Ile Arg Leu Glu Asp Gly Phe Ser Val Ile
210 215 220

Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Ala Gln

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

Cys Gly Leu Ser Thr His Thr Ile Gly Gly Arg Ile Val Gly Gly Gln
435 440 445

Pro Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Leu Leu Gly Gln
450 455 460

Thr Thr Ala Ala Ala Gly Ala Leu Ile His Asp Asn Trp Val Leu Thr
465 470 475 480

Ala Ala His Ala Val Tyr Glu Lys Arg Met Ala Ala Ser Ser Leu Asn
485 490 495

Ile Arg Met Gly Ile Leu Lys Arg Leu Ser Pro His Tyr Thr Gln Ala
500 505 510

Trp Pro Glu Glu Ile Phe Ile His Glu Gly Tyr Thr His Gly Ala Gly
515 520 525

Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Lys Asn Lys Val Thr Ile
530 535 540

Asn Gly Ser Ile Met Pro Val Cys Leu Pro Arg Lys Glu Ala Ala Ser
545 550 555 560

Leu Met Arg Thr Asp Phe Thr Gly Thr Val Ala Gly Trp Gly Leu Thr
565 570 575

Gln Lys Gly Leu Leu Ala Arg Asn Leu Met Phe Val Asp Ile Pro Ile
580 585 590

Ala Asp His Gln Lys Cys Thr Thr Val Tyr Glu Lys Leu Tyr Pro Gly
595 600 605

Val Arg Val Ser Ala Asn Met Leu Cys Ala Gly Leu Glu Thr Gly Gly
610 615 620

Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe Leu Asp

625 630 635 640

Asn Glu Thr Gln Arg Trp Phe Val Gly Gly Ile Val Ser Trp Gly Ser
 645 650 655

Ile Asn Cys Gly Ala Ala Gly Gln Tyr Gly Val Tyr Thr Lys Val Ile
 660 665 670

Asn Tyr Ile Pro Trp Asn Glu Asn Ile Ile Ser Asn Phe
 675 680 685

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<211> 670
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<400> 52

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Ser Pro Gly Phe Pro Glu Lys Tyr Ala Asp His Gln Asp Arg Ser Trp
 20 25 30

Thr Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His
 35 40 45

Phe Asp Leu Glu Leu Ser Tyr Arg Cys Glu Tyr Asp Phe Val Lys Leu
 50 55 60

Ser Ser Gly Thr Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr
65 70 75 80

Asp Thr Glu Gln Ala Pro Gly Asn Asp Thr Phe Tyr Ser Leu Gly Pro
 85 90 95

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

Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Val Asp Glu Cys Arg
115 120 125

Val Ser Leu Gly Asp Ser Val Pro Cys Asp His Tyr Cys His Asn Tyr
130 135 140

Leu Gly Gly Tyr Tyr Cys Ser Cys Arg Ala Gly Tyr Ile Leu His Gln
145 150 155 160

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

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

Leu Ser Ser Cys Thr Tyr Ser Ile Arg Leu Glu Asp Gly Phe Ser Val
195 200 205

Ile Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Ala
210 215 220

Gln Cys Pro Tyr Asp Ser Leu Lys Ile Gln Thr Asp Lys Gly Glu His
225 230 235 240

Gly Pro Phe Cys Gly Lys Thr Leu Pro Pro Arg Ile Glu Thr Asp Ser
245 250 255

His Lys Val Thr Ile Thr Phe Ala Thr Asp Glu Ser Gly Asn His Thr
260 265 270

Gly Trp Lys Ile His Tyr Thr Ser Thr Ala Arg Pro Cys Pro Asp Pro
275 280 285

Thr Ala Pro Pro Asn Gly Ser Ile Ser Pro Val Gln Ala Thr Tyr Val
290 295 300

Leu Lys Asp Arg Phe Ser Val Phe Cys Lys Thr Gly Phe Glu Leu Leu
305 310 315 320

Gln Gly Ser Val Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp
325 330 335

Gly Ser Trp Asp Arg Pro Met Pro Glu Cys Ser Ile Ile Asp Cys Gly
340 345 350

Pro Pro Asp Asp Leu Pro Asn Gly His Val Asp Tyr Ile Thr Gly Pro
355 360 365

Gln Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr
370 375 380

Phe Tyr Thr Met Ser Ser Asn Gly Lys Tyr Val Cys Glu Ala Asp Gly
385 390 395 400

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

Val Cys Gly Leu Ser Thr His Thr Ile Gly Gly Arg Ile Val Gly Gly
420 425 430

Gln Pro Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Leu Leu Gly
435 440 445

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

Thr Ala Ala His Ala Val Tyr Glu Lys Arg Met Ala Ala Ser Ser Leu
465 470 475 480

Asn Ile Arg Met Gly Ile Leu Lys Arg Leu Ser Pro His Tyr Thr Gln
485 490 495

Ala Trp Pro Glu Glu Ile Phe Ile His Glu Gly Tyr Thr His Gly Ala
500 505 510

Gly Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Lys Asn Lys Val Thr
515 520 525

Ile Asn Gly Ser Ile Met Pro Val Cys Leu Pro Arg Lys Glu Ala Ala
530 535 540

Ser Leu Met Arg Thr Asp Phe Thr Gly Thr Val Ala Gly Trp Gly Leu
545 550 555 560

Thr Gln Lys Gly Leu Leu Ala Arg Asn Leu Met Phe Val Asp Ile Pro
565 570 575

Ile Ala Asp His Gln Lys Cys Thr Thr Val Tyr Glu Lys Leu Tyr Pro
580 585 590

Gly Val Arg Val Ser Ala Asn Met Leu Cys Ala Gly Leu Glu Thr Gly
595 600 605

Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe Leu
610 615 620

Asp Asn Glu Thr Gln Arg Trp Phe Val Gly Gly Ile Val Ser Trp Gly
625 630 635 640

Ser Ile Asn Cys Gly Ala Ala Gly Gln Tyr Gly Val Tyr Thr Lys Val
645 650 655

Ile Asn Tyr Ile Pro Trp Asn Glu Asn Ile Ile Ser Asn Phe
660 665 670

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<400> 53
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 Met Arg Leu Leu Ile Val Leu Gly Leu Leu Trp Ser Leu Val
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gcc aca ctt ttg ggc tcc aag tgg cct gag cct gta ttc ggg cgc ctg 99
 Ala Thr Leu Leu Gly Ser Lys Trp Pro Glu Pro Val Phe Gly Arg Leu
 15 20 25 30

gtg tcc ctg gcc ttc cca gag aag tat ggc aac cat cag gat cga tcc 147
 Val Ser Leu Ala Phe Pro Glu Lys Tyr Gly Asn His Gln Asp Arg Ser
 35 40 45

tgg acg ctg act gca ccc cct ggc ttc cgc ctg cgc ctc tac ttc acc 195
 Trp Thr Leu Thr Ala Pro Pro Gly Phe Arg Leu Arg Leu Tyr Phe Thr
 50 55 60

cac ttc aac ctg gaa ctc tct tac cgc tgc gag tat gac ttt gtc aag 243
 His Phe Asn Leu Glu Leu Ser Tyr Arg Cys Glu Tyr Asp Phe Val Lys
 65 70 75

ttg acc tca ggg acc aag gtg cta gcc acg ctg tgt ggg cag gag agt 291
 Leu Thr Ser Gly Thr Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser
 80 85 90

aca gat act gag cgg gca cct ggc aat gac acc ttc tac tca ctg ggt 339
 Thr Asp Thr Glu Arg Ala Pro Gly Asn Asp Thr Phe Tyr Ser Leu Gly
 95 100 105 110

ccc agc cta aag gtc acc ttc cac tcc gac tac tcc aat gag aag cca 387
 Pro Ser Leu Lys Val Thr Phe His Ser Asp Tyr Ser Asn Glu Lys Pro
 115 120 125

ttc aca gga ttt gag gcc ttc tat gca gcg gag gat gtg gat gaa tgc 435
 Phe Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Val Asp Glu Cys
 130 135 140

aga aca tcc ctg gga gac tca gtc cct tgt gac cat tat tgc cac aac 483
 Arg Thr Ser Leu Gly Asp Ser Val Pro Cys Asp His Tyr Cys His Asn
 145 150 155

tac ctg ggc ggc tac tac tgc tcc tgc cga gtg ggc tac att ctg cac 531
 Tyr Leu Gly Gly Tyr Tyr Cys Ser Cys Arg Val Gly Tyr Ile Leu His
 160 165 170

cag aac aag cat acc tgc tca gcc ctt tgt tca ggc cag gtg ttc act 579
 Gln Asn Lys His Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr
 175 180 185 190

ggg agg tct ggc ttt ctc agt agc cct gag tac cca cag cca tac ccc 627

Gly	Arg	Ser	Gly	Phe	Leu	Ser	Ser	Pro	Glu	Tyr	Pro	Gln	Pro	Tyr	Pro	
				195					200					205		
aaa	ctc	tcc	agc	tgc	gcc	tac	aac	atc	cgc	ctg	gag	gaa	ggc	ttc	agt	675
Lys	Leu	Ser	Ser	Cys	Ala	Tyr	Asn	Ile	Arg	Leu	Glu	Glu	Gly	Phe	Ser	
			210					215					220			
atc	acc	ctg	gac	ttc	gtg	gag	tcc	ttt	gat	gtg	gag	atg	cac	cct	gaa	723
Ile	Thr	Leu	Asp	Phe	Val	Glu	Ser	Phe	Asp	Val	Glu	Met	His	Pro	Glu	
		225					230					235				
gcc	cag	tgc	ccc	tac	gac	tcc	ctc	aag	att	caa	aca	gac	aag	agg	gaa	771
Ala	Gln	Cys	Pro	Tyr	Asp	Ser	Leu	Lys	Ile	Gln	Thr	Asp	Lys	Arg	Glu	
	240					245					250					
tac	ggc	ccg	ttt	tgt	ggg	aag	acg	ctg	ccc	ccc	agg	att	gaa	act	gac	819
Tyr	Gly	Pro	Phe	Cys	Gly	Lys	Thr	Leu	Pro	Pro	Arg	Ile	Glu	Thr	Asp	
255					260					265					270	
agc	aac	aag	gtg	acc	att	acc	ttt	acc	acc	gac	gag	tca	ggg	aac	cac	867
Ser	Asn	Lys	Val	Thr	Ile	Thr	Phe	Thr	Thr	Asp	Glu	Ser	Gly	Asn	His	
			275						280				285			
aca	ggc	tgg	aag	ata	cac	tac	aca	agc	aca	gca	cag	ccc	tgc	cct	gat	915
Thr	Gly	Trp	Lys	Ile	His	Tyr	Thr	Ser	Thr	Ala	Gln	Pro	Cys	Pro	Asp	
		290						295					300			
cca	acg	gcg	cca	cct	aat	ggc	cac	att	tca	cct	gtg	caa	gcc	acg	tat	963
Pro	Thr	Ala	Pro	Pro	Asn	Gly	His	Ile	Ser	Pro	Val	Gln	Ala	Thr	Tyr	
		305					310					315				
gtc	ctg	aag	gac	agc	ttt	tct	gtc	ttc	tgc	aag	act	ggc	ttc	gag	ctt	1011
Val	Leu	Lys	Asp	Ser	Phe	Ser	Val	Phe	Cys	Lys	Thr	Gly	Phe	Glu	Leu	
	320					325					330					
ctg	caa	ggc	tct	gtc	ccc	ctg	aag	tca	ttc	act	gct	gtc	tgt	cag	aaa	1059
Leu	Gln	Gly	Ser	Val	Pro	Leu	Lys	Ser	Phe	Thr	Ala	Val	Cys	Gln	Lys	
335					340					345					350	
gat	gga	tct	tgg	gac	cgg	ccg	ata	cca	gag	tgc	agc	att	att	gac	tgt	1107
Asp	Gly	Ser	Trp	Asp	Arg	Pro	Ile	Pro	Glu	Cys	Ser	Ile	Ile	Asp	Cys	
			355						360					365		
ggc	cct	ccc	gat	gac	cta	ccc	aat	ggc	cac	gtg	gac	tat	atc	aca	ggc	1155
Gly	Pro	Pro	Asp	Asp	Leu	Pro	Asn	Gly	His	Val	Asp	Tyr	Ile	Thr	Gly	
			370					375					380			
cct	gaa	gtg	acc	acc	tac	aaa	gct	gtg	att	cag	tac	agc	tgt	gaa	gag	1203
Pro	Glu	Val	Thr	Thr	Tyr	Lys	Ala	Val	Ile	Gln	Tyr	Ser	Cys	Glu	Glu	
		385					390					395				

act ttc tac aca atg agc agc aat ggt aaa tat gtg tgt gag gct gat	1251
Thr Phe Tyr Thr Met Ser Ser Asn Gly Lys Tyr Val Cys Glu Ala Asp	
400 405 410	
gga ttc tgg acg agc tcc aaa gga gaa aaa tcc ctc ccg gtt tgc aag	1299
Gly Phe Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Lys	
415 420 425 430	
cct gtc tgt gga ctg tcc aca cac act tca gga ggc cgt ata att gga	1347
Pro Val Cys Gly Leu Ser Thr His Thr Ser Gly Gly Arg Ile Ile Gly	
435 440 445	
gga cag cct gca aag cct ggt gac ttt cct tgg caa gtc ttg tta ctg	1395
Gly Gln Pro Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Leu Leu	
450 455 460	
ggt gaa act aca gca gca ggt gct ctt ata cat gac gac tgg gtc cta	1443
Gly Glu Thr Thr Ala Ala Gly Ala Leu Ile His Asp Asp Trp Val Leu	
465 470 475	
aca gcg gct cat gct gta tat ggg aaa aca gag gcg atg tcc tcc ctg	1491
Thr Ala Ala His Ala Val Tyr Gly Lys Thr Glu Ala Met Ser Ser Leu	
480 485 490	
gac atc cgc atg ggc atc ctc aaa agg ctc tcc ctc att tac act caa	1539
Asp Ile Arg Met Gly Ile Leu Lys Arg Leu Ser Leu Ile Tyr Thr Gln	
495 500 505 510	
gcc tgg cca gag gct gtc ttt atc cat gaa ggc tac act cac gga gct	1587
Ala Trp Pro Glu Ala Val Phe Ile His Glu Gly Tyr Thr His Gly Ala	
515 520 525	
ggt ttt gac aat gat ata gca ctg att aaa ctc aag aac aaa gtc aca	1635
Gly Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Lys Asn Lys Val Thr	
530 535 540	
atc aac aga aac atc atg ccg att tgt cta cca aga aaa gaa gct gca	1683
Ile Asn Arg Asn Ile Met Pro Ile Cys Leu Pro Arg Lys Glu Ala Ala	
545 550 555	
tcc tta atg aaa aca gac ttc gtt gga act gtg gct ggc tgg ggg tta	1731
Ser Leu Met Lys Thr Asp Phe Val Gly Thr Val Ala Gly Trp Gly Leu	
560 565 570	
acc cag aag ggg ttt ctt gct aga aac cta atg ttt gtg gac ata cca	1779
Thr Gln Lys Gly Phe Leu Ala Arg Asn Leu Met Phe Val Asp Ile Pro	
575 580 585 590	
att gtt gac cac caa aaa tgt gct act gcg tat aca aag cag ccc tac	1827

Ile Val Asp His	Gln Lys Cys Ala Thr	Ala Tyr Thr Lys Gln Pro Tyr	
	595	600	605
cca gga gca aaa gtg act gtt aac atg ctc tgt gct ggc cta gac cgc			1875
Pro Gly Ala Lys Val Thr Val Asn Met Leu Cys Ala Gly Leu Asp Arg	610	615	620
ggt ggc aag gac agc tgc aga ggt gac agc gga ggg gca tta gtg ttt			1923
Gly Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe	625	630	635
cta gac aat gaa aca cag aga tgg ttt gtg gga gga ata gtt tcc tgg			1971
Leu Asp Asn Glu Thr Gln Arg Trp Phe Val Gly Gly Ile Val Ser Trp	640	645	650
ggt tct att aac tgt ggg ggg tca gaa cag tat ggg gtc tac acg aaa			2019
Gly Ser Ile Asn Cys Gly Gly Ser Glu Gln Tyr Gly Val Tyr Thr Lys	655	660	665
gtc acg aac tat att ccc tgg att gag aac ata ata aat aat ttc taa			2067
Val Thr Asn Tyr Ile Pro Trp Ile Glu Asn Ile Ile Asn Asn Phe	675	680	685
tttgcaaaaaa aaaaaaaaaa aaaa			2091

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 <211> 685
 <212> PRT
 <213> Rat

<400> 54

Met Arg Leu Leu Ile Val Leu Gly Leu Leu Trp Ser Leu Val Ala Thr
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Leu Leu Gly Ser Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Val Ser
20 25 30

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

Leu Thr Ala Pro Pro Gly Phe Arg Leu Arg Leu Tyr Phe Thr His Phe
50 55 60

Asn Leu Glu Leu Ser Tyr Arg Cys Glu Tyr Asp Phe Val Lys Leu Thr

65				70				75				80				
Ser	Gly	Thr	Lys	Val	Leu	Ala	Thr	Leu	Cys	Gly	Gln	Glu	Ser	Thr	Asp	
				85					90					95		
Thr	Glu	Arg	Ala	Pro	Gly	Asn	Asp	Thr	Phe	Tyr	Ser	Leu	Gly	Pro	Ser	
				100					105					110		
Leu	Lys	Val	Thr	Phe	His	Ser	Asp	Tyr	Ser	Asn	Glu	Lys	Pro	Phe	Thr	
				115					120					125		
Gly	Phe	Glu	Ala	Phe	Tyr	Ala	Ala	Glu	Asp	Val	Asp	Glu	Cys	Arg	Thr	
				130					135					140		
Ser	Leu	Gly	Asp	Ser	Val	Pro	Cys	Asp	His	Tyr	Cys	His	Asn	Tyr	Leu	
145					150					155					160	
Gly	Gly	Tyr	Tyr	Cys	Ser	Cys	Arg	Val	Gly	Tyr	Ile	Leu	His	Gln	Asn	
				165					170					175		
Lys	His	Thr	Cys	Ser	Ala	Leu	Cys	Ser	Gly	Gln	Val	Phe	Thr	Gly	Arg	
				180					185					190		
Ser	Gly	Phe	Leu	Ser	Ser	Pro	Glu	Tyr	Pro	Gln	Pro	Tyr	Pro	Lys	Leu	
				195					200					205		
Ser	Ser	Cys	Ala	Tyr	Asn	Ile	Arg	Leu	Glu	Glu	Gly	Phe	Ser	Ile	Thr	
				210					215					220		
Leu	Asp	Phe	Val	Glu	Ser	Phe	Asp	Val	Glu	Met	His	Pro	Glu	Ala	Gln	
225					230					235					240	
Cys	Pro	Tyr	Asp	Ser	Leu	Lys	Ile	Gln	Thr	Asp	Lys	Arg	Glu	Tyr	Gly	
				245					250					255		
Pro	Phe	Cys	Gly	Lys	Thr	Leu	Pro	Pro	Arg	Ile	Glu	Thr	Asp	Ser	Asn	
				260					265					270		

Lys Val Thr Ile Thr Phe Thr Thr Asp Glu Ser Gly Asn His Thr Gly
275 280 285

Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Asp Pro Thr
290 295 300

Ala Pro Pro Asn Gly His Ile Ser Pro Val Gln Ala Thr Tyr Val Leu
305 310 315 320

Lys Asp Ser Phe Ser Val Phe Cys Lys Thr Gly Phe Glu Leu Leu Gln
325 330 335

Gly Ser Val Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp Gly
340 345 350

Ser Trp Asp Arg Pro Ile Pro Glu Cys Ser Ile Ile Asp Cys Gly Pro
355 360 365

Pro Asp Asp Leu Pro Asn Gly His Val Asp Tyr Ile Thr Gly Pro Glu
370 375 380

Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr Phe
385 390 395 400

Tyr Thr Met Ser Ser Asn Gly Lys Tyr Val Cys Glu Ala Asp Gly Phe
405 410 415

Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Lys Pro Val
420 425 430

Cys Gly Leu Ser Thr His Thr Ser Gly Gly Arg Ile Ile Gly Gly Gln
435 440 445

Pro Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Leu Leu Gly Glu
450 455 460

Thr Thr Ala Ala Gly Ala Leu Ile His Asp Asp Trp Val Leu Thr Ala

465		470		475		480
Ala His Ala Val Tyr Gly Lys Thr Glu Ala Met Ser Ser Leu Asp Ile						
		485		490		495
Arg Met Gly Ile Leu Lys Arg Leu Ser Leu Ile Tyr Thr Gln Ala Trp						
		500		505		510
Pro Glu Ala Val Phe Ile His Glu Gly Tyr Thr His Gly Ala Gly Phe						
		515		520		525
Asp Asn Asp Ile Ala Leu Ile Lys Leu Lys Asn Lys Val Thr Ile Asn						
		530		535		540
Arg Asn Ile Met Pro Ile Cys Leu Pro Arg Lys Glu Ala Ala Ser Leu						
545		550		555		560
Met Lys Thr Asp Phe Val Gly Thr Val Ala Gly Trp Gly Leu Thr Gln						
		565		570		575
Lys Gly Phe Leu Ala Arg Asn Leu Met Phe Val Asp Ile Pro Ile Val						
		580		585		590
Asp His Gln Lys Cys Ala Thr Ala Tyr Thr Lys Gln Pro Tyr Pro Gly						
		595		600		605
Ala Lys Val Thr Val Asn Met Leu Cys Ala Gly Leu Asp Arg Gly Gly						
		610		615		620
Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe Leu Asp						
625		630		635		640
Asn Glu Thr Gln Arg Trp Phe Val Gly Gly Ile Val Ser Trp Gly Ser						
		645		650		655
Ile Asn Cys Gly Gly Ser Glu Gln Tyr Gly Val Tyr Thr Lys Val Thr						
		660		665		670

Asn Tyr Ile Pro Trp Ile Glu Asn Ile Ile Asn Asn Phe
675 680 685

<210> 55
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<400> 55

Thr Leu Leu Gly Ser Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Val
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Ser Leu Ala Phe Pro Glu Lys Tyr Gly Asn His Gln Asp Arg Ser Trp
20 25 30

Thr Leu Thr Ala Pro Pro Gly Phe Arg Leu Arg Leu Tyr Phe Thr His
35 40 45

Phe Asn Leu Glu Leu Ser Tyr Arg Cys Glu Tyr Asp Phe Val Lys Leu
50 55 60

Thr Ser Gly Thr Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr
65 70 75 80

Asp Thr Glu Arg Ala Pro Gly Asn Asp Thr Phe Tyr Ser Leu Gly Pro
85 90 95

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

Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Val Asp Glu Cys Arg
115 120 125

Thr Ser Leu Gly Asp Ser Val Pro Cys Asp His Tyr Cys His Asn Tyr
130 135 140

Leu Gly Gly Tyr Tyr Cys Ser Cys Arg Val Gly Tyr Ile Leu His Gln
145 150 155 160

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

Arg Ser Gly Phe Leu Ser Ser Pro Glu Tyr Pro Gln Pro Tyr Pro Lys
180 185 190

Leu Ser Ser Cys Ala Tyr Asn Ile Arg Leu Glu Glu Gly Phe Ser Ile
195 200 205

Thr Leu Asp Phe Val Glu Ser Phe Asp Val Glu Met His Pro Glu Ala
210 215 220

Gln Cys Pro Tyr Asp Ser Leu Lys Ile Gln Thr Asp Lys Arg Glu Tyr
225 230 235 240

Gly Pro Phe Cys Gly Lys Thr Leu Pro Pro Arg Ile Glu Thr Asp Ser
245 250 255

Asn Lys Val Thr Ile Thr Phe Thr Thr Asp Glu Ser Gly Asn His Thr
260 265 270

Gly Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Asp Pro
275 280 285

Thr Ala Pro Pro Asn Gly His Ile Ser Pro Val Gln Ala Thr Tyr Val
290 295 300

Leu Lys Asp Ser Phe Ser Val Phe Cys Lys Thr Gly Phe Glu Leu Leu
305 310 315 320

Gln Gly Ser Val Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp
325 330 335

Gly Ser Trp Asp Arg Pro Ile Pro Glu Cys Ser Ile Ile Asp Cys Gly
340 345 350

Pro Pro Asp Asp Leu Pro Asn Gly His Val Asp Tyr Ile Thr Gly Pro
355 360 365

Glu Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr
370 375 380

Phe Tyr Thr Met Ser Ser Asn Gly Lys Tyr Val Cys Glu Ala Asp Gly
385 390 395 400

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

Val Cys Gly Leu Ser Thr His Thr Ser Gly Gly Arg Ile Ile Gly Gly
420 425 430

Gln Pro Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Leu Leu Gly
435 440 445

Glu Thr Thr Ala Ala Gly Ala Leu Ile His Asp Asp Trp Val Leu Thr
450 455 460

Ala Ala His Ala Val Tyr Gly Lys Thr Glu Ala Met Ser Ser Leu Asp
465 470 475 480

Ile Arg Met Gly Ile Leu Lys Arg Leu Ser Leu Ile Tyr Thr Gln Ala
485 490 495

Trp Pro Glu Ala Val Phe Ile His Glu Gly Tyr Thr His Gly Ala Gly
500 505 510

Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Lys Asn Lys Val Thr Ile
515 520 525

Asn Arg Asn Ile Met Pro Ile Cys Leu Pro Arg Lys Glu Ala Ala Ser
530 535 540

Leu Met Lys Thr Asp Phe Val Gly Thr Val Ala Gly Trp Gly Leu Thr
545 550 555 560

Gln Lys Gly Phe Leu Ala Arg Asn Leu Met Phe Val Asp Ile Pro Ile
565 570 575

Val Asp His Gln Lys Cys Ala Thr Ala Tyr Thr Lys Gln Pro Tyr Pro
580 585 590

Gly Ala Lys Val Thr Val Asn Met Leu Cys Ala Gly Leu Asp Arg Gly
595 600 605

Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe Leu
610 615 620

Asp Asn Glu Thr Gln Arg Trp Phe Val Gly Gly Ile Val Ser Trp Gly
625 630 635 640

Ser Ile Asn Cys Gly Gly Ser Glu Gln Tyr Gly Val Tyr Thr Lys Val
645 650 655

Thr Asn Tyr Ile Pro Trp Ile Glu Asn Ile Ile Asn Asn Phe
660 665 670

<210> 56
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo Sapiens

<400> 56
atgaggctgc tgaccctcct gggccttc

28

<210> 57
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo Sapiens

<400> 57
gtgccccctcc tgcgtcacct ctg 23

<210> 58
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo Sapiens

<400> 58
cagaggtgac gcaggagggg cac 23

<210> 59
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo Sapiens

<400> 59
ttaaaatcac taattatggt ctcgatc 27

<210> 60
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Murine

<400> 60
atgaggctac tcattcttcct gg 22

<210> 61
<211> 23
<212> DNA
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<220>
<223> Murine

<400> 61
ctgcagaggt gacgcagggg ggg 23

<210> 62
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Murine

<400> 62
ccccccctgc gtcacctctg cag 23

<210> 63
<211> 29
<212> DNA
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<220>
<223> Murine

<400> 63
ttagaaatta cttattatgt tctcaatcc 29

<210> 64
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Rat

<400> 64
gaggtgacgc aggaggggca ttagtgttt 29

<210> 65
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Rat

<400> 65
ctagaaacac taatgcccct cctgcgtcac ctctgca 37

<210> 66
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 66
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cagccccag ggaaggccct ggagtggctt gcacacattt tttcgagtga cgaaaaatcc 180
tacaggacat cgctgaagag caggctcacc atctccaagg acacctcaa aaaccaggtg 240
gtccttaca tgaccaacat ggaccctgtg gacacagcca cgtattactg tgcacggata 300
cgacgtggag gaattgacta ctggggccag ggaaccctgg tcactgtctc ctca 354

<210> 67
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 67

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

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Arg Gly
20 25 30

Lys Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Ser Asp Glu Lys Ser Tyr Arg Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Arg Arg Gly Gly Ile Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 68
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 68

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Thr
20 25 30

Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
35 40 45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60

Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80

Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Ala Arg Asp Pro Phe Gly Val Pro Phe Asp Ile Trp Gly
100 105 110

Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 69
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 69

Gln Pro Val Leu Thr Gln Pro Pro Ser Leu Ser Val Ser Pro Gly Gln
1 5 10 15

Thr Ala Ser Ile Thr Cys Ser Gly Glu Lys Leu Gly Asp Lys Tyr Ala
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu Val Met Tyr
35 40 45

Gln Asp Lys Gln Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Ser Thr Ala Val
85 90 95

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 70
<211> 324
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 70

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caggcccctg tgttgggtcat ctatgatgat agcgaccggc cctcagggat ccctgaccga      180
ttctctgcct ccaactctgg gaacacggcc accctgacca tcactagggg cgaagccggg      240
gatgaggccg actattattg tcagggtgtgg gacattgcta ctgatcatgt ggtcttcggc      300
ggaggggacca agctcaccgt ccta                                             324
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<210> 71

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 71

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

His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
          35          40          45

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Ala Ser
          50          55          60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Thr Arg Gly Glu Ala Gly
65          70          75          80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ile Ala Thr Asp His
          85          90          95
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Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ala Ala Ala Gly
100 105 110

Ser Glu Gln Lys Leu Ile Ser Glu
115 120

<210> 72
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 72

Leu Glu Val Thr Cys Glu Pro Gly Thr Thr Phe Lys Asp Lys Cys Asn
1 5 10 15

Thr Cys Arg Cys Gly Ser Asp Gly Lys Ser Ala Val Cys Thr Lys Leu
20 25 30

Trp Cys Asn Gln
35

<210> 73
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 73

Thr Cys Glu Pro Gly Thr Thr Phe Lys Asp Lys Cys Asn Thr Cys Arg
1 5 10 15

Cys Gly Ser Asp Gly Lys Ser Ala Val Cys Thr Lys Leu Trp Cys Asn
20 25 30

Gln

<210> 74
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 74

Thr Cys Arg Cys Gly Ser Asp Gly Lys Ser Ala Val Cys Thr Lys Leu
1 5 10 15

Trp Cys Asn Gln
20

<210> 75
<211> 491
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 75

Leu Glu Val Thr Cys Glu Pro Gly Thr Thr Phe Lys Asp Lys Cys Asn
1 5 10 15

Thr Cys Arg Cys Gly Ser Asp Gly Lys Ser Ala Val Cys Thr Lys Leu
20 25 30

Trp Cys Asn Gln Gly Thr Gly Gly Gly Ser Gly Ser Ser Ser Gln Val
35 40 45

Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu Thr Leu
50 55 60

Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Arg Gly Lys Met
65 70 75 80

Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu
85 90 95

Ala His Ile Phe Ser Ser Asp Glu Lys Ser Tyr Arg Thr Ser Leu Lys
100 105 110

Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Val Leu
115 120 125

Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala
130 135 140

Arg Ile Arg Arg Gly Gly Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val
145 150 155 160

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
165 170 175

Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu
180 185 190

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
195 200 205

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
210 215 220

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
225 230 235 240

Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr
245 250 255

Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
260 265 270

Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
275 280 285

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
290 295 300

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
305 310 315 320

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
325 330 335

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
340 345 350

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
355 360 365

Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
370 375 380

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
385 390 395 400

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
405 410 415

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
420 425 430

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
435 440 445

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
450 455 460

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465 470 475 480

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
485 490

<210> 76
<211> 491
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 76

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

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Arg Gly
20 25 30

Lys Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Ser Asp Glu Lys Ser Tyr Arg Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Arg Arg Gly Gly Ile Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

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

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
275 280 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
340 345 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385 390 395 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Ala Ala Gly
435 440 445

Gly Ser Gly Leu Glu Val Thr Cys Glu Pro Gly Thr Thr Phe Lys Asp
450 455 460

Lys Cys Asn Thr Cys Arg Cys Gly Ser Asp Gly Lys Ser Ala Val Cys
465 470 475 480

Thr Lys Leu Trp Cys Asn Gln Gly Ser Gly Ala
485 490

<210> 77

<211> 258

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 77

Leu Glu Val Thr Cys Glu Pro Gly Thr Thr Phe Lys Asp Lys Cys Asn
1 5 10 15

Thr Cys Arg Cys Gly Ser Asp Gly Lys Ser Ala Val Cys Thr Lys Leu
20 25 30

Trp Cys Asn Gln Gly Thr Gly Gly Gly Ser Gly Ser Ser Ser Gln Pro
35 40 45

Val Leu Thr Gln Pro Pro Ser Leu Ser Val Ser Pro Gly Gln Thr Ala
50 55 60

Ser Ile Thr Cys Ser Gly Glu Lys Leu Gly Asp Lys Tyr Ala Tyr Trp
65 70 75 80

Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu Val Met Tyr Gln Asp
85 90 95

Lys Gln Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser
100 105 110

Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met Asp Glu
115 120 125

Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Ser Thr Ala Val Phe Gly
130 135 140

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

Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala
165 170 175

Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val
180 185 190

Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr
195 200 205

Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu
210 215 220

Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln
225 230 235 240

Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu
245 250 255

Cys Ser

<210> 78
<211> 258
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 78

Gln Pro Val Leu Thr Gln Pro Pro Ser Leu Ser Val Ser Pro Gly Gln
1 5 10 15

Thr Ala Ser Ile Thr Cys Ser Gly Glu Lys Leu Gly Asp Lys Tyr Ala
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu Val Met Tyr
35 40 45

Gln Asp Lys Gln Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Ser Thr Ala Val
85 90 95

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala
100 105 110

Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn
115 120 125

Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val
130 135 140

Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu
145 150 155 160

Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser
165 170 175

Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser
180 185 190

Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro
195 200 205

Thr Glu Cys Ser Ala Ala Gly Gly Ser Gly Leu Glu Val Thr Cys Glu
210 215 220

Pro Gly Thr Thr Phe Lys Asp Lys Cys Asn Thr Cys Arg Cys Gly Ser
225 230 235 240

Asp Gly Lys Ser Ala Val Cys Thr Lys Leu Trp Cys Asn Gln Gly Ser
245 250 255

Gly Ala

<210> 79

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 79

Gly Thr Gly Gly Gly Ser Gly Ser Ser Ser
1 5 10

<210> 80

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 80

Ala Ala Gly Gly Ser Gly
1 5

<210> 81

<211> 4

<212> PRT

<213> Artificial Sequence

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<223> Synthetic

<400> 81

Gly Ser Gly Ala
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<210> 82

<211> 1533

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 82

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tcagatggga aatcggcggt ctgcacaaag ctctggtgta accagggcac cgggtggaggg 180

tcgggatcca gctcacaggt caccttgaag gagtctggtc ctgtgctggt gaaacccaca	240
gagacctca cgctgacctg caccgtctct gggttctcac tcagcagggg taaaatgggt	300
gtgagctgga tccgtcagcc cccaggggaag gccctggagt ggcttgcaca cattttttcg	360
agtgacgaaa aatcctacag gacatcgctg aagagcaggc tcaccatctc caaggacacc	420
tccaaaaacc aggtggtcct tacaatgacc aacatggacc ctgtggacac agccacgtat	480
tactgtgcac ggatacgacg tggaggaatt gactactggg gccaggggaac cctggtcact	540
gtctcctcag cctccaccaa gggcccatcc gtcttcccc tggcgccctg ctccaggagc	600
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<210> 83

<211> 1533

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 83

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tgcaccgtct ctgggttctc actcagcagg ggtaaaatgg gtgtgagctg gatccgtcag	180
ccccaggga aggccctgga gtggcttgca cacatTTTTT cgagtgcga aaaatcctac	240
aggacatcgc tgaagagcag gctcaccatc tccaaggaca cctccaaaaa ccagggtggtc	300
cttacaatga ccaacatgga ccctgtggac acagccacgt attactgtgc acggatacga	360
cgtggaggaa ttgactactg gggccaggga accctgggtca ctgtctcctc agcctccacc	420
aagggcccat ccgtcttccc cctggcgccc tgctccagga gcacctcca gagcacagcc	480
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgc gtggaactca	540
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tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcacgaagac ctacacctgc	660
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aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc	1260
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tcatagctccg tgatgcatga ggctctgcac aaccactaca cacagaagag cctctccctg	1380
tctctcggga aagccgctgg tggtagtggt ttggaagtga cgtgtgagcc cggaacgaca	1440
ttcaaagaca agtgcaatac ttgtcgggtgc ggttcagatg ggaaatcggc ggtctgcaca	1500
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<210> 84
 <211> 834
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 84	
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tcagatggga aatcggcggt ctgcacaaag ctctgggtga accagggcac cggtaggagg	180
tcgggatcca gctcacagcc agtgctgact cagccccct cactgtccgt gtccccagga	240
cagacagcca gcatcacctg ctctggagag aaattggggg ataaatatgc ttactggtat	300
cagcagaagc caggccagtc ccctgtgttg gtcattgtatc aagataaaca gcggccctca	360
gggatccctg agcgattctc tggctccaac tctgggaaca cagccactct gaccatcagc	420
gggacccagg ctatggatga ggctgactat tactgtcagg cgtgggacag cagcactgcg	480
gtattcggcg gagggacca gctgaccgtc ctaggccagc ctaaggcggc gccctcggtc	540
accctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc	600
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc	660
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc	720
agctatctga gcctgacgcc tgagcagtggt aagtcccaca gaagctacag ctgccaggtc	780
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc atag	834

<210> 85
 <211> 834

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 85

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