

SEQUENCE LISTING

<110> DAIICHI SANKYO COMPANY, LIMITED

<120> KLK5 INHIBITORY PEPTIDE

<130> FP1933

<150> JP2018-209729

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<160> 97

<170> PatentIn version 3.5

<210> 1

<211> 63

<212> PRT

<213> Homo sapiens

<400> 1

Asp Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro Asn Cys Ser
1 5 10 15

Gln Tyr Arg Leu Pro Gly Cys Pro Arg His Phe Asn Pro Val Cys Gly
20 25 30

Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys Met Lys Ile
35 40 45

Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly Pro Cys
50 55 60

<210> 2

<211> 227

<212> PRT

<213> Homo sapiens

<400> 2

Ile Ile Asn Gly Ser Asp Cys Asp Met His Thr Gln Pro Trp Gln Ala
1 5 10 15

Ala Leu Leu Leu Arg Pro Asn Gln Leu Tyr Cys Gly Ala Val Leu Val
20 25 30

His Pro Gln Trp Leu Leu Thr Ala Ala His Cys Arg Lys Lys Val Phe

35

40

45

Arg Val Arg Leu Gly His Tyr Ser Leu Ser Pro Val Tyr Glu Ser Gly
 50 55 60

Gln Gln Met Phe Gln Gly Val Lys Ser Ile Pro His Pro Gly Tyr Ser
 65 70 75 80

His Pro Gly His Ser Asn Asp Leu Met Leu Ile Lys Leu Asn Arg Arg
 85 90 95

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

Pro Ser Ala Gly Thr Lys Cys Leu Val Ser Gly Trp Gly Thr Thr Lys
 115 120 125

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

Val Leu Ser Gln Lys Arg Cys Glu Asp Ala Tyr Pro Arg Gln Ile Asp
 145 150 155 160

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

Gly Asp Ser Gly Gly Pro Val Val Cys Asn Gly Ser Leu Gln Gly Leu
 180 185 190

Val Ser Trp Gly Asp Tyr Pro Cys Ala Arg Pro Asn Arg Pro Gly Val
 195 200 205

Tyr Thr Asn Leu Cys Lys Phe Thr Lys Trp Ile Gln Glu Thr Ile Gln
 210 215 220

Ala Asn Ser
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<210> 3

<211> 224

<212> PRT

<213> Homo sapiens

<400> 3

Ile Ile Asp Gly Ala Pro Cys Ala Arg Gly Ser His Pro Trp Gln Val
 1 5 10 15

Ala Leu Leu Ser Gly Asn Gln Leu His Cys Gly Gly Val Leu Val Asn
 20 25 30

Glu Arg Trp Val Leu Thr Ala Ala His Cys Lys Met Asn Glu Tyr Thr
 35 40 45

Val His Leu Gly Ser Asp Thr Leu Gly Asp Arg Arg Ala Gln Arg Ile
 50 55 60

Lys Ala Ser Lys Ser Phe Arg His Pro Gly Tyr Ser Thr Gln Thr His
 65 70 75 80

Val Asn Asp Leu Met Leu Val Lys Leu Asn Ser Gln Ala Arg Leu Ser
 85 90 95

Ser Met Val Lys Lys Val Arg Leu Pro Ser Arg Cys Glu Pro Pro Gly
 100 105 110

Thr Thr Cys Thr Val Ser Gly Trp Gly Thr Thr Thr Ser Pro Asp Val
 115 120 125

Thr Phe Pro Ser Asp Leu Met Cys Val Asp Val Lys Leu Ile Ser Pro
 130 135 140

Gln Asp Cys Thr Lys Val Tyr Lys Asp Leu Leu Glu Asn Ser Met Leu
 145 150 155 160

Cys Ala Gly Ile Pro Asp Ser Lys Lys Asn Ala Cys Asn Gly Asp Ser
 165 170 175

Gly Gly Pro Leu Val Cys Arg Gly Thr Leu Gln Gly Leu Val Ser Trp
 180 185 190

Gly Thr Phe Pro Cys Gly Gln Pro Asn Asp Pro Gly Val Tyr Thr Gln
 195 200 205

Val Cys Lys Phe Thr Lys Trp Ile Asn Asp Thr Met Lys Lys His Arg
 210 215 220

<210> 4
 <211> 227
 <212> PRT
 <213> Homo sapiens

<400> 4

Ile Ile Gly Gly His Thr Cys Thr Arg Ser Ser Gln Pro Trp Gln Ala
 1 5 10 15

Ala Leu Leu Ala Gly Pro Arg Arg Arg Phe Leu Cys Gly Gly Ala Leu
 20 25 30

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

Leu Gln Val Ala Leu Gly Lys His Asn Leu Arg Arg Trp Glu Ala Thr
 50 55 60

Gln Gln Val Leu Arg Val Val Arg Gln Val Thr His Pro Asn Tyr Asn
 65 70 75 80

Ser Arg Thr His Asp Asn Asp Leu Met Leu Leu Gln Leu Gln Gln Pro
 85 90 95

Ala Arg Ile Gly Arg Ala Val Arg Pro Ile Glu Val Thr Gln Ala Cys
 100 105 110

Ala Ser Pro Gly Thr Ser Cys Arg Val Ser Gly Trp Gly Thr Ile Ser
 115 120 125

Ser Pro Ile Ala Arg Tyr Pro Ala Ser Leu Gln Cys Val Asn Ile Asn
 130 135 140

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

Pro Gly Met Val Cys Ala Gly Val Pro Gln Gly Gly Lys Asp Ser Cys

165

170

175

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

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

Val Tyr Thr Asn Leu Cys Lys Tyr Arg Ser Trp Ile Glu Glu Thr Met
 210 215 220

Arg Asp Lys
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<210> 5
 <211> 198
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> binder

<220>
 <221> CDS
 <222> (1)..(198)

<400> 5
 ggc ccg cag ttt ggt ctg ttt agc aaa tat cgt acc ccg aat tgt ctg 48
 Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro Asn Cys Leu
 1 5 10 15

aac tgg act gac cat cag tgt gaa cgt gac tac gac ccg gtt tgt ggt 96
 Asn Trp Thr Asp His Gln Cys Glu Arg Asp Tyr Asp Pro Val Cys Gly
 20 25 30

agc gat atg agc acc tat gca aat gaa tgt acc ctg tgc atg aaa att 144
 Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys Met Lys Ile
 35 40 45

cgt gaa ggt ggc cat aat att aaa att att cgc aat ggt ccg tgc ggc 192
 Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly Pro Cys Gly
 50 55 60

ggc taa 198
 Gly
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<210> 6
 <211> 65
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 6

Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro Asn Cys Leu
 1 5 10 15

Asn Trp Thr Asp His Gln Cys Glu Arg Asp Tyr Asp Pro Val Cys Gly
 20 25 30

Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys Met Lys Ile
 35 40 45

Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly Pro Cys Gly
 50 55 60

Gly
 65

<210> 7
 <211> 198
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> binder

<220>
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 <222> (1)..(198)

<400> 7

ggc ccg cag ttt ggt ctg ttt agc aaa tat cgt acc ccg aat tgt gct 48
 Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro Asn Cys Ala
 1 5 10 15

aac act atg aaa cag gac tgt act cgt gaa tac gac ccg gtt tgt ggt 96
 Asn Thr Met Lys Gln Asp Cys Thr Arg Glu Tyr Asp Pro Val Cys Gly
 20 25 30

agc gat atg agc acc tat gca aat gaa tgt acc ctg tgc atg aaa att 144
 Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys Met Lys Ile

35	40	45	
cgt gaa ggt ggc cat aat att aaa att att cgc aat ggt ccg tgc ggc			192
Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly Pro Cys Gly			
50	55	60	

ggc taa	198
Gly	
65	

<210> 8
 <211> 65
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 8

Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro Asn Cys Ala
1 5 10 15

Asn Thr Met Lys Gln Asp Cys Thr Arg Glu Tyr Asp Pro Val Cys Gly
20 25 30

Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys Met Lys Ile
35 40 45

Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly Pro Cys Gly
50 55 60

Gly
 65

<210> 9
 <211> 198
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> binder

<220>
 <221> CDS
 <222> (1)..(198)

<400> 9
 ggc ccg cag ttt ggt ctg ttt agc aaa tat cgt acc ccg aat tgt cag 48
 Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro Asn Cys Gln
 1 5 10 15

gaa gac atg act gaa tac tgt gct cgt gac ttc gac ccg gtt tgt ggt 96
 Glu Asp Met Thr Glu Tyr Cys Ala Arg Asp Phe Asp Pro Val Cys Gly
 20 25 30

agc gat atg agc acc tat gca aat gaa tgt acc ctg tgc atg aaa att 144
 Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys Met Lys Ile
 35 40 45

cgt gaa ggt ggc cat aat att aaa att att cgc aat ggt ccg tgc ggc 192
 Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly Pro Cys Gly
 50 55 60

ggc taa 198
 Gly
 65

<210> 10
 <211> 65
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 10
 Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro Asn Cys Gln
 1 5 10 15

Glu Asp Met Thr Glu Tyr Cys Ala Arg Asp Phe Asp Pro Val Cys Gly
 20 25 30

Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys Met Lys Ile
 35 40 45

Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly Pro Cys Gly
 50 55 60

Gly
 65

<210> 11
 <211> 198

<212> DNA
 <213> Artificial Sequence

<220>
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<220>
 <221> CDS
 <222> (1)..(198)

<400> 11
 ggc ccg cag ttt ggt ctg ttt agc aaa tat cgt acc ccg aat tgt tct 48
 Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro Asn Cys Ser
 1 5 10 15
 cag tgg cag tac tct tct tgt gac cgt gtt tac gac ccg gtt tgt ggt 96
 Gln Trp Gln Tyr Ser Ser Cys Asp Arg Val Tyr Asp Pro Val Cys Gly
 20 25 30
 agc gat atg agc acc tat gca aat gaa tgt acc ctg tgc atg aaa att 144
 Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys Met Lys Ile
 35 40 45
 cgt gaa ggt ggc cat aat att aaa att att cgc aat ggt ccg tgc ggc 192
 Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly Pro Cys Gly
 50 55 60
 ggc taa 198
 Gly
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<210> 12
 <211> 65
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 12
 Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro Asn Cys Ser
 1 5 10 15
 Gln Trp Gln Tyr Ser Ser Cys Asp Arg Val Tyr Asp Pro Val Cys Gly
 20 25 30
 Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys Met Lys Ile
 35 40 45

Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly Pro Cys Gly
 50 55 60

Gly
 65

<210> 13
 <211> 198
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> binder

<220>
 <221> CDS
 <222> (1)..(198)

<400> 13
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 Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro Asn Cys Gly
 1 5 10 15

cgt tac act act ggt ggt tgt aac aaa gaa tac gaa ccg gtt tgt ggt 96
 Arg Tyr Thr Thr Gly Gly Cys Asn Lys Glu Tyr Glu Pro Val Cys Gly
 20 25 30

agc gat atg agc acc tat gca aat gaa tgt acc ctg tgc atg aaa att 144
 Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys Met Lys Ile
 35 40 45

cgt gaa ggt ggc cat aat att aaa att att cgc aat ggt ccg tgc ggc 192
 Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly Pro Cys Gly
 50 55 60

ggc taa 198
 Gly
 65

<210> 14
 <211> 65
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 14

Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro Asn Cys Gly
 1 5 10 15

Arg Tyr Thr Thr Gly Gly Cys Asn Lys Glu Tyr Glu Pro Val Cys Gly
 20 25 30

Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys Met Lys Ile
 35 40 45

Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly Pro Cys Gly
 50 55 60

Gly
 65

<210> 15
 <211> 198
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> binder

<220>
 <221> CDS
 <222> (1)..(198)

<400> 15
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 Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro Asn Cys Gln
 1 5 10 15

cag tac cgt gaa ctg ggt tgt ggt cgt cag tac gac ccg gtt tgt ggt 96
 Gln Tyr Arg Glu Leu Gly Cys Gly Arg Gln Tyr Asp Pro Val Cys Gly
 20 25 30

agc gat atg agc acc tat gca aat gaa tgt acc ctg tgc atg aaa att 144
 Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys Met Lys Ile
 35 40 45

cgt gaa ggt ggc cat aat att aaa att att cgc aat ggt ccg tgc ggc 192
 Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly Pro Cys Gly
 50 55 60

ggc taa 198
 Gly
 65

<210> 16
 <211> 65
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 16

Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro Asn Cys Gln
 1 5 10 15

Gln Tyr Arg Glu Leu Gly Cys Gly Arg Gln Tyr Asp Pro Val Cys Gly
 20 25 30

Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys Met Lys Ile
 35 40 45

Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly Pro Cys Gly
 50 55 60

Gly
 65

<210> 17
 <211> 198
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> binder

<220>
 <221> CDS
 <222> (1)..(198)

<400> 17

ggc ccg caa ttt ggt ctg ttt agc aaa tat cgt acc ccg aat tgt gac 48
 Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro Asn Cys Asp
 1 5 10 15

gaa atc ggt aaa tac ggt tgt ggt cgt tct tac gac ccg gtt tgt ggt 96
 Glu Ile Gly Lys Tyr Gly Cys Gly Arg Ser Tyr Asp Pro Val Cys Gly
 20 25 30

agc gat atg agc acc tat gca aat gaa tgt acc ctg tgc atg aaa att 144

Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys Met Lys Ile
 35 40 45

cgt gaa ggt ggc cat aat att aaa att att cgc aat ggt ccg tgc ggc
 Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly Pro Cys Gly
 50 55 60

192

ggc taa
 Gly
 65

198

<210> 18
 <211> 65
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 18

Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro Asn Cys Asp
 1 5 10 15

Glu Ile Gly Lys Tyr Gly Cys Gly Arg Ser Tyr Asp Pro Val Cys Gly
 20 25 30

Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys Met Lys Ile
 35 40 45

Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly Pro Cys Gly
 50 55 60

Gly
 65

<210> 19
 <211> 198
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> binder

<220>
 <221> CDS
 <222> (1)..(198)

<400> 19

ggc	ccg	cag	ttt	ggc	ctg	ttt	agc	aaa	tat	cgt	acc	ccg	aat	tgt	act	48
Gly	Pro	Gln	Phe	Gly	Leu	Phe	Ser	Lys	Tyr	Arg	Thr	Pro	Asn	Cys	Thr	
1				5					10					15		

tct	cag	act	ctg	ggc	tct	tgt	tct	cgt	gaa	tac	gac	ccg	gtt	tgt	ggc	96
Ser	Gln	Thr	Leu	Gly	Ser	Cys	Ser	Arg	Glu	Tyr	Asp	Pro	Val	Cys	Gly	
			20					25					30			

agc	gat	atg	agc	acc	tat	gca	aat	gaa	tgt	acc	ctg	tgc	atg	aaa	att	144
Ser	Asp	Met	Ser	Thr	Tyr	Ala	Asn	Glu	Cys	Thr	Leu	Cys	Met	Lys	Ile	
		35					40					45				

cgt	gaa	ggc	ggc	cat	aat	att	aaa	att	att	cgc	aat	ggc	ccg	tgc	ggc	192
Arg	Glu	Gly	Gly	His	Asn	Ile	Lys	Ile	Ile	Arg	Asn	Gly	Pro	Cys	Gly	
	50					55					60					

ggc	taa															198
Gly																
65																

<210> 20

<211> 65

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 20

Gly	Pro	Gln	Phe	Gly	Leu	Phe	Ser	Lys	Tyr	Arg	Thr	Pro	Asn	Cys	Thr
1				5					10					15	

Ser	Gln	Thr	Leu	Gly	Ser	Cys	Ser	Arg	Glu	Tyr	Asp	Pro	Val	Cys	Gly
			20					25					30		

Ser	Asp	Met	Ser	Thr	Tyr	Ala	Asn	Glu	Cys	Thr	Leu	Cys	Met	Lys	Ile
		35					40					45			

Arg	Glu	Gly	Gly	His	Asn	Ile	Lys	Ile	Ile	Arg	Asn	Gly	Pro	Cys	Gly
	50					55					60				

Gly
65

<210> 21

<211> 198
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> binder

<220>
 <221> CDS
 <222> (1)..(198)

<400> 21
 ggc ccg cag ttt ggt ctg ttt agc aaa tat cgt acc ccg aat tgt tac 48
 Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro Asn Cys Tyr
 1 5 10 15
 cag tac cgt tct aaa ggt tgt act cat gaa tac gac ccg gtt tgt ggt 96
 Gln Tyr Arg Ser Lys Gly Cys Thr His Glu Tyr Asp Pro Val Cys Gly
 20 25 30
 agc gat atg agc acc tat gca aat gaa tgt acc ctg tgc atg aaa att 144
 Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys Met Lys Ile
 35 40 45
 cgt gaa ggt ggc cat aat att aaa att att cgc aat ggt ccg tgc ggc 192
 Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly Pro Cys Gly
 50 55 60
 ggc taa 198
 Gly
 65

<210> 22
 <211> 65
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 22
 Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro Asn Cys Tyr
 1 5 10 15
 Gln Tyr Arg Ser Lys Gly Cys Thr His Glu Tyr Asp Pro Val Cys Gly
 20 25 30
 Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys Met Lys Ile
 35 40 45

Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly Pro Cys Gly
 50 55 60

Gly
 65

<210> 23
 <211> 198
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> binder

<220>
 <221> CDS
 <222> (1)..(198)

<400> 23
 ggc ccg cag ttt ggt ctg ttt agc aaa tat cgt acc ccg aat tgt atg 48
 Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro Asn Cys Met
 1 5 10 15
 cag cat gct cgt cag ggt tgt cat tac gac tac gac ccg gtt tgt ggt 96
 Gln His Ala Arg Gln Gly Cys His Tyr Asp Tyr Asp Pro Val Cys Gly
 20 25 30
 agc gat atg agc acc tat gca aat gaa tgt acc ctg tgc atg aaa att 144
 Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys Met Lys Ile
 35 40 45
 cgt gaa ggt ggc cat aat att aaa att att cgc aat ggt ccg tgc ggc 192
 Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly Pro Cys Gly
 50 55 60
 ggc taa 198
 Gly
 65

<210> 24
 <211> 65
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 24

Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro Asn Cys Met
 1 5 10 15

Gln His Ala Arg Gln Gly Cys His Tyr Asp Tyr Asp Pro Val Cys Gly
 20 25 30

Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys Met Lys Ile
 35 40 45

Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly Pro Cys Gly
 50 55 60

Gly
 65

<210> 25
 <211> 198
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> binder

<220>
 <221> CDS
 <222> (1)..(198)

<400> 25
 ggc ccg cag ttt ggt ctg ttt agc aaa tat cgt acc ccg aat tgt ggt 48
 Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro Asn Cys Gly
 1 5 10 15

gaa tac aaa ggt cgt ggt tgt tac tac cat tac gac ccg gtt tgt ggt 96
 Glu Tyr Lys Gly Arg Gly Cys Tyr Tyr His Tyr Asp Pro Val Cys Gly
 20 25 30

agc gat atg agc acc tat gca aat gaa tgt acc ctg tgc atg aaa att 144
 Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys Met Lys Ile
 35 40 45

cgt gaa ggt ggc cat aat att aaa att att cgc aat ggt ccg tgc ggc 192
 Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly Pro Cys Gly
 50 55 60

ggc taa 198
 Gly
 65

<210> 26
 <211> 65
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 26

Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro Asn Cys Gly
 1 5 10 15

Glu Tyr Lys Gly Arg Gly Cys Tyr Tyr His Tyr Asp Pro Val Cys Gly
 20 25 30

Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys Met Lys Ile
 35 40 45

Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly Pro Cys Gly
 50 55 60

Gly
 65

<210> 27
 <211> 198
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> binder

<220>
 <221> CDS
 <222> (1)..(198)

<400> 27

ggc ccg cag ttt ggt ctg ttt agc aaa tat cgt acc ccg aat tgt ggt 48
 Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro Asn Cys Gly
 1 5 10 15

act atg cag ggt tct ggt tgt act tac cat tac gaa ccg gtt tgt ggt 96
 Thr Met Gln Gly Ser Gly Cys Thr Tyr His Tyr Glu Pro Val Cys Gly
 20 25 30

agc gat atg agc acc tat gca aat gaa tgt acc ctg tgc atg aaa att 144
 Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys Met Lys Ile
 35 40 45

cgt gaa ggt ggc cat aat att aaa att att cgc aat ggt ccg tgc ggc 192
 Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly Pro Cys Gly
 50 55 60

ggc taa 198
 Gly
 65

<210> 28
 <211> 65
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 28

Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro Asn Cys Gly
 1 5 10 15

Thr Met Gln Gly Ser Gly Cys Thr Tyr His Tyr Glu Pro Val Cys Gly
 20 25 30

Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys Met Lys Ile
 35 40 45

Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly Pro Cys Gly
 50 55 60

Gly
 65

<210> 29
 <211> 198
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> binder

<220>
 <221> CDS

<222> (1)..(198)

<400> 29

ggc ccg cag ttt ggt ctg ttt agc aaa tat cgt acc ccg aat tgt tct 48
Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro Asn Cys Ser
1 5 10 15

cag gtt gtt gaa act tac tgt aac cgt gac tac gac ccg gtt tgt ggt 96
Gln Val Val Glu Thr Tyr Cys Asn Arg Asp Tyr Asp Pro Val Cys Gly
20 25 30

agc gat atg agc acc tat gca aat gaa tgt acc ctg tgc atg aaa att 144
Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys Met Lys Ile
35 40 45

cgt gaa ggt ggc cat aat att aaa att att cgc aat ggt ccg tgc ggc 192
Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly Pro Cys Gly
50 55 60

ggc taa 198
Gly
65

<210> 30

$\langle 211 \rangle$	65
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<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthetic Construct

<400> 30

Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro Asn Cys Ser
1 5 10 15

Gln Val Val Glu Thr Tyr Cys Asn Arg Asp Tyr Asp Pro Val Cys Gly
20 25 30

Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys Met Lys Ile
35 40 45

Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly Pro Cys Gly
50 55 60

Gly
65

<210> 31
 <211> 198
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> binder

<220>
 <221> CDS
 <222> (1)..(198)

<400> 31
 ggc ccg cag ttt ggt ctg ttt agc aaa tat cgt acc ccg aat tgt tac 48
 Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro Asn Cys Tyr
 1 5 10 15
 gac act act act cat tac tgt tct cgt gaa tac gac ccg gtt tgt ggt 96
 Asp Thr Thr Thr His Tyr Cys Ser Arg Glu Tyr Asp Pro Val Cys Gly
 20 25 30
 agc gat atg agc acc tat gca aat gaa tgt acc ctg tgc atg aaa att 144
 Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys Met Lys Ile
 35 40 45
 cgt gaa ggt ggc cat aat att aaa att att cgc aat ggt ccg tgc ggc 192
 Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly Pro Cys Gly
 50 55 60
 ggc taa 198
 Gly
 65

<210> 32
 <211> 65
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 32
 Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro Asn Cys Tyr
 1 5 10 15
 Asp Thr Thr Thr His Tyr Cys Ser Arg Glu Tyr Asp Pro Val Cys Gly
 20 25 30
 Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys Met Lys Ile

35

40

45

Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly Pro Cys Gly
 50 55 60

Gly
 65

<210> 33
 <211> 897
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> binder

<220>
 <221> CDS
 <222> (1)..(897)

<400> 33
 gat gac gac ggc cct cag ttc ggc ctg ttc agc aag tac aga acc cct 48
 Asp Asp Asp Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro
 1 5 10 15
 aac tgc ctg cag tgg act gac cat cag tgt gaa cgt gac tac gac cct 96
 Asn Cys Leu Gln Trp Thr Asp His Gln Cys Glu Arg Asp Tyr Asp Pro
 20 25 30
 gtg tgc ggc agc gac atg agc acc tac gcc aat gag tgc acc ctg tgc 144
 Val Cys Gly Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys
 35 40 45
 atg aag atc aga gaa ggc ggc cac aac atc aag atc atc cgg aat ggc 192
 Met Lys Ile Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly
 50 55 60
 ccc tgc gaa ccc aag agc tgc gac aag acc cac acc tgt ccc cct tgt 240
 Pro Cys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 65 70 75 80
 cct gcc ccc gaa ctg ctg gga gga cct agc gtg ttc ctg ttc ccc cca 288
 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 85 90 95
 aag ccc aag gac acc ctg atg atc agc cgg acc ccc gaa gtg acc tgc 336
 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 100 105 110
 gtg gtg gtg gat gtg tcc cac gag gac cct gaa gtg aag ttc aat tgg 384

Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	
		115					120					125				
tac	gtg	gac	ggc	gtg	gaa	gtg	cac	aac	gcc	aag	acc	aag	cct	aga	gag	432
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	
	130					135					140					
gaa	cag	tac	aac	tcc	acc	tac	cgg	gtg	gtg	tct	gtg	ctg	aca	gtg	ctg	480
Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	
145				150						155					160	
cat	cag	gac	tgg	ctg	aac	ggc	aaa	gag	tac	aag	tgc	aag	gtg	tcc	aac	528
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	
				165					170					175		
aag	gcc	ctg	cct	gcc	ccc	atc	gag	aaa	acc	atc	agc	aag	gcc	aag	ggc	576
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	
			180					185					190			
cag	ccc	cgc	gaa	ccc	cag	gtg	tac	aca	ctg	ccc	cct	agc	cgg	gaa	gag	624
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	
			195				200					205				
atg	acc	aag	aac	cag	gtg	tcc	ctg	acc	tgt	ctc	gtg	aaa	ggc	ttc	tac	672
Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	
	210					215					220					
ccc	agc	gac	att	gcc	gtg	gaa	tgg	gag	agc	aac	ggc	cag	ccc	gag	aac	720
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	
225					230					235					240	
aac	tac	aag	acc	acc	ccc	cct	gtg	ctg	gac	agc	gac	ggc	tca	ttc	ttc	768
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	
				245					250					255		
ctg	tac	agc	aag	ctg	acc	gtg	gac	aag	agc	cgg	tgg	cag	cag	ggc	aac	816
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	
			260					265					270			
gtg	ttc	agc	tgc	agc	gtg	atg	cac	gag	gcc	ctg	cac	aac	cac	tac	acc	864
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	
		275					280					285				
cag	aag	tcc	ctg	agc	ctg	agc	ccc	ggc	aaa	tga						897
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys							
	290					295										

<210> 34

<211> 298

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 34

Asp Asp Asp Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro
 1 5 10 15

Asn Cys Leu Gln Trp Thr Asp His Gln Cys Glu Arg Asp Tyr Asp Pro
 20 25 30

Val Cys Gly Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys
 35 40 45

Met Lys Ile Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly
 50 55 60

Pro Cys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 65 70 75 80

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 85 90 95

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 100 105 110

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 115 120 125

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 130 135 140

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 145 150 155 160

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 165 170 175

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

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 195 200 205

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 210 215 220

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 225 230 235 240

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 245 250 255

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

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 275 280 285

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 290 295

<210> 35
 <211> 897
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> binder

<220>
 <221> CDS
 <222> (1)..(897)

<400> 35
 gat gac gac ggc cct cag ttc ggc ctg ttc agc aag tac aga acc cct 48
 Asp Asp Asp Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro
 1 5 10 15

aac tgc gct aac act atg aaa cag gac tgt act cgt gaa tac gac cct 96
 Asn Cys Ala Asn Thr Met Lys Gln Asp Cys Thr Arg Glu Tyr Asp Pro
 20 25 30

gtg tgc ggc agc gac atg agc acc tac gcc aat gag tgc acc ctg tgc 144
 Val Cys Gly Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys
 35 40 45

atg aag atc aga gaa ggc ggc cac aac atc aag atc atc cgg aat ggc 192
 Met Lys Ile Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly

50	55	60	
ccc tgc gaa ccc aag agc tgc gac aag acc cac acc tgt ccc cct tgt Pro Cys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys 65 70 75 80			240
cct gcc ccc gaa ctg ctg gga gga cct agc gtg ttc ctg ttc ccc cca Pro Ala Pro Glu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro 85 90 95			288
aag ccc aag gac acc ctg atg atc agc cgg acc ccc gaa gtg acc tgc Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys 100 105 110			336
gtg gtg gtg gat gtg tcc cac gag gac cct gaa gtg aag ttc aat tgg Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp 115 120 125			384
tac gtg gac ggc gtg gaa gtg cac aac gcc aag acc aag cct aga gag Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu 130 135 140			432
gaa cag tac aac tcc acc tac cgg gtg gtg tct gtg ctg aca gtg ctg Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu 145 150 155 160			480
cat cag gac tgg ctg aac ggc aaa gag tac aag tgc aag gtg tcc aac His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn 165 170 175			528
aag gcc ctg cct gcc ccc atc gag aaa acc atc agc aag gcc aag ggc Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly 180 185 190			576
cag ccc cgc gaa ccc cag gtg tac aca ctg ccc cct agc cgg gaa gag Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu 195 200 205			624
atg acc aag aac cag gtg tcc ctg acc tgt ctc gtg aaa ggc ttc tac Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr 210 215 220			672
ccc agc gac att gcc gtg gaa tgg gag agc aac ggc cag ccc gag aac Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn 225 230 235 240			720
aac tac aag acc acc ccc cct gtg ctg gac agc gac ggc tca ttc ttc Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe 245 250 255			768
ctg tac agc aag ctg acc gtg gac aag agc cgg tgg cag cag ggc aac Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn 260 265 270			816

864

897

$\langle 210 \rangle$	36
$\langle 211 \rangle$	298
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	Artificial Sequence

<220>
<223> Synthetic Construct

<400> 36

Asp Asp Asp Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro
1 5 10 15

Asn Cys Ala Asn Thr Met Lys Gln Asp Cys Thr Arg Glu Tyr Asp Pro
20 25 30

Val Cys Gly Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys
35 40 45

Met Lys Ile Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly
50 55 60

Pro Cys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
65 70 75 80

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
85 90 95

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
100 105 110

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
115 120 125

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
130 135 140

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 145 150 155 160

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 165 170 175

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

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 195 200 205

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 210 215 220

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 225 230 235 240

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 245 250 255

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

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 275 280 285

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 290 295

<210> 37
 <211> 897
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> binder

<220>
 <221> CDS
 <222> (1)..(897)

Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr		
210						215					220						
ccc	agc	gac	att	gcc	gtg	gaa	tgg	gag	agc	aac	ggc	cag	ccc	gag	aac	720	
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn		
225					230					235					240		
aac	tac	aag	acc	acc	ccc	cct	gtg	ctg	gac	agc	gac	ggc	tca	ttc	ttc	768	
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe		
				245					250					255			
ctg	tac	agc	aag	ctg	acc	gtg	gac	aag	agc	cgg	tgg	cag	cag	ggc	aac	816	
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn		
			260					265					270				
gtg	ttc	agc	tgc	agc	gtg	atg	cac	gag	gcc	ctg	cac	aac	cac	tac	acc	864	
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr		
		275					280					285					
cag	aag	tcc	ctg	agc	ctg	agc	ccc	ggc	aaa	tga						897	
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys								
	290					295											

<210> 38
 <211> 298
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 38

Asp	Asp	Asp	Gly	Pro	Gln	Phe	Gly	Leu	Phe	Ser	Lys	Tyr	Arg	Thr	Pro		
1				5					10					15			
Asn	Cys	Gln	Glu	Asp	Met	Thr	Glu	Tyr	Cys	Ala	Arg	Asp	Phe	Asp	Pro		
		20						25					30				
Val	Cys	Gly	Ser	Asp	Met	Ser	Thr	Tyr	Ala	Asn	Glu	Cys	Thr	Leu	Cys		
		35					40					45					
Met	Lys	Ile	Arg	Glu	Gly	Gly	His	Asn	Ile	Lys	Ile	Ile	Arg	Asn	Gly		
	50					55					60						
Pro	Cys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys		
65					70					75					80		

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
85 90 95

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
100 105 110

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
115 120 125

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
130 135 140

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
145 150 155 160

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
165 170 175

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

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
195 200 205

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
210 215 220

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
225 230 235 240

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
245 250 255

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

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
275 280 285

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
290 295

<210> 39
 <211> 897
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> binder

<220>
 <221> CDS
 <222> (1)..(897)

<400> 39
 gat gac gac ggc cct cag ttc ggc ctg ttc agc aag tac aga acc cct 48
 Asp Asp Asp Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro
 1 5 10 15

aac tgc ggc cag tgg cag tac tct tct tgt gac cgt gtt tac gac cct 96
 Asn Cys Gly Gln Trp Gln Tyr Ser Ser Cys Asp Arg Val Tyr Asp Pro
 20 25 30

gtg tgc ggc agc gac atg agc acc tac gcc aat gag tgc acc ctg tgc 144
 Val Cys Gly Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys
 35 40 45

atg aag atc aga gaa ggc ggc cac aac atc aag atc atc cgg aat ggc 192
 Met Lys Ile Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly
 50 55 60

ccc tgc gaa ccc aag agc tgc gac aag acc cac acc tgt ccc cct tgt 240
 Pro Cys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 65 70 75 80

cct gcc ccc gaa ctg ctg gga gga cct agc gtg ttc ctg ttc ccc cca 288
 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 85 90 95

aag ccc aag gac acc ctg atg atc agc cgg acc ccc gaa gtg acc tgc 336
 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 100 105 110

gtg gtg gtg gat gtg tcc cac gag gac cct gaa gtg aag ttc aat tgg 384
 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 115 120 125

tac gtg gac ggc gtg gaa gtg cac aac gcc aag acc aag cct aga gag 432
 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 130 135 140

gaa cag tac aac tcc acc tac cgg gtg gtg tct gtg ctg aca gtg ctg 480
 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu

145	150	155	160	
cat cag gac tgg	ctg aac ggc aaa	gag tac aag tgc aag	gtg tcc aac	528
His Gln Asp Trp	Leu Asn Gly Lys	Glu Tyr Lys Cys Lys	Val Ser Asn	
	165	170	175	
aag gcc ctg cct	gcc ccc atc gag	aaa acc atc agc	aag gcc aag ggc	576
Lys Ala Leu Pro	Ala Pro Ile Glu	Lys Thr Ile Ser Lys	Ala Lys Gly	
	180	185	190	
cag ccc cgc gaa	ccc cag gtg tac	aca ctg ccc cct	agc cgg gaa gag	624
Gln Pro Arg Glu	Pro Gln Val Tyr	Thr Leu Pro Pro	Ser Arg Glu Glu	
	195	200	205	
atg acc aag aac	cag gtg tcc ctg	acc tgt ctc gtg	aaa ggc ttc tac	672
Met Thr Lys Asn	Gln Val Ser Leu	Thr Cys Leu Val	Lys Gly Phe Tyr	
	210	215	220	
ccc agc gac att	gcc gtg gaa tgg	gag agc aac ggc	cag ccc gag aac	720
Pro Ser Asp Ile	Ala Val Glu Trp	Glu Ser Asn Gly	Gln Pro Glu Asn	
	225	230	235	240
aac tac aag acc	acc ccc cct gtg	ctg gac agc gac	ggc tca ttc ttc	768
Asn Tyr Lys Thr	Thr Pro Pro Val	Leu Asp Ser Asp	Gly Ser Phe Phe	
	245	250	255	
ctg tac agc aag	ctg acc gtg gac	aag agc cgg tgg	cag cag ggc aac	816
Leu Tyr Ser Lys	Leu Thr Val Asp	Lys Ser Arg Trp	Gln Gln Gly Asn	
	260	265	270	
gtg ttc agc tgc	agc gtg atg cac	gag gcc ctg cac	aac cac tac acc	864
Val Phe Ser Cys	Ser Val Met His	Glu Ala Leu His	Asn His Tyr Thr	
	275	280	285	
cag aag tcc ctg	agc ctg agc ccc	ggc aaa tga		897
Gln Lys Ser Leu	Ser Leu Ser Pro	Gly Lys		
	290	295		

<210> 40
 <211> 298
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 40

Asp Asp Asp Gly	Pro Gln Phe Gly	Leu Phe Ser Lys	Tyr Arg Thr Pro
1	5	10	15

Asn Cys Gly Gln Trp Gln Tyr Ser Ser Cys Asp Arg Val Tyr Asp Pro

20

25

30

Val Cys Gly Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys
 35 40 45

Met Lys Ile Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly
 50 55 60

Pro Cys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 65 70 75 80

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 85 90 95

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 100 105 110

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 115 120 125

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 130 135 140

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 145 150 155 160

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 165 170 175

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

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 195 200 205

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 210 215 220

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 225 230 235 240

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 245 250 255

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

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 275 280 285

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 290 295

<210> 41
 <211> 897
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> binder

<220>
 <221> CDS
 <222> (1)..(897)

<400> 41
 gat gac gac ggc cct cag ttc ggc ctg ttc agc aag tac aga acc cct 48
 Asp Asp Asp Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro
 1 5 10 15
 aac tgc ggt cgt tac act act ggt ggt tgt aac aaa gaa tac gaa cct 96
 Asn Cys Gly Arg Tyr Thr Thr Gly Gly Cys Asn Lys Glu Tyr Glu Pro
 20 25 30
 gtg tgc ggc agc gac atg agc acc tac gcc aat gag tgc acc ctg tgc 144
 Val Cys Gly Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys
 35 40 45
 atg aag atc aga gaa ggc ggc cac aac atc aag atc atc cgg aat ggc 192
 Met Lys Ile Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly
 50 55 60
 ccc tgc gaa ccc aag agc tgc gac aag acc cac acc tgt ccc cct tgt 240
 Pro Cys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 65 70 75 80
 cct gcc ccc gaa ctg ctg gga gga cct agc gtg ttc ctg ttc ccc cca 288
 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 85 90 95

aag ccc aag gac acc ctg atg atc agc cgg acc ccc gaa gtg acc tgc	336
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys	
100 105 110	
gtg gtg gtg gat gtg tcc cac gag gac cct gaa gtg aag ttc aat tgg	384
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp	
115 120 125	
tac gtg gac ggc gtg gaa gtg cac aac gcc aag acc aag cct aga gag	432
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu	
130 135 140	
gaa cag tac aac tcc acc tac cgg gtg gtg tct gtg ctg aca gtg ctg	480
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu	
145 150 155 160	
cat cag gac tgg ctg aac ggc aaa gag tac aag tgc aag gtg tcc aac	528
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn	
165 170 175	
aag gcc ctg cct gcc ccc atc gag aaa acc atc agc aag gcc aag ggc	576
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly	
180 185 190	
cag ccc cgc gaa ccc cag gtg tac aca ctg ccc cct agc cgg gaa gag	624
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu	
195 200 205	
atg acc aag aac cag gtg tcc ctg acc tgt ctc gtg aaa ggc ttc tac	672
Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr	
210 215 220	
ccc agc gac att gcc gtg gaa tgg gag agc aac ggc cag ccc gag aac	720
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn	
225 230 235 240	
aac tac aag acc acc ccc cct gtg ctg gac agc gac ggc tca ttc ttc	768
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe	
245 250 255	
ctg tac agc aag ctg acc gtg gac aag agc cgg tgg cag cag ggc aac	816
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn	
260 265 270	
gtg ttc agc tgc agc gtg atg cac gag gcc ctg cac aac cac tac acc	864
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr	
275 280 285	
cag aag tcc ctg agc ctg agc ccc ggc aaa tga	897
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys	
290 295	

<210> 42
 <211> 298
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 42

Asp Asp Asp Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro
 1 5 10 15

Asn Cys Gly Arg Tyr Thr Thr Gly Gly Cys Asn Lys Glu Tyr Glu Pro
 20 25 30

Val Cys Gly Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys
 35 40 45

Met Lys Ile Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly
 50 55 60

Pro Cys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 65 70 75 80

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 85 90 95

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 100 105 110

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 115 120 125

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 130 135 140

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 145 150 155 160

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 165 170 175

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

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 195 200 205

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 210 215 220

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 225 230 235 240

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 245 250 255

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

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 275 280 285

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 290 295

<210> 43
 <211> 897
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> binder

<220>
 <221> CDS
 <222> (1)..(897)

<400> 43
 gat gac gac ggc cct cag ttc ggc ctg ttc agc aag tac aga acc cct 48
 Asp Asp Asp Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro
 1 5 10 15

aac tgc cag cag tac cgt gaa ctg ggt tgt ggt cgt cag tac gac cct 96
 Asn Cys Gln Gln Tyr Arg Glu Leu Gly Cys Gly Arg Gln Tyr Asp Pro
 20 25 30

gtg tgc ggc agc gac atg agc acc tac gcc aat gag tgc acc ctg tgc Val Cys Gly Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys 35 40 45	144
atg aag atc aga gaa ggc ggc cac aac atc aag atc atc cgg aat ggc Met Lys Ile Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly 50 55 60	192
ccc tgc gaa ccc aag agc tgc gac aag acc cac acc tgt ccc cct tgt Pro Cys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys 65 70 75 80	240
cct gcc ccc gaa ctg ctg gga gga cct agc gtg ttc ctg ttc ccc cca Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro 85 90 95	288
aag ccc aag gac acc ctg atg atc agc cgg acc ccc gaa gtg acc tgc Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys 100 105 110	336
gtg gtg gtg gat gtg tcc cac gag gac cct gaa gtg aag ttc aat tgg Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp 115 120 125	384
tac gtg gac ggc gtg gaa gtg cac aac gcc aag acc aag cct aga gag Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu 130 135 140	432
gaa cag tac aac tcc acc tac cgg gtg gtg tct gtg ctg aca gtg ctg Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu 145 150 155 160	480
cat cag gac tgg ctg aac ggc aaa gag tac aag tgc aag gtg tcc aac His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn 165 170 175	528
aag gcc ctg cct gcc ccc atc gag aaa acc atc agc aag gcc aag ggc Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly 180 185 190	576
cag ccc cgc gaa ccc cag gtg tac aca ctg ccc cct agc cgg gaa gag Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu 195 200 205	624
atg acc aag aac cag gtg tcc ctg acc tgt ctc gtg aaa ggc ttc tac Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr 210 215 220	672
ccc agc gac att gcc gtg gaa tgg gag agc aac ggc cag ccc gag aac Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn 225 230 235 240	720
aac tac aag acc acc ccc cct gtg ctg gac agc gac ggc tca ttc ttc Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe 245 250 255 260	768

245								250								255								
ctg	tac	agc	aag	ctg	acc	gtg	gac	aag	agc	cgg	tgg	cag	cag	ggc	aac		816							
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn									
			260					265						270										
gtg	ttc	agc	tgc	agc	gtg	atg	cac	gag	gcc	ctg	cac	aac	cac	tac	acc		864							
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr									
			275				280					285												
cag	aag	tcc	ctg	agc	ctg	agc	ccc	ggc	aaa	tga							897							
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys															
			290				295																	

<210> 44
 <211> 298
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 44

Asp	Asp	Asp	Gly	Pro	Gln	Phe	Gly	Leu	Phe	Ser	Lys	Tyr	Arg	Thr	Pro
1				5					10					15	

Asn	Cys	Gln	Gln	Tyr	Arg	Glu	Leu	Gly	Cys	Gly	Arg	Gln	Tyr	Asp	Pro
			20					25					30		

Val	Cys	Gly	Ser	Asp	Met	Ser	Thr	Tyr	Ala	Asn	Glu	Cys	Thr	Leu	Cys
		35					40					45			

Met	Lys	Ile	Arg	Glu	Gly	Gly	His	Asn	Ile	Lys	Ile	Ile	Arg	Asn	Gly
	50					55					60				

Pro	Cys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys
65					70					75					80

Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro
				85					90					95	

Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys
			100					105					110		

Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115

120

125

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 130 135 140

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 145 150 155 160

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 165 170 175

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

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 195 200 205

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 210 215 220

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 225 230 235 240

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 245 250 255

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

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 275 280 285

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 290 295

<210> 45

<211> 897

<212> DNA

<213> Artificial Sequence

<220>

<223> binder

<220>

<221> CDS

<222> (1)..(897)

<400> 45

gat	gac	gac	ggc	cct	cag	ttc	ggc	ctg	ttc	agc	aag	tac	aga	acc	cct	48
Asp	Asp	Asp	Gly	Pro	Gln	Phe	Gly	Leu	Phe	Ser	Lys	Tyr	Arg	Thr	Pro	
1				5				10						15		

aac	tgc	gac	gaa	atc	ggc	aaa	tac	ggc	tgt	ggc	cgt	tct	tac	gac	cct	96
Asn	Cys	Asp	Glu	Ile	Gly	Lys	Tyr	Gly	Cys	Gly	Arg	Ser	Tyr	Asp	Pro	
			20					25					30			

gtg	tgc	ggc	agc	gac	atg	agc	acc	tac	gcc	aat	gag	tgc	acc	ctg	tgc	144
Val	Cys	Gly	Ser	Asp	Met	Ser	Thr	Tyr	Ala	Asn	Glu	Cys	Thr	Leu	Cys	
		35					40					45				

atg	aag	atc	aga	gaa	ggc	ggc	cac	aac	atc	aag	atc	atc	cgg	aat	ggc	192
Met	Lys	Ile	Arg	Glu	Gly	Gly	His	Asn	Ile	Lys	Ile	Ile	Arg	Asn	Gly	
	50					55					60					

ccc	tgc	gaa	ccc	aag	agc	tgc	gac	aag	acc	cac	acc	tgt	ccc	cct	tgt	240
Pro	Cys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	
65					70					75					80	

cct	gcc	ccc	gaa	ctg	ctg	gga	gga	cct	agc	gtg	ttc	ctg	ttc	ccc	cca	288
Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	
			85					90						95		

aag	ccc	aag	gac	acc	ctg	atg	atc	agc	cgg	acc	ccc	gaa	gtg	acc	tgc	336
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	
			100					105					110			

gtg	gtg	gtg	gat	gtg	tcc	cac	gag	gac	cct	gaa	gtg	aag	ttc	aat	tgg	384
Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	
		115					120					125				

tac	gtg	gac	ggc	gtg	gaa	gtg	cac	aac	gcc	aag	acc	aag	cct	aga	gag	432
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	
	130					135					140					

gaa	cag	tac	aac	tcc	acc	tac	cgg	gtg	gtg	tct	gtg	ctg	aca	gtg	ctg	480
Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	
145					150					155					160	

cat	cag	gac	tgg	ctg	aac	ggc	aaa	gag	tac	aag	tgc	aag	gtg	tcc	aac	528
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	
				165					170					175		

aag	gcc	ctg	cct	gcc	ccc	atc	gag	aaa	acc	atc	agc	aag	gcc	aag	ggc	576
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	
			180					185					190			

Pro Cys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
65 70 75 80

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
85 90 95

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
100 105 110

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
115 120 125

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
130 135 140

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
145 150 155 160

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
165 170 175

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

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
195 200 205

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
210 215 220

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
225 230 235 240

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
245 250 255

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

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 275 280 285

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 290 295

<210> 47
 <211> 897
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> binder

<220>
 <221> CDS
 <222> (1)..(897)

<400> 47
 gat gac gac ggc cct cag ttc ggc ctg ttc agc aag tac aga acc cct 48
 Asp Asp Asp Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro
 1 5 10 15
 aac tgc ggc tct cag act ctg ggt tct tgt tct cgt gaa tac gac cct 96
 Asn Cys Gly Ser Gln Thr Leu Gly Ser Cys Ser Arg Glu Tyr Asp Pro
 20 25 30
 gtg tgc ggc agc gac atg agc acc tac gcc aat gag tgc acc ctg tgc 144
 Val Cys Gly Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys
 35 40 45
 atg aag atc aga gaa ggc ggc cac aac atc aag atc atc cgg aat ggc 192
 Met Lys Ile Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly
 50 55 60
 ccc tgc gaa ccc aag agc tgc gac aag acc cac acc tgt ccc cct tgt 240
 Pro Cys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 65 70 75 80
 cct gcc ccc gaa ctg ctg gga gga cct agc gtg ttc ctg ttc ccc cca 288
 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 85 90 95
 aag ccc aag gac acc ctg atg atc agc cgg acc ccc gaa gtg acc tgc 336
 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 100 105 110
 gtg gtg gtg gat gtg tcc cac gag gac cct gaa gtg aag ttc aat tgg 384
 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 115 120 125

tac gtg gac ggc gtg gaa gtg cac aac gcc aag acc aag cct aga gag Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu 130 135 140	432
gaa cag tac aac tcc acc tac cgg gtg gtg tct gtg ctg aca gtg ctg Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu 145 150 155 160	480
cat cag gac tgg ctg aac ggc aaa gag tac aag tgc aag gtg tcc aac His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn 165 170 175	528
aag gcc ctg cct gcc ccc atc gag aaa acc atc agc aag gcc aag ggc Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly 180 185 190	576
cag ccc cgc gaa ccc cag gtg tac aca ctg ccc cct agc cgg gaa gag Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu 195 200 205	624
atg acc aag aac cag gtg tcc ctg acc tgt ctc gtg aaa ggc ttc tac Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr 210 215 220	672
ccc agc gac att gcc gtg gaa tgg gag agc aac ggc cag ccc gag aac Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn 225 230 235 240	720
aac tac aag acc acc ccc cct gtg ctg gac agc gac ggc tca ttc ttc Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe 245 250 255	768
ctg tac agc aag ctg acc gtg gac aag agc cgg tgg cag cag ggc aac Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn 260 265 270	816
gtg ttc agc tgc agc gtg atg cac gag gcc ctg cac aac cac tac acc Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr 275 280 285	864
cag aag tcc ctg agc ctg agc ccc ggc aaa tga Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys 290 295	897

<210> 48

<211> 298

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 48

Asp Asp Asp Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro
 1 5 10 15

Asn Cys Gly Ser Gln Thr Leu Gly Ser Cys Ser Arg Glu Tyr Asp Pro
 20 25 30

Val Cys Gly Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys
 35 40 45

Met Lys Ile Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly
 50 55 60

Pro Cys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 65 70 75 80

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 85 90 95

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 100 105 110

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 115 120 125

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 130 135 140

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 145 150 155 160

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 165 170 175

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

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 195 200 205

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

210

215

220

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 225 230 235 240

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 245 250 255

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

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 275 280 285

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 290 295

<210> 49
 <211> 897
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> binder

<220>
 <221> CDS
 <222> (1)..(897)

<400> 49
 gat gac gac ggc cct cag ttc ggc ctg ttc agc aag tac aga acc cct 48
 Asp Asp Asp Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro
 1 5 10 15

aac tgc tac cag tac aga agc aag ggc tgc acc cac gag tac gat cct 96
 Asn Cys Tyr Gln Tyr Arg Ser Lys Gly Cys Thr His Glu Tyr Asp Pro
 20 25 30

gtg tgc ggc agc gac atg agc acc tac gcc aat gag tgc acc ctg tgc 144
 Val Cys Gly Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys
 35 40 45

atg aag atc aga gaa ggc ggc cac aac atc aag atc atc cgg aat ggc 192
 Met Lys Ile Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly
 50 55 60

ccc tgc gaa ccc aag agc tgc gac aag acc cac acc tgt ccc cct tgt 240

Pro 65	Cys	Glu	Pro	Lys	Ser 70	Cys	Asp	Lys	Thr	His 75	Thr	Cys	Pro	Pro	Cys 80	
cct Pro	gcc Ala	ccc Pro	gaa Glu	ctg Leu 85	ctg Leu	gga Gly	gga Gly	cct Pro	agc Ser 90	gtg Val	ttc Phe	ctg Leu	ttc Phe 95	ccc Pro	cca Pro	288
aag Lys	ccc Pro	aag Lys	gac Asp 100	acc Thr	ctg Leu	atg Met	atc Ile	agc Ser 105	cgg Arg	acc Thr	ccc Pro	gaa Glu	gtg Val 110	acc Thr	tgc Cys	336
gtg Val	gtg Val	gtg Val	gat Asp 115	gtg Val	tcc Ser	cac His	gag Glu 120	gac Asp	cct Pro	gaa Glu	gtg Val	aag Lys 125	ttc Phe	aat Asn	tgg Trp	384
tac Tyr 130	gtg Val	gac Asp	ggc Gly	gtg Val	gaa Glu	gtg Val 135	cac His	aac Asn	gcc Ala	aag Lys	acc Thr 140	aag Lys	cct Pro	aga Arg	gag Glu	432
gaa Glu 145	cag Gln	tac Tyr	aac Asn	tcc Ser	acc Thr 150	tac Tyr	cgg Arg	gtg Val	gtg Val	tct Ser 155	gtg Val	ctg Leu	aca Thr	gtg Val	ctg Leu 160	480
cat His	cag Gln	gac Asp	tgg Trp 165	ctg Leu	aac Asn	ggc Gly	aaa Lys	gag Glu	tac Tyr 170	aag Lys	tgc Cys	aag Lys	gtg Val 175	tcc Ser	aac Asn	528
aag Lys	gcc Ala	ctg Leu	cct Pro 180	gcc Ala	ccc Pro	atc Ile	gag Glu 185	aaa Lys	acc Thr	atc Ile	agc Ser	aag Lys	gcc Ala 190	aag Lys	ggc Gly	576
cag Gln	ccc Pro	cgc Arg 195	gaa Glu	ccc Pro	cag Gln	gtg Val	tac Tyr 200	aca Thr	ctg Leu	ccc Pro	cct Pro	agc Ser 205	cgg Arg	gaa Glu	gag Glu	624
atg Met 210	acc Thr	aag Lys	aac Asn	cag Gln	gtg Val	tcc Ser 215	ctg Leu	acc Thr	tgt Cys	ctc Leu	gtg Val 220	aaa Lys	ggc Gly	ttc Phe	tac Tyr	672
ccc Pro 225	agc Ser	gac Asp	att Ile	gcc Ala	gtg Val 230	gaa Glu	tgg Trp	gag Glu	agc Ser	aac Asn 235	ggc Gly	cag Gln	ccc Pro	gag Glu	aac Asn 240	720
aac Asn	tac Tyr	aag Lys	acc Thr	acc Thr 245	ccc Pro	cct Pro	gtg Val	ctg Leu	gac Asp 250	agc Ser	gac Asp	ggc Gly	tca Ser	ttc Phe 255	ttc Phe	768
ctg Leu	tac Tyr	agc Ser	aag Lys 260	ctg Leu	acc Thr	gtg Val	gac Asp 265	aag Lys	agc Ser	cgg Arg	tgg Trp	cag Gln	cag Gln	ggc Gly	aac Asn	816
gtg Val	ttc Phe	agc Ser 275	tgc Cys	agc Ser	gtg Val	atg Met	cac His 280	gag Glu	gcc Ala	ctg Leu	cac His	aac Asn 285	cac His	tac Tyr	acc Thr	864

cag aag tcc ctg agc ctg agc ccc ggc aaa tga
 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 290 295

<210> 50
 <211> 298
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 50

Asp Asp Asp Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro
 1 5 10 15

Asn Cys Tyr Gln Tyr Arg Ser Lys Gly Cys Thr His Glu Tyr Asp Pro
 20 25 30

Val Cys Gly Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys
 35 40 45

Met Lys Ile Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly
 50 55 60

Pro Cys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 65 70 75 80

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 85 90 95

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 100 105 110

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 115 120 125

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 130 135 140

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 145 150 155 160

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 165 170 175

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

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 195 200 205

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 210 215 220

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 225 230 235 240

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 245 250 255

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

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 275 280 285

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 290 295

<210> 51
 <211> 897
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> binder

<220>
 <221> CDS
 <222> (1)..(897)

<400> 51
 gat gac gac ggc cct cag ttc ggc ctg ttc agc aag tac aga acc cct
 Asp Asp Asp Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro

1	5				10				15							
aac tgc atg cag cat gct cgt cag ggt tgt cat tac gac tac gac cct	Asn Cys Met Gln His Ala Arg Gln Gly Cys His Tyr Asp Tyr Asp Pro				20 25				30							96
gtg tgc ggc agc gac atg agc acc tac gcc aat gag tgc acc ctg tgc	Val Cys Gly Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys				35 40				45							144
atg aag atc aga gaa ggc ggc cac aac atc aag atc atc cgg aat ggc	Met Lys Ile Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly				50 55				60							192
ccc tgc gaa ccc aag agc tgc gac aag acc cac acc tgt ccc cct tgt	Pro Cys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys				65 70				75 80							240
cct gcc ccc gaa ctg ctg gga gga cct agc gtg ttc ctg ttc ccc cca	Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro				85 90				95							288
aag ccc aag gac acc ctg atg atc agc cgg acc ccc gaa gtg acc tgc	Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys				100 105				110							336
gtg gtg gtg gat gtg tcc cac gag gac cct gaa gtg aag ttc aat tgg	Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp				115 120				125							384
tac gtg gac ggc gtg gaa gtg cac aac gcc aag acc aag cct aga gag	Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu				130 135				140							432
gaa cag tac aac tcc acc tac cgg gtg gtg tct gtg ctg aca gtg ctg	Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu				145 150				155 160							480
cat cag gac tgg ctg aac ggc aaa gag tac aag tgc aag gtg tcc aac	His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn				165 170				175							528
aag gcc ctg cct gcc ccc atc gag aaa acc atc agc aag gcc aag ggc	Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly				180 185				190							576
cag ccc cgc gaa ccc cag gtg tac aca ctg ccc cct agc cgg gaa gag	Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu				195 200				205							624
atg acc aag aac cag gtg tcc ctg acc tgt ctc gtg aaa ggc ttc tac	Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr				210 215				220							672

ccc agc gac att gcc gtg gaa tgg gag agc aac ggc cag ccc gag aac 720
 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 225 230 235 240

aac tac aag acc acc ccc cct gtg ctg gac agc gac ggc tca ttc ttc 768
 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 245 250 255

ctg tac agc aag ctg acc gtg gac aag agc cgg tgg cag cag ggc aac 816
 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 260 265 270

gtg ttc agc tgc agc gtg atg cac gag gcc ctg cac aac cac tac acc 864
 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 275 280 285

cag aag tcc ctg agc ctg agc ccc ggc aaa tga 897
 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 290 295

<210> 52
 <211> 298
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 52

Asp Asp Asp Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro
 1 5 10 15

Asn Cys Met Gln His Ala Arg Gln Gly Cys His Tyr Asp Tyr Asp Pro
 20 25 30

Val Cys Gly Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys
 35 40 45

Met Lys Ile Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly
 50 55 60

Pro Cys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 65 70 75 80

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 85 90 95

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 100 105 110

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 115 120 125

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 130 135 140

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 145 150 155 160

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 165 170 175

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

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 195 200 205

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 210 215 220

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 225 230 235 240

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 245 250 255

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

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 275 280 285

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 290 295

<211> 897
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> binder

<220>
 <221> CDS
 <222> (1)..(897)

<400> 53
 gat gac gac ggc cct cag ttc ggc ctg ttc agc aag tac aga acc cct 48
 Asp Asp Asp Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro
 1 5 10 15

aac tgc ggt gaa tac aaa ggt cgt ggt tgt tac tac cat tac gac cct 96
 Asn Cys Gly Glu Tyr Lys Gly Arg Gly Cys Tyr Tyr His Tyr Asp Pro
 20 25 30

gtg tgc ggc agc gac atg agc acc tac gcc aat gag tgc acc ctg tgc 144
 Val Cys Gly Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys
 35 40 45

atg aag atc aga gaa ggc ggc cac aac atc aag atc atc cgg aat ggc 192
 Met Lys Ile Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly
 50 55 60

ccc tgc gaa ccc aag agc tgc gac aag acc cac acc tgt ccc cct tgt 240
 Pro Cys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 65 70 75 80

cct gcc ccc gaa ctg ctg gga gga cct agc gtg ttc ctg ttc ccc cca 288
 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 85 90 95

aag ccc aag gac acc ctg atg atc agc cgg acc ccc gaa gtg acc tgc 336
 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 100 105 110

gtg gtg gtg gat gtg tcc cac gag gac cct gaa gtg aag ttc aat tgg 384
 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 115 120 125

tac gtg gac ggc gtg gaa gtg cac aac gcc aag acc aag cct aga gag 432
 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 130 135 140

gaa cag tac aac tcc acc tac cgg gtg gtg tct gtg ctg aca gtg ctg 480
 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 145 150 155 160

cat cag gac tgg ctg aac ggc aaa gag tac aag tgc aag gtg tcc aac 528

His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn		
				165					170					175			
aag	gcc	ctg	cct	gcc	ccc	atc	gag	aaa	acc	atc	agc	aag	gcc	aag	ggc		576
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly		
			180					185					190				
cag	ccc	cgc	gaa	ccc	cag	gtg	tac	aca	ctg	ccc	cct	agc	cgg	gaa	gag		624
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu		
		195					200					205					
atg	acc	aag	aac	cag	gtg	tcc	ctg	acc	tgt	ctc	gtg	aaa	ggc	ttc	tac		672
Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr		
	210					215					220						
ccc	agc	gac	att	gcc	gtg	gaa	tgg	gag	agc	aac	ggc	cag	ccc	gag	aac		720
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn		
225					230					235					240		
aac	tac	aag	acc	acc	ccc	cct	gtg	ctg	gac	agc	gac	ggc	tca	ttc	ttc		768
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe		
				245					250					255			
ctg	tac	agc	aag	ctg	acc	gtg	gac	aag	agc	cgg	tgg	cag	cag	ggc	aac		816
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn		
			260					265					270				
gtg	ttc	agc	tgc	agc	gtg	atg	cac	gag	gcc	ctg	cac	aac	cac	tac	acc		864
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr		
		275					280					285					
cag	aag	tcc	ctg	agc	ctg	agc	ccc	ggc	aaa	tga							897
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys								
	290					295											

<210> 54
 <211> 298
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 54

Asp	Asp	Asp	Gly	Pro	Gln	Phe	Gly	Leu	Phe	Ser	Lys	Tyr	Arg	Thr	Pro		
1				5					10					15			

Asn	Cys	Gly	Glu	Tyr	Lys	Gly	Arg	Gly	Cys	Tyr	Tyr	His	Tyr	Asp	Pro		
		20						25					30				

Val Cys Gly Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys
 35 40 45

Met Lys Ile Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly
 50 55 60

Pro Cys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 65 70 75 80

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 85 90 95

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 100 105 110

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 115 120 125

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 130 135 140

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 145 150 155 160

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 165 170 175

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

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 195 200 205

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 210 215 220

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 225 230 235 240

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 245 250 255

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

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 275 280 285

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 290 295

<210> 55
 <211> 897
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> binder

<220>
 <221> CDS
 <222> (1)..(897)

<400> 55
 gat gac gac ggc cct cag ttc ggc ctg ttc agc aag tac aga acc cct 48
 Asp Asp Asp Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro
 1 5 10 15

aac tgc ggt act atg cag ggt tct ggt tgt act tac cat tac gaa cct 96
 Asn Cys Gly Thr Met Gln Gly Ser Gly Cys Thr Tyr His Tyr Glu Pro
 20 25 30

gtg tgc ggc agc gac atg agc acc tac gcc aat gag tgc acc ctg tgc 144
 Val Cys Gly Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys
 35 40 45

atg aag atc aga gaa ggc ggc cac aac atc aag atc atc cgg aat ggc 192
 Met Lys Ile Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly
 50 55 60

ccc tgc gaa ccc aag agc tgc gac aag acc cac acc tgt ccc cct tgt 240
 Pro Cys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 65 70 75 80

cct gcc ccc gaa ctg ctg gga gga cct agc gtg ttc ctg ttc ccc cca 288
 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 85 90 95

aag ccc aag gac acc ctg atg atc agc cgg acc ccc gaa gtg acc tgc 336
 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

100	105	110	
gtg gtg gtg gat gtg tcc cac gag gac cct gaa gtg aag ttc aat tgg Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp 115 120 125			384
tac gtg gac ggc gtg gaa gtg cac aac gcc aag acc aag cct aga gag Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu 130 135 140			432
gaa cag tac aac tcc acc tac cgg gtg gtg tct gtg ctg aca gtg ctg Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu 145 150 155 160			480
cat cag gac tgg ctg aac ggc aaa gag tac aag tgc aag gtg tcc aac His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn 165 170 175			528
aag gcc ctg cct gcc ccc atc gag aaa acc atc agc aag gcc aag ggc Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly 180 185 190			576
cag ccc cgc gaa ccc cag gtg tac aca ctg ccc cct agc cgg gaa gag Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu 195 200 205			624
atg acc aag aac cag gtg tcc ctg acc tgt ctc gtg aaa ggc ttc tac Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr 210 215 220			672
ccc agc gac att gcc gtg gaa tgg gag agc aac ggc cag ccc gag aac Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn 225 230 235 240			720
aac tac aag acc acc ccc cct gtg ctg gac agc gac ggc tca ttc ttc Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe 245 250 255			768
ctg tac agc aag ctg acc gtg gac aag agc cgg tgg cag cag ggc aac Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn 260 265 270			816
gtg ttc agc tgc agc gtg atg cac gag gcc ctg cac aac cac tac acc Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr 275 280 285			864
cag aag tcc ctg agc ctg agc ccc ggc aaa tga Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys 290 295			897

<210> 56

<211> 298

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 56

Asp Asp Asp Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro
1 5 10 15

Asn Cys Gly Thr Met Gln Gly Ser Gly Cys Thr Tyr His Tyr Glu Pro
20 25 30

Val Cys Gly Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys
35 40 45

Met Lys Ile Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly
50 55 60

Pro Cys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
65 70 75 80

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
85 90 95

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
100 105 110

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
115 120 125

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
130 135 140

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
145 150 155 160

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
165 170 175

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

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 195 200 205

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 210 215 220

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 225 230 235 240

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 245 250 255

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

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 275 280 285

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 290 295

<210> 57
 <211> 897
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> binder

<220>
 <221> CDS
 <222> (1)..(897)

<400> 57
 gat gac gac ggc cct cag ttc ggc ctg ttc agc aag tac aga acc cct 48
 Asp Asp Asp Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro
 1 5 10 15

aac tgc ggc cag gtt gtt gaa act tac tgt aac cgt gac tac gac cct 96
 Asn Cys Gly Gln Val Val Glu Thr Tyr Cys Asn Arg Asp Tyr Asp Pro
 20 25 30

gtg tgc ggc agc gac atg agc acc tac gcc aat gag tgc acc ctg tgc 144
 Val Cys Gly Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys
 35 40 45

atg aag atc aga gaa ggc ggc cac aac atc aag atc atc cgg aat ggc Met Lys Ile Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly 50 55 60	192
ccc tgc gaa ccc aag agc tgc gac aag acc cac acc tgt ccc cct tgt Pro Cys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys 65 70 75 80	240
cct gcc ccc gaa ctg ctg gga gga cct agc gtg ttc ctg ttc ccc cca Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro 85 90 95	288
aag ccc aag gac acc ctg atg atc agc cgg acc ccc gaa gtg acc tgc Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys 100 105 110	336
gtg gtg gtg gat gtg tcc cac gag gac cct gaa gtg aag ttc aat tgg Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp 115 120 125	384
tac gtg gac ggc gtg gaa gtg cac aac gcc aag acc aag cct aga gag Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu 130 135 140	432
gaa cag tac aac tcc acc tac cgg gtg gtg tct gtg ctg aca gtg ctg Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu 145 150 155 160	480
cat cag gac tgg ctg aac ggc aaa gag tac aag tgc aag gtg tcc aac His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn 165 170 175	528
aag gcc ctg cct gcc ccc atc gag aaa acc atc agc aag gcc aag ggc Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly 180 185 190	576
cag ccc cgc gaa ccc cag gtg tac aca ctg ccc cct agc cgg gaa gag Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu 195 200 205	624
atg acc aag aac cag gtg tcc ctg acc tgt ctc gtg aaa ggc ttc tac Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr 210 215 220	672
ccc agc gac att gcc gtg gaa tgg gag agc aac ggc cag ccc gag aac Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn 225 230 235 240	720
aac tac aag acc acc ccc cct gtg ctg gac agc gac ggc tca ttc ttc Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe 245 250 255	768
ctg tac agc aag ctg acc gtg gac aag agc cgg tgg cag cag ggc aac	816

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

gtg ttc agc tgc agc gtg atg cac gag gcc ctg cac aac cac tac acc 864
 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 275 280 285

cag aag tcc ctg agc ctg agc ccc ggc aaa tga 897
 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 290 295

<210> 58
 <211> 298
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 58

Asp Asp Asp Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro
 1 5 10 15

Asn Cys Gly Gln Val Val Glu Thr Tyr Cys Asn Arg Asp Tyr Asp Pro
 20 25 30

Val Cys Gly Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys
 35 40 45

Met Lys Ile Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly
 50 55 60

Pro Cys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 65 70 75 80

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 85 90 95

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 100 105 110

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 115 120 125

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 130 135 140

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 145 150 155 160

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 165 170 175

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

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 195 200 205

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 210 215 220

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 225 230 235 240

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 245 250 255

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

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 275 280 285

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 290 295

<210> 59
 <211> 897
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> binder

<220>

<221> CDS

<222> (1)..(897)

<400> 59

gat	gac	gac	ggc	cct	cag	ttc	ggc	ctg	ttc	agc	aag	tac	aga	acc	cct	48
Asp	Asp	Asp	Gly	Pro	Gln	Phe	Gly	Leu	Phe	Ser	Lys	Tyr	Arg	Thr	Pro	
1				5				10					15			

aac	tgc	tac	gac	act	act	act	cat	tac	tgt	tct	cgt	gaa	tac	gac	cct	96
Asn	Cys	Tyr	Asp	Thr	Thr	Thr	His	Tyr	Cys	Ser	Arg	Glu	Tyr	Asp	Pro	
			20					25					30			

gtg	tgc	ggc	agc	gac	atg	agc	acc	tac	gcc	aat	gag	tgc	acc	ctg	tgc	144
Val	Cys	Gly	Ser	Asp	Met	Ser	Thr	Tyr	Ala	Asn	Glu	Cys	Thr	Leu	Cys	
		35					40					45				

atg	aag	atc	aga	gaa	ggc	ggc	cac	aac	atc	aag	atc	atc	cgg	aat	ggc	192
Met	Lys	Ile	Arg	Glu	Gly	Gly	His	Asn	Ile	Lys	Ile	Ile	Arg	Asn	Gly	
	50					55					60					

ccc	tgc	gaa	ccc	aag	agc	tgc	gac	aag	acc	cac	acc	tgt	ccc	cct	tgt	240
Pro	Cys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	
65				70					75						80	

cct	gcc	ccc	gaa	ctg	ctg	gga	gga	cct	agc	gtg	ttc	ctg	ttc	ccc	cca	288
Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	
			85					90					95			

aag	ccc	aag	gac	acc	ctg	atg	atc	agc	cgg	acc	ccc	gaa	gtg	acc	tgc	336
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	
			100					105					110			

gtg	gtg	gtg	gat	gtg	tcc	cac	gag	gac	cct	gaa	gtg	aag	ttc	aat	tgg	384
Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	
		115					120					125				

tac	gtg	gac	ggc	gtg	gaa	gtg	cac	aac	gcc	aag	acc	aag	cct	aga	gag	432
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	
	130					135					140					

gaa	cag	tac	aac	tcc	acc	tac	cgg	gtg	gtg	tct	gtg	ctg	aca	gtg	ctg	480
Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	
145				150					155						160	

cat	cag	gac	tgg	ctg	aac	ggc	aaa	gag	tac	aag	tgc	aag	gtg	tcc	aac	528
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	
			165					170					175			

aag	gcc	ctg	cct	gcc	ccc	atc	gag	aaa	acc	atc	agc	aag	gcc	aag	ggc	576
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	
			180					185					190			

cag	ccc	cgc	gaa	ccc	cag	gtg	tac	aca	ctg	ccc	cct	agc	cgg	gaa	gag	624
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	

195	200	205	
atg acc aag aac cag gtg tcc	ctg acc tgt ctc gtg aaa ggc ttc tac		672
Met Thr Lys Asn Gln Val Ser	Leu Thr Cys Leu Val Lys Gly Phe Tyr		
210	215	220	
ccc agc gac att gcc gtg gaa tgg gag agc aac ggc cag ccc gag aac			720
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn			
225	230	235	240
aac tac aag acc acc ccc cct gtg ctg gac agc gac ggc tca ttc ttc			768
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe			
245	250	255	
ctg tac agc aag ctg acc gtg gac aag agc cgg tgg cag cag ggc aac			816
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn			
260	265	270	
gtg ttc agc tgc agc gtg atg cac gag gcc ctg cac aac cac tac acc			864
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr			
275	280	285	
cag aag tcc ctg agc ctg agc ccc ggc aaa tga			897
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys			
290	295		

<210> 60
 <211> 298
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 60

Asp Asp Asp Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro
1 5 10 15

Asn Cys Tyr Asp Thr Thr Thr His Tyr Cys Ser Arg Glu Tyr Asp Pro
20 25 30

Val Cys Gly Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys
35 40 45

Met Lys Ile Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly
50 55 60

Pro Cys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys

65		70		75		80	
Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly
			85				90
							95
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile
			100				105
							110
Val	Val	Val	Asp	Val	Ser	His	Glu
			115				120
							125
Tyr	Val	Asp	Gly	Val	Glu	Val	His
			130				135
							140
Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg
							150
							155
							160
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys
							170
							175
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu
							180
							185
							190
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr
							200
							205
Met	Thr	Lys	Asn	Gln	Val	Ser	Leu
							210
							215
							220
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp
							225
							230
							235
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val
							245
							250
							255
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp
							260
							265
							270
Val	Phe	Ser	Cys	Ser	Val	Met	His
							275
							280
							285

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 290 295

<210> 61
 <211> 63
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fomula

<220>
 <221> DOMAIN
 <222> (16)..(22)
 <223> Xaa is any amino acid

<220>
 <221> DOMAIN
 <222> (24)..(28)
 <223> Xaa is any amino acid

<400> 61

Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro Asn Cys Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Pro Val Cys Gly
 20 25 30

Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys Met Lys Ile
 35 40 45

Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly Pro Cys
 50 55 60

<210> 62
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 62
 aaaaggatcc ctggacaaac gtggcccgca gtttggtctg tttag

<210> 63
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 63
 aaaactcgag ttagccgccg cacggacat tgcgaataa 39

<210> 64
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 64
 ggcgattata aagatgacga tgataaacac catcaccacc atc 43

<210> 65
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 65
 gtttaaaactc aatgatggtg gtgatggtgt ttatcatcgt cat 43

<210> 66
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 66
 aaaatctaga gccgccacca tggccacagc tagaccccct 40

<210> 67
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Primer

<400> 67

cgatcatcttt ataatcgccg ctgttggcct ggatggtttc ctg

43

<210> 68

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 68

aaaatctaga gccgccacca tggccagatc tctgctgctg ccc

43

<210> 69

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 69

cgatcatcttt ataatcgccc cgggtgttct tcatggtgtc gtt

43

<210> 70

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 70

aaaatctaga gccgccacca tggtcctcct cctcaccgcc ctc

43

<210> 71

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 71

cgatcatcttt ataatcgccc ttgtcgcgca tggtctcctc gat

43

<210> 72
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 72
 aaaagtttaa actcaatgat ggtggtgatg gtgt 34

<210> 73
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 73
 aaaatctaga gccgccacca tgggagtgtg gctgctgagc ctg 43

<210> 74
 <211> 58
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 74
 aaaagtttaa actcaatgat ggtggtgatg gtgccggtgg gtcttcatgg tttccatg 58

<210> 75
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 75
 aaaatctaga gccgccacca tgtttctgct gctgatcatc ctg 43

<210> 76
 <211> 56
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Primer

<400> 76

aaaagtttaa actcaatgat ggtggtgatg gtggttgctc tgcattggtcc gctgaa

56

<210> 77

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Substrate

<220>

<221> PEPTIDE

<222> (7)..(7)

<223> Xaa is Nva

<400> 77

Arg	Pro	Lys	Pro	Val	Glu	Xaa	Trp	Arg	Lys
1				5					10

<210> 78

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Substrate

<400> 78

Leu	Leu	Val	Tyr
1			

<210> 79

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Substrate

<400> 79

Ala	Ala	Pro	Val
1			

<210> 80
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Substrate

<400> 80

Leu Ser Thr Arg
 1

<210> 81
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 81
 agatgggtgt tgtctgatga cgacggccct cagttcggcc tgttc 45

<210> 82
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 82
 gcaggggcca ttccggat 18

<210> 83
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 83
 aaaatctaga gccgccacca tgaagcacct gtggttcttt ctgctgct 48

<210> 84
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Primer

<400> 84

agacaacacc catctaggag cggccaccag cagcagaaag aacc

44

<210> 85

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 85

atccggaatg gccctgcga acccaagagc tgcgac

36

<210> 86

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 86

aaaagtttaa actcatttgc cggggctcag

30

<210> 87

<211> 232

<212> PRT

<213> Homo sapiens

<400> 87

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 88
<211> 62
<212> PRT
<213> Homo sapiens

<400> 88

Glu Ala Ala Lys Glu Ile Cys Ser Glu Phe Arg Asp Gln Val Arg Asn
1 5 10 15

Gly Thr Leu Ile Cys Thr Arg Glu His Asn Pro Val Arg Gly Pro Asp
 20 25 30

Gly Lys Met His Gly Asn Lys Cys Ala Met Cys Ala Ser Val Phe Lys
 35 40 45

Leu Glu Glu Glu Glu Lys Lys Asn Asp Lys Glu Glu Lys Gly
 50 55 60

<210> 89

<211> 62

<212> PRT

<213> Homo sapiens

<400> 89

Glu Ala Val Gln Glu Leu Cys Ser Glu Tyr Arg His Tyr Val Arg Asn
 1 5 10 15

Gly Arg Leu Pro Cys Thr Arg Glu Asn Asp Pro Ile Glu Gly Leu Asp
 20 25 30

Gly Lys Ile His Gly Asn Thr Cys Ser Met Cys Glu Ala Phe Phe Gln
 35 40 45

Gln Glu Ala Lys Glu Lys Glu Arg Ala Glu Pro Arg Ala Lys
 50 55 60

<210> 90

<211> 67

<212> PRT

<213> Homo sapiens

<400> 90

Ile Glu Cys Ala Lys Gln Thr Lys Gln Met Val Asp Cys Ser His Tyr
 1 5 10 15

Lys Lys Leu Pro Pro Gly Gln Gln Arg Phe Cys His His Met Tyr Asp
 20 25 30

Pro Ile Cys Gly Ser Asp Gly Lys Thr Tyr Lys Asn Asp Cys Phe Phe
 35 40 45

Cys Ser Lys Val Lys Lys Thr Asp Gly Thr Leu Lys Phe Val His Phe
 50 55 60

Gly Lys Cys
 65

<210> 91
 <211> 227
 <212> PRT
 <213> Mus musculus

<400> 91

Arg Ile Val Asn Gly Ser Asp Cys Gln Lys Asp Ala Gln Pro Trp Gln
 1 5 10 15

Gly Ala Leu Leu Leu Gly Pro Asn Lys Leu Tyr Cys Gly Ala Val Leu
 20 25 30

Ile Ser Pro Gln Trp Leu Leu Thr Ala Ala His Cys Arg Lys Pro Val
 35 40 45

Phe Arg Ile Arg Leu Gly His His Ser Met Ser Pro Val Tyr Glu Ser
 50 55 60

Gly Gln Gln Met Phe Gln Gly Ile Lys Ser Ile Pro His Pro Gly Tyr
 65 70 75 80

Ser His Pro Gly His Ser Asn Asp Leu Met Leu Ile Lys Met Asn Arg
 85 90 95

Lys Ile Arg Asp Ser His Ser Val Lys Pro Val Glu Ile Ala Cys Asp
 100 105 110

Cys Ala Thr Glu Gly Thr Arg Cys Met Val Ser Gly Trp Gly Thr Thr
 115 120 125

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

Thr Val Leu Ser Glu Glu Arg Cys Lys Asn Ser Tyr Pro Gly Gln Ile

145 150 155 160
 Asp Lys Thr Met Phe Cys Ala Gly Asp Glu Glu Gly Arg Asp Ser Cys
 165 170 175
 Gln Gly Asp Ser Gly Gly Pro Val Val Cys Asn Gly Lys Leu Gln Gly
 180 185 190
 Leu Val Ser Trp Gly Asp Phe Pro Cys Ala Gln Arg Asn Arg Pro Gly
 195 200 205
 Val Tyr Thr Asn Leu Cys Glu Phe Val Lys Trp Ile Lys Asp Thr Met
 210 215 220

 Asn Ser Asn
 225

 <210> 92
 <211> 225
 <212> PRT
 <213> Mus musculus

 <400> 92

 Arg Ile Ile Asp Gly Tyr Lys Cys Lys Glu Gly Ser His Pro Trp Gln
 1 5 10 15

 Val Ala Leu Leu Lys Gly Asn Gln Leu His Cys Gly Gly Val Leu Val
 20 25 30

 Asp Lys Tyr Trp Val Leu Thr Ala Ala His Cys Lys Met Gly Gln Tyr
 35 40 45

 Gln Val Gln Leu Gly Ser Asp Lys Ile Gly Asp Gln Ser Ala Gln Lys
 50 55 60

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

 His Val Asn Asp Ile Met Leu Val Arg Leu Asp Glu Pro Val Lys Met
 85 90 95

Ser Ser Lys Val Glu Ala Val Gln Leu Pro Glu His Cys Glu Pro Pro
 100 105 110

Gly Thr Ser Cys Thr Val Ser Gly Trp Gly Thr Thr Thr Ser Pro Asp
 115 120 125

Val Thr Phe Pro Ser Asp Leu Met Cys Ser Asp Val Lys Leu Ile Ser
 130 135 140

Ser Arg Glu Cys Lys Lys Val Tyr Lys Asp Leu Leu Gly Lys Thr Met
 145 150 155 160

Leu Cys Ala Gly Ile Pro Asp Ser Lys Thr Asn Thr Cys Asn Gly Asp
 165 170 175

Ser Gly Gly Pro Leu Val Cys Asn Asp Thr Leu Gln Gly Leu Val Ser
 180 185 190

Trp Gly Thr Tyr Pro Cys Gly Gln Pro Asn Asp Pro Gly Val Tyr Thr
 195 200 205

Gln Val Cys Lys Tyr Lys Arg Trp Val Met Glu Thr Met Lys Thr His
 210 215 220

Arg
 225

<210> 93
 <211> 227
 <212> PRT
 <213> Mus musculus

<400> 93

Ile Ile Gly Gly Tyr Arg Cys Val Arg Asn Ser Gln Pro Trp Gln Val
 1 5 10 15

Ala Leu Gln Ala Gly Pro Gly His Arg Phe Leu Cys Gly Gly Val Leu
 20 25 30

Leu Ser Asp Gln Trp Val Ile Thr Ala Ala His Cys Ala Arg Pro Ile
 35 40 45

Leu His Val Ala Leu Gly Lys His Asn Ile Arg Arg Trp Glu Ala Thr
 50 55 60

Gln Gln Val Val Arg Val Ala Arg Gln Val Pro His Pro Gln Tyr Gln
 65 70 75 80

Pro Gln Ala His Asp Asn Asp Leu Met Leu Leu Lys Leu Gln Lys Lys
 85 90 95

Val Arg Leu Gly Arg Ala Val Lys Thr Ile Ser Val Ala Ser Ser Cys
 100 105 110

Ala Ser Pro Gly Thr Pro Cys Arg Val Ser Gly Trp Gly Thr Ile Ala
 115 120 125

Ser Pro Ile Ala Arg Tyr Pro Thr Ala Leu Gln Cys Val Asn Val Asn
 130 135 140

Ile Met Ser Glu Gln Ala Cys His Arg Ala Tyr Pro Gly Ile Ile Thr
 145 150 155 160

Ser Gly Met Val Cys Ala Gly Val Pro Glu Gly Gly Lys Asp Ser Cys
 165 170 175

Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly Gln Leu Gln Gly
 180 185 190

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

Val Tyr Ala Asn Leu Cys Asn Tyr His Ser Trp Ile Gln Arg Thr Met
 210 215 220

Gln Ser Asn
 225

<210> 94

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 94

agatgggtgt tgtctgacgg ccctcagttc ggcctgttc

39

<210> 95

<211> 891

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion

<220>

<221> CDS

<222> (1)..(891)

<400> 95

gac	ggc	cct	cag	ttc	ggc	ctg	ttc	agc	aag	tac	aga	acc	cct	aac	tgc	48
Asp	Gly	Pro	Gln	Phe	Gly	Leu	Phe	Ser	Lys	Tyr	Arg	Thr	Pro	Asn	Cys	
1			5						10					15		

gct	aac	act	atg	aaa	cag	gac	tgt	act	cgt	gaa	tac	gac	cct	gtg	tgc	96
Ala	Asn	Thr	Met	Lys	Gln	Asp	Cys	Thr	Arg	Glu	Tyr	Asp	Pro	Val	Cys	
		20						25					30			

ggc	agc	gac	atg	agc	acc	tac	gcc	aat	gag	tgc	acc	ctg	tgc	atg	aag	144
Gly	Ser	Asp	Met	Ser	Thr	Tyr	Ala	Asn	Glu	Cys	Thr	Leu	Cys	Met	Lys	
	35						40					45				

atc	aga	gaa	ggc	ggc	cac	aac	atc	aag	atc	atc	cgg	aat	ggc	ccc	tgc	192
Ile	Arg	Glu	Gly	Gly	His	Asn	Ile	Lys	Ile	Ile	Arg	Asn	Gly	Pro	Cys	
	50					55					60					

gaa	ccc	aag	agc	tgc	gac	aag	acc	cac	acc	tgt	ccc	cct	tgt	cct	gcc	240
Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	
65					70					75					80	

ccc	gaa	ctg	ctg	gga	gga	cct	agc	gtg	ttc	ctg	ttc	ccc	cca	aag	ccc	288
Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	
				85					90					95		

aag	gac	acc	ctg	atg	atc	agc	cgg	acc	ccc	gaa	gtg	acc	tgc	gtg	gtg	336
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	
			100					105					110			

gtg	gat	gtg	tcc	cac	gag	gac	cct	gaa	gtg	aag	ttc	aat	tgg	tac	gtg	384
Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	
		115					120					125				

gac	ggc	gtg	gaa	gtg	cac	aac	gcc	aag	acc	aag	cct	aga	gag	gaa	cag	432
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Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln		
130						135					140						
tac	aac	tcc	acc	tac	cgg	gtg	gtg	tct	gtg	ctg	aca	gtg	ctg	cat	cag	480	
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln		
145					150					155					160		
gac	tgg	ctg	aac	ggc	aaa	gag	tac	aag	tgc	aag	gtg	tcc	aac	aag	gcc	528	
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala		
				165					170					175			
ctg	cct	gcc	ccc	atc	gag	aaa	acc	atc	agc	aag	gcc	aag	ggc	cag	ccc	576	
Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro		
			180					185					190				
cgc	gaa	ccc	cag	gtg	tac	aca	ctg	ccc	cct	agc	cgg	gaa	gag	atg	acc	624	
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr		
		195					200					205					
aag	aac	cag	gtg	tcc	ctg	acc	tgt	ctc	gtg	aaa	ggc	ttc	tac	ccc	agc	672	
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser		
	210					215					220						
gac	att	gcc	gtg	gaa	tgg	gag	agc	aac	ggc	cag	ccc	gag	aac	aac	tac	720	
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr		
225					230					235					240		
aag	acc	acc	ccc	cct	gtg	ctg	gac	agc	gac	ggc	tca	ttc	ttc	ctg	tac	768	
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr		
				245					250					255			
agc	aag	ctg	acc	gtg	gac	aag	agc	cgg	tgg	cag	cag	ggc	aac	gtg	ttc	816	
Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe		
			260					265					270				
agc	tgc	agc	gtg	atg	cac	gag	gcc	ctg	cac	aac	cac	tac	acc	cag	aag	864	
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys		
		275				280						285					
tcc	ctg	agc	ctg	agc	ccc	ggc	aaa	tga								891	
Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys										
	290					295											

<210> 96

<211> 296

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 96

Asp Gly Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro Asn Cys
 1 5 10 15

Ala Asn Thr Met Lys Gln Asp Cys Thr Arg Glu Tyr Asp Pro Val Cys
 20 25 30

Gly Ser Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys Met Lys
 35 40 45

Ile Arg Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly Pro Cys
 50 55 60

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

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 85 90 95

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 100 105 110

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

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 130 135 140

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 145 150 155 160

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 165 170 175

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 180 185 190

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
 195 200 205

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 210 215 220

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 225 230 235 240

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 245 250 255

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 275 280 285

Ser Leu Ser Leu Ser Pro Gly Lys
 290 295

<210> 97
 <211> 62
 <212> PRT
 <213> Homo sapiens

<400> 97

Pro Gln Phe Gly Leu Phe Ser Lys Tyr Arg Thr Pro Asn Cys Ser Gln
 1 5 10 15

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

Asp Met Ser Thr Tyr Ala Asn Glu Cys Thr Leu Cys Met Lys Ile Arg
 35 40 45

Glu Gly Gly His Asn Ile Lys Ile Ile Arg Asn Gly Pro Cys
 50 55 60