

SEQUENCE LISTING

<110> NANKAI UNIVERSITY

<120> ANTI-CD40 ANTIBODY AND USE THEREOF

<130> PF 200148PCT

<160> 76

<170> PatentIn version 3.3

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Gly Tyr Thr Phe Thr Gly Tyr Tyr
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Gly Phe Thr Phe Gly Asp Ser Ala
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Ile Asn Pro Asn Ser Gly Gly Thr
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Ile Ser Arg Asn Ser Asp Thr Ile
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Ala Arg Glu Arg Val Gly Ala Thr Pro Thr Tyr Tyr Tyr Tyr Met Asp
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Val

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Ala Arg Arg Ser Gly Asp His His Ala Met Asp Val
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Gln Ser Leu Leu Tyr Ser Asn Gly Tyr Asn Tyr
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Gln Ser Val Asn Thr Tyr
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Leu Gly Ser
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Asp Ser Ser
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Met Gln Gly Leu Glu Thr Pro Tyr Thr
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Gln Gln Tyr Ser Thr Val Pro Leu Thr
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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

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

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Arg Val Gly Ala Thr Pro Thr Tyr Tyr Tyr Tyr Met Asp
100 105 110

Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120

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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Ile Ser Cys Ala Gly Ser Gly Phe Thr Phe Gly Asp Ser
20 25 30

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

Ser Gly Ile Ser Arg Asn Ser Asp Thr Ile Val Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Arg Arg Ser Gly Asp His His Ala Met Asp Val Trp Gly Pro Gly
100 105 110

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

Glu Ser Ala Thr Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Tyr Ser
20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Leu Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

65		70		75		80									
Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Leu	Tyr	Tyr	Cys	Met	Gln	Gly
			85						90					95	

Leu	Glu	Thr	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys
			100					105					110		

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Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Asn	Thr	Tyr
			20					25					30		

Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Met
		35					40					45			

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

Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu	Pro
65					70					75				80	

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

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

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Arg Val Gly Ala Thr Pro Thr Tyr Tyr Tyr Tyr Met Asp
100 105 110

Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys
115 120 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
130 135 140

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
145 150 155 160

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
165 170 175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
180 185 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
195 200 205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
210 215 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
225 230 235 240

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

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
290 295 300

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr

385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
435 440 445

Ser Leu Ser Pro Gly Lys
450

<210>	18
<211>	454
<212>	PRT
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<400> 18

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr

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

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Arg Val Gly Ala Thr Pro Thr Tyr Tyr Tyr Tyr Met Asp
100 105 110

Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys
115 120 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
130 135 140

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
145 150 155 160

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
165 170 175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
180 185 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
195 200 205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
210 215 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Asp
225 230 235 240

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

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
260 265 270

Val Ser Asp Glu Asp Gly Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
290 295 300

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
325 330 335

Arg Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
435 440 445

Ser Leu Ser Pro Gly Lys
450

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<400> 19

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

1	5	10	15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr	20	25	30
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met	35	40	45
Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe	50	55	60
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr	65	70	75
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys	85	90	95
Ala Arg Glu Arg Val Gly Ala Thr Pro Thr Tyr Tyr Tyr Tyr Met Asp	100	105	110
Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys	115	120	125
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly	130	135	140
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro	145	150	155
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr	165	170	175
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val	180	185	190
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn	195	200	205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
210 215 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
225 230 235 240

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

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
260 265 270

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

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
290 295 300

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Phe Pro
325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys

405

410

415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 435 440 445

Ser Leu Ser Pro Gly Lys
 450

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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Ile Ser Cys Ala Gly Ser Gly Phe Thr Phe Gly Asp Ser
 20 25 30

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

Ser Gly Ile Ser Arg Asn Ser Asp Thr Ile Val Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95

Ala Arg Arg Ser Gly Asp His His Ala Met Asp Val Trp Gly Pro Gly
 100 105 110

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

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

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

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

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

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

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

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225 230 235 240

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

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

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

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

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
325 330 335

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

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

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

Lys

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<400> 21

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

Glu Ser Ala Thr Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Tyr Ser

20

25

30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Leu Lys Pro Gly Gln Ser
 35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
 50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Leu Tyr Tyr Cys Met Gln Gly
 85 90 95

Leu Glu Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
 115 120 125

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

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
 145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
 165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
 180 185 190

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

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215

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<400> 22

Glu Thr Thr Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Asn Thr Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met
35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65 70 75 80

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

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

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

Phe Asn Arg Gly Glu Cys
210

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<400> 23

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

Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

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<400> 24

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Ile Ser Cys Ala Gly Ser
20 25

<210> 25
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<213> synthetic construct

<400> 25

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
1 5 10 15

Trp

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<400> 26

Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
1 5 10 15

Gly

<210> 27
<211> 38
<212> PRT
<213> synthetic construct

<400> 27

Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr
1 5 10 15

Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp
20 25 30

Thr Ala Val Tyr Tyr Cys
35

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<400> 28

Val Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
1 5 10 15

Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
20 25 30

Thr Ala Leu Tyr Tyr Cys
35

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<400> 29

Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
1 5 10

<210> 30
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<400> 30

Trp Gly Pro Gly Thr Thr Val Thr Val Ser Ser
1 5 10

<210> 31
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<212> PRT
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<400> 31

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

Glu Ser Ala Thr Ile Ser Cys Arg Ser Ser
20 25

<210> 32

<211> 26
<212> PRT
<213> synthetic construct

<400> 32

Glu Thr Thr Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser
20 25

<210> 33
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<213> synthetic construct

<400> 33

Leu Asp Trp Tyr Leu Leu Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile
1 5 10 15

Tyr

<210> 34
<211> 17
<212> PRT
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<400> 34

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Met
1 5 10 15

Tyr

<210> 35
<211> 36
<212> PRT
<213> synthetic construct

<400> 35

Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly
20 25 30

Leu Tyr Tyr Cys
35

<210> 36
<211> 36
<212> PRT
<213> synthetic construct

<400> 36

Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala
20 25 30

Val Tyr Tyr Cys
35

<210> 37
<211> 10
<212> PRT
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<400> 37

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
1 5 10

<210> 38
<211> 10
<212> PRT
<213> synthetic construct

<400> 38

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
1 5 10

<210> 39
<211> 372
<212> DNA
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<400> 39
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cctggacaag ggcttgagtg gatgggatgg atcaacccta acagtgggtg cacaactat 180
gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240
atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gagagaaaga 300
gtgggagcta ctccgaccta ctactactac atggacgtct ggggcaaagg gaccacggtc 360
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372

<210> 40
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<400> 40
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tcctgtgcag gctctggatt cacctttggc gattcggcca tgcactgggt ccggcaagct 120
ccaggtaagg gcctggagtg ggtctcaggt attagtagga atagtgatac catagtctat 180
gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgc aaggcggtcg 300
ggtgatcacc acgctatgga cgtctggggc ccagggacca cggtcaccgt ctctca 357

<210> 41
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atctcctgca ggtctagtca gagcctcctg tacagtaatg gatacaacta tttggattgg 120
tacctgctga agccagggca gtctccacaa ctctgatct atttgggttc taatcgggcc 180
tccgggggtcc ctgacagggtt cagtggcagt ggatcaggca cagattttac actgaagatc 240
agcagagtgg aggctgagga tgttggcctt tattactgca tgcaaggctt agaaactccg 300
tacacttttg gccagggggac caagctggag atcaaaa 336

<210> 42
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<400> 42
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ctctcctgca gggccagtca gagtgttaac acttatttag cctggtacca acagaaacct 120
ggccaggctc ccaggctcct catgtatgat tcatccagca gggccactgg catcccagac 180
aggttcagtg gcagtgggtc tgggacagac ttactctca ccatcagcag actggagcct 240
gaagattttg cagtgtatta ctgtcagcag tatagtaccg taccgctcac tttcggcgga 300
gggaccaagc tggagatcaa acgt 324

<210> 43
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<400> 43

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
1 5 10 15

Val Thr Asn Ser
20

<210> 44
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<212> DNA

<213> synthetic construct

<400> 44

atgtacagga tgcaactcct gtcttgcatt gcactaagtc ttgcacttgt cacgaattcg 60

<210> 45

<211> 464

<212> PRT

<213> synthetic construct

<400> 45

Met Met Val Leu Ser Leu Leu Tyr Leu Leu Thr Ala Leu Pro Gly Ile
1 5 10 15

Leu Ser Glu Val Gln Leu Glu Gln Ser Gly Ala Glu Leu Met Lys Pro
20 25 30

Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Thr Gly Tyr Thr Phe Thr
35 40 45

Thr Tyr Trp Ile Glu Trp Ile Lys Gln Arg Pro Gly His Ser Leu Glu
50 55 60

Trp Ile Gly Glu Ile Leu Pro Gly Ser Asp Ser Thr Tyr Tyr Asn Glu
65 70 75 80

Lys Val Lys Gly Lys Val Thr Phe Thr Ala Asp Ala Ser Ser Asn Thr
85 90 95

Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr
100 105 110

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

Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
130 135 140

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly

145		150		155		160									
Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn
				165					170					175	
Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln
			180					185					190		
Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser
		195					200					205			
Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser
	210					215					220				
Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr
225					230					235					240
His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser
			245						250					255	
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
		260						265					270		
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro
		275					280					285			
Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
	290					295					300				
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val
305					310					315					320
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
				325					330					335	
Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr
			340					345					350		

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
355 360 365

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
370 375 380

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
385 390 395 400

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
405 410 415

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
420 425 430

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
435 440 445

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460

<210> 46
<211> 234
<212> PRT
<213> synthetic construct

<400> 46

Met Asp Ser Gln Ala Gln Val Leu Met Leu Leu Leu Trp Val Ser
1 5 10 15

Gly Thr Cys Gly Asp Ile Glu Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Val Thr Pro Gly Asp Ser Val Ser Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

Ile Ser Asn Asn Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro
50 55 60

Arg Leu Leu Ile Lys Tyr Thr Ser Gln Ser Met Ser Gly Ile Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn
85 90 95

Ser Val Glu Thr Glu Asp Phe Gly Val Tyr Phe Cys Gln Gln Ser Gly
100 105 110

Ser Trp Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Asp Ile Lys Arg
115 120 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130 135 140

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

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
180 185 190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
195 200 205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 47

<211> 1392

<212> DNA

<213> synthetic construct

<400> 47

atgatgggcc	tgagcctgct	gtatctgctg	actgcactgc	ctggaatcct	gagcgaggtc	60
cagctggaac	agagcggggc	tgaactgatg	aaacccggag	caagtgtgaa	aatctcctgc	120
aaggccacag	gctacacttt	caccacatat	tggatcgagt	ggattaagca	gcgaccagga	180
cacagcctgg	agtggatcgg	cgaaattctg	cctgggtcag	acagcaccta	ctataacgaa	240
aaggtgaaaag	gcaagggtcac	ttttaccgcc	gatgctagct	ccaataccgc	ttacatgcag	300
ctgtctagtc	tgacatccga	ggactctgcc	gtctactatt	gtgccagggg	ggatggggtt	360
tatgtgtatt	gggggcaggg	caccactctg	accgtgtcct	cagcctccac	taagggccca	420
tccgtgttcc	ctctggcacc	ctccagcaag	agcacaagcg	gaggcaccgc	cgactggggc	480
tgccctcgtga	aggactactt	cccagaaccc	gtgaccgtca	gctggaatag	cggcgctctg	540
accagcggag	tccacacttt	ccccgcagt	ctgcagtcca	gcggcctgta	cagcctgagc	600
agcgtgggtca	ctgtgccaag	cagcagcctg	ggcactcaga	cctacatctg	caacgtcaac	660
cacaagccca	gcaacacaaa	ggtggacaag	aaggtcgagc	ccaagtcctg	cgataagacc	720
cacacctgcc	ctccatgtcc	cgcccccgag	ctgctggggag	gacccagcgt	cttcctgttt	780
ccccccaagc	caaaggacac	cctgatgatc	agcaggaccc	ccgaagtgac	ctgcgtcgtg	840
gtggacgtga	gccacgaaga	tcccggagtg	aagttcaact	ggtacgtgga	cggcgtggaa	900
gtgcacaacg	ccaagacaaa	acccagggag	gagcagtatg	ccagcaccta	cagggtcgtg	960
agcgtcctga	ccgtgctgca	ccaagactgg	ctgaacggca	aggagtataa	gtgcaagggtg	1020
agcaacaagg	cactgcccgc	ccccatcgag	aagaccat	ccaaggccaa	ggggcaacct	1080
aggagaccac	aggtctacac	tctgccccct	agcagggacg	agctgaccaa	gaaccagggtc	1140
tccctgactt	gcctggtgaa	ggggttttat	cccagcgaca	tcgccgtcga	gtgggagagc	1200
aatggccagc	ccgaaaacaa	ctacaagacc	acaccccctg	tgctggacag	cgacggcagc	1260
ttctttctgt	atagcaaaact	gacagtggat	aagagcagat	ggcagcaggg	caacgtgttc	1320
tcctgctccg	tgatgcacga	ggccctgcac	aatcactaca	cccagaagtc	cctgagcctg	1380
tccccgggaa	aa					1392

<210> 48
 <211> 702
 <212> DNA
 <213> synthetic construct

<400> 48
 atggatagcc aggcccaggt gctgatgctg ctgctgctgt ggggtgtccgg aacttgcggc 60
 gatattgaac tgaccagag ccctgccact ctgtccgtga cccagggcga cagcgtctcc 120
 ctgtcttgca gggccagtca gtcaatcagc aacaatctgc actggtacca gcagaagtct 180
 catgagagtc cccggctgct gatcaaatat acatcccagt ctatgagtgg cattcctagc 240
 agattctcag gcagcgggtc cggaaccgac tttaactgt ctattaacag cgtggagacc 300
 gaagatttcg ggggtctactt ttgtcagcag agcgggtcat ggcctcggac attcggcggg 360
 gggactaaac tggacatcaa acgaaccgtg gccgcaccaa gcgtcttcat cttcccgcc 420
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 480
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 540
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 600
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 660
 ctgagctcgc ccgtcacaaa gagctttaac agaggcgagt gc 702

<210> 49
 <211> 472
 <212> PRT
 <213> synthetic construct

<400> 49

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

Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr
			20					25					30		

Ser	Tyr	Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu
			35				40					45			

Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr Gly Asn Tyr Ala Gln
50 55 60

Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr
65 70 75 80

Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Ala Arg Glu Glu Glu Gln Gln Phe Ser Leu Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Gly Leu Ser
115 120 125

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

Thr Val Thr Ile Ser Cys Thr Arg Ser Ser Gly Ser Ile Ala Ser Asn
145 150 155 160

Ser Val His Trp Tyr Gln Gln Arg Pro Gly Ser Ala Pro Thr Thr Val
165 170 175

Ile Ser Glu Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
180 185 190

Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
195 200 205

Leu Lys Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser
210 215 220

Asn Phe His Trp Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu Gly
225 230 235 240

Gly Leu Gly Gly Leu Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

245

250

255

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 260 265 270

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 275 280 285

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 290 295 300

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 305 310 315 320

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 325 330 335

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 340 345 350

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 355 360 365

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 370 375 380

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 385 390 395 400

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 405 410 415

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 420 425 430

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 435 440 445

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 450 455 460

Ser Leu Ser Leu Ser Pro Gly Lys
 465 470

<210> 50
 <211> 1416
 <212> DNA
 <213> synthetic construct

<400> 50
 atggcacagg ttcagctggg acagtctggg gctgaggtga agaagcctgg ggcctcagtg 60
 aaggtctcct gcaaggcttc tggatacacc ttcaccagct actatatgca ctgggtgcga 120
 caggcccctg gacaagggct tgagtggatg ggaggggatca tccctatctt tggtagcagga 180
 aactacgcac agaagttcca gggcagagtc acgattaccg cggacgaatc cacgagcaca 240
 gcctacatgg agctgagcag cctgagatct gaggacacgg ccgtgtatta ctgtgcgaga 300
 gaggaggagc agcagttcag cttggactac tggggccagg gaaccctggg caccgtctcc 360
 tcaggcggcg gcggtggctt atccaatttt atgctgactc agccccactc tgtgtcggag 420
 tctccgggga agacgggtac catctcctgc accgcagca gtggcagcat tgccagcaac 480
 tctgtgcatt ggtaccagca gcgcccgggc agtgcccca ccactgtgat ctctgaaaat 540
 aaccaacgac cctctggggg cctgatcgg ttctctggct ccatcgacag ctctccaac 600
 tctgcctccc tcaccatctc tggactgaag actgaggacg aggctgacta ctactgtcag 660
 tcttatgaca gcaactttca ttgggtgttc ggcggaggga cccagctcac cgtttttaggt 720
 ggcctcgggg gcctggacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 780
 gggggaccgt cagtcttcct cttccccca aaacccaagg acaccctcat gatctcccgg 840
 acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 900
 aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 960
 tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1020
 ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1080

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1140
 gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1200
 gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1260
 cccgtgctgg actccgacgg ctcttcttc ctctacagca agctcaccgt ggacaagagc 1320
 aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1380
 tacacgcaga agagcctctc cctgtctccg ggtaaa 1416

<210> 51
 <211> 17
 <212> PRT
 <213> synthetic construct

<400> 51

Ala	Arg	Glu	Arg	Val	Gly	Ala	Thr	Pro	Thr	Tyr	Tyr	Tyr	Trp	Trp	Asp
1				5					10					15	

Val

<210> 52
 <211> 17
 <212> PRT
 <213> synthetic construct

<400> 52

Ala	Arg	Glu	Arg	Val	Gly	Ala	Asn	Pro	Thr	Tyr	Tyr	Tyr	Tyr	Trp	Asp
1				5					10					15	

Val

<210> 53
 <211> 9
 <212> PRT
 <213> synthetic construct

<400> 53

Met Asn Gly Leu Glu Val Pro Tyr Thr
1 5

<210> 54
<211> 9
<212> PRT
<213> synthetic construct

<400> 54

Met Gln Gln Leu Glu Gln Pro Tyr Thr
1 5

<210> 55
<211> 17
<212> PRT
<213> synthetic construct

<220>
<221> misc_feature
<222> (8)..(8)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (14)..(15)
<223> Xaa can be any naturally occurring amino acid

<400> 55

Ala Arg Glu Arg Val Gly Ala Xaa Pro Thr Tyr Tyr Tyr Xaa Xaa Asp
1 5 10 15

Val

<210> 56
<211> 9
<212> PRT
<213> synthetic construct

<220>
<221> misc_feature

<222> (2)..(3)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (5)..(6)
<223> Xaa can be any naturally occurring amino acid

<400> 56

Met Xaa Xaa Leu Xaa Xaa Pro Tyr Thr
1 5

<210> 57
<211> 372
<212> DNA
<213> synthetic construct

<400> 57
cagggtacagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaagg cttctggata caccttcacc ggctactata tgcactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggatgg atcaacccta acagtgggtg cacaaactat 180
gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240
atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gagagaaaga 300
gtgggagcta ctccgaccta ctactactgg tgggacgtct ggggcaaagg gaccacggtc 360
accgtctcct ca 372

<210> 58
<211> 124
<212> PRT
<213> synthetic construct

<400> 58

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

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

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Arg Val Gly Ala Thr Pro Thr Tyr Tyr Tyr Trp Trp Asp
100 105 110

Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 59
<211> 372
<212> DNA
<213> synthetic construct

<400> 59
cagggtacagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaagg cttctggata caccttcacc ggctactata tgcactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggatgg atcaacccta acagtgggtg cacaaactat 180
gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240
atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gagagaaaaga 300
gtgggagcta atccgacctt ctactactac tgggacgtct ggggcaaagg gaccacggtc 360
accgtctcct ca 372

<210> 60
<211> 124
<212> PRT
<213> synthetic construct

<400> 60

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

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

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Arg Val Gly Ala Asn Pro Thr Tyr Tyr Tyr Tyr Trp Asp
100 105 110

Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 61

<211> 372

<212> DNA

<213> synthetic construct

<400> 61

cagggtacagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata caccttcacc ggctactata tgtactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcaacccta acagtgggtg cacaaactat 180

gcacagaagt ttcagggcag ggtcaccatg accaggggaca cgtccatcag cacagcctac 240

atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gagagaaaga 300

gtgggagcta atccgaccta ctactactac tgggacgtct ggggcaaagg gaccacggtc 360
accgtctcct ca 372

<210> 62
<211> 124
<212> PRT
<213> synthetic construct

<400> 62

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Arg Val Gly Ala Asn Pro Thr Tyr Tyr Tyr Tyr Trp Asp
100 105 110

Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 63
<211> 336
<212> DNA
<213> synthetic construct

<400> 63

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gatgttgtga tgactcagtc tccactctcc ctgcccgtca cccctggaga gtcggccacc      60
atctcctgca ggtctagtca gagcctcctg tacagtaatg gatacaacta tttggattgg      120
tacctgctga agccagggca gtctccacaa ctctgatct atttgggttc taatcgggcc      180
tccgggggtcc ctgacagggt cagtggcagt ggatcaggca cagattttac actgaagatc      240
agcagagtgg aggctgagga tgttggcctt tattactgca tgaatggctt agaagtgccg      300
tacacttttg gccaggggac caagctggag atcaaaa                                336

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<210> 64
<211> 112
<212> PRT
<213> synthetic construct

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<400> 64

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

```

```

Glu Ser Ala Thr Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Tyr Ser
              20              25              30

```

```

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Leu Lys Pro Gly Gln Ser
35              40              45

```

```

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50              55              60

```

```

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65              70              75              80

```

```

Ser Arg Val Glu Ala Glu Asp Val Gly Leu Tyr Tyr Cys Met Asn Gly
85              90              95

```

```

Leu Glu Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100             105             110

```

```

<210> 65
<211> 336

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<212> DNA
<213> synthetic construct

<400> 65
gatgttgtga tgactcagtc tccactctcc ctgcccgtca cccctggaga gtcggccacc 60
atctcctgca ggtctagtca gagcctcctg tacagtaatg gatacaacta tttggattgg 120
tacctgctga agccagggca gtctccacaa ctctgatct atttgggttc taatcgggcc 180
tccgggggtcc ctgacagggt cagtggcagt ggatcaggca cagattttac actgaagatc 240
agcagagtgg aggctgagga tgttggcctt tattactgca tgcaacagct agaacagccg 300
tacacttttg gccaggggac caagctggag atcaaa 336

<210> 66
<211> 112
<212> PRT
<213> synthetic construct

<400> 66

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

Glu Ser Ala Thr Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Tyr Ser
20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Leu Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Leu Tyr Tyr Cys Met Gln Gln
85 90 95

Leu Glu Gln Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 67
<211> 454
<212> PRT
<213> synthetic construct

<400> 67

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

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

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Arg Val Gly Ala Thr Pro Thr Tyr Tyr Tyr Trp Trp Asp
100 105 110

Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys
115 120 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
130 135 140

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
145 150 155 160

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr

165

170

175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
 180 185 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
 195 200 205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
 210 215 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
 225 230 235 240

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

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
 275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
 290 295 300

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
 305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
 325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
 340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
 355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
435 440 445

Ser Leu Ser Pro Gly Lys
450

<210> 68
<211> 219
<212> PRT
<213> synthetic construct

<400> 68

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

Glu Ser Ala Thr Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Tyr Ser
20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Leu Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Leu Tyr Tyr Cys Met Asn Gly
85 90 95

Leu Glu Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

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

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

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

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 69
<211> 454
<212> PRT
<213> synthetic construct

<400> 69

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr

20

25

30

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

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Glu Arg Val Gly Ala Asn Pro Thr Tyr Tyr Tyr Tyr Trp Asp
 100 105 110

Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys
 115 120 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
 130 135 140

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
 145 150 155 160

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
 165 170 175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
 180 185 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
 195 200 205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
 210 215 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
225 230 235 240

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

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
290 295 300

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys

420

425

430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 435 440 445

Ser Leu Ser Pro Gly Lys
 450

<210> 70
 <211> 454
 <212> PRT
 <213> synthetic construct

<400> 70

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
 20 25 30

Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Glu Arg Val Gly Ala Asn Pro Thr Tyr Tyr Tyr Tyr Trp Asp
 100 105 110

Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys
 115 120 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
130 135 140

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
145 150 155 160

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
165 170 175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
180 185 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
195 200 205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
210 215 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
225 230 235 240

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

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
290 295 300

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
435 440 445

Ser Leu Ser Pro Gly Lys
450

<210> 71
<211> 219
<212> PRT
<213> synthetic construct

<400> 71

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

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

<210> 72
 <211> 663
 <212> DNA
 <213> synthetic construct

<400> 72	
gatgttgtga tgactcagtc tccactctcc ctgcccgtca cccctggaga gtcggccacc	60
atctcctgca ggtctagtca gagcctcctg tacagtaatg gatacaacta tttggattgg	120
tacctgctga agccagggca gtctccacaa ctctgatct atttgggttc taatcgggcc	180
tccgggggtcc ctgacagggt cagtggcagt ggatcaggca cagattttac actgaagatc	240
agcagagtgg aggctgagga tgttggcctt tattactgca tgcaaggctc atgaactccg	300
tacacttttg gccaggggac caagctggag atcaaacgaa ctgtggctgc accatctgtc	360
ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt cgtgtgcctg	420
ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa	480
tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagctc	540
agcagcacc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa	600
gtcaccatc agggcctgtc ctgcccgtc acaaagagct tcaacagggg agagtgttga	660
taa	663

<210> 73
<211> 693
<212> DNA
<213> synthetic construct

<400> 73
caggtagcagc tggtagcagc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaagg cttctggata caccttcacc ggctactata tgcactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggatgg atcaacccta acagtgggtg cacaactat 180
gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240
atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gagagaaaaga 300
gtgggagcta cttgaaccta ctactactac atggacgtct ggggcaaagg gaccacggtc 360
accgtctcct cagcctccac caagggccca tcggtcttcc ccctggcacc ctctccaag 420
agcacctctg ggggcacagc ggccctgggc tgcctgggtca aggactactt cccgaaccg 480
gtgacgggtg cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc 540
ctacagtcct caggactcta ctccctcagc agcgtgggtga ctgtgccctc tagcagcttg 600
ggcaccaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag 660
aaagttgagc ccaaattctg tgacaaaact cac 693

<210> 74
<211> 746
<212> DNA
<213> synthetic construct

<400> 74
atgaaaaaga cagctatcgc gattgcagtg gcaactggctg gtttcgctac cgtggcccag 60
gcggccgagc tcgatgttgt gatgactcag tctccactct ccctgcccgt caccctgga 120
gagtcggcca ccatctcctg caggcttagt cagagcctcc tgtacagtaa tggatacaac 180
tatttggtt ggtacctgct gaagccaggc cagtctccac aactcctgat ctatttggtt 240
tctaatacggg cctccgggggt ccctgacagg ttcagtggca gtggatcagg cacagatttt 300
aactgaaga tcagcagagt ggaggctgag gatgttggcc ttattactg catgcaagg 360

ctagaaaactc cgtacacttt tggccagggg accaagctgg agatcaaacg aactgtggct	420
gcaccatctg tcttcatctt cccgccatct gatgagcagt tgaaatctgg aactgcctct	480
gtcgtgtgcc tgctgaataa cttctatccc agagaggcca aagtacagtg gaagggtgat	540
aacgccctcc aatcgggtaa ctcccaggag agtgtcacag agcaggacag caaggacagc	600
acctacagcc tcagcagcac cctgacgctg agcaaagcag actacgagaa acacaaagtc	660
tacgcctgcg aagtcaccca tcagggcctg tcctcgcccc tcacaaagag cttcaacagg	720
ggagagtgat ttaattaatc tagata	746

<210> 75

<211> 746

<212> DNA

<213> synthetic construct

<400> 75

gccgctggat tgttattact cgctgccc aa ccagccatgg ccgaggtgca gctgctcgag	60
caggtacagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc	120
tcctgcaagg cttctggata caccttcacc ggctactata tgcactgggt gcgacaggcc	180
cctggacaag ggcttgagtg gatgggatgg atcaacccta acagtgggtg cacaactat	240
gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac	300
atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gagagaaaga	360
gtgggagcta ctccgaccta ctactactac atggacgtct ggggcaaagg gaccacggtc	420
accgtctcct cagcctccac caagggccca tcggtcttcc ccctggcacc ctctccaag	480
agcacctctg ggggcacagc ggccctgggc tgcctgggtca aggactactt ccccgaaccg	540
gtgacgggtg cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc	600
ctacagtcct caggactcta ctccctcagc agcgtgggtga ctgtgccctc tagcagcttg	660
ggcaccaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag	720
aaagttgaca aaactagtgg ccaggc	746

<210> 76

<211> 17
<212> PRT
<213> synthetic construct

<400> 76

Met	Tyr	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	Gly
1				5					10					15	

Trp