

SEQUENCE LISTING

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<120> METHODS FOR TREATING AND/OR PREVENTING
GRAFT-VERSUS-HOST DISEASE AND/OR DIFFUSE
ALVEOLAR HEMORRHAGE AND/OR VENO-OCCLUSIVE
DISEASE ASSOCIATED WITH
HEMATOPOIETIC STEM CELL TRANSPLANT

<130> MP.1.0278.PCT

<150> 62/545,864

<151> 2017-08-15

<150> 62/574,690

<151> 2017-10-19

<150> 62/630,756

<151> 2018-02-14

<150> 62/637,281

<151> 2018-03-01

<160> 71

<170> PatentIn version 3.5

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<212> DNA

<213> Homo sapiens

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<222> (27)..(584)

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Cys Gly Gln Glu Ser Thr Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr	
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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	
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Ser Asn Glu Lys Pro Phe Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu	
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His His Cys His Asn His Leu Gly Gly Phe Tyr Cys Ser Cys Arg Ala	
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Gly Tyr Val Leu His Arg Asn Lys Arg Thr Cys Ser Glu Gln Ser Leu	
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Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
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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
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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
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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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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
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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
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 Cys Gly Ser Val Ala Thr Pro Leu Gly Pro Lys Trp Pro Glu Pro Val 25
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 Phe Gly Arg Leu Ala Ser Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp 40
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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 55
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 Asp Phe Val Lys Leu Ser Ser Gly Ala Lys Val Leu Ala Thr Leu Cys 90
 75 80 85
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 Gly Gln Glu Ser Thr Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe 105
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 Tyr Ser Leu Gly Ser Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser 120
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ctc	cca	gtc	tgt	gag	cct	gtt	tgt	gga	cta	tca	gcc	cgc	aca	aca	gga	1347
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gat	gca	tcc	gcc	ctg	gac	att	cga	atg	ggc	acc	ctg	aaa	aga	cta	tca	1539
Asp	Ala	Ser	Ala	Leu	Asp	Ile	Arg	Met	Gly	Thr	Leu	Lys	Arg	Leu	Ser	
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cct	cat	tat	aca	caa	gcc	tgg	tct	gaa	gct	gtt	ttt	ata	cat	gaa	ggc	1587
Pro	His	Tyr	Thr	Gln	Ala	Trp	Ser	Glu	Ala	Val	Phe	Ile	His	Glu	Gly	
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Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
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Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser
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Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr Asp
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Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser
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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
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Lys Arg Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gln Arg
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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
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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

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360

365

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

Ile Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Thr
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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
260 265 270

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

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

Leu Lys Asp Ser Phe Ser Ile Phe Cys Glu Thr Gly Tyr Glu Leu Leu
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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
340 345 350

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
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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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Ile Val Asp His Gln Lys Cys Thr Ala Ala Tyr Glu Lys Pro Pro Tyr
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Pro Arg Gly Ser Val Thr Ala Asn Met Leu Cys Ala Gly Leu Glu Ser
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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
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
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>

<221> CDS

<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 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

[illegible]

<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	
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aagtggcctg aacctgtgtt cgggcgcctg gcatcccccg gctttccagg ggagtatgcc	120
aatgaccagg agcggcgctg gaccctgact gcaccccccg gctaccgcct gcgcctctac	180

ttcacccact tcgacctgga gctctccac ctctgcgagt acgacttcgt caagctgagc	240
tcggggggcca aggtgctggc cacgctgtgc gggcaggaga gcacagacac ggagcggggcc	300
cctggcaagg acactttcta ctcgctgggc tccagcctgg acattacctt ccgctccgac	360
tactccaacg agaagccgtt cacgggggtt gaggccttct atgcagccga ggacattgac	420
gagtgccagg tggccccggg agaggcgccc acctgcgacc accactgcca caaccacctg	480
ggcggtttct actgctcctg ccgcgaggc 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
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 33	
agcagccctg aatacccacg gccgtatccc aaa	33

<210> 34
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 34
cgggatccat gaggctgctg accctc

26

<210> 35
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 35
ggaattccta ggctgcata

19

<210> 36
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 36
ggaattccta cagggcgct

19

<210> 37
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 37
ggaattccta gtagtggat

19

<210> 38
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 38
tgcggccgct gtaggtgctg tcttt

25

<210> 39
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 39
ggaattcact cgttattctc gga

23

<210> 40
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 40
tccgagaata acgagtg

17

<210> 41
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 41
cattgaaagc tttggggtag aagttgttc

29

<210> 42
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 42
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<220>
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						1				5						
ggt	ctg	ctg	tgg	agt	ttg	gtg	gcc	aca	ctt	ctg	ggt	tca	aag	tgg	cct	101
Gly	Leu	Leu	Trp	Ser	Leu	Val	Ala	Thr	Leu	Leu	Gly	Ser	Lys	Trp	Pro	
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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	
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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	
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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	
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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	
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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	
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Asp Tyr Ser Asn Glu Lys Pro Phe Thr Gly Phe Glu Ala Phe Tyr Ala	
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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	
155 160 165	
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	
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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	
265 270 275	
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	
280 285 290 295	
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	

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tgc aag aca ggc ttc gag ctt ctg caa ggt 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			
345	350	355	
gag tgc agc att att gat tgt ggc cct ccc gat gac cta ccc aat ggc			1157
Glu Cys Ser Ile Ile Asp Cys Gly Pro Pro Asp Asp Leu Pro Asn Gly			
360	365	370	375
cat gtg gac tat atc aca ggc cct caa gtg act acc tac aaa gct gtg			1205
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	
aaa ctc ccc ccg gtt tgt gag cct gtt tgt ggg ctg tcc aca cac act			1349
Lys Leu Pro Pro Val Cys Glu Pro Val Cys Gly Leu Ser Thr His Thr			
425	430	435	
ata gga gga cgc ata gtt gga ggg cag cct gca aag cct ggt gac ttt			1397
Ile Gly Gly Arg Ile Val Gly Gly Gln Pro Ala Lys Pro Gly Asp Phe			
440	445	450	455
cct tgg caa gtc ttg ttg ctg ggt caa act aca gca gca gca ggt gca			1445
Pro Trp Gln Val Leu Leu Leu Gly Gln Thr Thr Ala Ala Ala Gly Ala			
460	465	470	
ctt ata cat gac aat tgg gtc cta aca gcc gct cat gct gta tat gag			1493
Leu Ile His Asp Asn Trp Val Leu Thr Ala Ala His Ala Val Tyr Glu			
475	480	485	
aaa aga atg gca gcg tcc tcc ctg aac atc cga atg ggc atc ctc aaa			1541
Lys Arg Met Ala Ala Ser Ser Leu Asn Ile Arg Met Gly Ile Leu Lys			
490	495	500	
agg ctc tca cct cat tac act caa gcc tgg ccc gag gaa atc ttt ata			1589
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

tgc cta ccg cga aaa gaa gct gca tcc tta atg aga aca gac ttc act 1733
Cys Leu Pro Arg Lys Glu Ala Ala Ser Leu Met Arg Thr Asp Phe Thr
555 560 565

aac cta atg ttt gtg gac ata cca att gct gac cac caa aaa tgt acc 1829
Asn Leu Met Phe Val Asp Ile Pro Ile Ala Asp His Gln Lys Cys Thr
585 590 595

ctc tgt gct ggc tta gag act ggt ggc aag gac agc tgc aga ggt gac 1925
Leu Cys Ala Gly Leu Glu Thr Gly Gly Lys Asp Ser Cys Arg Gly Asp
620 625 630

gtg gga gga ata gtt tcc tgg ggt tcc att aat tgt ggg gcg gca ggc 2021
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aac ata ata agt aat ttc taa 2090
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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
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Thr Glu Gln Ala Pro Gly Asn Asp Thr Phe Tyr Ser Leu Gly Pro Ser
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Leu Lys Val Thr Phe His Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
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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
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Cys Gly Leu Ser Thr His Thr Ile Gly Gly Arg Ile Val Gly Gly Gln
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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
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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
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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
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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

<211> 2091
<212> DNA
<213> Rat

<220>
<221> CDS
<222> (10)..(2067)

<400> 53
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Met Arg Leu Leu Ile Val Leu Gly Leu Leu Trp Ser Leu Val
1 5 10

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 Tyr Leu Gly Gly Tyr Tyr Cys Ser Cys Arg Val Gly Tyr Ile Leu His 160 165 170	531
cag aac aag cat acc tgc tca gcc ctt tgt tca ggc cag gtg ttc act Gln Asn Lys His Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr 175 180 185 190	579
ggg agg tct ggc ttt ctc agt agc cct gag tac cca cag cca tac ccc Gly Arg Ser Gly Phe Leu Ser Ser Pro Glu Tyr Pro Gln Pro Tyr Pro 195 200 205	627
aaa ctc tcc agc tgc gcc tac aac atc cgc ctg gag gaa ggc ttc agt Lys Leu Ser Ser Cys Ala Tyr Asn Ile Arg Leu Glu Glu Gly Phe Ser 210 215 220	675
atc acc ctg gac ttc gtg gag tcc ttt gat gtg gag atg cac cct gaa Ile Thr Leu Asp Phe Val Glu Ser Phe Asp Val Glu Met His Pro Glu 225 230 235	723
gcc cag tgc ccc tac gac tcc ctc aag att caa aca gac aag agg gaa Ala Gln Cys Pro Tyr Asp Ser Leu Lys Ile Gln Thr Asp Lys Arg Glu 240 245 250	771
tac ggc ccg ttt tgt ggg aag acg ctg ccc ccc agg att gaa act gac Tyr Gly Pro Phe Cys Gly Lys Thr Leu Pro Pro Arg Ile Glu Thr Asp 255 260 265 270	819
agc aac aag gtg acc att acc ttt acc acc gac gag tca ggg aac cac Ser Asn Lys Val Thr Ile Thr Phe Thr Thr Asp Glu Ser Gly Asn His 275 280 285	867
aca ggc tgg aag ata cac tac aca agc aca gca cag ccc tgc cct gat Thr Gly Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Asp 290 295 300	915
cca acg gcg cca cct aat ggt cac att tca cct gtg caa gcc acg tat Pro Thr Ala Pro Pro Asn Gly His Ile Ser Pro Val Gln Ala Thr Tyr 305 310 315	963
gtc ctg aag gac agc ttt tct gtc ttc tgc aag act ggc ttc gag ctt Val Leu Lys Asp Ser Phe Ser Val Phe Cys Lys Thr Gly Phe Glu Leu 320 325 330	1011
ctg caa ggt tct gtc ccc ctg aag tca ttc act gct gtc tgt cag aaa Leu Gln Gly Ser Val Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys 335 340 345 350	1059
gat gga tct tgg gac cgg ccg ata cca gag tgc agc att att gac tgt Asp Gly Ser Trp Asp Arg Pro Ile Pro Glu Cys Ser Ile Ile Asp Cys	1107

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	
655 660 665 670	

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	

tttgcaaaaa aaaaaaaaaa aaaa	2091
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<210> 54
 <211> 685
 <212> PRT
 <213> Rat

<400> 54

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

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

<211> 670

<212> PRT

<213> Rat

<400> 55

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

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

<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
<213> Artificial Sequence

<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
<213> Artificial Sequence

<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

caggtcacct tgaaggagtc tggtcctgtg ctggtgaaac ccacagagac cctcacgctg 60

acctgcaccg tctctggggtt ctactcagc aggggtaaaa tgggtgtgag ctggatccgt 120

cagccccag ggaaggccct ggagtggctt gcacacattt tttcgagtga cgaaaaatcc 180

tacaggacat cgctgaagag caggctcacc atctccaagg acacctccaa aaaccagggtg 240

gtccttaciaa 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> 318
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic

<220>
 <221> misc_feature
 <222> (246)..(246)
 <223> n is a, c, g, or t

<400> 69	
cagccagtgc tgactcagcc cccctcactg tccgtgtccc caggacagac agccagcatc	60
acctgctctg gagagaaaatt gggggataaa tatgcttact ggtatcagca gaagccaggc	120
cagtcccctg tgttggtcat gtatcaagat aaacagcggc cctcagggat ccctgagcga	180
ttctctggct ccaactctgg gaacacagcc actctgacca tcagcgggac ccaggctatg	240
gatgangctg actattactg tcaggcgtgg gacagcagca ctgcggtatt cggcggaggg	300
accaagctga ccgtccta	318

<210> 70
 <211> 106
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic

<400> 70

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> 71

<211> 120

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic

<400> 71

Ser Tyr Glu Leu Ile Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15

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

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