

SEQUENCE LISTING

<110> Kite Pharma, Inc.

<120> TGF-Beta Receptors and Methods of Use

<130> K1075.P/82352-321521

<140> K1075.P

<141> 2020-06-17

<160> 58

<170> PatentIn version 3.5

<210> 1

<211> 1509

<212> DNA

<213> Homo sapiens

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<210> 2
<211> 503
<212> PRT
<213> Homo sapiens

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<400> 2

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Met Glu Ala Ala Val Ala Ala Pro Arg Pro Arg Leu Leu Leu Leu Val
1           5           10           15

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Leu Ala Ala Ala Ala Ala Ala Ala Ala Ala Leu Leu Pro Gly Ala Thr
          20           25           30

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Ala Leu Gln Cys Phe Cys His Leu Cys Thr Lys Asp Asn Phe Thr Cys
          35           40           45

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

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Val Ile His Asn Ser Met Cys Ile Ala Glu Ile Asp Leu Ile Pro Arg
65           70           75           80

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Asp Arg Pro Phe Val Cys Ala Pro Ser Ser Lys Thr Gly Ser Val Thr
85 90 95

Thr Thr Tyr Cys Cys Asn Gln Asp His Cys Asn Lys Ile Glu Leu Pro
100 105 110

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

Val Ile Ala Gly Pro Val Cys Phe Val Cys Ile Ser Leu Met Leu Met
130 135 140

Val Tyr Ile Cys His Asn Arg Thr Val Ile His His Arg Val Pro Asn
145 150 155 160

Glu Glu Asp Pro Ser Leu Asp Arg Pro Phe Ile Ser Glu Gly Thr Thr
165 170 175

Leu Lys Asp Leu Ile Tyr Asp Met Thr Thr Ser Gly Ser Gly Ser Gly
180 185 190

Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Arg Thr Ile Val Leu Gln
195 200 205

Glu Ser Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly Lys Trp
210 215 220

Arg Gly Glu Glu Val Ala Val Lys Ile Phe Ser Ser Arg Glu Glu Arg
225 230 235 240

Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu Arg His
245 250 255

Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn Gly Thr
260 265 270

Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly Ser Leu

275

280

285

Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Val Glu Gly Met Ile Lys
 290 295 300

Leu Ala Leu Ser Thr Ala Ser Gly Leu Ala His Leu His Met Glu Ile
 305 310 315 320

Val Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser
 325 330 335

Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp Leu
 340 345 350

Gly Leu Ala Val Arg His Asp Ser Ala Thr Asp Thr Ile Asp Ile Ala
 355 360 365

Pro Asn His Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu
 370 375 380

Asp Asp Ser Ile Asn Met Lys His Phe Glu Ser Phe Lys Arg Ala Asp
 385 390 395 400

Ile Tyr Ala Met Gly Leu Val Phe Trp Glu Ile Ala Arg Arg Cys Ser
 405 410 415

Ile Gly Gly Ile His Glu Asp Tyr Gln Leu Pro Tyr Tyr Asp Leu Val
 420 425 430

Pro Ser Asp Pro Ser Val Glu Glu Met Arg Lys Val Val Cys Glu Gln
 435 440 445

Lys Leu Arg Pro Asn Ile Pro Asn Arg Trp Gln Ser Cys Glu Ala Leu
 450 455 460

Arg Val Met Ala Lys Ile Met Arg Glu Cys Trp Tyr Ala Asn Gly Ala
 465 470 475 480

Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln Leu Ser
485 490 495

Gln Gln Glu Gly Ile Lys Met
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<210> 3
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Extracellular Domain

<400> 3

Leu Gln Cys Phe Cys His Leu Cys Thr Lys Asp Asn Phe Thr Cys Val
1 5 10 15

Thr Asp Gly Leu Cys Phe Val Ser Val Thr Glu Thr Thr Asp Lys Val
20 25 30

Ile His Asn Ser Met Cys Ile Ala Glu Ile Asp Leu Ile Pro Arg Asp
35 40 45

Arg Pro Phe Val Cys Ala Pro Ser Ser Lys Thr Gly Ser Val Thr Thr
50 55 60

Thr Tyr Cys Cys Asn Gln Asp His Cys Asn Lys Ile Glu Leu Pro Thr
65 70 75 80

Thr Val Lys Ser Ser Pro Gly Leu Gly Pro Val Glu Leu
85 90

<210> 4
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Transmembrane Domain

<400> 4

Ala Ala Val Ile Ala Gly Pro Val Cys Phe Val Cys Ile Ser Leu Met
1 5 10 15

Leu Met Val Tyr Ile
20

<210> 5

<211> 114

<212> PRT

<213> Artificial Sequence

<220>

<223> Extracellular Domain + Transmembrane Domain

<400> 5

Leu Gln Cys Phe Cys His Leu Cys Thr Lys Asp Asn Phe Thr Cys Val
1 5 10 15

Thr Asp Gly Leu Cys Phe Val Ser Val Thr Glu Thr Thr Asp Lys Val
20 25 30

Ile His Asn Ser Met Cys Ile Ala Glu Ile Asp Leu Ile Pro Arg Asp
35 40 45

Arg Pro Phe Val Cys Ala Pro Ser Ser Lys Thr Gly Ser Val Thr Thr
50 55 60

Thr Tyr Cys Cys Asn Gln Asp His Cys Asn Lys Ile Glu Leu Pro Thr
65 70 75 80

Thr Val Lys Ser Ser Pro Gly Leu Gly Pro Val Glu Leu Ala Ala Val
85 90 95

Ile Ala Gly Pro Val Cys Phe Val Cys Ile Ser Leu Met Leu Met Val
100 105 110

Tyr Ile

<210> 6
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Intracellular Domain

<400> 6

Arg Val Asn Arg Gln
1 5

<210> 7
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Extracellular Domain + Transmembrane Domain + Intracellular
Domain

<400> 7

Leu Gln Cys Phe Cys His Leu Cys Thr Lys Asp Asn Phe Thr Cys Val
1 5 10 15

Thr Asp Gly Leu Cys Phe Val Ser Val Thr Glu Thr Thr Asp Lys Val
20 25 30

Ile His Asn Ser Met Cys Ile Ala Glu Ile Asp Leu Ile Pro Arg Asp
35 40 45

Arg Pro Phe Val Cys Ala Pro Ser Ser Lys Thr Gly Ser Val Thr Thr
50 55 60

Thr Tyr Cys Cys Asn Gln Asp His Cys Asn Lys Ile Glu Leu Pro Thr
65 70 75 80

Thr Val Lys Ser Ser Pro Gly Leu Gly Pro Val Glu Leu Ala Ala Val
85 90 95

Ala Leu Gln Cys Phe Cys His Leu Cys Thr Lys Asp Asn Phe Thr Cys
35 40 45

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

Val Ile His Asn Ser Met Cys Ile Ala Glu Ile Asp Leu Ile Pro Arg
65 70 75 80

Asp Arg Pro Phe Val Cys Ala Pro Ser Ser Lys Thr Gly Ser Val Thr
85 90 95

Thr Thr Tyr Cys Cys Asn Gln Asp His Cys Asn Lys Ile Glu Leu Pro
100 105 110

Thr Thr Val Lys Ser Ser Pro Gly Leu Gly Pro Val Glu Leu
115 120 125

<210> 10

<211> 152

<212> PRT

<213> Artificial Sequence

<220>

<223> Signal + Extracellular Domain + Transmembrane Domain +
Intracellular Domain

<400> 10

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1 5 10 15

Leu Ala Ala Ala Ala Ala Ala Ala Ala Leu Leu Pro Gly Ala Thr
20 25 30

Ala Leu Gln Cys Phe Cys His Leu Cys Thr Lys Asp Asn Phe Thr Cys
35 40 45

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

Val Ile His Asn Ser Met Cys Ile Ala Glu Ile Asp Leu Ile Pro Arg
65 70 75 80

Asp Arg Pro Phe Val Cys Ala Pro Ser Ser Lys Thr Gly Ser Val Thr
85 90 95

Thr Thr Tyr Cys Cys Asn Gln Asp His Cys Asn Lys Ile Glu Leu Pro
100 105 110

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

Val Ile Ala Gly Pro Val Cys Phe Val Cys Ile Ser Leu Met Leu Met
130 135 140

Val Tyr Ile Arg Val Asn Arg Gln
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<210> 11
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<223> Extracellular Domain + Transmembrane Domain

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<210> 12
<211> 1701
<212> DNA

<213> Homo sapiens

<400> 12

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<210> 13
 <211> 567
 <212> PRT
 <213> Homo sapiens

<400> 13

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Trp	Thr	Arg	Ile	Ala	Ser	Thr	Ile	Pro	Pro	His	Val	Gln	Lys	Ser	Val
			20					25					30		

Asn	Asn	Asp	Met	Ile	Val	Thr	Asp	Asn	Asn	Gly	Ala	Val	Lys	Phe	Pro
		35					40					45			

Gln	Leu	Cys	Lys	Phe	Cys	Asp	Val	Arg	Phe	Ser	Thr	Cys	Asp	Asn	Gln
	50					55					60				

Lys	Ser	Cys	Met	Ser	Asn	Cys	Ser	Ile	Thr	Ser	Ile	Cys	Glu	Lys	Pro
65					70					75					80

Gln	Glu	Val	Cys	Val	Ala	Val	Trp	Arg	Lys	Asn	Asp	Glu	Asn	Ile	Thr
				85					90					95	

Leu	Glu	Thr	Val	Cys	His	Asp	Pro	Lys	Leu	Pro	Tyr	His	Asp	Phe	Ile
			100					105					110		

Leu	Glu	Asp	Ala	Ala	Ser	Pro	Lys	Cys	Ile	Met	Lys	Glu	Lys	Lys	Lys
		115					120					125			

Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn
130 135 140

Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Leu
145 150 155 160

Leu Leu Val Ile Phe Gln Val Thr Gly Ile Ser Leu Leu Pro Pro Leu
165 170 175

Gly Val Ala Ile Ser Val Ile Ile Ile Phe Tyr Cys Tyr Arg Val Asn
180 185 190

Arg Gln Gln Lys Leu Ser Ser Thr Trp Glu Thr Gly Lys Thr Arg Lys
195 200 205

Leu Met Glu Phe Ser Glu His Cys Ala Ile Ile Leu Glu Asp Asp Arg
210 215 220

Ser Asp Ile Ser Ser Thr Cys Ala Asn Asn Ile Asn His Asn Thr Glu
225 230 235 240

Leu Leu Pro Ile Glu Leu Asp Thr Leu Val Gly Lys Gly Arg Phe Ala
245 250 255

Glu Val Tyr Lys Ala Lys Leu Lys Gln Asn Thr Ser Glu Gln Phe Glu
260 265 270

Thr Val Ala Val Lys Ile Phe Pro Tyr Glu Glu Tyr Ala Ser Trp Lys
275 280 285

Thr Glu Lys Asp Ile Phe Ser Asp Ile Asn Leu Lys His Glu Asn Ile
290 295 300

Leu Gln Phe Leu Thr Ala Glu Glu Arg Lys Thr Glu Leu Gly Lys Gln
305 310 315 320

Tyr Trp Leu Ile Thr Ala Phe His Ala Lys Gly Asn Leu Gln Glu Tyr

325

330

335

Leu Thr Arg His Val Ile Ser Trp Glu Asp Leu Arg Lys Leu Gly Ser
 340 345 350

Ser Leu Ala Arg Gly Ile Ala His Leu His Ser Asp His Thr Pro Cys
 355 360 365

Gly Arg Pro Lys Met Pro Ile Val His Arg Asp Leu Lys Ser Ser Asn
 370 375 380

Ile Leu Val Lys Asn Asp Leu Thr Cys Cys Leu Cys Asp Phe Gly Leu
 385 390 395 400

Ser Leu Arg Leu Asp Pro Thr Leu Ser Val Asp Asp Leu Ala Asn Ser
 405 410 415

Gly Gln Val Gly Thr Ala Arg Tyr Met Ala Pro Glu Val Leu Glu Ser
 420 425 430

Arg Met Asn Leu Glu Asn Val Glu Ser Phe Lys Gln Thr Asp Val Tyr
 435 440 445

Ser Met Ala Leu Val Leu Trp Glu Met Thr Ser Arg Cys Asn Ala Val
 450 455 460

Gly Glu Val Lys Asp Tyr Glu Pro Pro Phe Gly Ser Lys Val Arg Glu
 465 470 475 480

His Pro Cys Val Glu Ser Met Lys Asp Asn Val Leu Arg Asp Arg Gly
 485 490 495

Arg Pro Glu Ile Pro Ser Phe Trp Leu Asn His Gln Gly Ile Gln Met
 500 505 510

Val Cys Glu Thr Leu Thr Glu Cys Trp Asp His Asp Pro Glu Ala Arg
 515 520 525

Leu Thr Ala Gln Cys Val Ala Glu Arg Phe Ser Glu Leu Glu His Leu
530 535 540

Asp Arg Leu Ser Gly Arg Ser Cys Ser Glu Glu Lys Ile Pro Glu Asp
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Gly Ser Leu Asn Thr Thr Lys
565

<210> 14
<211> 194
<212> PRT
<213> Artificial Sequence

<220>
<223> Truncated TGF beta R2

<400> 14

Met Gly Arg Gly Leu Leu Arg Gly Leu Trp Pro Leu His Ile Val Leu
1 5 10 15

Trp Thr Arg Ile Ala Ser Thr Ile Pro Pro His Val Gln Lys Ser Val
20 25 30

Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro
35 40 45

Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln
50 55 60

Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro
65 70 75 80

Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr
85 90 95

Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile
100 105 110

Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys
115 120 125

Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn
130 135 140

Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Leu
145 150 155 160

Leu Leu Val Ile Phe Gln Val Thr Gly Ile Ser Leu Leu Pro Pro Leu
165 170 175

Gly Val Ala Ile Ser Val Ile Ile Ile Phe Tyr Cys Tyr Arg Val Asn
180 185 190

Arg Gln

<210> 15

<211> 137

<212> PRT

<213> Artificial Sequence

<220>

<223> Extracellular Domain

<400> 15

Thr Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile Val
1 5 10 15

Thr Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys
20 25 30

Asp Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn
35 40 45

Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala
50 55 60

Val Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His
65 70 75 80

Asp Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser
85 90 95

Pro Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe
100 105 110

Met Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser
115 120 125

Glu Glu Tyr Asn Thr Ser Asn Pro Asp
130 135

<210> 16
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Transmembrane Domain

<400> 16

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

Leu Gly Val Ala Ile Ser Val Ile Ile Ile Phe Tyr Cys Tyr
20 25 30

<210> 17
<211> 167
<212> PRT
<213> Artificial Sequence

<220>
<223> Extracellular Domain + Transmembrane Domain

<400> 17

Thr Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile Val

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

<210> 18
 <211> 20
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> IL7Ralpha Transmembrane Domain

<400> 18

Pro Ile Leu Leu Thr Ile Ser Ile Leu Ser Phe Phe Ser Val Ala Leu
1 5 10 15

Leu Val Ile Leu
20

<210> 19

<211> 159

<212> PRT

<213> Artificial Sequence

<220>

<223> Extracellular Domain + IL7Ralpha Transmembrane Domain

<400> 19

Thr Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile Val
1 5 10 15

Thr Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys
20 25 30

Asp Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn
35 40 45

Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala
50 55 60

Val Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His
65 70 75 80

Asp Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser
85 90 95

Pro Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe
100 105 110

Met Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser

115

120

125

Glu Glu Tyr Asn Thr Ser Asn Pro Asp Ser Gly Pro Ile Leu Leu Thr
 130 135 140

Ile Ser Ile Leu Ser Phe Phe Ser Val Ala Leu Leu Val Ile Leu
 145 150 155

<210> 20
 <211> 23
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IL7Ralpha "CPT" Transmembrane Domain

<400> 20

Pro Ile Leu Leu Thr Cys Pro Thr Ile Ser Ile Leu Ser Phe Phe Ser
 1 5 10 15

Val Ala Leu Leu Val Ile Leu
 20

<210> 21
 <211> 162
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Extracellular Domain + IL7Ralpha "CPT"

<400> 21

Thr Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile Val
 1 5 10 15

Thr Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys
 20 25 30

Asp Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn
 35 40 45

Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala
50 55 60

Val Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His
65 70 75 80

Asp Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser
85 90 95

Pro Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe
100 105 110

Met Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser
115 120 125

Glu Glu Tyr Asn Thr Ser Asn Pro Asp Ser Gly Pro Ile Leu Leu Thr
130 135 140

Cys Pro Thr Ile Ser Ile Leu Ser Phe Phe Ser Val Ala Leu Leu Val
145 150 155 160

Ile Leu

<210> 22

<211> 200

<212> PRT

<213> Artificial Sequence

<220>

<223> IL7Ralpha Intracellular Domain

<400> 22

Ala Cys Val Leu Trp Lys Lys Arg Ile Lys Pro Ile Val Trp Pro Ser
1 5 10 15

Leu Pro Asp His Lys Lys Thr Leu Glu His Leu Cys Lys Lys Pro Arg
20 25 30

Lys Asn Leu Asn Val Ser Phe Asn Pro Glu Ser Phe Leu Asp Cys Gln
35 40 45

Ile His Arg Val Asp Asp Ile Gln Ala Arg Asp Glu Val Glu Gly Phe
50 55 60

Leu Gln Asp Thr Phe Pro Gln Gln Leu Glu Glu Ser Glu Lys Gln Arg
65 70 75 80

Leu Gly Gly Asp Val Gln Ser Pro Asn Cys Pro Ser Glu Asp Val Val
85 90 95

Ile Thr Pro Glu Ser Phe Gly Arg Asp Ser Ser Leu Thr Cys Leu Ala
100 105 110

Gly Asn Val Ser Ala Cys Asp Ala Pro Ile Leu Ser Ser Ser Arg Ser
115 120 125

Leu Asp Cys Arg Glu Ser Gly Lys Asn Gly Pro His Val Tyr Gln Asp
130 135 140

Leu Leu Leu Ser Leu Gly Thr Thr Asn Ser Thr Leu Pro Pro Pro Phe
145 150 155 160

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

Pro Ile Leu Thr Ser Leu Gly Ser Asn Gln Glu Glu Ala Tyr Val Thr
180 185 190

Met Ser Ser Phe Tyr Gln Asn Gln
195 200

<210> 23

<211> 359

<212> PRT

<213> Artificial Sequence

<220>

<223> Extracellular Domain + IL7Ralpha + Transmembrane Domain +
IL7Ralpha ICD

<400> 23

Thr Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile Val
1 5 10 15

Thr Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys
20 25 30

Asp Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn
35 40 45

Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala
50 55 60

Val Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His
65 70 75 80

Asp Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser
85 90 95

Pro Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe
100 105 110

Met Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser
115 120 125

Glu Glu Tyr Asn Thr Ser Asn Pro Asp Ser Gly Pro Ile Leu Leu Thr
130 135 140

Ile Ser Ile Leu Ser Phe Phe Ser Val Ala Leu Leu Val Ile Leu Ala
145 150 155 160

Cys Val Leu Trp Lys Lys Arg Ile Lys Pro Ile Val Trp Pro Ser Leu
165 170 175

Pro Asp His Lys Lys Thr Leu Glu His Leu Cys Lys Lys Pro Arg Lys
180 185 190

Asn Leu Asn Val Ser Phe Asn Pro Glu Ser Phe Leu Asp Cys Gln Ile
195 200 205

His Arg Val Asp Asp Ile Gln Ala Arg Asp Glu Val Glu Gly Phe Leu
210 215 220

Gln Asp Thr Phe Pro Gln Gln Leu Glu Glu Ser Glu Lys Gln Arg Leu
225 230 235 240

Gly Gly Asp Val Gln Ser Pro Asn Cys Pro Ser Glu Asp Val Val Ile
245 250 255

Thr Pro Glu Ser Phe Gly Arg Asp Ser Ser Leu Thr Cys Leu Ala Gly
260 265 270

Asn Val Ser Ala Cys Asp Ala Pro Ile Leu Ser Ser Ser Arg Ser Leu
275 280 285

Asp Cys Arg Glu Ser Gly Lys Asn Gly Pro His Val Tyr Gln Asp Leu
290 295 300

Leu Leu Ser Leu Gly Thr Thr Asn Ser Thr Leu Pro Pro Pro Phe Ser
305 310 315 320

Leu Gln Ser Gly Ile Leu Thr Leu Asn Pro Val Ala Gln Gly Gln Pro
325 330 335

Ile Leu Thr Ser Leu Gly Ser Asn Gln Glu Glu Ala Tyr Val Thr Met
340 345 350

Ser Ser Phe Tyr Gln Asn Gln
355

<210> 24
<211> 362

<212> PRT

<213> Artificial Sequence

<220>

<223> Extracellular Domain + IL7Ralpha "CPT" Transmembrane Domain +
IL7Ralpha Intracellular Domain

<400> 24

Thr Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile Val
1 5 10 15

Thr Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys
20 25 30

Asp Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn
35 40 45

Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala
50 55 60

Val Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His
65 70 75 80

Asp Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser
85 90 95

Pro Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe
100 105 110

Met Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser
115 120 125

Glu Glu Tyr Asn Thr Ser Asn Pro Asp Ser Gly Pro Ile Leu Leu Thr
130 135 140

Cys Pro Thr Ile Ser Ile Leu Ser Phe Phe Ser Val Ala Leu Leu Val
145 150 155 160

Ile Leu Ala Cys Val Leu Trp Lys Lys Arg Ile Lys Pro Ile Val Trp

165

170

175

Pro Ser Leu Pro Asp His Lys Lys Thr Leu Glu His Leu Cys Lys Lys
 180 185 190

Pro Arg Lys Asn Leu Asn Val Ser Phe Asn Pro Glu Ser Phe Leu Asp
 195 200 205

Cys Gln Ile His Arg Val Asp Asp Ile Gln Ala Arg Asp Glu Val Glu
 210 215 220

Gly Phe Leu Gln Asp Thr Phe Pro Gln Gln Leu Glu Glu Ser Glu Lys
 225 230 235 240

Gln Arg Leu Gly Gly Asp Val Gln Ser Pro Asn Cys Pro Ser Glu Asp
 245 250 255

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

Leu Ala Gly Asn Val Ser Ala Cys Asp Ala Pro Ile Leu Ser Ser Ser
 275 280 285

Arg Ser Leu Asp Cys Arg Glu Ser Gly Lys Asn Gly Pro His Val Tyr
 290 295 300

Gln Asp Leu Leu Leu Ser Leu Gly Thr Thr Asn Ser Thr Leu Pro Pro
 305 310 315 320

Pro Phe Ser Leu Gln Ser Gly Ile Leu Thr Leu Asn Pro Val Ala Gln
 325 330 335

Gly Gln Pro Ile Leu Thr Ser Leu Gly Ser Asn Gln Glu Glu Ala Tyr
 340 345 350

Val Thr Met Ser Ser Phe Tyr Gln Asn Gln
 355 360

<210> 25
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> TGF beta R2 signal sequence

<400> 25

Met Gly Arg Gly Leu Leu Arg Gly Leu Trp Pro Leu His Ile Val Leu
1 5 10 15

Trp Thr Arg Ile Ala Ser
20

<210> 26
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> CSF2Ralpha signal sequence

<400> 26

Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro
20

<210> 27
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> CSF2Ralpha signal + Myc tag

<400> 27

Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
20 25 30

<210> 28
<211> 159
<212> PRT
<213> Artificial Sequence

<220>
<223> CSF2Ralpha signal + Extracellular Domain

<400> 28

Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro Thr Ile Pro Pro His Val Gln Lys Ser Val
20 25 30

Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro
35 40 45

Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln
50 55 60

Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro
65 70 75 80

Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr
85 90 95

Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile
100 105 110

Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys
115 120 125

Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn
130 135 140

Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp
145 150 155

<210> 29
<211> 169
<212> PRT
<213> Artificial Sequence

<220>
<223> CSF2Ralpha + Myc tag + Extracellular Domain

<400> 29

Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
20 25 30

Thr Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile Val
35 40 45

Thr Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys
50 55 60

Asp Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn
65 70 75 80

Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala
85 90 95

Val Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His
100 105 110

Asp Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser
115 120 125

Pro Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe
130 135 140

Met Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser
145 150 155 160

Glu Glu Tyr Asn Thr Ser Asn Pro Asp
165

<210> 30
<211> 381
<212> PRT
<213> Artificial Sequence

<220>
<223> CSF2Ralpha + Extracellular Domain + IL7Ralpha Transmembrane
Domain + IL7Ralpha Intracellular Domain

<400> 30

Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro Thr Ile Pro Pro His Val Gln Lys Ser Val
20 25 30

Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro
35 40 45

Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln
50 55 60

Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro
65 70 75 80

Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr
85 90 95

Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile
100 105 110

Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys
115 120 125

Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn
130 135 140

Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Ser
145 150 155 160

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

Leu Leu Val Ile Leu Ala Cys Val Leu Trp Lys Lys Arg Ile Lys Pro
180 185 190

Ile Val Trp Pro Ser Leu Pro Asp His Lys Lys Thr Leu Glu His Leu
195 200 205

Cys Lys Lys Pro Arg Lys Asn Leu Asn Val Ser Phe Asn Pro Glu Ser
210 215 220

Phe Leu Asp Cys Gln Ile His Arg Val Asp Asp Ile Gln Ala Arg Asp
225 230 235 240

Glu Val Glu Gly Phe Leu Gln Asp Thr Phe Pro Gln Gln Leu Glu Glu
245 250 255

Ser Glu Lys Gln Arg Leu Gly Gly Asp Val Gln Ser Pro Asn Cys Pro
260 265 270

Ser Glu Asp Val Val Ile Thr Pro Glu Ser Phe Gly Arg Asp Ser Ser
275 280 285

Leu Thr Cys Leu Ala Gly Asn Val Ser Ala Cys Asp Ala Pro Ile Leu
290 295 300

Ser Ser Ser Arg Ser Leu Asp Cys Arg Glu Ser Gly Lys Asn Gly Pro
305 310 315 320

His Val Tyr Gln Asp Leu Leu Leu Ser Leu Gly Thr Thr Asn Ser Thr
325 330 335

Leu Pro Pro Pro Phe Ser Leu Gln Ser Gly Ile Leu Thr Leu Asn Pro
340 345 350

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

Glu Ala Tyr Val Thr Met Ser Ser Phe Tyr Gln Asn Gln
370 375 380

<210> 31

<211> 391

<212> PRT

<213> Artificial Sequence

<220>

<223> CSF2Ralpha signal + Myc tag + Extracellular Domain + IL7Ralpha
Transmembrane Domain + IL7Ralpha Intracellular Domain

<400> 31

Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
20 25 30

Thr Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile Val
35 40 45

Thr Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys
50 55 60

Asp Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn
65 70 75 80

Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala
85 90 95

Val Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His
100 105 110

Asp Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser
115 120 125

Pro Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe
130 135 140

Met Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser
145 150 155 160

Glu Glu Tyr Asn Thr Ser Asn Pro Asp Ser Gly Pro Ile Leu Leu Thr
165 170 175

Ile Ser Ile Leu Ser Phe Phe Ser Val Ala Leu Leu Val Ile Leu Ala
180 185 190

Cys Val Leu Trp Lys Lys Arg Ile Lys Pro Ile Val Trp Pro Ser Leu
195 200 205

Pro Asp His Lys Lys Thr Leu Glu His Leu Cys Lys Lys Pro Arg Lys
210 215 220

Asn Leu Asn Val Ser Phe Asn Pro Glu Ser Phe Leu Asp Cys Gln Ile
225 230 235 240

His Arg Val Asp Asp Ile Gln Ala Arg Asp Glu Val Glu Gly Phe Leu
245 250 255

Gln Asp Thr Phe Pro Gln Gln Leu Glu Glu Ser Glu Lys Gln Arg Leu
260 265 270

Gly Gly Asp Val Gln Ser Pro Asn Cys Pro Ser Glu Asp Val Val Ile
275 280 285

Thr Pro Glu Ser Phe Gly Arg Asp Ser Ser Leu Thr Cys Leu Ala Gly

290

295

300

Asn Val Ser Ala Cys Asp Ala Pro Ile Leu Ser Ser Ser Arg Ser Leu
 305 310 315 320

Asp Cys Arg Glu Ser Gly Lys Asn Gly Pro His Val Tyr Gln Asp Leu
 325 330 335

Leu Leu Ser Leu Gly Thr Thr Asn Ser Thr Leu Pro Pro Pro Phe Ser
 340 345 350

Leu Gln Ser Gly Ile Leu Thr Leu Asn Pro Val Ala Gln Gly Gln Pro
 355 360 365

Ile Leu Thr Ser Leu Gly Ser Asn Gln Glu Glu Ala Tyr Val Thr Met
 370 375 380

Ser Ser Phe Tyr Gln Asn Gln
 385 390

<210> 32

<211> 381

<212> PRT

<213> Artificial Sequence

<220>

<223> CSF2Ralpha + Extracellular Domain + IL7Ralpha Transmembrane
 Domain + IL7Ralpha Intracellular Domain

<400> 32

Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
 1 5 10 15

Ala Phe Leu Leu Ile Pro Thr Ile Pro Pro His Val Gln Lys Ser Val
 20 25 30

Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro
 35 40 45

Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln
50 55 60

Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro
65 70 75 80

Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr
85 90 95

Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile
100 105 110

Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys
115 120 125

Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn
130 135 140

Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Ser
145 150 155 160

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

Leu Leu Val Ile Leu Ala Cys Val Leu Trp Lys Lys Arg Ile Lys Pro
180 185 190

Ile Val Trp Pro Ser Leu Pro Asp His Lys Lys Thr Leu Glu His Leu
195 200 205

Cys Lys Lys Pro Arg Lys Asn Leu Asn Val Ser Phe Asn Pro Glu Ser
210 215 220

Phe Leu Asp Cys Gln Ile His Arg Val Asp Asp Ile Gln Ala Arg Asp
225 230 235 240

Glu Val Glu Gly Phe Leu Gln Asp Thr Phe Pro Gln Gln Leu Glu Glu
245 250 255

Ser Glu Lys Gln Arg Leu Gly Gly Asp Val Gln Ser Pro Asn Cys Pro
260 265 270

Ser Glu Asp Val Val Ile Thr Pro Glu Ser Phe Gly Arg Asp Ser Ser
275 280 285

Leu Thr Cys Leu Ala Gly Asn Val Ser Ala Cys Asp Ala Pro Ile Leu
290 295 300

Ser Ser Ser Arg Ser Leu Asp Cys Arg Glu Ser Gly Lys Asn Gly Pro
305 310 315 320

His Val Tyr Gln Asp Leu Leu Leu Ser Leu Gly Thr Thr Asn Ser Thr
325 330 335

Leu Pro Pro Pro Phe Ser Leu Gln Ser Gly Ile Leu Thr Leu Asn Pro
340 345 350

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

Glu Ala Tyr Val Thr Met Ser Ser Phe Tyr Gln Asn Gln
370 375 380

<210> 33
<211> 394
<212> PRT
<213> Artificial Sequence

<220>
<223> CSF2Ralpha signal + Myc tag + Extracellular Domain + IL7Ralpha
"CPT" Transmembrane Domain + IL7Ralpha Intracellular Domain

<400> 33

Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu

20

25

30

Thr Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile Val
 35 40 45

Thr Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys
 50 55 60

Asp Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn
 65 70 75 80

Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala
 85 90 95

Val Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His
 100 105 110

Asp Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser
 115 120 125

Pro Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe
 130 135 140

Met Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser
 145 150 155 160

Glu Glu Tyr Asn Thr Ser Asn Pro Asp Ser Gly Pro Ile Leu Leu Thr
 165 170 175

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

Ile Leu Ala Cys Val Leu Trp Lys Lys Arg Ile Lys Pro Ile Val Trp
 195 200 205

Pro Ser Leu Pro Asp His Lys Lys Thr Leu Glu His Leu Cys Lys Lys
 210 215 220

Pro Arg Lys Asn Leu Asn Val Ser Phe Asn Pro Glu Ser Phe Leu Asp
225 230 235 240

Cys Gln Ile His Arg Val Asp Asp Ile Gln Ala Arg Asp Glu Val Glu
245 250 255

Gly Phe Leu Gln Asp Thr Phe Pro Gln Gln Leu Glu Glu Ser Glu Lys
260 265 270

Gln Arg Leu Gly Gly Asp Val Gln Ser Pro Asn Cys Pro Ser Glu Asp
275 280 285

Val Val Ile Thr Pro Glu Ser Phe Gly Arg Asp Ser Ser Leu Thr Cys
290 295 300

Leu Ala Gly Asn Val Ser Ala Cys Asp Ala Pro Ile Leu Ser Ser Ser
305 310 315 320

Arg Ser Leu Asp Cys Arg Glu Ser Gly Lys Asn Gly Pro His Val Tyr
325 330 335

Gln Asp Leu Leu Leu Ser Leu Gly Thr Thr Asn Ser Thr Leu Pro Pro
340 345 350

Pro Phe Ser Leu Gln Ser Gly Ile Leu Thr Leu Asn Pro Val Ala Gln
355 360 365

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

Val Thr Met Ser Ser Phe Tyr Gln Asn Gln
385 390

<210> 34
<211> 384
<212> PRT
<213> Artificial Sequence

<220>

<223> CSF2Ralpha signal + Extracellular Domain + IL7Ralpha "CPT"
Transmembrane Domain + IL7Ralpha Intracellular Domain

<400> 34

Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro Thr Ile Pro Pro His Val Gln Lys Ser Val
20 25 30

Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro
35 40 45

Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln
50 55 60

Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro
65 70 75 80

Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr
85 90 95

Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile
100 105 110

Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys
115 120 125

Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn
130 135 140

Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Ser
145 150 155 160

Gly Pro Ile Leu Leu Thr Cys Pro Thr Ile Ser Ile Leu Ser Phe Phe
165 170 175

Ser Val Ala Leu Leu Val Ile Leu Ala Cys Val Leu Trp Lys Lys Arg
180 185 190

Ile Lys Pro Ile Val Trp Pro Ser Leu Pro Asp His Lys Lys Thr Leu
195 200 205

Glu His Leu Cys Lys Lys Pro Arg Lys Asn Leu Asn Val Ser Phe Asn
210 215 220

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

Ala Arg Asp Glu Val Glu Gly Phe Leu Gln Asp Thr Phe Pro Gln Gln
245 250 255

Leu Glu Glu Ser Glu Lys Gln Arg Leu Gly Gly Asp Val Gln Ser Pro
260 265 270

Asn Cys Pro Ser Glu Asp Val Val Ile Thr Pro Glu Ser Phe Gly Arg
275 280 285

Asp Ser Ser Leu Thr Cys Leu Ala Gly Asn Val Ser Ala Cys Asp Ala
290 295 300

Pro Ile Leu Ser Ser Ser Arg Ser Leu Asp Cys Arg Glu Ser Gly Lys
305 310 315 320

Asn Gly Pro His Val Tyr Gln Asp Leu Leu Leu Ser Leu Gly Thr Thr
325 330 335

Asn Ser Thr Leu Pro Pro Pro Phe Ser Leu Gln Ser Gly Ile Leu Thr
340 345 350

Leu Asn Pro Val Ala Gln Gly Gln Pro Ile Leu Thr Ser Leu Gly Ser
355 360 365

Asn Gln Glu Glu Ala Tyr Val Thr Met Ser Ser Phe Tyr Gln Asn Gln
370 375 380

<210> 35
<211> 573
<212> DNA
<213> Artificial Sequence

<220>
<223> CSF2Ralpha signal + Myc tag + Extracellular Domain + IL7Ralpha
Transmembrane Domain

<400> 35
atgctgctgc tggtgaccag cctgctgctg tgcgagctgc cccaccccg cttcctgctg 60
atccccgagc agaagctgat cagcgaggag gacctgacca tccccccca cgtgcagaag 120
agcgtgaaca acgacatgat cgtgaccgac aacaacggcg ccgtgaagtt cccccagctg 180
tgcaagttct gcgacgtgag gttcagcacc tgcgacaacc agaagagctg catgagcaac 240
tgcagcatca ccagcatctg cgagaagccc caggaggtgt gcgtggccgt gtggaggaag 300
aacgacgaga acatcacctt ggagaccgtg tgccacgacc ccaagctgcc ctaccacgac 360
ttcatcctgg aggacgccgc cagccccaag tgcacatga aggagaagaa gaagcccggc 420
gagaccttct tcatgtgcag ctgcagcagc gacgagtgc acgacaacat catcttcagc 480
gaggagtaca acaccagcaa ccccgacccc agcccatcc tgctgaccat cagcatcctg 540
agcttcttca gcgtggccct gctggtgatc ctg 573

<210> 36
<211> 582
<212> DNA
<213> Artificial Sequence

<220>
<223> CSF2Ralpha signal + Myc tag + Extracellular Domain + IL7Ralpha
"CPT" Transmembrane Domain

<400> 36
atgctgctgc tggtgaccag cctgctgctg tgcgagctgc cccaccccg cttcctgctg 60
atccccgagc agaagctgat cagcgaggag gacctgacca tccccccca cgtgcagaag 120
agcgtgaaca acgacatgat cgtgaccgac aacaacggcg ccgtgaagtt cccccagctg 180
tgcaagttct gcgacgtgag gttcagcacc tgcgacaacc agaagagctg catgagcaac 240

tgcagcatca ccagcatctg cgagaagccc caggaggtgt gcgtggccgt gtggaggaag	300
aacgacgaga acatcacctt ggagaccgtg tgccacgacc ccaagctgcc ctaccacgac	360
ttcatccttg aggacgccgc cagccccaag tgcacatga aggagaagaa gaagcccggc	420
gagaccttct tcatgtgcag ctgcagcagc gacgagtga acgacaacat catcttcagc	480
gaggagtaca acaccagcaa ccccgacccc agcggcatcc tgctgacctg cccaccatc	540
agcatcctga gcttcttcag cgtggccctg ctggtgatcc tg	582

<210> 37
 <211> 473
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Artificial Sequence

<400> 37

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

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

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

Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Ser	Arg	Glu	Ser	Gly	Val
	50					55					60				

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

Ile	Ser	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys	Gln	Gln
			85						90					95	

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

Lys Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser
115 120 125

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

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
145 150 155 160

Asn Lys Asn Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
165 170 175

Glu Trp Val Gly Arg Ile Arg Asn Lys Thr Asn Asn Tyr Ala Thr Tyr
180 185 190

Tyr Ala Asp Ser Val Lys Ala Arg Phe Thr Ile Ser Arg Asp Asp Ser
195 200 205

Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr
210 215 220

Ala Val Tyr Tyr Cys Val Ala Gly Asn Ser Phe Ala Tyr Trp Gly Gln
225 230 235 240

Gly Thr Leu Val Thr Val Ser Ser Gly Ser Thr Thr Thr Pro Ala Pro
245 250 255

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
260 265 270

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
275 280 285

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
290 295 300

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys
305 310 315 320

Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg
325 330 335

Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro
340 345 350

Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser
355 360 365

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
370 375 380

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
385 390 395 400

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
405 410 415

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
420 425 430

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
435 440 445

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
450 455 460

Leu His Met Gln Ala Leu Pro Pro Arg
465 470

<210> 38

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Sequence

<400> 38

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Asn
20 25 30

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

Gly Arg Ile Arg Asn Lys Thr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

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

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Ala Gly Asn Ser Phe Ala Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 39

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Sequence

<400> 39

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ser Arg Glu Ser Gly Val
50 55 60

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

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

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

Lys

<210> 40
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence

<400> 40

Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
1 5 10 15

Lys Gly

<210> 41
<211> 45
<212> PRT
<213> Artificial Sequence

<220>

<223> Artificial Sequence

<400> 41

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1 5 10 15

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
20 25 30

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
35 40 45

<210> 42

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Sequence

<400> 42

Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
1 5 10 15

Ser Leu Val Ile Thr Leu Tyr Cys
20

<210> 43

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Sequence

<400> 43

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
1 5 10 15

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
20 25 30

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
35 40 45

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
50 55 60

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
65 70 75 80

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
85 90 95

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
100 105 110

Arg

<210> 44

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Sequence

<400> 44

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
1 5 10 15

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

Pro Glu Glu Glu Glu Gly Gly Cys Glu
35 40

<210> 45
<211> 483
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence

<400> 45

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asp Ile Val Met Thr Gln
1 5 10 15

Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn
20 25 30

Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser Ser Asn Gln Lys Asn Tyr
35 40 45

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
50 55 60

Tyr Trp Ala Ser Ser Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly
65 70 75 80

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala
85 90 95

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Asn Tyr Pro Leu
100 105 110

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser Gly
115 120 125

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Gln
130 135 140

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
145 150 155 160

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Asn Ala Met Asn
165 170 175

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Arg Ile
180 185 190

Arg Asn Lys Thr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys
195 200 205

Ala Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser Leu Tyr Leu
210 215 220

Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val
225 230 235 240

Ala Gly Asn Ser Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
245 250 255

Ser Ser Gly Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
260 265 270

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
275 280 285

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
290 295 300

Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
305 310 315 320

Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu
325 330 335

Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln
340 345 350

Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly
355 360 365

Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
370 375 380

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
385 390 395 400

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
405 410 415

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
420 425 430

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
435 440 445

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
450 455 460

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
465 470 475 480

Pro Pro Arg

<210> 46
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence

<400> 46

Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
1 5 10 15

Gly Pro

<210> 47
<211> 688
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence

<400> 47

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

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

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

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ser Arg Glu Ser Gly Val
50 55 60

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

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

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

Lys Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser
115 120 125

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

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
145 150 155 160

Asn Lys Asn Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
165 170 175

Glu Trp Val Gly Arg Ile Arg Asn Lys Thr Asn Asn Tyr Ala Thr Tyr
180 185 190

Tyr Ala Asp Ser Val Lys Ala Arg Phe Thr Ile Ser Arg Asp Asp Ser
195 200 205

Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr
210 215 220

Ala Val Tyr Tyr Cys Val Ala Gly Asn Ser Phe Ala Tyr Trp Gly Gln
225 230 235 240

Gly Thr Leu Val Thr Val Ser Ser Gly Ser Thr Thr Thr Pro Ala Pro
245 250 255

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
260 265 270

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
275 280 285

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
290 295 300

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys
305 310 315 320

Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg
325 330 335

Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro
340 345 350

Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser
355 360 365

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
370 375 380

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
385 390 395 400

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
405 410 415

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
420 425 430

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
435 440 445

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
450 455 460

Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly
465 470 475 480

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Gly
485 490 495

Arg Gly Leu Leu Arg Gly Leu Trp Pro Leu His Ile Val Leu Trp Thr
500 505 510

Arg Ile Ala Ser Thr Ile Pro Pro His Val Gln Lys Ser Val Asn Asn
515 520 525

Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu
530 535 540

Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser
545 550 555 560

Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu
565 570 575

Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu
580 585 590

Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu
595 600 605

Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly
610 615 620

Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn
625 630 635 640

Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Leu Leu Leu
645 650 655

Val Ile Phe Gln Val Thr Gly Ile Ser Leu Leu Pro Pro Leu Gly Val
660 665 670

Ala Ile Ser Val Ile Ile Ile Phe Tyr Cys Tyr Arg Val Asn Arg Gln
675 680 685

<210> 48
<211> 582
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence

<400> 48
atgggcaggg gcctgctgag gggcctgtgg cccctgcaca tcgtgctgtg gaccaggatc 60
gccagcacca tcccccccca cgtgcagaag agcgtgaaca acgacatgat cgtgaccgac 120
aacaacggcg ccgtaagtt cccccagctg tgcaagttct gcgacgtgag gttcagcacc 180
tgcgacaacc agaagagctg catgagcaac tgcagcatca ccagcatctg cgagaagccc 240

caggaggtgt gcgtagccgt gtggaggaag aacgacgaga acatcacctt ggagaccgtg	300
tgccacgacc ccaagctgcc ctaccacgac ttcattcttg aggacgccgc cagccccaag	360
tgcattcatga aggagaagaa gaagcccggc gagaccttct tcatgtgcag ctgcagcagc	420
gacgagtgc acgacaacat catcttcagc gaggagtaca acaccagcaa ccccgacctg	480
ctgctggtga tcttccaggt gaccggcatc agcctgctgc cccccctggg cgtggccatc	540
agcgtgatca tcatcttcta ctgctacagg gtgaacaggc ag	582

<210> 49
 <211> 1449
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial Sequence

<400> 49	
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ttagctgtgt ctttaggaga gagggccaca atcaactgca agagcagcca gagcctcctc	120
tacagcagca accagaagaa ctatttagct tggtagcagc aaaagcccgg ccagcccccc	180
aagctgctga tctactgggc cagcagcaga gagagcggcg tgcccgatag attcagcgga	240
agcggctccg gcacagattt caccctcacc attagctctt tacaagctga ggacgtggcc	300
gtgtactact gccagcagta ctacaactac cctttaacct tcggccaagg taccaagctg	360
gagatcaagg gctccacatc cggatccggc aagcccggta gcggagaagg cagcacaag	420
ggagaggtgc agctggtgga gagcggaggc ggactggtcc agcccgttg atctttaagg	480
ctgtcttggt ccgccagcgg ctttaccttt aacaagaacg ctatgaactg ggtgaggcaa	540
gctcccggta agggtttaga gtgggtgggt cgtattcgta ataagaccaa caactacgcc	600
acctactatg ccgactccgt gaaggctcgt ttcaccatct ctcgtgacga cagcaagaac	660
agcctctatt tacagatgaa ctctttaaag accgaggaca ccgccgtgta ctattgcgtg	720
gctggcaact ccttcgccta ctggggccaa ggcacttttag tgaccgtgag ctccgggtcc	780
accacgacgc cagcggcgcg accaccaaca ccggcgccca ccatcgctc gcagcccctg	840

tccctgcgcc cagaggcgtg ccggccagcg gcggggggcg cagtgcacac gagggggctg	900
gacttcgcct gtgatatcta catctgggcg cccttggccg ggacttgtgg ggtccttctc	960
ctgtcactgg ttatcacctt ttactgcaaa cggggcagaa agaaactcct gtatatattc	1020
aaacaaccat ttatgagacc agtacaaact actcaagagg aagatggctg tagctgccga	1080
tttccagaag aagaagaagg aggatgtgaa ctgagagtga agttcagcag gagcgcagac	1140
gccccgcgt accagcaggg ccagaaccag ctctataacg agctcaatct aggacgaaga	1200
gaggagtacg atgttttggg caagaggcgt ggccgggacc ctgagatggg gggaaagccg	1260
agaaggaaga accctcagga aggcctgtac aatgaactgc agaaagataa gatggcggag	1320
gcctacagtg agattgggat gaaaggcgag cgccggaggg gcaaggggca cgatggcctt	1380
taccagggtc tcagtacagc caccaaggac acctacgacg cccttcacat gcaggccctg	1440
ccccctcgc	1449

<210> 50
 <211> 2094
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial Sequence

<400> 50	
gagcagaagc tgatcagcga ggaggacctc gatatcgtga tgacccagag ccccgactct	60
ttagctgtgt ctttaggaga gagggccaca atcaactgca agagcagcca gaggctcctc	120
tacagcagca accagaagaa ctatttagct tggtagcagc aaaagcccgg ccagcccccc	180
aagctgctga tctactgggc cagcagcaga gagagcggcg tgcccgatag attcagcggg	240
agcggctccg gcacagattt caccctcacc attagctctt tacaagctga ggacgtggcc	300
gtgtactact gccagcagta ctacaactac cttttaacct tcggccaagg taccaagctg	360
gagatcaagg gctccacatc cggatccggc aagcccggta gcggagaagg cagcacaag	420
ggagaggtgc agctgggtgga gagcggaggc ggactgggtc agcccgggtg atctttaagg	480
ctgtcttgtg ccgccagcgg ctttaccttt aacaagaacg ctatgaactg ggtgaggcaa	540

gctcccggta agggtttaga gtgggtgggt cgtattcgta ataagaccaa caactacgcc	600
acctactatg ccgactccgt gaaggctcgt ttcaccatct ctcgtgacga cagcaagaac	660
agcctctatt tacagatgaa ctcttttaaag accgaggaca ccgccgtgta ctattgcgtg	720
gctggcaact ccttcgccta ctggggccaa ggcacttttag tgaccgtgag ctccgggtcc	780
accacgacgc cagcgccgcg accaccaaca ccggcgccca ccatcgcgtc gcagcccctg	840
tccctgcgcc cagaggcgtg ccggccagcg gcggggggcg cagtgcacac gagggggctg	900
gacttcgcct gtgatatcta catctgggcg cccttggccg ggacttgtgg ggtccttctc	960
ctgtcactgg ttatcacctt ttactgcaaa cggggcagaa agaaactcct gtatatattc	1020
aaacaaccat ttatgagacc agtacaaact actcaagagg aagatggctg tagctgccga	1080
tttccagaag aagaagaagg aggatgtgaa ctgagagtga agttcagcag gagcgcagac	1140
gccccgcgt accagcaggg ccagaaccag ctctataacg agctcaatct aggacgaaga	1200
gaggagtacg atgttttggg caagaggcgt ggccgggacc ctgagatggg gggaaagccg	1260
agaaggaaga accctcagga aggcctgtac aatgaactgc agaaagataa gatggcggag	1320
gcctacagtg agattgggat gaaaggcgag cgccggagggg gcaaggggca cgatggcctt	1380
taccagggtc tcagtacagc caccaaggac acctacgacg cccttcacat gcaggccctg	1440
ccccctcgcg gctctggaga gggcagaggc tctctgctga cctgcggcga cgtggaagag	1500
aaccagggcc ccatgggaag aggtttactg agaggactgt ggcctttaca catcgtgctg	1560
tggactcgta tcgccagcac catcccccc catgtgcaga agagcgtgaa caacgacatg	1620
atcgtgaccg acaacaatgg cgccgtgaag ttcccccagc tgtgcaagtt ctgcgacgtg	1680
aggttcagca cttgtgacaa ccagaagagc tgcatgagca actgcagcat cacctccatc	1740
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ttagagacag tgtgccacga cccaagctg ccctaccacg acttcatttt agaagatgcc	1860
gccagcccca agtgcatcat gaaggagaag aagaagcccg gcgagacctt cttcatgtgc	1920
agctgcagct ccgacgagtg caacgataac atcatcttca gcgaggagta caacaccagc	1980
aaccccgatt tactgctggt gatcttccaa gttaccggca tttctttact gcctccttta	2040

ggcgtggcta tcagcgtgat catcatcttc tactgctata gggagaacag acag 2094

<210> 51

<211> 1419

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial Sequence

<400> 51

gatatcgtga tgaccagag cccgactct ttagctgtga gccttggaga gagggccaca 60

atcaactgca agagcagcca gagcctcctc tacagcagca accagaagaa ctatttagct 120

tggtaccagc aaaagcccgg ccagcccccc aagctgctga tctactgggc cagcagcaga 180

gagagcggcg tgcccgatag attcagcggga agcggctccg gcacagattt caccctcacc 240

attagctctt tacaagctga ggacgtggcc gtgtactact gccagcagta ctacaactac 300

cctttaacct tcggccaagg aacaaagctg gagatcaagg gctccacatc cggatccggc 360

aagcccggta gcggagaagg cagcacaaag ggagaggtgc agctgggtgga gagcggaggc 420

ggactgggtcc agcccgggtgg atctttaagg ctgtcttgtg ccgccagcgg ctttaccttt 480

aacaagaacg ctatgaactg ggtccgacaa gctcccggaa aaggtttaga gtgggtgggt 540

cgtattcgta ataagaccaa caactacgcc acctactatg ccgactccgt gaaggctcgt 600

ttcaccatct ctcgtgacga cagcaagaac agcctctatt taaaaatgaa ctctttaaag 660

accgaggaca ccgccgtgta ctattgcgtg gctggcaact ctttcgccta ctggggccaa 720

ggcactttag tgaccgtgag ctccgggtcc accacgacgc cagcgccgcg accaccaaca 780

ccggcgccca ccacgcgtc gcaaccctg tccctgcgcc ccgaggcgtg ccggccagcg 840

gcggggggcg cagtgcacac gagggggctg gacttcgcct gtgatatcta catctgggcg 900

cccttggccg ggacttgtgg ggtccttctc ctgtcactgg ttatcacctt ttattgcaaa 960

cggggcagaa agaaactcct gtatatattc aaacaaccat ttatgagacc agtacaact 1020

actcaagagg aagatggctg tagctgccga tttccagaag aagaagaagg aggatgtgaa 1080

ttgagagtga agttcagcag gagcgcagac gccccgcct atcagcaagg ccagaaccag 1140

ctctataacg agctcaatth agggcgaaga gaggagtacg atgttttgga caagaggcgt	1200
ggccgggacc ccgaaatggg gggaaagccg agaaggaaga accctcagga aggcttgtag	1260
aatgaattgc agaaggataa gatggcggag gcatacagtg agattgggat gaaaggcgag	1320
cgccggaggg gcaaggggca cgatggcctt tatcagggtc tcagtacagc caccaaggac	1380
acctacgacg cccttcacat gcaagccctg cccctcgc	1419

<210> 52
 <211> 2064
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial Sequence

<400> 52	
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tggtaccagc aaaagcccg ccagcccccc aagctgctga tctactgggc cagcagcaga	180
gagagcggcg tgcccgatag attcagcgga agcggctccg gcacagattt caccctcacc	240
attagctctt tacaagctga ggacgtggcc gtgtactact gccagcagta ctacaactac	300
cctttaacct tcggccaagg aacaaagctg gagatcaagg gctccacatc cggatccggc	360
aagcccggta gcggagaagg cagcacaag ggagagggtgc agctgggtgga gagcggaggc	420
ggactgggtcc agcccgggtg atctttaagg ctgtcttggt ccgccagcgg ctttaccttt	480
aacaagaacg ctatgaactg ggtccgacaa gctcccggaa aaggtttaga gtgggtgggt	540
cgtattcgta ataagaccaa caactacgcc acctactatg ccgactccgt gaaggctcgt	600
ttcaccatct ctctgacga cagcaagaac agcctctatt tacaaatgaa ctctttaaag	660
accgaggaca ccgccgtgta ctattgcgtg gctggcaact ctttcgccta ctggggccaa	720
ggcacttttag tgaccgtgag ctccgggtcc accacgacgc cagcgccgcg accaccaaca	780
ccggcgccca ccatcgctc gcaaccctg tccctgcgcc ccgaggcgtg ccggccagcg	840
gcggggggcg cagtgcacac gagggggctg gacttcgcct gtgatatacta catctgggcg	900

cccttggccg ggacttgtgg ggtccttctc ctgtcactgg ttatcacctt ttattgcaaa	960
cggggcagaa agaaactcct gtatatattc aaacaaccat ttatgagacc agtacaaact	1020
actcaagagg aagatggctg tagctgccga tttccagaag aagaagaagg aggatgtgaa	1080
ttgagagtga agttcagcag gagcgcagac gccccgcct atcagcaagg ccagaaccag	1140
ctctataacg agctcaattt agggcgaaga gaggagtacg atgttttgga caagaggcgt	1200
ggccgggacc ccgaaatggg gggaaagccg agaaggaaga accctcagga aggcttgtac	1260
aatgaattgc agaaggataa gatggcggag gcatacagtg agattgggat gaaaggcgag	1320
cgccggaggg gcaaggggca cgatggcctt tatcagggtc tcagtacagc caccaaggac	1380
acctacgacg cccttcacat gcaagccctg cccctcgcg gctctggaga gggcagaggc	1440
tctctgctga cctgcggcga cgtggaagag aaccaggcc ccatgggaag aggtttactg	1500
agaggactgt ggcctttaca catcgtgctg tggactcgta tcgccagcac catcccccc	1560
catgtccaaa agagcgtgaa caacgacatg atcgtgaccg acaacaatgg cgccgtgaag	1620
ttcccccagc tgtgcaagtt ctgcgacgtg aggttcagca cttgtgacaa ccagaagagc	1680
tgcattgagca actgcagcat cacctccatc tgcgagaagc cccaagaagt gtgcgtggcc	1740
gtgtggagga agaacgacga gaacatcact ttagagacag tgtgccacga cccaagctg	1800
ccctaccacg acttcatttt agaagatgcc gccagcccca agtgcatcat gaaggagaag	1860
aagaagcccc gcgagacctt cttcatgtgt tcttgttcgt ctgatgagtg caacgataac	1920
atcatcttca gcgaggagta caacaccagc aaccccgatt tactgctggt gatcttccaa	1980
gttaccggca tttctttact gcctccgttg ggcgtggcta tcagcgtgat catcatcttc	2040
tactgctatc gtgttaatcg tcaa	2064

<210> 53
 <211> 1476
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Artificial Sequence

<400> 53

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atccccacata tggaggtgca gcttggtgag tctgggtggag gattgggtgca gcctggaggg	120
tcattgagac tctcatgtgc agcctctgga ttcaccttca ataagaatgc catgaattgg	180
gtccgccagg ctccaggaaa gggtttggaa tgggttggcc gcataagaaa taaaactaat	240
aattatgcaa catattatgc cgattcagtg aaagccaggt ttaccatctc cagagatgat	300
tcaaagaact cactctatct gcaaatgaac agcttgaaaa ccgaggacac agccgtgtac	360
tattgtgtgg ctggttaactc gtttgcttac tggggccaag ggactctggg cactgtctct	420
gcaggcggag gcggatcagg tggtggcgga tctggaggtg gcggaagcga cattgtgatg	480
acccagtctc cagactccct agctgtgtca ctgggagaga gggccactat caactgcaag	540
tccagtcaga gccttttata tagcagcaat caaaagaact acttggcctg gtaccaacag	600
aaaccagggc agcctcctaa actgctgatt tactgggcat ccagtaggga atctggggtc	660
cctgatcgct tcagtggcag tggatctggg acagatttca ctctcaccat cagcagtctg	720
caggctgaag acgtggcagt ttattactgt cagcaatatt ataactatcc gctcacgttc	780
ggtcagggga ccaagttgga gatcaaaact agtaccacga cgccagcgcc gcgaccacca	840
acaccggcgc ccaccatcgc gtcgcagccc ctgtccctgc gccagaggc gtgccggcca	900
gcggcggggg gcgcagtgca cacgaggggg ctggacttcg cctgtgacat ctacatctgg	960
gcgcccttgg ccgggacttg tggggtcctt ctcctgtcac tggttatcac caaacggggc	1020
agaaagaaac tcctgtatat attcaaaca ccatthtatga gaccagtaca aactactcaa	1080
gaggaagatg gctgtagctg ccgatttcca gaagaagaag aaggaggatg tgaactgaga	1140
gtgaagttca gcaggagcgc agacgcccc gcgtaccagc agggccagaa ccagctctat	1200
aacgagctca atctaggacg aagagaggag tacgatgttt tggacaagag acgtggccgg	1260
gacctgaga tggggggaaa gccgagaagg aagaaccctc aggaaggcct gtacaatgaa	1320
ctgcagaaaag ataagatggc ggaggcctac agtgagattg ggatgaaagg cgagcgccgg	1380
aggggcaagg ggcacgatgg cctttaccag ggtctcagta cagccaccaa ggacacctac	1440
gacgcccttc acatgcaggc cctgccccct cgctga	1476

<210> 54
<211> 1476
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence

<400> 54
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tcattgagac tctcatgtgc agcctctgga ttcaccttca ataagaatgc catgaattgg 180
gtccgccagg ctccaggaaa gggtttggaa tgggttggcc gcataagaaa taaaactaat 240
aattatgcaa catattatgc cgattcagtg aaagccagggt ttaccatctc cagagatgat 300
tcaaagaact cactctatct gcaaatgaac agcttgaaaa ccgaggacac agccgtgtac 360
tattgtgtgg ctggaaaactc gtttgcttac tggggccaag ggactctggg cactgtcagc 420
gctggaggag gcggatcagg tggtagcgga tctggagggtg gcggaagcga cattgtgatg 480
accagtcctc cagactccct agctgtgtca ctgggagaga gggccactat caactgcaag 540
tccagtcaga gccttttata tagcagcaat caaaagaact acttggcctg gtaccagcaa 600
aagccagggc agcctcctaa actgctgatt tactgggcat ccagtaggga atctggggtc 660
cctgatcgct tcagtggcag tggatctggg acagatttca ctctcaccat cagcagtctg 720
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gcggcggggg gcgcagtgca cacgaggggg ctggacttcg cctgtgacat ctacatctgg 960
gcgcccttgg ccgggacttg tggggtcctt ctctgtcac tggttatcac caaacggggc 1020
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gaggaagatg gctgtagctg ccgatttcca gaagaagaag aaggaggatg tgaactgaga 1140
gtgaagttca gcaggagcgc agacgcccc gcgtaccagc aagggcagaa ccagctctat 1200

aacgagctca atctaggacg aagagaggag tacgatgttt tggacaagag gcgtggccgg	1260
gaccttgaga tgggggggaaa gccgagaagg aagaaccctc aggaaggcct gtacaatgaa	1320
ctgcagaaaag ataagatggc ggaggcctac agtgagattg ggatgaaagg cgagcgccgg	1380
aggggcaagg ggcacgatgg cttttaccag ggtctcagta cagccaccaa ggacacctac	1440
gacgcccttc acatgcaagc tctgccccct cgctga	1476

<210> 55
 <211> 2112
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial Sequence

<400> 55	
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tcattgagac tctcatgtgc agcctctgga ttcaccttca ataagaatgc catgaattgg	180
gtccgccagg ctccaggaaa gggtttgga tgggttgcc gcataagaaa taaaactaat	240
aattatgcaa catattatgc cgattcagtg aaagccaggt ttaccatctc cagagatgat	300
tcaaagaact cactctatct gcaaatgaac agcttgaaaa ccgaggacac agccgtgtac	360
tattgtgtgg ctggtaactc gtttgcttac tggggccaag ggactctggg cactgtctct	420
gcaggcggag gcggatcagg tgggtggcga tctggagggtg gcggaagcga cattgtgatg	480
accagtcctc cagactccct agctgtgtca ctgggagaga gggccactat caactgcaag	540
tccagtcaga gccttttata tagcagcaat caaaagaact acttggcctg gtaccaacag	600
aaaccagggc agcctcctaa actgctgatt tactgggcat ccagtaggga atctggggtc	660
cctgatcgct tcagtggcag tggatctggg acagatttca ctctcaccat cagcagtctg	720
caggctgaag acgtggcagt ttattactgt cagcaatatt ataactatcc gctcacgttc	780
ggtcagggga ccaagttgga gatcaaaact agtaccacga cgccagcgcc gcgaccacca	840
acaccggcgc ccaccatcgc gtcgcagccc ctgtccctgc gcccagaggc gtgccggcca	900

gcggcggggg gcgcagtgca cacgaggggg ctggacttcg cctgtgacat ctacatctgg	960
gcgcccttgg ccgggacttg tggggtcctt ctcctgtcac tggttatcac caaacggggc	1020
agaaagaaac tcctgtatat attcaaaca ccatttatga gaccagtaca aactactcaa	1080
gaggaagatg gctgtagctg ccgatttcca gaagaagaag aaggaggatg tgaactgaga	1140
gtgaagttca gcaggagcgc agacgcccc gcgtaccagc agggccagaa ccagctctat	1200
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ctgcagaaaag ataagatggc ggaggcctac agtgagattg ggatgaaagg cgagcgccgg	1380
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aagttctgcg acgtgagggt cagcacttgt gacaaccaga agagctgcat gagcaactgc	1740
agcatcacct ccatctgcga gaagccccaa gaagtgtgcg tggccgtgtg gaggaagaac	1800
gacgagaaca tcactttaga gacagtgtgc cacgacccca agctgcccta ccacgacttc	1860
attttagaag atgccgccag cccaagtgc atcatgaagg agaagaagaa gcccggcgag	1920
accttcttca tgtgttcttg ttcgtctgat gagtgaacg ataacatcat cttcagcgag	1980
gagtacaaca ccagcaaccc cgatttactg ctggtgatct tccaagttac cggcatttct	2040
ttactgcctc cgttgggcgt ggctatcagc gtgatcatca tcttctactg ctatcgtgtt	2100
aatcgtcaat ga	2112

<210> 56
 <211> 491
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Artificial Sequence

<400> 56

Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro His Met Glu Val Gln Leu Val Glu Ser Gly
20 25 30

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

Ser Gly Phe Thr Phe Asn Lys Asn Ala Met Asn Trp Val Arg Gln Ala
50 55 60

Pro Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg Asn Lys Thr Asn
65 70 75 80

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Ala Arg Phe Thr Ile
85 90 95

Ser Arg Asp Asp Ser Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu
100 105 110

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Ala Gly Asn Ser Phe
115 120 125

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met
145 150 155 160

Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr
165 170 175

Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser Ser Asn Gln Lys
180 185 190

Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu
195 200 205

Leu Ile Tyr Trp Ala Ser Ser Arg Glu Ser Gly Val Pro Asp Arg Phe
210 215 220

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
225 230 235 240

Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Asn Tyr
245 250 255

Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Thr Ser Thr
260 265 270

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
275 280 285

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
290 295 300

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
305 310 315 320

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
325 330 335

Thr Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
340 345 350

Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg
355 360 365

Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser
370 375 380

Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr
385 390 395 400

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
405 410 415

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
420 425 430

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
435 440 445

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
450 455 460

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
465 470 475 480

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 57
<211> 491
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence

<400> 57

Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro His Met Glu Val Gln Leu Val Glu Ser Gly
20 25 30

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

Ser Gly Phe Thr Phe Asn Lys Asn Ala Met Asn Trp Val Arg Gln Ala
50 55 60

Pro Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg Asn Lys Thr Asn
65 70 75 80

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Ala Arg Phe Thr Ile
85 90 95

Ser Arg Asp Asp Ser Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu
100 105 110

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Ala Gly Asn Ser Phe
115 120 125

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met
145 150 155 160

Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr
165 170 175

Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser Ser Asn Gln Lys
180 185 190

Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu
195 200 205

Leu Ile Tyr Trp Ala Ser Ser Arg Glu Ser Gly Val Pro Asp Arg Phe
210 215 220

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
225 230 235 240

Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Asn Tyr
245 250 255

Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Thr Ser Thr
260 265 270

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
275 280 285

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
290 295 300

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
305 310 315 320

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
325 330 335

Thr Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
340 345 350

Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg
355 360 365

Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser
370 375 380

Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr
385 390 395 400

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
405 410 415

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
420 425 430

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
435 440 445

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
450 455 460

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
465 470 475 480

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 58
<211> 491
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence

<400> 58

Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro His Met Glu Val Gln Leu Val Glu Ser Gly
20 25 30

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

Ser Gly Phe Thr Phe Asn Lys Asn Ala Met Asn Trp Val Arg Gln Ala
50 55 60

Pro Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg Asn Lys Thr Asn
65 70 75 80

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Ala Arg Phe Thr Ile
85 90 95

Ser Arg Asp Asp Ser Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu
100 105 110

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Ala Gly Asn Ser Phe
115 120 125

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met
145 150 155 160

Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr
165 170 175

Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser Ser Asn Gln Lys
180 185 190

Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu
195 200 205

Leu Ile Tyr Trp Ala Ser Ser Arg Glu Ser Gly Val Pro Asp Arg Phe
210 215 220

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
225 230 235 240

Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Asn Tyr
245 250 255

Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Thr Ser Thr
260 265 270

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
275 280 285

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
290 295 300

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
305 310 315 320

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
325 330 335

Thr Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
340 345 350

Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg
355 360 365

Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser
370 375 380

Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr
385 390 395 400

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
405 410 415

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
420 425 430

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
435 440 445

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
450 455 460

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
465 470 475 480

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490