

464173SEQLIST

SEQUENCE LISTING

<110> Malek, Thomas

<120> INTERLEUKIN-2/INTERLEUKIN-2 RECEPTOR
 ALPHA FUSION PROTEINS AND METHODS OF USE

<130> 060569-464173

<150> US 62/033,726

<151> 2014-08-06

<160> 65

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 153

<212> PRT

<213> Homo sapeins

<400> 1

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Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
 1             5             10             15
Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu
      20             25             30
Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile
      35             40             45
Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe
      50             55             60
Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu
65             70             75             80
Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys
      85             90             95
Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile
      100            105            110
Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala
      115            120            125
Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe
      130            135            140
Cys Gln Ser Ile Ile Ser Thr Leu Thr
145            150

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<210> 2

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<211> 133

<212> PRT

<213> Homo sapiens

<400> 2

Ala	Pro	Thr	Ser	Ser	Ser	Thr	Lys	Lys	Thr	Gln	Leu	Gln	Leu	Glu	His
1				5					10					15	
Leu	Leu	Leu	Asp	Leu	Gln	Met	Ile	Leu	Asn	Gly	Ile	Asn	Asn	Tyr	Lys
			20					25					30		
Asn	Pro	Lys	Leu	Thr	Arg	Met	Leu	Thr	Phe	Lys	Phe	Tyr	Met	Pro	Lys
		35					40					45			
Lys	Ala	Thr	Glu	Leu	Lys	His	Leu	Gln	Cys	Leu	Glu	Glu	Glu	Leu	Lys
	50					55					60				
Pro	Leu	Glu	Glu	Val	Leu	Asn	Leu	Ala	Gln	Ser	Lys	Asn	Phe	His	Leu
65					70					75					80
Arg	Pro	Arg	Asp	Leu	Ile	Ser	Asn	Ile	Asn	Val	Ile	Val	Leu	Glu	Leu
			85						90					95	
Lys	Gly	Ser	Glu	Thr	Thr	Phe	Met	Cys	Glu	Tyr	Ala	Asp	Glu	Thr	Ala
			100					105					110		
Thr	Ile	Val	Glu	Phe	Leu	Asn	Arg	Trp	Ile	Thr	Phe	Cys	Gln	Ser	Ile
	115						120					125			
Ile	Ser	Thr	Leu	Thr											
	130														

<210> 3

<211> 169

<212> PRT

<213> Mus musculus

<400> 3

Met	Tyr	Ser	Met	Gln	Leu	Ala	Ser	Cys	Val	Thr	Leu	Thr	Leu	Val	Leu
1				5					10					15	
Leu	Val	Asn	Ser	Ala	Pro	Thr	Ser	Ser	Ser	Thr	Ser	Ser	Ser	Thr	Ala
			20					25					30		
Glu	Ala	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	His	Leu
	35						40					45			
Glu	Gln	Leu	Leu	Met	Asp	Leu	Gln	Glu	Leu	Leu	Ser	Arg	Met	Glu	Asn
	50					55					60				
Tyr	Arg	Asn	Leu	Lys	Leu	Pro	Arg	Met	Leu	Thr	Phe	Lys	Phe	Tyr	Leu
65					70					75					80
Pro	Lys	Gln	Ala	Thr	Glu	Leu	Lys	Asp	Leu	Gln	Cys	Leu	Glu	Asp	Glu
			85					90						95	
Leu	Gly	Pro	Leu	Arg	His	Val	Leu	Asp	Leu	Thr	Gln	Ser	Lys	Ser	Phe
			100					105					110		
Gln	Leu	Glu	Asp	Ala	Glu	Asn	Phe	Ile	Ser	Asn	Ile	Arg	Val	Thr	Val
	115						120					125			
Val	Lys	Leu	Lys	Gly	Ser	Asp	Asn	Thr	Phe	Glu	Cys	Gln	Phe	Asp	Asp

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130 135 140
 Glu Ser Ala Thr Val Val Asp Phe Leu Arg Arg Trp Ile Ala Phe Cys
 145 150 155 160
 Gln Ser Ile Ile Ser Thr Ser Pro Gln
 165

<210> 4
 <211> 169
 <212> PRT
 <213> Mus musculus

<400> 4
 Met Tyr Ser Met Gln Leu Ala Ser Cys Val Thr Leu Thr Leu Val Leu
 1 5 10 15
 Leu Val Asn Ser Ala Pro Thr Ser Ser Ser Thr Ser Ser Ser Thr Ala
 20 25 30
 Glu Ala Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln His Leu
 35 40 45
 Glu Gln Leu Leu Met Asp Leu Gln Glu Leu Leu Ser Arg Met Glu Asn
 50 55 60
 Tyr Arg Asn Leu Lys Leu Pro Arg Met Leu Thr Phe Lys Phe Tyr Leu
 65 70 75 80
 Pro Lys Gln Ala Thr Glu Leu Lys Asp Leu Gln Cys Leu Glu Asp Glu
 85 90 95
 Leu Gly Pro Leu Arg His Val Leu Asp Leu Thr Gln Ser Lys Ser Phe
 100 105 110
 Gln Leu Glu Asp Ala Glu Asn Phe Ile Ser Asn Ile Arg Val Thr Val
 115 120 125
 Val Lys Leu Lys Gly Ser Asp Asn Thr Phe Glu Cys Gln Phe Asp Asp
 130 135 140
 Glu Ser Ala Thr Val Val Asp Phe Leu Arg Arg Trp Ile Ala Phe Cys
 145 150 155 160
 Gln Ser Ile Ile Ser Thr Ser Pro Gln
 165

<210> 5
 <211> 272
 <212> PRT
 <213> Homo sapiens

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

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      35              40              45
Cys Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr
  50              55              60
Met Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp Asp Asn Gln Cys
  65              70              75              80
Gln Cys Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys Gln Val Thr Pro
      85              90              95
Gln Pro Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Pro
  100              105              110
Met Gln Pro Val Asp Gln Ala Ser Leu Pro Gly His Cys Arg Glu Pro
  115              120              125
Pro Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val
  130              135              140
Gly Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His
  145              150              155              160
Arg Gly Pro Ala Glu Ser Val Cys Lys Met Thr His Gly Lys Thr Arg
      165              170              175
Trp Thr Gln Pro Gln Leu Ile Cys Thr Gly Glu Met Glu Thr Ser Gln
  180              185              190
Phe Pro Gly Glu Glu Lys Pro Gln Ala Ser Pro Glu Gly Arg Pro Glu
  195              200              205
Ser Glu Thr Ser Cys Leu Val Thr Thr Thr Asp Phe Gln Ile Gln Thr
  210              215              220
Glu Met Ala Ala Thr Met Glu Thr Ser Ile Phe Thr Thr Glu Tyr Gln
  225              230              235              240
Val Ala Val Ala Gly Cys Val Phe Leu Leu Ile Ser Val Leu Leu Leu
      245              250              255
Ser Gly Leu Thr Trp Gln Arg Arg Gln Arg Lys Ser Arg Arg Thr Ile
  260              265              270

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<210> 6

<211> 251

<212> PRT

<213> Homo sapiens

<400> 6

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

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

<210> 7

<211> 219

<212> PRT

<213> Homo sapiens

<400> 7

Glu	Leu	Cys	Asp	Asp	Asp	Pro	Pro	Glu	Ile	Pro	His	Ala	Thr	Phe	Lys		
1				5				10						15			
Ala	Met	Ala	Tyr	Lys	Glu	Gly	Thr	Met	Leu	Asn	Cys	Glu	Cys	Lys	Arg		
		20						25					30				
Gly	Phe	Arg	Arg	Ile	Lys	Ser	Gly	Ser	Leu	Tyr	Met	Leu	Cys	Thr	Gly		
	35					40					45						
Asn	Ser	Ser	His	Ser	Ser	Trp	Asp	Asn	Gln	Cys	Gln	Cys	Thr	Ser	Ser		
	50				55				60								
Ala	Thr	Arg	Asn	Thr	Thr	Lys	Gln	Val	Thr	Pro	Gln	Pro	Glu	Glu	Gln		
65				70				75					80				
Lys	Glu	Arg	Lys	Thr	Thr	Glu	Met	Gln	Ser	Pro	Met	Gln	Pro	Val	Asp		
			85					90					95				
Gln	Ala	Ser	Leu	Pro	Gly	His	Cys	Arg	Glu	Pro	Pro	Pro	Trp	Glu	Asn		
	100						105						110				
Glu	Ala	Thr	Glu	Arg	Ile	Tyr	His	Phe	Val	Val	Gly	Gln	Met	Val	Tyr		
	115					120						125					
Tyr	Gln	Cys	Val	Gln	Gly	Tyr	Arg	Ala	Leu	His	Arg	Gly	Pro	Ala	Glu		
	130				135						140						
Ser	Val	Cys	Lys	Met	Thr	His	Gly	Lys	Thr	Arg	Trp	Thr	Gln	Pro	Gln		

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

<210> 8

<211> 268

<212> PRT

<213> Mus musculus

<400> 8

Met	Glu	Pro	Arg	Leu	Leu	Met	Leu	Gly	Phe	Leu	Ser	Leu	Thr	Ile	Val
1				5				10						15	
Pro	Ser	Cys	Arg	Ala	Glu	Leu	Cys	Leu	Tyr	Asp	Pro	Pro	Glu	Val	Pro
			20					25					30		
Asn	Ala	Thr	Phe	Lys	Ala	Leu	Ser	Tyr	Lys	Asn	Gly	Thr	Ile	Leu	Asn
			35					40					45		
Cys	Glu	Cys	Lys	Arg	Gly	Phe	Arg	Arg	Leu	Lys	Glu	Leu	Val	Tyr	Met
			50			55					60				
Arg	Cys	Leu	Gly	Asn	Ser	Trp	Ser	Ser	Asn	Cys	Gln	Cys	Thr	Ser	Asn
				70						75					80
Ser	His	Asp	Lys	Ser	Arg	Lys	Gln	Val	Thr	Ala	Gln	Leu	Glu	His	Gln
				85						90					95
Lys	Glu	Gln	Gln	Thr	Thr	Thr	Asp	Met	Gln	Lys	Pro	Thr	Gln	Ser	Met
			100					105							110
His	Gln	Glu	Asn	Leu	Thr	Gly	His	Cys	Arg	Glu	Pro	Pro	Pro	Trp	Lys
			115				120								125
His	Glu	Asp	Ser	Lys	Arg	Ile	Tyr	His	Phe	Val	Glu	Gly	Gln	Ser	Val
			130			135					140				
His	Tyr	Glu	Cys	Ile	Pro	Gly	Tyr	Lys	Ala	Leu	Gln	Arg	Gly	Pro	Ala
				150						155					160
Ile	Ser	Ile	Cys	Lys	Met	Lys	Cys	Gly	Lys	Thr	Gly	Trp	Thr	Gln	Pro
			165						170						175
Gln	Leu	Thr	Cys	Val	Asp	Glu	Arg	Glu	His	His	Arg	Phe	Leu	Ala	Ser
			180					185						190	
Glu	Glu	Ser	Gln	Gly	Ser	Arg	Asn	Ser	Ser	Pro	Glu	Ser	Glu	Thr	Ser
			195				200					205			
Cys	Pro	Ile	Thr	Thr	Thr	Asp	Phe	Pro	Gln	Pro	Thr	Glu	Thr	Thr	Ala
			210			215					220				
Met	Thr	Glu	Thr	Phe	Val	Leu	Thr	Met	Glu	Tyr	Lys	Val	Ala	Val	Ala
				230						235					240
Ser	Cys	Leu	Phe	Leu	Leu	Ile	Ser	Ile	Leu	Leu	Leu	Ser	Gly	Leu	Thr

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245 250 255
 Trp Gln His Arg Trp Arg Lys Ser Arg Arg Thr Ile
 260 265

<210> 9
 <211> 247
 <212> PRT
 <213> Mus musculus

<400> 9
 Glu Leu Cys Leu Tyr Asp Pro Pro Glu Val Pro Asn Ala Thr Phe Lys
 1 5 10 15
 Ala Leu Ser Tyr Lys Asn Gly Thr Ile Leu Asn Cys Glu Cys Lys Arg
 20 25 30
 Gly Phe Arg Arg Leu Lys Glu Leu Val Tyr Met Arg Cys Leu Gly Asn
 35 40 45
 Ser Trp Ser Ser Asn Cys Gln Cys Thr Ser Asn Ser His Asp Lys Ser
 50 55 60
 Arg Lys Gln Val Thr Ala Gln Leu Glu His Gln Lys Glu Gln Gln Thr
 65 70 75 80
 Thr Thr Asp Met Gln Lys Pro Thr Gln Ser Met His Gln Glu Asn Leu
 85 90 95
 Thr Gly His Cys Arg Glu Pro Pro Pro Trp Lys His Glu Asp Ser Lys
 100 105 110
 Arg Ile Tyr His Phe Val Glu Gly Gln Ser Val His Tyr Glu Cys Ile
 115 120 125
 Pro Gly Tyr Lys Ala Leu Gln Arg Gly Pro Ala Ile Ser Ile Cys Lys
 130 135 140
 Met Lys Cys Gly Lys Thr Gly Trp Thr Gln Pro Gln Leu Thr Cys Val
 145 150 155 160
 Asp Glu Arg Glu His His Arg Phe Leu Ala Ser Glu Glu Ser Gln Gly
 165 170 175
 Ser Arg Asn Ser Ser Pro Glu Ser Glu Thr Ser Cys Pro Ile Thr Thr
 180 185 190
 Thr Asp Phe Pro Gln Pro Thr Glu Thr Thr Ala Met Thr Glu Thr Phe
 195 200 205
 Val Leu Thr Met Glu Tyr Lys Val Ala Val Ala Ser Cys Leu Phe Leu
 210 215 220
 Leu Ile Ser Ile Leu Leu Leu Ser Gly Leu Thr Trp Gln His Arg Trp
 225 230 235 240
 Arg Lys Ser Arg Arg Thr Ile
 245

<210> 10
 <211> 215
 <212> PRT

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<213> Mus musculus

<400> 10

Glu	Leu	Cys	Leu	Tyr	Asp	Pro	Pro	Glu	Val	Pro	Asn	Ala	Thr	Phe	Lys
1				5					10					15	
Ala	Leu	Ser	Tyr	Lys	Asn	Gly	Thr	Ile	Leu	Asn	Cys	Glu	Cys	Lys	Arg
			20					25					30		
Gly	Phe	Arg	Arg	Leu	Lys	Glu	Leu	Val	Tyr	Met	Arg	Cys	Leu	Gly	Asn
		35				40						45			
Ser	Trp	Ser	Ser	Asn	Cys	Gln	Cys	Thr	Ser	Asn	Ser	His	Asp	Lys	Ser
	50					55					60				
Arg	Lys	Gln	Val	Thr	Ala	Gln	Leu	Glu	His	Gln	Lys	Glu	Gln	Gln	Thr
65					70					75				80	
Thr	Thr	Asp	Met	Gln	Lys	Pro	Thr	Gln	Ser	Met	His	Gln	Glu	Asn	Leu
				85					90					95	
Thr	Gly	His	Cys	Arg	Glu	Pro	Pro	Pro	Trp	Lys	His	Glu	Asp	Ser	Lys
			100					105					110		
Arg	Ile	Tyr	His	Phe	Val	Glu	Gly	Gln	Ser	Val	His	Tyr	Glu	Cys	Ile
		115					120					125			
Pro	Gly	Tyr	Lys	Ala	Leu	Gln	Arg	Gly	Pro	Ala	Ile	Ser	Ile	Cys	Lys
	130					135					140				
Met	Lys	Cys	Gly	Lys	Thr	Gly	Trp	Thr	Gln	Pro	Gln	Leu	Thr	Cys	Val
145					150					155					160
Asp	Glu	Arg	Glu	His	His	Arg	Phe	Leu	Ala	Ser	Glu	Glu	Ser	Gln	Gly
				165					170					175	
Ser	Arg	Asn	Ser	Ser	Pro	Glu	Ser	Glu	Thr	Ser	Cys	Pro	Ile	Thr	Thr
		180						185					190		
Thr	Asp	Phe	Pro	Gln	Pro	Thr	Glu	Thr	Thr	Ala	Met	Thr	Glu	Thr	Phe
	195						200						205		
Val	Leu	Thr	Met	Glu	Tyr	Lys									
	210					215									

<210> 11

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> (Gly3Ser)4 linker

<400> 11

Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser
1				5				10						15	

<210> 12

<211> 8

464173SEQLIST

<212> PRT

<213> Artificial Sequence

<220>

<223> (Gly3Ser)2 linker

<400> 12

Gly Gly Gly Ser Gly Gly Gly Ser

1

5

<210> 13

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> (Gly3Ser)3 linker

<400> 13

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser

1

5

10

<210> 14

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> (Gly3Ser)5 linker

<400> 14

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser

1

5

10

15

Gly Gly Gly Ser

20

<210> 15

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Gly3 linker

<400> 15

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Gly Gly Gly
1

<210> 16

<211> 384

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized Mature form of IL-2

(Gly4Ser)4-extracellular domain of IL-2 R

<400> 16

Ala	Pro	Thr	Ser	Ser	Ser	Thr	Ser	Ser	Ser	Thr	Ala	Glu	Ala	Gln	Gln
1				5				10						15	
Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	His	Leu	Glu	Gln	Leu	Leu
			20					25					30		
Met	Asp	Leu	Gln	Glu	Leu	Leu	Ser	Arg	Met	Glu	Asn	Tyr	Arg	Asn	Leu
	35						40					45			
Lys	Leu	Pro	Arg	Met	Leu	Thr	Phe	Lys	Phe	Tyr	Leu	Pro	Lys	Gln	Ala
	50					55					60				
Thr	Glu	Leu	Lys	Asp	Leu	Gln	Cys	Leu	Glu	Asp	Glu	Leu	Gly	Pro	Leu
65					70					75					80
Arg	His	Val	Leu	Asp	Leu	Thr	Gln	Ser	Lys	Ser	Phe	Gln	Leu	Glu	Asp
				85					90					95	
Ala	Glu	Asn	Phe	Ile	Ser	Asn	Ile	Arg	Val	Thr	Val	Val	Lys	Leu	Lys
			100					105					110		
Gly	Ser	Asp	Asn	Thr	Phe	Glu	Cys	Gln	Phe	Asp	Asp	Glu	Ser	Ala	Thr
	115						120					125			
Val	Val	Asp	Phe	Leu	Arg	Arg	Trp	Ile	Ala	Phe	Cys	Gln	Ser	Ile	Ile
	130					135					140				
Ser	Thr	Ser	Pro	Gln	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly
145					150					155					160
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Leu	Cys	Leu	Tyr	Asp	Pro
			165						170					175	
Pro	Glu	Val	Pro	Asn	Ala	Thr	Phe	Lys	Ala	Leu	Ser	Tyr	Lys	Asn	Gly
			180					185					190		
Thr	Ile	Leu	Asn	Cys	Glu	Cys	Lys	Arg	Gly	Phe	Arg	Arg	Leu	Lys	Glu
	195						200					205			
Leu	Val	Tyr	Met	Arg	Cys	Leu	Gly	Asn	Ser	Trp	Ser	Ser	Asn	Cys	Gln
	210					215					220				
Cys	Thr	Ser	Asn	Ser	His	Asp	Lys	Ser	Arg	Lys	Gln	Val	Thr	Ala	Gln
225					230					235					240
Leu	Glu	His	Gln	Lys	Glu	Gln	Gln	Thr	Thr	Thr	Asp	Met	Gln	Lys	Pro
			245						250					255	
Thr	Gln	Ser	Met	His	Gln	Glu	Asn	Leu	Thr	Gly	His	Cys	Arg	Glu	Pro
			260					265						270	

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Pro Pro Trp Lys His Glu Asp Ser Lys Arg Ile Tyr His Phe Val Glu
    275                                280                285
Gly Gln Ser Val His Tyr Glu Cys Ile Pro Gly Tyr Lys Ala Leu Gln
    290                                295                300
Arg Gly Pro Ala Ile Ser Ile Cys Lys Met Lys Cys Gly Lys Thr Gly
305                                310                315                320
Trp Thr Gln Pro Gln Leu Thr Cys Val Asp Glu Arg Glu His His Arg
    325                                330                335
Phe Leu Ala Ser Glu Glu Ser Gln Gly Ser Arg Asn Ser Ser Pro Glu
    340                                345                350
Ser Glu Thr Ser Cys Pro Ile Thr Thr Thr Asp Phe Pro Gln Pro Thr
    355                                360                365
Glu Thr Thr Ala Met Thr Glu Thr Phe Val Leu Thr Met Glu Tyr Lys
    370                                375                380

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<210> 17

<211> 404

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized unprocessed form of IL-2
(Gly4Ser)4-extracellular domain of IL-2 R

<400> 17

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Met Asp Ser Met Gln Leu Ala Ser Cys Val Thr Leu Thr Leu Val Leu
  1                                5                10                15
Leu Val Asn Ser Ala Pro Thr Ser Ser Ser Thr Ser Ser Ser Thr Ala
    20                                25                30
Glu Ala Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln His Leu
    35                                40                45
Glu Gln Leu Leu Met Asp Leu Gln Glu Leu Leu Ser Arg Met Glu Asn
    50                                55                60
Tyr Arg Asn Leu Lys Leu Pro Arg Met Leu Thr Phe Lys Phe Tyr Leu
65                                70                75                80
Pro Lys Gln Ala Thr Glu Leu Lys Asp Leu Gln Cys Leu Glu Asp Glu
    85                                90                95
Leu Gly Pro Leu Arg His Val Leu Asp Leu Thr Gln Ser Lys Ser Phe
    100                               105                110
Gln Leu Glu Asp Ala Glu Asn Phe Ile Ser Asn Ile Arg Val Thr Val
    115                               120                125
Val Lys Leu Lys Gly Ser Asp Asn Thr Phe Glu Cys Gln Phe Asp Asp
    130                               135                140
Glu Ser Ala Thr Val Val Asp Phe Leu Arg Arg Trp Ile Ala Phe Cys
145                               150                155                160
Gln Ser Ile Ile Ser Thr Ser Pro Gln Gly Gly Gly Gly Ser Gly Gly
    165                               170                175

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Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu Cys
    180                      185                      190
Leu Tyr Asp Pro Pro Glu Val Pro Asn Ala Thr Phe Lys Ala Leu Ser
    195                      200                      205
Tyr Lys Asn Gly Thr Ile Leu Asn Cys Glu Cys Lys Arg Gly Phe Arg
    210                      215                      220
Arg Leu Lys Glu Leu Val Tyr Met Arg Cys Leu Gly Asn Ser Trp Ser
    225                      230                      235                      240
Ser Asn Cys Gln Cys Thr Ser Asn Ser His Asp Lys Ser Arg Lys Gln
    245                      250                      255
Val Thr Ala Gln Leu Glu His Gln Lys Glu Gln Gln Thr Thr Thr Asp
    260                      265                      270
Met Gln Lys Pro Thr Gln Ser Met His Gln Glu Asn Leu Thr Gly His
    275                      280                      285
Cys Arg Glu Pro Pro Pro Trp Lys His Glu Asp Ser Lys Arg Ile Tyr
    290                      295                      300
His Phe Val Glu Gly Gln Ser Val His Tyr Glu Cys Ile Pro Gly Tyr
    305                      310                      315                      320
Lys Ala Leu Gln Arg Gly Pro Ala Ile Ser Ile Cys Lys Met Lys Cys
    325                      330                      335
Gly Lys Thr Gly Trp Thr Gln Pro Gln Leu Thr Cys Val Asp Glu Arg
    340                      345                      350
Glu His His Arg Phe Leu Ala Ser Glu Glu Ser Gln Gly Ser Arg Asn
    355                      360                      365
Ser Ser Pro Glu Ser Glu Thr Ser Cys Pro Ile Thr Thr Thr Asp Phe
    370                      375                      380
Pro Gln Pro Thr Glu Thr Thr Ala Met Thr Glu Thr Phe Val Leu Thr
    385                      390                      395                      400
Met Glu Tyr Lys

```

<210> 18

<211> 389

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized mature form of IL-2 (Gly4Ser)5-
extracellular domain of IL-2 R

<400> 18

```

Ala Pro Thr Ser Ser Ser Thr Ser Ser Ser Thr Ala Glu Ala Gln Gln
  1                      5                      10                      15
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln His Leu Glu Gln Leu Leu
    20                      25                      30
Met Asp Leu Gln Glu Leu Leu Ser Arg Met Glu Asn Tyr Arg Asn Leu
    35                      40                      45

```

464173SEQLIST

Lys Leu Pro Arg Met Leu Thr Phe Lys Phe Tyr Leu Pro Lys Gln Ala
 50 55 60
 Thr Glu Leu Lys Asp Leu Gln Cys Leu Glu Asp Glu Leu Gly Pro Leu
 65 70 75 80
 Arg His Val Leu Asp Leu Thr Gln Ser Lys Ser Phe Gln Leu Glu Asp
 85 90 95
 Ala Glu Asn Phe Ile Ser Asn Ile Arg Val Thr Val Val Lys Leu Lys
 100 105 110
 Gly Ser Asp Asn Thr Phe Glu Cys Gln Phe Asp Asp Glu Ser Ala Thr
 115 120 125
 Val Val Asp Phe Leu Arg Arg Trp Ile Ala Phe Cys Gln Ser Ile Ile
 130 135 140
 Ser Thr Ser Pro Gln Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 145 150 155 160
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu
 165 170 175
 Cys Leu Tyr Asp Pro Pro Glu Val Pro Asn Ala Thr Phe Lys Ala Leu
 180 185 190
 Ser Tyr Lys Asn Gly Thr Ile Leu Asn Cys Glu Cys Lys Arg Gly Phe
 195 200 205
 Arg Arg Leu Lys Glu Leu Val Tyr Met Arg Cys Leu Gly Asn Ser Trp
 210 215 220
 Ser Ser Asn Cys Gln Cys Thr Ser Asn Ser His Asp Lys Ser Arg Lys
 225 230 235 240
 Gln Val Thr Ala Gln Leu Glu His Gln Lys Glu Gln Gln Thr Thr Thr
 245 250 255
 Asp Met Gln Lys Pro Thr Gln Ser Met His Gln Glu Asn Leu Thr Gly
 260 265 270
 His Cys Arg Glu Pro Pro Pro Trp Lys His Glu Asp Ser Lys Arg Ile
 275 280 285
 Tyr His Phe Val Glu Gly Gln Ser Val His Tyr Glu Cys Ile Pro Gly
 290 295 300
 Tyr Lys Ala Leu Gln Arg Gly Pro Ala Ile Ser Ile Cys Lys Met Lys
 305 310 315 320
 Cys Gly Lys Thr Gly Trp Thr Gln Pro Gln Leu Thr Cys Val Asp Glu
 325 330 335
 Arg Glu His His Arg Phe Leu Ala Ser Glu Glu Ser Gln Gly Ser Arg
 340 345 350
 Asn Ser Ser Pro Glu Ser Glu Thr Ser Cys Pro Ile Thr Thr Thr Asp
 355 360 365
 Phe Pro Gln Pro Thr Glu Thr Thr Ala Met Thr Glu Thr Phe Val Leu
 370 375 380
 Thr Met Glu Tyr Lys
 385

<210> 19

<211> 409

464173SEQLIST

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthesized unprocessed form of IL-2 (Gly4Ser)5-extracellular domain of IL-2 B

<400> 19

Met 1	Asp	Ser	Met	Gln 5	Leu	Ala	Ser	Cys	Val 10	Thr	Leu	Thr	Leu	Val 15	Leu
Leu	Val	Asn	Ser 20	Ala	Pro	Thr	Ser	Ser 25	Ser	Thr	Ser	Ser	Ser 30	Thr	Ala
Glu	Ala	Gln 35	Gln	Gln	Gln	Gln	Gln 40	Gln	Gln	Gln	Gln	Gln 45	Gln	His	Leu
Glu	Gln 50	Leu	Leu	Met	Asp 55	Leu	Gln	Glu	Leu	Leu	Ser 60	Arg	Met	Glu	Asn
Tyr 65	Arg	Asn	Leu	Lys 70	Leu	Pro	Arg	Met	Leu	Thr 75	Phe	Lys	Phe	Tyr 80	Leu
Pro	Lys	Gln	Ala	Thr 85	Glu	Leu	Lys	Asp 90	Leu	Gln	Cys	Leu	Glu 95	Asp	Glu
Leu	Gly	Pro	Leu 100	Arg	His	Val	Leu	Asp 105	Leu	Thr	Gln	Ser	Lys 110	Ser	Phe
Gln	Leu	Glu 115	Asp	Ala	Glu	Asn	Phe 120	Ile	Ser	Asn	Ile	Arg 125	Val	Thr	Val
Val	Lys 130	Leu	Lys	Gly	Ser	Asp 135	Asn	Thr	Phe	Glu	Cys 140	Gln	Phe	Asp	Asp
Glu 145	Ser	Ala	Thr	Val	Val 150	Asp	Phe	Leu	Arg	Arg 155	Trp	Ile	Ala	Phe	Cys 160
Gln	Ser	Ile	Ile	Ser 165	Thr	Ser	Pro	Gln	Gly 170	Gly	Gly	Gly	Ser	Gly 175	Gly
Gly	Gly	Ser	Gly 180	Gly	Gly	Gly	Ser	Gly 185	Gly	Gly	Gly	Ser	Gly 190	Gly	Gly
Gly	Ser	Glu 195	Leu	Cys	Leu	Tyr	Asp 200	Pro	Pro	Glu	Val 205	Pro	Asn	Ala	Thr
Phe	Lys 210	Ala	Leu	Ser	Tyr	Lys 215	Asn	Gly	Thr	Ile	Leu 220	Asn	Cys	Glu	Cys
Lys 225	Arg	Gly	Phe	Arg	Arg 230	Leu	Lys	Glu	Leu	Val 235	Tyr	Met	Arg	Cys	Leu 240
Gly	Asn	Ser	Trp	Ser 245	Ser	Asn	Cys	Gln	Cys 250	Thr	Ser	Asn	Ser	His 255	Asp
Lys	Ser	Arg	Lys 260	Gln	Val	Thr	Ala	Gln 265	Leu	Glu	His	Gln	Lys 270	Glu	Gln
Gln	Thr	Thr 275	Thr	Asp	Met	Gln	Lys 280	Pro	Thr	Gln	Ser	Met 285	His	Gln	Glu
Asn	Leu 290	Thr	Gly	His	Cys	Arg 295	Glu	Pro	Pro	Pro	Trp 300	Lys	His	Glu	Asp
Ser 305	Lys	Arg	Ile	Tyr	His 310	Phe	Val	Glu	Gly	Gln 315	Ser	Val	His	Tyr	Glu 320

464173SEQLIST

```

Cys Ile Pro Gly Tyr Lys Ala Leu Gln Arg Gly Pro Ala Ile Ser Ile
      325              330              335
Cys Lys Met Lys Cys Gly Lys Thr Gly Trp Thr Gln Pro Gln Leu Thr
      340              345              350
Cys Val Asp Glu Arg Glu His His Arg Phe Leu Ala Ser Glu Glu Ser
      355              360              365
Gln Gly Ser Arg Asn Ser Ser Pro Glu Ser Glu Thr Ser Cys Pro Ile
      370              375              380
Thr Thr Thr Asp Phe Pro Gln Pro Thr Glu Thr Thr Ala Met Thr Glu
385              390              395              400
Thr Phe Val Leu Thr Met Glu Tyr Lys
      405

```

<210> 20

<211> 380

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized mature form of IL-2 (Gly3Ser)4-
extracellular domain of IL-2 R

<400> 20

```

Ala Pro Thr Ser Ser Ser Thr Ser Ser Ser Thr Ala Glu Ala Gln Gln
 1              5              10              15
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln His Leu Glu Gln Leu Leu
      20              25              30
Met Asp Leu Gln Glu Leu Leu Ser Arg Met Glu Asn Tyr Arg Asn Leu
      35              40              45
Lys Leu Pro Arg Met Leu Thr Phe Lys Phe Tyr Leu Pro Lys Gln Ala
      50              55              60
Thr Glu Leu Lys Asp Leu Gln Cys Leu Glu Asp Glu Leu Gly Pro Leu
65              70              75              80
Arg His Val Leu Asp Leu Thr Gln Ser Lys Ser Phe Gln Leu Glu Asp
      85              90              95
Ala Glu Asn Phe Ile Ser Asn Ile Arg Val Thr Val Val Lys Leu Lys
      100             105             110
Gly Ser Asp Asn Thr Phe Glu Cys Gln Phe Asp Asp Glu Ser Ala Thr
      115             120             125
Val Val Asp Phe Leu Arg Arg Trp Ile Ala Phe Cys Gln Ser Ile Ile
      130             135             140
Ser Thr Ser Pro Gln Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
145             150             155             160
Ser Gly Gly Gly Ser Glu Leu Cys Leu Tyr Asp Pro Pro Glu Val Pro
      165             170             175
Asn Ala Thr Phe Lys Ala Leu Ser Tyr Lys Asn Gly Thr Ile Leu Asn
      180             185             190

```

464173SEQLIST

Cys	Glu	Cys	Lys	Arg	Gly	Phe	Arg	Arg	Leu	Lys	Glu	Leu	Val	Tyr	Met
	195						200					205			
Arg	Cys	Leu	Gly	Asn	Ser	Trp	Ser	Ser	Asn	Cys	Gln	Cys	Thr	Ser	Asn
	210					215					220				
Ser	His	Asp	Lys	Ser	Arg	Lys	Gln	Val	Thr	Ala	Gln	Leu	Glu	His	Gln
225					230					235					240
Lys	Glu	Gln	Gln	Thr	Thr	Thr	Asp	Met	Gln	Lys	Pro	Thr	Gln	Ser	Met
				245					250						255
His	Gln	Glu	Asn	Leu	Thr	Gly	His	Cys	Arg	Glu	Pro	Pro	Pro	Trp	Lys
			260					265							270
His	Glu	Asp	Ser	Lys	Arg	Ile	Tyr	His	Phe	Val	Glu	Gly	Gln	Ser	Val
		275					280					285			
His	Tyr	Glu	Cys	Ile	Pro	Gly	Tyr	Lys	Ala	Leu	Gln	Arg	Gly	Pro	Ala
	290					295					300				
Ile	Ser	Ile	Cys	Lys	Met	Lys	Cys	Gly	Lys	Thr	Gly	Trp	Thr	Gln	Pro
305					310					315					320
Gln	Leu	Thr	Cys	Val	Asp	Glu	Arg	Glu	His	His	Arg	Phe	Leu	Ala	Ser
				325					330						335
Glu	Glu	Ser	Gln	Gly	Ser	Arg	Asn	Ser	Ser	Pro	Glu	Ser	Glu	Thr	Ser
			340					345					350		
Cys	Pro	Ile	Thr	Thr	Thr	Asp	Phe	Pro	Gln	Pro	Thr	Glu	Thr	Thr	Ala
		355					360					365			
Met	Thr	Glu	Thr	Phe	Val	Leu	Thr	Met	Glu	Tyr	Lys				
	370					375					380				

<210> 21

<211> 400

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized unprocessed form of IL-2 (Gly3Ser)4-extracellular domain of IL-2 R

<400> 21

Met	Asp	Ser	Met	Gln	Leu	Ala	Ser	Cys	Val	Thr	Leu	Thr	Leu	Val	Leu
1				5					10					15	
Leu	Val	Asn	Ser	Ala	Pro	Thr	Ser	Ser	Ser	Thr	Ser	Ser	Ser	Thr	Ala
			20					25					30		
Glu	Ala	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	His	Leu
		35				40						45			
Glu	Gln	Leu	Leu	Met	Asp	Leu	Gln	Glu	Leu	Leu	Ser	Arg	Met	Glu	Asn
	50				55						60				
Tyr	Arg	Asn	Leu	Lys	Leu	Pro	Arg	Met	Leu	Thr	Phe	Lys	Phe	Tyr	Leu
65				70						75					80
Pro	Lys	Gln	Ala	Thr	Glu	Leu	Lys	Asp	Leu	Gln	Cys	Leu	Glu	Asp	Glu
			85					90						95	

464173SEQLIST

```

Leu Gly Pro Leu Arg His Val Leu Asp Leu Thr Gln Ser Lys Ser Phe
    100                      105                      110
Gln Leu Glu Asp Ala Glu Asn Phe Ile Ser Asn Ile Arg Val Thr Val
    115                      120                      125
Val Lys Leu Lys Gly Ser Asp Asn Thr Phe Glu Cys Gln Phe Asp Asp
    130                      135                      140
Glu Ser Ala Thr Val Val Asp Phe Leu Arg Arg Trp Ile Ala Phe Cys
    145                      150                      155                      160
Gln Ser Ile Ile Ser Thr Ser Pro Gln Gly Gly Gly Ser Gly Gly Gly
    165                      170                      175
Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Leu Cys Leu Tyr Asp Pro
    180                      185                      190
Pro Glu Val Pro Asn Ala Thr Phe Lys Ala Leu Ser Tyr Lys Asn Gly
    195                      200                      205
Thr Ile Leu Asn Cys Glu Cys Lys Arg Gly Phe Arg Arg Leu Lys Glu
    210                      215                      220
Leu Val Tyr Met Arg Cys Leu Gly Asn Ser Trp Ser Ser Asn Cys Gln
    225                      230                      235                      240
Cys Thr Ser Asn Ser His Asp Lys Ser Arg Lys Gln Val Thr Ala Gln
    245                      250                      255
Leu Glu His Gln Lys Glu Gln Gln Thr Thr Thr Asp Met Gln Lys Pro
    260                      265                      270
Thr Gln Ser Met His Gln Glu Asn Leu Thr Gly His Cys Arg Glu Pro
    275                      280                      285
Pro Pro Trp Lys His Glu Asp Ser Lys Arg Ile Tyr His Phe Val Glu
    290                      295                      300
Gly Gln Ser Val His Tyr Glu Cys Ile Pro Gly Tyr Lys Ala Leu Gln
    305                      310                      315                      320
Arg Gly Pro Ala Ile Ser Ile Cys Lys Met Lys Cys Gly Lys Thr Gly
    325                      330                      335
Trp Thr Gln Pro Gln Leu Thr Cys Val Asp Glu Arg Glu His His Arg
    340                      345                      350
Phe Leu Ala Ser Glu Glu Ser Gln Gly Ser Arg Asn Ser Ser Pro Glu
    355                      360                      365
Ser Glu Thr Ser Cys Pro Ile Thr Thr Thr Asp Phe Pro Gln Pro Thr
    370                      375                      380
Glu Thr Thr Ala Met Thr Glu Thr Phe Val Leu Thr Met Glu Tyr Lys
    385                      390                      395                      400

```

<210> 22

<211> 372

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized mature form IL-2 (Gly4Ser)4-
extracellular domain of IL-2 R

464173SEQLIST

<400> 22

Ala	Pro	Thr	Ser	Ser	Ser	Thr	Lys	Lys	Thr	Gln	Leu	Gln	Leu	Glu	His
1				5					10					15	
Leu	Leu	Leu	Asp	Leu	Gln	Met	Ile	Leu	Asn	Gly	Ile	Asn	Asn	Tyr	Lys
			20					25					30		
Asn	Pro	Lys	Leu	Thr	Arg	Met	Leu	Thr	Phe	Lys	Phe	Tyr	Met	Pro	Lys
		35					40					45			
Lys	Ala	Thr	Glu	Leu	Lys	His	Leu	Gln	Cys	Leu	Glu	Glu	Glu	Leu	Lys
	50					55					60				
Pro	Leu	Glu	Glu	Val	Leu	Asn	Leu	Ala	Gln	Ser	Lys	Asn	Phe	His	Leu
65					70					75					80
Arg	Pro	Arg	Asp	Leu	Ile	Ser	Asn	Ile	Asn	Val	Ile	Val	Leu	Glu	Leu
			85						90					95	
Lys	Gly	Ser	Glu	Thr	Thr	Phe	Met	Cys	Glu	Tyr	Ala	Asp	Glu	Thr	Ala
			100					105					110		
Thr	Ile	Val	Glu	Phe	Leu	Asn	Arg	Trp	Ile	Thr	Phe	Cys	Gln	Ser	Ile
		115					120					125			
Ile	Ser	Thr	Leu	Thr	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly
	130					135					140				
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Leu	Cys	Asp	Asp	Asp	Pro
145					150					155					160
Pro	Glu	Ile	Pro	His	Ala	Thr	Phe	Lys	Ala	Met	Ala	Tyr	Lys	Glu	Gly
				165					170					175	
Thr	Met	Leu	Asn	Cys	Glu	Cys	Lys	Arg	Gly	Phe	Arg	Arg	Ile	Lys	Ser
			180					185					190		
Gly	Ser	Leu	Tyr	Met	Leu	Cys	Thr	Gly	Asn	Ser	Ser	His	Ser	Ser	Trp
		195					200					205			
Asp	Asn	Gln	Cys	Gln	Cys	Thr	Ser	Ser	Ala	Thr	Arg	Asn	Thr	Thr	Lys
	210					215					220				
Gln	Val	Thr	Pro	Gln	Pro	Glu	Glu	Gln	Lys	Glu	Arg	Lys	Thr	Thr	Glu
225					230					235					240
Met	Gln	Ser	Pro	Met	Gln	Pro	Val	Asp	Gln	Ala	Ser	Leu	Pro	Gly	His
				245					250					255	
Cys	Arg	Glu	Pro	Pro	Pro	Trp	Glu	Asn	Glu	Ala	Thr	Glu	Arg	Ile	Tyr
		260						265					270		
His	Phe	Val	Val	Gly	Gln	Met	Val	Tyr	Tyr	Gln	Cys	Val	Gln	Gly	Tyr
		275				280						285			
Arg	Ala	Leu	His	Arg	Gly	Pro	Ala	Glu	Ser	Val	Cys	Lys	Met	Thr	His
	290					295					300				
Gly	Lys	Thr	Arg	Trp	Thr	Gln	Pro	Gln	Leu	Ile	Cys	Thr	Gly	Glu	Met
305					310					315					320
Glu	Thr	Ser	Gln	Phe	Pro	Gly	Glu	Glu	Lys	Pro	Gln	Ala	Ser	Pro	Glu
				325					330					335	
Gly	Arg	Pro	Glu	Ser	Glu	Thr	Ser	Cys	Leu	Val	Thr	Thr	Thr	Asp	Phe
		340						345					350		
Gln	Ile	Gln	Thr	Glu	Met	Ala	Ala	Thr	Met	Glu	Thr	Ser	Ile	Phe	Thr
		355					360						365		

464173SEQLIST

Thr Glu Tyr Gln
370

```
<210> 23
<211> 392
<212> PRT
<213> Artificial Sequence
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<220>
<223> Synthesized unprocessed form IL-2 (Gly4Ser)4-extracellular domain of IL-2 R

<400> 23															
Met 1	Asp	Arg	Met	Gln 5	Leu	Leu	Ser	Cys 10	Ile	Ala	Leu	Ser	Leu	Ala 15	Leu
Val	Thr	Asn 20	Ser	Ala	Pro	Thr	Ser	Ser 25	Ser	Thr	Lys	Lys	Thr 30	Gln	Leu
Gln	Leu	Glu 35	His	Leu	Leu	Leu	Asp 40	Leu	Gln	Met	Ile	Leu	Asn 45	Gly	Ile
Asn	Asn 50	Tyr	Lys	Asn	Pro	Lys 55	Leu	Thr	Arg	Met	Leu	Thr	Phe	Lys	Phe
Tyr 65	Met	Pro	Lys	Lys	Ala 70	Thr	Glu	Leu	Lys	His 75	Leu	Gln	Cys	Leu	Glu 80
Glu	Glu	Leu	Lys	Pro 85	Leu	Glu	Glu	Val	Leu	Asn 90	Leu	Ala	Gln	Ser 95	Lys
Asn	Phe	His 100	Leu	Arg	Pro	Arg	Asp 105	Leu	Ile	Ser	Asn	Ile	Asn 110	Val	Ile
Val	Leu	Glu 115	Leu	Lys	Gly	Ser	Glu	Thr	Thr	Phe	Met	Cys	Glu	Tyr	Ala
Asp	Glu 130	Thr	Ala	Thr	Ile	Val	Glu	Phe	Leu	Asn	Arg 140	Trp	Ile	Thr	Phe
Cys 145	Gln	Ser	Ile	Ile	Ser	Thr	Leu	Thr	Gly	Gly 155	Gly	Gly	Ser	Gly	Gly 160
Gly	Gly	Ser	Gly	Gly 165	Gly	Gly	Ser	Gly	Gly	Gly 170	Gly	Ser	Glu	Leu	Cys
Asp	Asp	Asp 180	Pro	Pro	Glu	Ile	Pro	His 185	Ala	Thr	Phe	Lys	Ala 190	Met	Ala
Tyr	Lys	Glu 195	Gly	Thr	Met	Leu	Asn	Cys 200	Glu	Cys	Lys	Arg 205	Gly	Phe	Arg
Arg	Ile 210	Lys	Ser	Gly	Ser	Leu	Tyr	Met	Leu	Cys	Thr 220	Gly	Asn	Ser	Ser
His 225	Ser	Ser	Trp	Asp	Asn	Gln	Cys	Gln	Cys	Thr 235	Ser	Ser	Ala	Thr	Arg
Asn	Thr	Thr	Lys	Gln 245	Val	Thr	Pro	Gln	Pro	Glu	Glu	Gln	Lys	Glu	Arg
Lys	Thr	Thr	Glu	Met	Gln	Ser	Pro	Met	Gln	Pro	Val	Asp	Gln	Ala	Ser
<270>															

464173SEQLIST

```

Leu Pro Gly His Cys Arg Glu Pro Pro Pro Trp Glu Asn Glu Ala Thr
    275                      280                      285
Glu Arg Ile Tyr His Phe Val Val Gly Gln Met Val Tyr Tyr Gln Cys
    290                      295                      300
Val Gln Gly Tyr Arg Ala Leu His Arg Gly Pro Ala Glu Ser Val Cys
    305                      310                      315                      320
Lys Met Thr His Gly Lys Thr Arg Trp Thr Gln Pro Gln Leu Ile Cys
    325                      330                      335
Thr Gly Glu Met Glu Thr Ser Gln Phe Pro Gly Glu Glu Lys Pro Gln
    340                      345                      350
Ala Ser Pro Glu Gly Arg Pro Glu Ser Glu Thr Ser Cys Leu Val Thr
    355                      360                      365
Thr Thr Asp Phe Gln Ile Gln Thr Glu Met Ala Ala Thr Met Glu Thr
    370                      375                      380
Ser Ile Phe Thr Thr Glu Tyr Gln
    385                      390

```

<210> 24

<211> 368

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized mature form IL-2 (Gly3Ser)4-
extracellular domain of IL-2 R

<400> 24

```

Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
  1                      5                      10                      15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
    20                      25                      30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
    35                      40                      45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Leu Lys
    50                      55                      60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
    65                      70                      75                      80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
    85                      90                      95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
    100                      105                      110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
    115                      120                      125
Ile Ser Thr Leu Thr Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
    130                      135                      140
Ser Gly Gly Gly Ser Glu Leu Cys Asp Asp Asp Pro Pro Glu Ile Pro
    145                      150                      155                      160

```

464173SEQLIST

```

His Ala Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly Thr Met Leu Asn
      165                      170                      175
Cys Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr
      180                      185                      190
Met Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp Asp Asn Gln Cys
      195                      200                      205
Gln Cys Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys Gln Val Thr Pro
      210                      215                      220
Gln Pro Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Pro
      225                      230                      235                      240
Met Gln Pro Val Asp Gln Ala Ser Leu Pro Gly His Cys Arg Glu Pro
      245                      250                      255
Pro Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val
      260                      265                      270
Gly Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His
      275                      280                      285
Arg Gly Pro Ala Glu Ser Val Cys Lys Met Thr His Gly Lys Thr Arg
      290                      295                      300
Trp Thr Gln Pro Gln Leu Ile Cys Thr Gly Glu Met Glu Thr Ser Gln
      305                      310                      315                      320
Phe Pro Gly Glu Glu Lys Pro Gln Ala Ser Pro Glu Gly Arg Pro Glu
      325                      330                      335
Ser Glu Thr Ser Cys Leu Val Thr Thr Thr Asp Phe Gln Ile Gln Thr
      340                      345                      350
Glu Met Ala Ala Thr Met Glu Thr Ser Ile Phe Thr Thr Glu Tyr Gln
      355                      360                      365

```

<210> 25

<211> 388

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized unprocessed form IL-2 (Gly3Ser)4-
extracellular domain of IL-2 R

<400> 25

```

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

```

464173SEQLIST

Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys
 85 90 95
 Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile
 100 105 110
 Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala
 115 120 125
 Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe
 130 135 140
 Cys Gln Ser Ile Ile Ser Thr Leu Thr Gly Gly Gly Ser Gly Gly Gly
 145 150 155 160
 Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Leu Cys Asp Asp Asp Pro
 165 170 175
 Pro Glu Ile Pro His Ala Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly
 180 185 190
 Thr Met Leu Asn Cys Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser
 195 200 205
 Gly Ser Leu Tyr Met Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp
 210 215 220
 Asp Asn Gln Cys Gln Cys Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys
 225 230 235 240
 Gln Val Thr Pro Gln Pro Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu
 245 250 255
 Met Gln Ser Pro Met Gln Pro Val Asp Gln Ala Ser Leu Pro Gly His
 260 265 270
 Cys Arg Glu Pro Pro Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr
 275 280 285
 His Phe Val Val Gly Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr
 290 295 300
 Arg Ala Leu His Arg Gly Pro Ala Glu Ser Val Cys Lys Met Thr His
 305 310 315 320
 Gly Lys Thr Arg Trp Thr Gln Pro Gln Leu Ile Cys Thr Gly Glu Met
 325 330 335
 Glu Thr Ser Gln Phe Pro Gly Glu Glu Lys Pro Gln Ala Ser Pro Glu
 340 345 350
 Gly Arg Pro Glu Ser Glu Thr Ser Cys Leu Val Thr Thr Thr Asp Phe
 355 360 365
 Gln Ile Gln Thr Glu Met Ala Ala Thr Met Glu Thr Ser Ile Phe Thr
 370 375 380
 Thr Glu Tyr Gln
 385

<210> 26

<211> 364

<212> PRT

<213> Artificial Sequence

<220>

464173SEQLIST

<223> Synthesized mature form IL-2 (Gly3Ser)3-
extracellular domain of IL-2 R

<400> 26

Ala	Pro	Thr	Ser	Ser	Ser	Thr	Lys	Lys	Thr	Gln	Leu	Gln	Leu	Glu	His
1				5					10					15	
Leu	Leu	Leu	Asp	Leu	Gln	Met	Ile	Leu	Asn	Gly	Ile	Asn	Asn	Tyr	Lys
			20					25					30		
Asn	Pro	Lys	Leu	Thr	Arg	Met	Leu	Thr	Phe	Lys	Phe	Tyr	Met	Pro	Lys
		35					40					45			
Lys	Ala	Thr	Glu	Leu	Lys	His	Leu	Gln	Cys	Leu	Glu	Glu	Glu	Leu	Lys
	50					55					60				
Pro	Leu	Glu	Glu	Val	Leu	Asn	Leu	Ala	Gln	Ser	Lys	Asn	Phe	His	Leu
65					70					75					80
Arg	Pro	Arg	Asp	Leu	Ile	Ser	Asn	Ile	Asn	Val	Ile	Val	Leu	Glu	Leu
				85					90					95	
Lys	Gly	Ser	Glu	Thr	Thr	Phe	Met	Cys	Glu	Tyr	Ala	Asp	Glu	Thr	Ala
			100					105					110		
Thr	Ile	Val	Glu	Phe	Leu	Asn	Arg	Trp	Ile	Thr	Phe	Cys	Gln	Ser	Ile
		115					120					125			
Ile	Ser	Thr	Leu	Thr	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly
	130					135					140				
Ser	Glu	Leu	Cys	Asp	Asp	Asp	Pro	Pro	Glu	Ile	Pro	His	Ala	Thr	Phe
145					150					155					160
Lys	Ala	Met	Ala	Tyr	Lys	Glu	Gly	Thr	Met	Leu	Asn	Cys	Glu	Cys	Lys
				165					170					175	
Arg	Gly	Phe	Arg	Arg	Ile	Lys	Ser	Gly	Ser	Leu	Tyr	Met	Leu	Cys	Thr
			180					185					190		
Gly	Asn	Ser	Ser	His	Ser	Ser	Trp	Asp	Asn	Gln	Cys	Gln	Cys	Thr	Ser
	195						200					205			
Ser	Ala	Thr	Arg	Asn	Thr	Thr	Lys	Gln	Val	Thr	Pro	Gln	Pro	Glu	Glu
	210					215					220				
Gln	Lys	Glu	Arg	Lys	Thr	Thr	Glu	Met	Gln	Ser	Pro	Met	Gln	Pro	Val
225					230					235					240
Asp	Gln	Ala	Ser	Leu	Pro	Gly	His	Cys	Arg	Glu	Pro	Pro	Pro	Trp	Glu
				245					250					255	
Asn	Glu	Ala	Thr	Glu	Arg	Ile	Tyr	His	Phe	Val	Val	Gly	Gln	Met	Val
			260					265					270		
Tyr	Tyr	Gln	Cys	Val	Gln	Gly	Tyr	Arg	Ala	Leu	His	Arg	Gly	Pro	Ala
		275					280					285			
Glu	Ser	Val	Cys	Lys	Met	Thr	His	Gly	Lys	Thr	Arg	Trp	Thr	Gln	Pro
	290					295					300				
Gln	Leu	Ile	Cys	Thr	Gly	Glu	Met	Glu	Thr	Ser	Gln	Phe	Pro	Gly	Glu
305					310					315					320
Glu	Lys	Pro	Gln	Ala	Ser	Pro	Glu	Gly	Arg	Pro	Glu	Ser	Glu	Thr	Ser
				325					330					335	
Cys	Leu	Val	Thr	Thr	Thr	Asp	Phe	Gln	Ile	Gln	Thr	Glu	Met	Ala	Ala
			340					345					350		

Thr Met Glu Thr Ser Ile Phe Thr Thr Glu Tyr Gln
355 360

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<210> 27
<211> 384
<212> PRT
<213> Artificial Sequence
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<220>
<223> Synthesized unprocessed form of IL-2 (Gly3Ser)3-
extracellular domain of IL-2 R

<400> 27															
Met 1	Asp	Arg	Met	Gln 5	Leu	Leu	Ser	Cys	Ile 10	Ala	Leu	Ser	Leu	Ala 15	Leu
Val	Thr	Asn	Ser 20	Ala	Pro	Thr	Ser	Ser 25	Ser	Thr	Lys	Lys	Thr 30	Gln	Leu
Gln	Leu	Glu	His	Leu	Leu	Leu	Asp 40	Leu	Gln	Met	Ile	Leu	Asn 45	Gly	Ile
Asn	Asn	Tyr	Lys	Asn	Pro	Lys	Leu	Thr	Arg	Met	Leu	Thr	Phe	Lys	Phe
Tyr 65	Met	Pro	Lys	Lys	Ala 70	Thr	Glu	Leu	Lys	His	Leu	Gln	Cys	Leu	Glu 80
Glu	Glu	Leu	Lys	Pro	Leu	Glu	Glu	Val	Leu	Asn	Leu	Ala	Gln	Ser	Lys
Asn	Phe	His	Leu	Arg	Pro	Arg	Asp	Leu	Ile	Ser	Asn	Ile	Asn	Val	Ile
Val	Leu	Glu	Leu	Lys	Gly	Ser	Glu	Thr	Thr	Phe	Met	Cys	Glu	Tyr	Ala
Asp	Glu	Thr	Ala	Thr	Ile	Val	Glu	Phe	Leu	Asn	Arg	Trp	Ile	Thr	Phe
Cys 145	Gln	Ser	Ile	Ile	Ser	Thr	Leu	Thr	Gly	Gly	Gly	Ser	Gly	Gly	Gly 160
Ser	Gly	Gly	Gly	Ser	Glu	Leu	Cys	Asp	Asp	Asp	Pro	Pro	Glu	Ile	Pro
His	Ala	Thr	Phe	Lys	Ala	Met	Ala	Tyr	Lys	Glu	Gly	Thr	Met	Leu	Asn
Cys	Glu	Cys	Lys	Arg	Gly	Phe	Arg	Arg	Ile	Lys	Ser	Gly	Ser	Leu	Tyr
Met	Leu	Cys	Thr	Gly	Asn	Ser	Ser	His	Ser	Ser	Trp	Asp	Asn	Gln	Cys
Gln 225	Cys	Thr	Ser	Ser	Ala	Thr	Arg	Asn	Thr	Thr	Lys	Gln	Val	Thr	Pro
Gln	Pro	Glu	Glu	Gln	Lys	Glu	Arg	Lys	Thr	Thr	Glu	Met	Gln	Ser	Pro
Met	Gln	Pro	Val	Asp	Gln	Ala	Ser	Leu	Pro	Gly	His	Cys	Arg	Glu	Pro

464173SEQLIST

```

Pro Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val
    275                                280                                285
Gly Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His
    290                                295                                300
Arg Gly Pro Ala Glu Ser Val Cys Lys Met Thr His Gly Lys Thr Arg
    305                                310                                315                                320
Trp Thr Gln Pro Gln Leu Ile Cys Thr Gly Glu Met Glu Thr Ser Gln
    325                                330                                335
Phe Pro Gly Glu Glu Lys Pro Gln Ala Ser Pro Glu Gly Arg Pro Glu
    340                                345                                350
Ser Glu Thr Ser Cys Leu Val Thr Thr Thr Asp Phe Gln Ile Gln Thr
    355                                360                                365
Glu Met Ala Ala Thr Met Glu Thr Ser Ile Phe Thr Thr Glu Tyr Gln
    370                                375                                380

```

<210> 28

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> IL-2 leader optimized Kozak sequence

<400> 28

```

gccaccatgg acaggatgca actcctgtct tgcattgcac taagtcttgc acttgtcaca 60
aacagt                                           66

```

<210> 29

<211> 1239

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized unprocessed form of IL-2
(Gly4Ser)4-extracellular domain of IL-2 R

<400> 29

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atggacagca tgcagctcgc atcctgtgtc acattgacac ttgtgctcct tgtcaacagc 60
gcacccactt caagctctac ttcaagctct acagcggaag cacagcagca gcagcagcag 120
cagcagcagc agcagcacct ggagcagctg ttgatggacc tacaggagct cctgagcagg 180
atggagaatt acaggaacct gaaactcccc aggatgctca cttcaaatt ttacttgccc 240
aagcaggcca cagaattgaa agatcttcag tgcctagaag atgaacttgg acctctgcgg 300
catgttctgg atttgactca aagcaaaagc tttcaattgg aagatgctga gaatttcac 360
agcaatatca gagtaactgt tgtaaaaacta aagggtctg acaacacatt tgagtgccaa 420
ttcgaatgat agtcagcaac tgtggtggac tttctgagga gatggatagc cttctgtcaa 480
agcatcatct caacaagccc tcaaggtgga ggtggatctg gtggagggtg atcagggtgga 540
ggtggatccg gtggagggtg atctgaactg tgtctgtatg acccaccga ggtccccaat 600

```

464173SEQLIST

```
gccacattca aagccctctc ctacaagaac ggcaccatcc taaactgtga atgcaagaga 660
ggttttccgaa gactaaagga attggtctat atgcgttgct taggaaactc ctggagcagc 720
aactgccagt gcaccagcaa ctcccatgac aaatcgagaa agcaagttac agctcaactt 780
gaacaccaga aagagcaaca aaccacaaca gacatgcaga agccaacaca gtctatgcac 840
caagagaacc ttacagggtca ctgcagggag ccacctcctt ggaaacatga agattccaag 900
agaatctatc atttcgtgga aggacagagt gttcactacg agtgtattcc gggatacaag 960
gctctacaga gaggtcctgc tattagcatc tgcaagatga agtgtgggaa aacgggggtgg 1020
actcagcccc agctcacatg tgtagatgaa agagaacacc accgatttct ggctagttag 1080
gaatctcaag gaagcagaaa ttcttctccc gagagtgaga cttcctgccc cataaccacc 1140
acagacttcc cacaaccacac agaaacaact gcaatgacgg agacatttgt gctcacaatg 1200
gagtataagg gtggacatca ccatcaccat cactaataa 1239
```

<210> 30

<211> 1227

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized unprocessed form of IL-2 (Gly3Ser)4-extracellular domain of IL-2 R

<400> 30

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atggacagca tgcagctcgc atcctgtgtc acattgacac ttgtgctcct tgtcaacagc 60
gcaccactt caagctctac ttcaagctct acagcggaag cacagcagca gcagcagcag 120
cagcagcagc agcagcacct ggagcagctg ttgatggacc tacaggagct cctgagcagg 180
atggagaatt acaggaacct gaaactcccc aggatgctca ctttcaaatt ttacttgccc 240
aagcaggcca cagaattgaa agatcttcag tgcctagaag atgaacttgg acctctgcgg 300
catgttctgg atttgactca aagcaaaagc tttcaattgg aagatgctga gaatttcatc 360
agcaatatca gagtaactgt tgtaaaaacta aagggtcttg acaacacatt tgagtgccaa 420
ttcgtatgat agtcagcaac tgtggtggac tttctgagga gatggatagc cttctgtcaa 480
agcatcatct caacaagccc tcaagggtgga gggttctggtg gaggttcagg tggaggttcg 540
ggtggagggt ctgaactgtg tctgtatgac ccaccgagg tccccaatgc cacattcaaa 600
gccctctcct acaagaacgg caccatccta aactgtgaat gcaagagagg tttccgaaga 660
ctaaaggaat tgggtctatat gcgttgctta ggaaactcct ggagcagcaa ctgccagtgc 720
accagcaact cccatgacaa atcgagaaag caagttacag ctcaacttga acaccagaaa 780
gagcaacaaa ccacaacaga catgcagaag ccaacacagt ctatgcacca agagaacctt 840
acaggtcact gcaggagacc acctccttgg aaacatgaag attccaagag aatctatcat 900
ttcgtggaag gacagagtgt tctactacgag tgtattccgg gatacaaggc tctacagaga 960
ggtcctgcta ttagcatctg caagatgaag tgtgggaaaa cggggtggac tcagccccag 1020
ctcacatgtg tagatgaaag agaaccacc cgatttcttg ctagtgagga atctcaagga 1080
agcagaaatt cttctcccga gagtgagact tcctgcccc taaccaccac agacttccca 1140
caaccacag aaacaactgc aatgacggag acatttgtgc tcacaatgga gtataagggt 1200
ggacatcacc atcacatca ctaataa 1227
```

<210> 31

<211> 1254

<212> DNA

<213> Artificial Sequence

464173SEQLIST

<220>

<223> Synthesized unprocessed form of IL-2 (Gly4Ser)5-
extracellular domain of IL-2 R

<400> 31

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atggacagca tgcagctcgc atcctgtgtc acattgacac ttgtgctcct tgtcaacagc 60
gcacccactt caagctctac ttcaagctct acagcgggaag cacagcagca gcagcagcag 120
cagcagcagc agcagcacct ggagcagctg ttgatggacc tacaggagct cctgagcagg 180
atggagaatt acaggaacct gaaactcccc aggatgctca ctttcaaatt ttacttgccc 240
aagcaggcca cagaattgaa agatcttcag tgcctagaag atgaacttgg acctctgcgg 300
catgttcttg atttgactca aagcaaaagc tttcaattgg aagatgctga gaatttcac 360
agcaatatca gagtaactgt tgtaaaacta aagggtcttg acaacacatt tgagtgccaa 420
ttcgaatgat agtcagcaac tgtggtggac tttctgagga gatggatagc cttctgtcaa 480
agcatcatct caacaagccc tcaagggtga ggtggatcag gtggaggtgg atctggtgga 540
ggtggatcag gtggaggtgg atccggtgga ggtggatctg aactgtgtct gtatgacca 600
cccgaggctc ccaatgccac attcaaagcc ctctcctaca agaacggcac catcctaaac 660
tgtgaatgca agagagggtt ccgaagacta aaggaattgg tctatatgcg ttgcttagga 720
aactcctgga gcagcaactg ccagtgcacc agcaactccc atgacaaatc gagaaagcaa 780
gttacagctc aacttgaaca ccagaaagag caacaaacca caacagacat gcagaagcca 840
acacagtcta tgcaccaaga gaaccttaca ggtcactgca gggagccacc tccttgga 900
catgaagatt ccaagagaat ctatcatctt gtggaaggac agagtgttca ctacgagtgt 960
attccgggat acaaggctct acagagaggc cctgctatta gcatctgcaa gatgaagtgt 1020
gggaaaacgg ggtggactca gccccagctc acatgtgtag atgaaagaga acaccaccga 1080
tttctggcta gtgaggaatc tcaaggaagc agaaattctt ctcccagag tgagacttcc 1140
tgccccataa ccaccacaga cttcccacaa cccacagaaa caactgcaat gacggagaca 1200
tttgtgctca caatggagta taagggtgga catcaccatc accatcacta ataa 1254

```

<210> 32

<211> 1206

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized unprocessed form IL-2 (Gly4Ser)4-
extracellular domain of IL-2 R

<400> 32

```

atggacagga tgcaactcct gtcttgcatt gcactaagtc ttgcacttgt cacaacacagt 60
gcacctactt caagttctac aaagaaaaca cagctacaac tggagcatct actgctggat 120
ttacagatga ttttgaatgg aattaataat tacaagaatc ccaaactcac caggatgctc 180
acatttaagt tttacatgcc caagaaggcc acagaactga aacatcttca gtgtctagaa 240
gaagaactca aacctctgga ggaagtgcta aatttagctc aaagcaaaaa ctttacttta 300
agaccaggga acttaatcag caatatcaac gtaatagttc tggaactaaa gggatctgaa 360
acaacattca tgtgtgaata tgctgatgag acagcaacca ttgtagaatt tctgaacaga 420
tggtattact tttgtcaaag catcatctca acactgactg gtggaggtgg atctggtgga 480
ggtggatcag gtggaggtgg atccggtgga ggtggatctg agctctgtga cgatgacccg 540
ccagagatcc cacacgccac attcaaagcc atggcctaca aggaaggaac catgttgaac 600

```

464173SEQLIST

```

tgtgaatgca agagagggtt cgcagaata aaaaagcgggt cactctatat gctctgtaca 660
ggaaaactcta gccactcgtc ctgggacaac caatgtcaat gcacaagctc tgccactcgg 720
aacacaacga aacaagtga acctcaacct gaagaacaga aagaaaaggaa aaccacagaa 780
atgcaaagtc caatgcagcc agtggacca ggcagccttc caggctactg cagggaacct 840
ccaccatggg aaaatgaagc cacagagaga atttatcatt tcgtgggtggg gcagatgggt 900
tattatcagt gcgtccaggg atacagggct ctacacagag gtcctgctga gagcgtctgc 960
aaaatgaccc acgggaagac aagggtggacc cagccccagc tcatatgcac aggtgaaatg 1020
gagaccagtc agtttccagg tgaagagaag cctcaggcaa gccccgaagg ccgtcctgag 1080
agtgaagactt cctgcctcgt cacaacaaca gattttcaaa tacagacaga aatggctgca 1140
accatggaga cgtccatatt tacaacagag taccaggggtg gacatcacca tcaccatcac 1200
taataa                                     1206

```

<210> 33

<211> 1194

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized unprocessed form IL-2 (Gly3Ser)4-
extracellular domain of IL-2 R

<400> 33

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atggacagga tgcaactcct gtcttgcat gactaagtc ttgcacttgt cacaacagct 60
gcacctactt caagttctac aaagaaaaca cagctacaac tggagcattt actgctggat 120
ttacagatga ttttgaatgg aattaataat tacaagaatc ccaaactcac caggatgctc 180
acatttaagt tttacatgcc caagaaggcc acagaactga aacatcttca gtgtctagaa 240
gaagaactca aacctctgga ggaagtgcta aatttagctc aaagcaaaaa ctttacttta 300
agaccagggg acttaatcag caatatcaac gtaatagttc tggaactaaa gggatctgaa 360
acaacattca tgtgtgaata tgctgatgag acagcaacca ttgtagaatt tctgaacaga 420
tggattacct tttgtcaaag catcatctca aactgactg gtggagggtt tgggtggagg 480
tcagggtggg gttcgggtgg aggttctgag ctctgtgacg atgacccgcc agagatccca 540
cacgccacat tcaaagccat ggcctacaag gaaggaacca tgttgaactg tgaatgcaag 600
agaggtttcc gcagaataaa aagcgggtca ctctatatgc tctgtacagg aaactctagc 660
cactcgtcct gggacaacca atgtcaatgc acaagctctg ccactcggaa cacaacgaaa 720
caagtgaac ctcaacctga agaacagaaa gaaaggaaaa ccacagaaat gcaaagtcca 780
atgcagccag tggaccaagc gagccttcca ggtcactgca gggaacctcc accatgggaa 840
aatgaagcca cagagagaat ttatcatctt gtggtggggc agatggttta ttatcagtgc 900
gtccagggat acagggtctt acacagaggt cctgctgaga gcgtctgcaa aatgaccac 960
gggaagacaa ggtggaccca gccccagctc atatgcacag gtgaaatgga gaccagtcag 1020
tttccagggtg aagagaagcc tcaggcaagc cccgaaggcc gtcctgagag tgagacttcc 1080
tgccctgtca caacaacaga ttttcaaata cagacagaaa tggctgcaac catggagacg 1140
tccatattta caacagagta ccagggtgga catcaccatc accatcacta ataa 1194

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<210> 34

<211> 1182

<212> DNA

<213> Artificial Sequence

464173SEQLIST

<220>

<223> Synthesized unprocessed form of IL-2 (Gly3Ser)3-
extracellular domain of IL-2 R

<400> 34

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atggacagga tgcaactcct gtcttgcatt gcactaagtc ttgcacttgt cacaacacagt 60
gcacctactt caagttctac aaagaaaaca cagctacaac tggagcattt actgctggat 120
ttacagatga ttttgaatgg aattaataat tacaagaatc ccaaactcac caggatgctc 180
acatttaagt ttacatgcc caagaaggcc acagaactga aacatcttca gtgtctagaa 240
gaagaactca aacctctgga ggaagtgcta aatttagctc aaagcaaaaa ctttacttta 300
agaccagagg acttaatcag caatatcaac gtaatagttc tggaactaaa gggatctgaa 360
acaacattca tgtgtgaata tgctgatgag acagcaacca ttgtagaatt tctgaacaga 420
tggtattacc tttgtcaaag catcatctca aactgactg gtggagggtt tggtggagggt 480
tcagggtggag gttcggagct ctgtgacgat gaccgccag agatcccaca cgccacattc 540
aaagccatgg cctacaagga aggaaccatg ttgaactgtg aatgcaagag aggtttccgc 600
agaataaaaa gcgggtcact ctatatgctc tgtacaggaa actctagcca ctcgtcctgg 660
gacaaccaat gtcaatgcac aagctctgcc actcggaaaca caacgaaaca agtgacacct 720
caacctgaag aacagaaaga aaggaaaacc acagaaatgc aaagtccaat gcagccagtg 780
gaccaagcga gccttccagg tctactgcagg gaacctccac catgggaaaa tgaagccaca 840
gagagaattt atcatttcgt ggtggggcag atggtttatt atcagtgcgt ccagggatac 900
agggctctac acagagggtc tgctgagagc gtctgcaaaa tgaccacagg gaagacaagg 960
tggtaccagc cccagctcat atgcacaggt gaaatggaga ccagtcagtt tccaggtgaa 1020
gagaagcctc aggcaagccc cgaaggccgt cctgagagtg agacttcctg cctcgtcaca 1080
acaacagatt ttcaaatata gacagaaatg gctgcaacca tggagacgct catatttaca 1140
acagagtacc aggggtggaca tcaccatcac catcactaat aa 1182
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<210> 35

<211> 13

<212> DNA

<213> Artificial Sequence

<220>

<223> Kozak consensus

<400> 35

gccgccrcca ugg

13

<210> 36

<211> 396

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized unprocessed form of IL-2 (Gly3Ser)3-
extracellular domain of IL-2 R

<400> 36

Met Tyr Ser Met Gln Leu Ala Ser Cys Val Thr Leu Thr Leu Val Leu

464173SEQLIST

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Leu Val Asn Ser Ala Pro Thr Ser Ser Ser Thr Ser Ser Ser Thr Ala			
	20	25	30
Glu Ala Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln His Leu			
	35	40	45
Glu Gln Leu Leu Met Asp Leu Gln Glu Leu Leu Ser Arg Met Glu Asn			
	50	55	60
Tyr Arg Asn Leu Lys Leu Pro Arg Met Leu Thr Phe Lys Phe Tyr Leu			
65	70	75	80
Pro Lys Gln Ala Thr Glu Leu Lys Asp Leu Gln Cys Leu Glu Asp Glu			
	85	90	95
Leu Gly Pro Leu Arg His Val Leu Asp Leu Thr Gln Ser Lys Ser Phe			
	100	105	110
Gln Leu Glu Asp Ala Glu Asn Phe Ile Ser Asn Ile Arg Val Thr Val			
	115	120	125
Val Lys Leu Lys Gly Ser Asp Asn Thr Phe Glu Cys Gln Phe Asp Asp			
	130	135	140
Glu Ser Ala Thr Val Val Asp Phe Leu Arg Arg Trp Ile Ala Phe Cys			
145	150	155	160
Gln Ser Ile Ile Ser Thr Ser Pro Gln Gly Gly Gly Ser Gly Gly Gly			
	165	170	175
Ser Gly Gly Gly Ser Glu Leu Cys Leu Tyr Asp Pro Pro Glu Val Pro			
	180	185	190
Asn Ala Thr Phe Lys Ala Leu Ser Tyr Lys Asn Gly Thr Ile Leu Asn			
	195	200	205
Cys Glu Cys Lys Arg Gly Phe Arg Arg Leu Lys Glu Leu Val Tyr Met			
	210	215	220
Arg Cys Leu Gly Asn Ser Trp Ser Ser Asn Cys Gln Cys Thr Ser Asn			
225	230	235	240
Ser His Asp Lys Ser Arg Lys Gln Val Thr Ala Gln Leu Glu His Gln			
	245	250	255
Lys Glu Gln Gln Thr Thr Thr Asp Met Gln Lys Pro Thr Gln Ser Met			
	260	265	270
His Gln Glu Asn Leu Thr Gly His Cys Arg Glu Pro Pro Pro Trp Lys			
	275	280	285
His Glu Asp Ser Lys Arg Ile Tyr His Phe Val Glu Gly Gln Ser Val			
	290	295	300
His Tyr Glu Cys Ile Pro Gly Tyr Lys Ala Leu Gln Arg Gly Pro Ala			
305	310	315	320
Ile Ser Ile Cys Lys Met Lys Cys Gly Lys Thr Gly Trp Thr Gln Pro			
	325	330	335
Gln Leu Thr Cys Val Asp Glu Arg Glu His His Arg Phe Leu Ala Ser			
	340	345	350
Glu Glu Ser Gln Gly Ser Arg Asn Ser Ser Pro Glu Ser Glu Thr Ser			
	355	360	365
Cys Pro Ile Thr Thr Thr Asp Phe Pro Gln Pro Thr Glu Thr Thr Ala			
	370	375	380
Met Thr Glu Thr Phe Val Leu Thr Met Glu Tyr Lys			

464173SEQLIST

385

390

395

<210> 37

<211> 396

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized mature form of IL-2 (Gly3Ser)3-
extracellular domain of IL-2 R

<400> 37

```

Met Asp Ser Met Gln Leu Ala Ser Cys Val Thr Leu Thr Leu Val Leu
 1           5           10           15
Leu Val Asn Ser Ala Pro Thr Ser Ser Ser Thr Ser Ser Ser Thr Ala
          20           25           30
Glu Ala Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln His Leu
          35           40           45
Glu Gln Leu Leu Met Asp Leu Gln Glu Leu Leu Ser Arg Met Glu Asn
 50           55           60
Tyr Arg Asn Leu Lys Leu Pro Arg Met Leu Thr Phe Lys Phe Tyr Leu
 65           70           75           80
Pro Lys Gln Ala Thr Glu Leu Lys Asp Leu Gln Cys Leu Glu Asp Glu
          85           90           95
Leu Gly Pro Leu Arg His Val Leu Asp Leu Thr Gln Ser Lys Ser Phe
          100          105          110
Gln Leu Glu Asp Ala Glu Asn Phe Ile Ser Asn Ile Arg Val Thr Val
          115          120          125
Val Lys Leu Lys Gly Ser Asp Asn Thr Phe Glu Cys Gln Phe Asp Asp
          130          135          140
Glu Ser Ala Thr Val Val Asp Phe Leu Arg Arg Trp Ile Ala Phe Cys
 145          150          155          160
Gln Ser Ile Ile Ser Thr Ser Pro Gln Gly Gly Gly Ser Gly Gly Gly
          165          170          175
Ser Gly Gly Gly Ser Glu Leu Cys Leu Tyr Asp Pro Pro Glu Val Pro
          180          185          190
Asn Ala Thr Phe Lys Ala Leu Ser Tyr Lys Asn Gly Thr Ile Leu Asn
          195          200          205
Cys Glu Cys Lys Arg Gly Phe Arg Arg Leu Lys Glu Leu Val Tyr Met
          210          215          220
Arg Cys Leu Gly Asn Ser Trp Ser Ser Asn Cys Gln Cys Thr Ser Asn
 225          230          235          240
Ser His Asp Lys Ser Arg Lys Gln Val Thr Ala Gln Leu Glu His Gln
          245          250          255
Lys Glu Gln Gln Thr Thr Thr Asp Met Gln Lys Pro Thr Gln Ser Met
          260          265          270
His Gln Glu Asn Leu Thr Gly His Cys Arg Glu Pro Pro Trp Lys

```

464173SEQLIST

```

      275      280      285
His Glu Asp Ser Lys Arg Ile Tyr His Phe Val Glu Gly Gln Ser Val
 290      295      300
His Tyr Glu Cys Ile Pro Gly Tyr Lys Ala Leu Gln Arg Gly Pro Ala
305      310      315      320
Ile Ser Ile Cys Lys Met Lys Cys Gly Lys Thr Gly Trp Thr Gln Pro
      325      330      335
Gln Leu Thr Cys Val Asp Glu Arg Glu His His Arg Phe Leu Ala Ser
 340      345      350
Glu Glu Ser Gln Gly Ser Arg Asn Ser Ser Pro Glu Ser Glu Thr Ser
 355      360      365
Cys Pro Ile Thr Thr Thr Asp Phe Pro Gln Pro Thr Glu Thr Thr Ala
 370      375      380
Met Thr Glu Thr Phe Val Leu Thr Met Glu Tyr Lys
385      390      395

```

<210> 38

<211> 397

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized unprocessed form of IL-2 (Gly4Ser)5-
extracellular domain of IL-2 R

<400> 38

```

Met Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
 1      5      10      15
Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu
      20      25      30
Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile
 35      40      45
Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe
 50      55      60
Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu
65      70      75      80
Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys
      85      90      95
Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile
      100      105      110
Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala
      115      120      125
Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe
      130      135      140
Cys Gln Ser Ile Ile Ser Thr Leu Thr Gly Gly Gly Gly Ser Gly Gly
145      150      155      160
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

```

464173SEQLIST

				165					170					175			
Gly	Ser	Glu	Leu	Cys	Asp	Asp	Asp	Pro	Pro	Glu	Ile	Pro	His	Ala	Thr		
			180					185					190				
Phe	Lys	Ala	Met	Ala	Tyr	Lys	Glu	Gly	Thr	Met	Leu	Asn	Cys	Glu	Cys		
		195					200					205					
Lys	Arg	Gly	Phe	Arg	Arg	Ile	Lys	Ser	Gly	Ser	Leu	Tyr	Met	Leu	Cys		
	210					215					220						
Thr	Gly	Asn	Ser	Ser	His	Ser	Ser	Trp	Asp	Asn	Gln	Cys	Gln	Cys	Thr		
225					230				235						240		
Ser	Ser	Ala	Thr	Arg	Asn	Thr	Thr	Lys	Gln	Val	Thr	Pro	Gln	Pro	Glu		
				245					250					255			
Glu	Gln	Lys	Glu	Arg	Lys	Thr	Thr	Glu	Met	Gln	Ser	Pro	Met	Gln	Pro		
		260						265					270				
Val	Asp	Gln	Ala	Ser	Leu	Pro	Gly	His	Cys	Arg	Glu	Pro	Pro	Pro	Trp		
	275						280					285					
Glu	Asn	Glu	Ala	Thr	Glu	Arg	Ile	Tyr	His	Phe	Val	Val	Gly	Gln	Met		
	290					295					300						
Val	Tyr	Tyr	Gln	Cys	Val	Gln	Gly	Tyr	Arg	Ala	Leu	His	Arg	Gly	Pro		
305					310					315					320		
Ala	Glu	Ser	Val	Cys	Lys	Met	Thr	His	Gly	Lys	Thr	Arg	Trp	Thr	Gln		
				325					330					335			
Pro	Gln	Leu	Ile	Cys	Thr	Gly	Glu	Met	Glu	Thr	Ser	Gln	Phe	Pro	Gly		
			340					345					350				
Glu	Glu	Lys	Pro	Gln	Ala	Ser	Pro	Glu	Gly	Arg	Pro	Glu	Ser	Glu	Thr		
		355					360					365					
Ser	Cys	Leu	Val	Thr	Thr	Thr	Asp	Phe	Gln	Ile	Gln	Thr	Glu	Met	Ala		
	370					375					380						
Ala	Thr	Met	Glu	Thr	Ser	Ile	Phe	Thr	Thr	Glu	Tyr	Gln					
385					390					395							

<210> 39

<211> 377

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized mature form of human IL-2 (Gly4Ser)5-
extracellular domain of IL-2 R

<400> 39

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

464173SEQLIST

50	55	60													
Pro	Leu	Glu	Glu	Val	Leu	Asn	Leu	Ala	Gln	Ser	Lys	Asn	Phe	His	Leu
65					70					75					80
Arg	Pro	Arg	Asp	Leu	Ile	Ser	Asn	Ile	Asn	Val	Ile	Val	Leu	Glu	Leu
				85					90					95	
Lys	Gly	Ser	Glu	Thr	Thr	Phe	Met	Cys	Glu	Tyr	Ala	Asp	Glu	Thr	Ala
			100					105					110		
Thr	Ile	Val	Glu	Phe	Leu	Asn	Arg	Trp	Ile	Thr	Phe	Cys	Gln	Ser	Ile
		115					120					125			
Ile	Ser	Thr	Leu	Thr	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly
		130				135					140				
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Leu
145					150				155					160	
Cys	Asp	Asp	Asp	Pro	Pro	Glu	Ile	Pro	His	Ala	Thr	Phe	Lys	Ala	Met
				165					170					175	
Ala	Tyr	Lys	Glu	Gly	Thr	Met	Leu	Asn	Cys	Glu	Cys	Lys	Arg	Gly	Phe
			180					185					190		
Arg	Arg	Ile	Lys	Ser	Gly	Ser	Leu	Tyr	Met	Leu	Cys	Thr	Gly	Asn	Ser
		195					200						205		
Ser	His	Ser	Ser	Trp	Asp	Asn	Gln	Cys	Gln	Cys	Thr	Ser	Ser	Ala	Thr
	210					215					220				
Arg	Asn	Thr	Thr	Lys	Gln	Val	Thr	Pro	Gln	Pro	Glu	Glu	Gln	Lys	Glu
225					230				235					240	
Arg	Lys	Thr	Thr	Glu	Met	Gln	Ser	Pro	Met	Gln	Pro	Val	Asp	Gln	Ala
				245					250					255	
Ser	Leu	Pro	Gly	His	Cys	Arg	Glu	Pro	Pro	Pro	Trp	Glu	Asn	Glu	Ala
			260					265					270		
Thr	Glu	Arg	Ile	Tyr	His	Phe	Val	Val	Gly	Gln	Met	Val	Tyr	Tyr	Gln
		275					280					285			
Cys	Val	Gln	Gly	Tyr	Arg	Ala	Leu	His	Arg	Gly	Pro	Ala	Glu	Ser	Val
	290					295					300				
Cys	Lys	Met	Thr	His	Gly	Lys	Thr	Arg	Trp	Thr	Gln	Pro	Gln	Leu	Ile
305					310					315				320	
Cys	Thr	Gly	Glu	Met	Glu	Thr	Ser	Gln	Phe	Pro	Gly	Glu	Glu	Lys	Pro
				325					330					335	
Gln	Ala	Ser	Pro	Glu	Gly	Arg	Pro	Glu	Ser	Glu	Thr	Ser	Cys	Leu	Val
			340					345					350		
Thr	Thr	Thr	Asp	Phe	Gln	Ile	Gln	Thr	Glu	Met	Ala	Ala	Thr	Met	Glu
		355					360					365			
Thr	Ser	Ile	Phe	Thr	Thr	Glu	Tyr	Gln							
	370					375									

<210> 40

<211> 20

<212> PRT

<213> Artificial Sequence

464173SEQLIST

<220>

<223> Linker sequence (Gly4Ser)4

<400> 40

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1 5 10 15
 Gly Gly Gly Ser
 20

<210> 41

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker sequence (Gly4Ser)5

<400> 41

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1 5 10 15
 Gly Gly Gly Ser Gly Gly Gly Gly Ser
 20 25

<210> 42

<211> 1215

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized unprocessed form IL-2 (Gly3Ser)3-extracellular domain of IL-2 R

<400> 42

atggacagca tgcagctcgc atcctgtgtc acattgacac ttgtgctcct tgtcaacagc 60
 gcacccactt caagctctac ttcaagctct acagcgggaag cacagcagca gcagcagcag 120
 cagcagcagc agcagcacct ggagcagctg ttgatggacc tacaggagct cctgagcagg 180
 atggagaatt acaggaacct gaaactcccc aggatgctca cttcaaatt ttacttgccc 240
 aagcaggcca cagaattgaa agatcttcag tgcctagaag atgaacttgg acctctgcgg 300
 catgttctgg atttgactca aagcaaaagc tttcaattgg aagatgctga gaatttcac 360
 agcaatatca gagtaactgt tgtaaaacta aagggtcttg acaacacatt tgagtgccaa 420
 ttcgatgatg agtcagcaac tgtggtggac tttctgagga gatggatagc cttctgtcaa 480
 agcatcatct caacaagccc tcaaggtgga gggttctggtg gaggttcagg tggagggttcg 540
 gaactgtgtc tgtatgaccc acccgaggtc cccaatgcc aattcaaagc cctctcctac 600
 aagaacggca ccatcctaaa ctgtgaatgc aagagagggt tccgaagact aaaggaattg 660
 gtctatatgc gttgcttagg aaactcctgg agcagcaact gccagtgcac cagcaactcc 720
 catgacaaat cgagaaagca agttacagct caacttgaac accagaaaga gcaacaaacc 780

464173SEQLIST

```

acaacagaca tgcagaagcc aacacagtct atgcaccaag agaacccttac aggtcactgc 840
agggaagccac ctcccttgga acatgaagat tccaagagaa tctatcattt cgtggaagga 900
cagagtgttc actacgagtg tattccggga tacaaggctc tacagagagg tcctgctatt 960
agcatctgca agatgaagtg tgggaaaacg ggggtggactc agccccagct cacatgtgta 1020
gatgaaagag aacaccaccg atttctggct agtgaggaat ctcaaggaag cagaaattct 1080
tctcccgaga gtgagacttc ctgccccata accaccacag acttcccaca acccacagaa 1140
acaactgcaa tgacggagac atttgtgctc acaatggagt ataagggtgg acatcaccat 1200
caccatcact aataa 1215

```

<210> 43

<211> 360

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized mature form IL-2 (Gly3Ser)2-
extracellular domain of IL-2 R

<400> 43

```

Ala Pro Thr Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
1          5          10          15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
20          25          30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
35          40          45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
50          55          60
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65          70          75          80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
85          90          95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
100          105          110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
115          120          125
Ile Ser Thr Leu Thr Gly Gly Gly Ser Gly Gly Gly Ser Glu Leu Cys
130          135          140
Asp Asp Asp Pro Pro Glu Ile Pro His Ala Thr Phe Lys Ala Met Ala
145          150          155          160
Tyr Lys Glu Gly Thr Met Leu Asn Cys Glu Cys Lys Arg Gly Phe Arg
165          170          175
Arg Ile Lys Ser Gly Ser Leu Tyr Met Leu Cys Thr Gly Asn Ser Ser
180          185          190
His Ser Ser Trp Asp Asn Gln Cys Gln Cys Thr Ser Ser Ala Thr Arg
195          200          205
Asn Thr Thr Lys Gln Val Thr Pro Gln Pro Glu Glu Gln Lys Glu Arg
210          215          220
Lys Thr Thr Glu Met Gln Ser Pro Met Gln Pro Val Asp Gln Ala Ser

```

464173SEQLIST

```

225          230          235          240
Leu Pro Gly His Cys Arg Glu Pro Pro Trp Glu Asn Glu Ala Thr
          245          250          255
Glu Arg Ile Tyr His Phe Val Val Gly Gln Met Val Tyr Tyr Gln Cys
          260          265          270
Val Gln Gly Tyr Arg Ala Leu His Arg Gly Pro Ala Glu Ser Val Cys
          275          280          285
Lys Met Thr His Gly Lys Thr Arg Trp Thr Gln Pro Gln Leu Ile Cys
          290          295          300
Thr Gly Glu Met Glu Thr Ser Gln Phe Pro Gly Glu Glu Lys Pro Gln
305          310          315          320
Ala Ser Pro Glu Gly Arg Pro Glu Ser Glu Thr Ser Cys Leu Val Thr
          325          330          335
Thr Thr Asp Phe Gln Ile Gln Thr Glu Met Ala Ala Thr Met Glu Thr
          340          345          350
Ser Ile Phe Thr Thr Glu Tyr Gln
          355          360

```

<210> 44

<211> 380

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized unprocessed form IL-2 (Gly3Ser)2-
extracellular domain of IL-2 R

<400> 44

```

Met Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
 1          5          10          15
Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu
          20          25          30
Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile
          35          40          45
Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe
          50          55          60
Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu
65          70          75          80
Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys
          85          90          95
Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile
          100          105          110
Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala
          115          120          125
Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe
          130          135          140
Cys Gln Ser Ile Ile Ser Thr Leu Thr Gly Gly Gly Ser Gly Gly Gly

```

464173SEQLIST

```

145          150          155          160
Ser Glu Leu Cys Asp Asp Asp Pro Pro Glu Ile Pro His Ala Thr Phe
          165          170          175
Lys Ala Met Ala Tyr Lys Glu Gly Thr Met Leu Asn Cys Glu Cys Lys
          180          185          190
Arg Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr Met Leu Cys Thr
          195          200          205
Gly Asn Ser Ser His Ser Ser Trp Asp Asn Gln Cys Gln Cys Thr Ser
          210          215          220
Ser Ala Thr Arg Asn Thr Thr Lys Gln Val Thr Pro Gln Pro Glu Glu
225          230          235          240
Gln Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Pro Met Gln Pro Val
          245          250          255
Asp Gln Ala Ser Leu Pro Gly His Cys Arg Glu Pro Pro Pro Trp Glu
          260          265          270
Asn Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val Gly Gln Met Val
          275          280          285
Tyr Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His Arg Gly Pro Ala
          290          295          300
Glu Ser Val Cys Lys Met Thr His Gly Lys Thr Arg Trp Thr Gln Pro
305          310          315          320
Gln Leu Ile Cys Thr Gly Glu Met Glu Thr Ser Gln Phe Pro Gly Glu
          325          330          335
Glu Lys Pro Gln Ala Ser Pro Glu Gly Arg Pro Glu Ser Glu Thr Ser
          340          345          350
Cys Leu Val Thr Thr Thr Asp Phe Gln Ile Gln Thr Glu Met Ala Ala
          355          360          365
Thr Met Glu Thr Ser Ile Phe Thr Thr Glu Tyr Gln
          370          375          380

```

<210> 45

<211> 355

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized mature form IL-2 (Gly3)- extracellular
domain of IL-2 R

<400> 45

```

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

```

464173SEQLIST

50	55	60													
Pro	Leu	Glu	Glu	Val	Leu	Asn	Leu	Ala	Gln	Ser	Lys	Asn	Phe	His	Leu
65					70					75					80
Arg	Pro	Arg	Asp	Leu	Ile	Ser	Asn	Ile	Asn	Val	Ile	Val	Leu	Glu	Leu
				85					90					95	
Lys	Gly	Ser	Glu	Thr	Thr	Phe	Met	Cys	Glu	Tyr	Ala	Asp	Glu	Thr	Ala
			100					105					110		
Thr	Ile	Val	Glu	Phe	Leu	Asn	Arg	Trp	Ile	Thr	Phe	Cys	Gln	Ser	Ile
		115					120					125			
Ile	Ser	Thr	Leu	Thr	Gly	Gly	Gly	Glu	Leu	Cys	Asp	Asp	Asp	Pro	Pro
	130					135					140				
Glu	Ile	Pro	His	Ala	Thr	Phe	Lys	Ala	Met	Ala	Tyr	Lys	Glu	Gly	Thr
145				150				155						160	
Met	Leu	Asn	Cys	Glu	Cys	Lys	Arg	Gly	Phe	Arg	Arg	Ile	Lys	Ser	Gly
			165					170						175	
Ser	Leu	Tyr	Met	Leu	Cys	Thr	Gly	Asn	Ser	Ser	His	Ser	Ser	Trp	Asp
		180					185						190		
Asn	Gln	Cys	Gln	Cys	Thr	Ser	Ser	Ala	Thr	Arg	Asn	Thr	Thr	Lys	Gln
	195						200					205			
Val	Thr	Pro	Gln	Pro	Glu	Glu	Gln	Lys	Glu	Arg	Lys	Thr	Thr	Glu	Met
	210				215				220						
Gln	Ser	Pro	Met	Gln	Pro	Val	Asp	Gln	Ala	Ser	Leu	Pro	Gly	His	Cys
225				230				235						240	
Arg	Glu	Pro	Pro	Pro	Trp	Glu	Asn	Glu	Ala	Thr	Glu	Arg	Ile	Tyr	His
			245					250						255	
Phe	Val	Val	Gly	Gln	Met	Val	Tyr	Tyr	Gln	Cys	Val	Gln	Gly	Tyr	Arg
		260					265					270			
Ala	Leu	His	Arg	Gly	Pro	Ala	Glu	Ser	Val	Cys	Lys	Met	Thr	His	Gly
	275					280						285			
Lys	Thr	Arg	Trp	Thr	Gln	Pro	Gln	Leu	Ile	Cys	Thr	Gly	Glu	Met	Glu
	290				295						300				
Thr	Ser	Gln	Phe	Pro	Gly	Glu	Glu	Lys	Pro	Gln	Ala	Ser	Pro	Glu	Gly
305				310					315					320	
Arg	Pro	Glu	Ser	Glu	Thr	Ser	Cys	Leu	Val	Thr	Thr	Thr	Asp	Phe	Gln
			325					330						335	
Ile	Gln	Thr	Glu	Met	Ala	Ala	Thr	Met	Glu	Thr	Ser	Ile	Phe	Thr	Thr
		340					345					350			
Glu	Tyr	Gln													
	355														

<210> 46

<211> 375

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized unprocessed form IL-2 (Gly3)-

464173SEQLIST

extracellular domain of IL-2 R

<400> 46

```

Met Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
 1           5           10           15
Val Thr Asn Ser Ala Pro Thr Ser Ser Thr Lys Lys Thr Gln Leu
      20           25           30
Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile
      35           40           45
Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe
      50           55           60
Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu
65           70           75           80
Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys
      85           90           95
Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile
      100          105          110
Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala
      115          120          125
Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe
      130          135          140
Cys Gln Ser Ile Ile Ser Thr Leu Thr Gly Gly Gly Glu Leu Cys Asp
145          150          155          160
Asp Asp Pro Pro Glu Ile Pro His Ala Thr Phe Lys Ala Met Ala Tyr
      165          170          175
Lys Glu Gly Thr Met Leu Asn Cys Glu Cys Lys Arg Gly Phe Arg Arg
      180          185          190
Ile Lys Ser Gly Ser Leu Tyr Met Leu Cys Thr Gly Asn Ser Ser His
      195          200          205
Ser Ser Trp Asp Asn Gln Cys Gln Cys Thr Ser Ser Ala Thr Arg Asn
      210          215          220
Thr Thr Lys Gln Val Thr Pro Gln Pro Glu Glu Gln Lys Glu Arg Lys
225          230          235          240
Thr Thr Glu Met Gln Ser Pro Met Gln Pro Val Asp Gln Ala Ser Leu
      245          250          255
Pro Gly His Cys Arg Glu Pro Pro Pro Trp Glu Asn Glu Ala Thr Glu
      260          265          270
Arg Ile Tyr His Phe Val Val Gly Gln Met Val Tyr Tyr Gln Cys Val
      275          280          285
Gln Gly Tyr Arg Ala Leu His Arg Gly Pro Ala Glu Ser Val Cys Lys
      290          295          300
Met Thr His Gly Lys Thr Arg Trp Thr Gln Pro Gln Leu Ile Cys Thr
305          310          315          320
Gly Glu Met Glu Thr Ser Gln Phe Pro Gly Glu Glu Lys Pro Gln Ala
      325          330          335
Ser Pro Glu Gly Arg Pro Glu Ser Glu Thr Ser Cys Leu Val Thr Thr
      340          345          350
Thr Asp Phe Gln Ile Gln Thr Glu Met Ala Ala Thr Met Glu Thr Ser

```

464173SEQLIST

355 360 365
Ile Phe Thr Thr Glu Tyr Gln
370 375

```
<210> 47
<211> 1170
<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthesized unprocessed form IL-2 (Gly3Ser)2-
extracellular domain of IL-2 R

<400> 47						
atggacagga	tgcaactcct	gtcttgcatt	gcactaagtc	ttgcacttgt	cacaaacagt	60
gcacctactt	caagttttac	aaagaaaaca	cagctacaac	tggagcattt	actgctggat	120
ttacagatga	ttttgaatgg	aattaataat	tacaagaatc	ccaaactcac	caggatgctc	180
acattttaagt	tttacatgcc	caagaaggcc	acagaactga	aacatcttca	gtgtctagaa	240
gaagaactca	aacctctgga	ggaagtgccta	aatttagctc	aaagcaaaaa	ctttcactta	300
agaccaggg	acttaatcag	caatatcaac	gtaatagttc	tggaaactaaa	gggatctgaa	360
acaacattca	tgtgtgaata	tgctgatgag	acagcaacca	ttgtagaatt	tctgaacaga	420
tggattacct	tttgtcaaag	catcatctca	acactgactg	gtggagggttc	tgggtggagggt	480
tcagagctct	gtgacgatga	cccgccagag	atcccacacg	ccacattcaa	agccatggcc	540
tacaaggaag	gaaccatggt	gaactgtgaa	tgcaagagag	gtttccgcag	aataaaaaagc	600
gggtcactct	atatgctctg	tacaggaaac	tctagccact	cgtcctggga	caaccaatgt	660
caatgcacaa	gctctgccac	tcggaacaca	acgaaacaag	tgacacctca	acctgaagaa	720
cagaaaagaaa	ggaaaaccac	agaaatgcaa	agtccaatgc	agccagtgga	ccaagcgagc	780
cttcagggtc	actgcaggga	acctccacca	tgggaaaatg	aagccacaga	gagaatttat	840
catttcgtgg	tggggcagat	ggttttattat	cagtgcgtcc	agggatacag	ggctctacac	900
agagggtcctg	ctgagagcgt	ctgcaaaaatg	accacgggga	agacaagggtg	gaccagagccc	960
cagctcatat	gcacagggtga	aatggagacc	agtcagtttc	cagggtgaaga	gaagcctcag	1020
gcaagccccg	aaggccgtcc	tgagagtgag	acttcctgcc	tcgtcacaaac	aacagattttt	1080
caaatacaga	cagaaatggc	tgcaaccatg	gagacgtcca	tattttacaac	agagtaccag	1140
ggtggacatc	accatcacca	tcactaataa				1170

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<210> 48
<211> 1155
<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthesized unprocessed form IL-2 (Gly3)-
extracellular domain of IL-2 R

<400> 48
atggacagga tgcaactcct gtcttgcatt gcactaagtc ttgcacttgt cacaaacagt 60
gcacctactt caagttctac aaagaaaaca cagctacaac tggagcattt actgctggat 120

464173SEQLIST

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ttacagatga ttttgaatgg aattaataat tacaagaatc ccaaactcac caggatgctc 180
acattttaagt tttacatgcc caagaaggcc acagaactga aacatcttca gtgtctagaa 240
gaagaactca aacctctgga ggaagtgcta aatttagctc aaagcaaaaa ctttacttta 300
agacccaggg acttaatcag caatatcaac gtaatagttc tggaactaaa gggatctgaa 360
acaacattca tgtgtgaata tgctgatgag acagcaacca ttgtagaatt tctgaacaga 420
tggattacct tttgtcaaag catcatctca acactgactg gtggagggtga gctctgtgac 480
gatgacccgc cagagatccc acacgccaca ttcaaagcca tggcctacaa ggaaggaacc 540
atgttgaact gtgaatgcaa gagaggtttc cgcagaataa aaagcgggtc actctatatg 600
ctctgtacag gaaactctag ccaactcgcc tgggacaacc aatgtcaatg cacaagctct 660
gccactcggg acacaacgaa acaagtgaca cctcaacctg aagaacagaa agaaaggaaa 720
accacagaaa tgcaaatgcc aatgcagcca gtggaccaag cgagccttcc aggtcactgc 780
agggaacctc caccatggga aaatgaagcc acagagagaa tttatcattt cgtgggtggg 840
cagatggttt attatcagtg cgtccaggga tacagggtc tacacagagg tcctgctgag 900
agcgtctgca aaatgacca cgggaagaca aggtggaccc agccccagct catatgcaca 960
ggtgaaatgg agaccagtca gtttccaggt gaagagaagc ctcaggcaag ccccgaggc 1020
cgtcctgaga gtgagacttc ctgcctcgtc acaacaacag attttcaaat acagacagaa 1080
atggctgcaa ccatggagac gtccatattt acaacagagt accagggtgg acatcaccat 1140
caccatcact aataa 1155

```

<210> 49

<211> 1221

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized unprocessed form IL-2 (Gly4Ser)5-
extracellular domain of IL-2 R

<400> 49

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atggacagga tgcaactcct gtcttgcatt gcactaagtc ttgcacttgt cacaacacagt 60
gcacctactt caagttctac aaagaaaaca cagctacaac tggagcattt actgctggat 120
ttacagatga ttttgaatgg aattaataat tacaagaatc ccaaactcac caggatgctc 180
acattttaagt tttacatgcc caagaaggcc acagaactga aacatcttca gtgtctagaa 240
gaagaactca aacctctgga ggaagtgcta aatttagctc aaagcaaaaa ctttacttta 300
agacccaggg acttaatcag caatatcaac gtaatagttc tggaactaaa gggatctgaa 360
acaacattca tgtgtgaata tgctgatgag acagcaacca ttgtagaatt tctgaacaga 420
tggattacct tttgtcaaag catcatctca acactgactg gtggagggtg atcagggtgga 480
ggtggatctg gtggagggtg atcagggtgga ggtggatccg gtggagggtg atctgagctc 540
tgtgacgatg acccgccaga gatccacac gccacattca aagccatggc ctacaaggaa 600
ggaacatgt tgaactgtga atgcaagaga ggtttccgca gaataaaaag cgggtcactc 660
tatatgctct gtacaggaaa ctctagccac tcgtcctggg acaaccaatg tcaatgcaca 720
agctctgcca ctcggaacac aacgaaacaa gtgacacctc aacctgaaga acagaaagaa 780
aggaaaacca cagaaatgca aagtccaatg cagccagtgg accaagcgag ccttccaggt 840
cactgcaggg aacctccacc atgggaaaat gaagccacag agagaattta tcatttcgtg 900
gtggggcaga tggtttatta tcagtgcgtc cagggataca gggctctaca cagaggctct 960
gctgagagcg tctgcaaaat gaccacggg aagacaaggt ggaccagcc ccagctcata 1020
tgcacagggtg aaatggagac cagtcagttt ccagggtgaag agaagcctca ggcaagcccc 1080
gaaggccgtc ctgagagtga gacttcctgc ctcgtcaca caacagattt tcaaatacag 1140

```

464173SEQLIST

acagaaatgg ctgcaaccat ggagacgtcc atatattacaa cagagtacca ggggtggacat 1200
caccatcacc atcactaata a 1221

<210> 50
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> (Gly4Ser)3 linker

<400> 50
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 51
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> (Gly4Ser)2 linker

<400> 51
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 52
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> (Gly4Ser)1 linker

<400> 52
Gly Gly Gly Gly Ser
1 5

<210> 53
<211> 10
<212> DNA
<213> Artificial Sequence

<220>

464173SEQLIST

<223> Kozak sequence

<400> 53

gccaccatgg

10

<210> 54

<211> 412

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized unprocessed form of IL-2

(Gly4Ser)4-extracellular domain of IL-2 R + glycine
spacer and poly-histidine region

<400> 54

Met	Asp	Ser	Met	Gln	Leu	Ala	Ser	Cys	Val	Thr	Leu	Thr	Leu	Val	Leu
1				5					10					15	
Leu	Val	Asn	Ser	Ala	Pro	Thr	Ser	Ser	Ser	Thr	Ser	Ser	Ser	Thr	Ala
			20					25					30		
Glu	Ala	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	His	Leu
		35				40						45			
Glu	Gln	Leu	Leu	Met	Asp	Leu	Gln	Glu	Leu	Leu	Ser	Arg	Met	Glu	Asn
	50					55					60				
Tyr	Arg	Asn	Leu	Lys	Leu	Pro	Arg	Met	Leu	Thr	Phe	Lys	Phe	Tyr	Leu
65					70					75					80
Pro	Lys	Gln	Ala	Thr	Glu	Leu	Lys	Asp	Leu	Gln	Cys	Leu	Glu	Asp	Glu
			85					90						95	
Leu	Gly	Pro	Leu	Arg	His	Val	Leu	Asp	Leu	Thr	Gln	Ser	Lys	Ser	Phe
		100						105					110		
Gln	Leu	Glu	Asp	Ala	Glu	Asn	Phe	Ile	Ser	Asn	Ile	Arg	Val	Thr	Val
		115				120						125			
Val	Lys	Leu	Lys	Gly	Ser	Asp	Asn	Thr	Phe	Glu	Cys	Gln	Phe	Asp	Asp
	130					135					140				
Glu	Ser	Ala	Thr	Val	Val	Asp	Phe	Leu	Arg	Arg	Trp	Ile	Ala	Phe	Cys
145					150					155					160
Gln	Ser	Ile	Ile	Ser	Thr	Ser	Pro	Gln	Gly	Gly	Gly	Gly	Ser	Gly	Gly
			165					170						175	
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Leu	Cys
		180						185					190		
Leu	Tyr	Asp	Pro	Pro	Glu	Val	Pro	Asn	Ala	Thr	Phe	Lys	Ala	Leu	Ser
		195						200					205		
Tyr	Lys	Asn	Gly	Thr	Ile	Leu	Asn	Cys	Glu	Cys	Lys	Arg	Gly	Phe	Arg
	210					215					220				
Arg	Leu	Lys	Glu	Leu	Val	Tyr	Met	Arg	Cys	Leu	Gly	Asn	Ser	Trp	Ser
225					230					235					240
Ser	Asn	Cys	Gln	Cys	Thr	Ser	Asn	Ser	His	Asp	Lys	Ser	Arg	Lys	Gln
			245						250					255	

464173SEQLIST

```

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

```

<210> 55

<211> 417

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized unprocessed form of IL-2 (Gly4Ser)5-
extracellular domain of IL-2 R + glycine spacer
and poly-histidine region

<400> 55

```

Met Asp Ser Met Gln Leu Ala Ser Cys Val Thr Leu Thr Leu Val Leu
 1          5          10          15
Leu Val Asn Ser Ala Pro Thr Ser Ser Ser Thr Ser Ser Ser Thr Ala
      20          25          30
Glu Ala Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln His Leu
      35          40          45
Glu Gln Leu Leu Met Asp Leu Gln Glu Leu Leu Ser Arg Met Glu Asn
      50          55          60
Tyr Arg Asn Leu Lys Leu Pro Arg Met Leu Thr Phe Lys Phe Tyr Leu
      65          70          75          80
Pro Lys Gln Ala Thr Glu Leu Lys Asp Leu Gln Cys Leu Glu Asp Glu
      85          90          95
Leu Gly Pro Leu Arg His Val Leu Asp Leu Thr Gln Ser Lys Ser Phe
      100         105         110
Gln Leu Glu Asp Ala Glu Asn Phe Ile Ser Asn Ile Arg Val Thr Val

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464173SEQLIST

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      115              120              125
Val  Lys  Leu  Lys  Gly  Ser  Asp  Asn  Thr  Phe  Glu  Cys  Gln  Phe  Asp  Asp
      130              135              140
Glu  Ser  Ala  Thr  Val  Val  Asp  Phe  Leu  Arg  Arg  Trp  Ile  Ala  Phe  Cys
145              150              155              160
Gln  Ser  Ile  Ile  Ser  Thr  Ser  Pro  Gln  Gly  Gly  Gly  Gly  Ser  Gly  Gly
      165              170              175
Gly  Gly  Ser  Gly  Gly  Gly  Gly  Ser  Gly  Gly  Gly  Gly  Ser  Gly  Gly  Gly
      180              185              190
Gly  Ser  Glu  Leu  Cys  Leu  Tyr  Asp  Pro  Pro  Glu  Val  Pro  Asn  Ala  Thr
      195              200              205
Phe  Lys  Ala  Leu  Ser  Tyr  Lys  Asn  Gly  Thr  Ile  Leu  Asn  Cys  Glu  Cys
      210              215              220
Lys  Arg  Gly  Phe  Arg  Arg  Leu  Lys  Glu  Leu  Val  Tyr  Met  Arg  Cys  Leu
225              230              235              240
Gly  Asn  Ser  Trp  Ser  Ser  Asn  Cys  Gln  Cys  Thr  Ser  Asn  Ser  His  Asp
      245              250              255
Lys  Ser  Arg  Lys  Gln  Val  Thr  Ala  Gln  Leu  Glu  His  Gln  Lys  Glu  Gln
      260              265              270
Gln  Thr  Thr  Thr  Asp  Met  Gln  Lys  Pro  Thr  Gln  Ser  Met  His  Gln  Glu
      275              280              285
Asn  Leu  Thr  Gly  His  Cys  Arg  Glu  Pro  Pro  Pro  Trp  Lys  His  Glu  Asp
      290              295              300
Ser  Lys  Arg  Ile  Tyr  His  Phe  Val  Glu  Gly  Gln  Ser  Val  His  Tyr  Glu
305              310              315              320
Cys  Ile  Pro  Gly  Tyr  Lys  Ala  Leu  Gln  Arg  Gly  Pro  Ala  Ile  Ser  Ile
      325              330              335
Cys  Lys  Met  Lys  Cys  Gly  Lys  Thr  Gly  Trp  Thr  Gln  Pro  Gln  Leu  Thr
      340              345              350
Cys  Val  Asp  Glu  Arg  Glu  His  His  Arg  Phe  Leu  Ala  Ser  Glu  Glu  Ser
      355              360              365
Gln  Gly  Ser  Arg  Asn  Ser  Ser  Pro  Glu  Ser  Glu  Thr  Ser  Cys  Pro  Ile
      370              375              380
Thr  Thr  Thr  Asp  Phe  Pro  Gln  Pro  Thr  Glu  Thr  Thr  Ala  Met  Thr  Glu
385              390              395              400
Thr  Phe  Val  Leu  Thr  Met  Glu  Tyr  Lys  Gly  Gly  His  His  His  His  His
      405              410              415
His

```

<210> 56

<211> 408

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized unprocessed form of IL-2 (Gly3Ser)4-

464173SEQLIST

extracellular domain of IL-2 R + glycine spacer
and poly-histidine region

<400> 56

```

Met Asp Ser Met Gln Leu Ala Ser Cys Val Thr Leu Thr Leu Val Leu
 1          5          10          15
Leu Val Asn Ser Ala Pro Thr Ser Ser Thr Ser Ser Thr Thr Ala
 20          25          30
Glu Ala Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln His Leu
 35          40          45
Glu Gln Leu Leu Met Asp Leu Gln Glu Leu Leu Ser Arg Met Glu Asn
 50          55          60
Tyr Arg Asn Leu Lys Leu Pro Arg Met Leu Thr Phe Lys Phe Tyr Leu
 65          70          75          80
Pro Lys Gln Ala Thr Glu Leu Lys Asp Leu Gln Cys Leu Glu Asp Glu
 85          90          95
Leu Gly Pro Leu Arg His Val Leu Asp Leu Thr Gln Ser Lys Ser Phe
100          105          110
Gln Leu Glu Asp Ala Glu Asn Phe Ile Ser Asn Ile Arg Val Thr Val
115          120          125
Val Lys Leu Lys Gly Ser Asp Asn Thr Phe Glu Cys Gln Phe Asp Asp
130          135          140
Glu Ser Ala Thr Val Val Asp Phe Leu Arg Arg Trp Ile Ala Phe Cys
145          150          155          160
Gln Ser Ile Ile Ser Thr Ser Pro Gln Gly Gly Gly Ser Gly Gly Gly
165          170          175
Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Leu Cys Leu Tyr Asp Pro
180          185          190
Pro Glu Val Pro Asn Ala Thr Phe Lys Ala Leu Ser Tyr Lys Asn Gly
195          200          205
Thr Ile Leu Asn Cys Glu Cys Lys Arg Gly Phe Arg Arg Leu Lys Glu
210          215          220
Leu Val Tyr Met Arg Cys Leu Gly Asn Ser Trp Ser Ser Asn Cys Gln
225          230          235          240
Cys Thr Ser Asn Ser His Asp Lys Ser Arg Lys Gln Val Thr Ala Gln
245          250          255
Leu Glu His Gln Lys Glu Gln Gln Thr Thr Thr Asp Met Gln Lys Pro
260          265          270
Thr Gln Ser Met His Gln Glu Asn Leu Thr Gly His Cys Arg Glu Pro
275          280          285
Pro Pro Trp Lys His Glu Asp Ser Lys Arg Ile Tyr His Phe Val Glu
290          295          300
Gly Gln Ser Val His Tyr Glu Cys Ile Pro Gly Tyr Lys Ala Leu Gln
305          310          315          320
Arg Gly Pro Ala Ile Ser Ile Cys Lys Met Lys Cys Gly Lys Thr Gly
325          330          335
Trp Thr Gln Pro Gln Leu Thr Cys Val Asp Glu Arg Glu His His Arg
340          345          350

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464173SEQLIST

Phe Leu Ala Ser Glu Glu Ser Gln Gly Ser Arg Asn Ser Ser Pro Glu
 355 360 365
 Ser Glu Thr Ser Cys Pro Ile Thr Thr Thr Asp Phe Pro Gln Pro Thr
 370 375 380
 Glu Thr Thr Ala Met Thr Glu Thr Phe Val Leu Thr Met Glu Tyr Lys
 385 390 395 400
 Gly Gly His His His His His His
 405

<210> 57

<211> 404

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized mature form of IL-2 (Gly3Ser)3-
 extracellular domain of IL-2 R + glycine spacer
 and poly-histidine region

<400> 57

Met Asp Ser Met Gln Leu Ala Ser Cys Val Thr Leu Thr Leu Val Leu
 1 5 10 15
 Leu Val Asn Ser Ala Pro Thr Ser Ser Ser Thr Ser Ser Ser Thr Ala
 20 25 30
 Glu Ala Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln His Leu
 35 40 45
 Glu Gln Leu Leu Met Asp Leu Gln Glu Leu Leu Ser Arg Met Glu Asn
 50 55 60
 Tyr Arg Asn Leu Lys Leu Pro Arg Met Leu Thr Phe Lys Phe Tyr Leu
 65 70 75 80
 Pro Lys Gln Ala Thr Glu Leu Lys Asp Leu Gln Cys Leu Glu Asp Glu
 85 90 95
 Leu Gly Pro Leu Arg His Val Leu Asp Leu Thr Gln Ser Lys Ser Phe
 100 105 110
 Gln Leu Glu Asp Ala Glu Asn Phe Ile Ser Asn Ile Arg Val Thr Val
 115 120 125
 Val Lys Leu Lys Gly Ser Asp Asn Thr Phe Glu Cys Gln Phe Asp Asp
 130 135 140
 Glu Ser Ala Thr Val Val Asp Phe Leu Arg Arg Trp Ile Ala Phe Cys
 145 150 155 160
 Gln Ser Ile Ile Ser Thr Ser Pro Gln Gly Gly Gly Ser Gly Gly Gly
 165 170 175
 Ser Gly Gly Gly Ser Glu Leu Cys Leu Tyr Asp Pro Pro Glu Val Pro
 180 185 190
 Asn Ala Thr Phe Lys Ala Leu Ser Tyr Lys Asn Gly Thr Ile Leu Asn
 195 200 205
 Cys Glu Cys Lys Arg Gly Phe Arg Arg Leu Lys Glu Leu Val Tyr Met

464173SEQLIST

210	215	220															
Arg Cys Leu Gly Asn Ser Trp Ser Ser Asn Cys Gln Cys Thr Ser Asn																	
225	230	235	240														
Ser His Asp Lys Ser Arg Lys Gln Val Thr Ala Gln Leu Glu His Gln																	
245	250	255															
Lys Glu Gln Gln Thr Thr Thr Asp Met Gln Lys Pro Thr Gln Ser Met																	
260	265	270															
His Gln Glu Asn Leu Thr Gly His Cys Arg Glu Pro Pro Pro Trp Lys																	
275	280	285															
His Glu Asp Ser Lys Arg Ile Tyr His Phe Val Glu Gly Gln Ser Val																	
290	295	300															
His Tyr Glu Cys Ile Pro Gly Tyr Lys Ala Leu Gln Arg Gly Pro Ala																	
305	310	315	320														
Ile Ser Ile Cys Lys Met Lys Cys Gly Lys Thr Gly Trp Thr Gln Pro																	
325	330	335															
Gln Leu Thr Cys Val Asp Glu Arg Glu His His Arg Phe Leu Ala Ser																	
340	345	350															
Glu Glu Ser Gln Gly Ser Arg Asn Ser Ser Pro Glu Ser Glu Thr Ser																	
355	360	365															
Cys Pro Ile Thr Thr Thr Asp Phe Pro Gln Pro Thr Glu Thr Thr Ala																	
370	375	380															
Met Thr Glu Thr Phe Val Leu Thr Met Glu Tyr Lys Gly Gly His His																	
385	390	395	400														
His His His His																	

<210> 58

<211> 388

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized unprocessed form IL-2 (Gly3Ser)2-
extracellular domain of IL-2 R + glycine spacer
and poly-histidine region

<400> 58

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

464173SEQLIST

Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys
 85 90 95
 Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile
 100 105 110
 Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala
 115 120 125
 Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe
 130 135 140
 Cys Gln Ser Ile Ile Ser Thr Leu Thr Gly Gly Gly Ser Gly Gly Gly
 145 150 155 160
 Ser Glu Leu Cys Asp Asp Asp Pro Pro Glu Ile Pro His Ala Thr Phe
 165 170 175
 Lys Ala Met Ala Tyr Lys Glu Gly Thr Met Leu Asn Cys Glu Cys Lys
 180 185 190
 Arg Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr Met Leu Cys Thr
 195 200 205
 Gly Asn Ser Ser His Ser Ser Trp Asp Asn Gln Cys Gln Cys Thr Ser
 210 215 220
 Ser Ala Thr Arg Asn Thr Thr Lys Gln Val Thr Pro Gln Pro Glu Glu
 225 230 235 240
 Gln Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Pro Met Gln Pro Val
 245 250 255
 Asp Gln Ala Ser Leu Pro Gly His Cys Arg Glu Pro Pro Pro Trp Glu
 260 265 270
 Asn Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val Gly Gln Met Val
 275 280 285
 Tyr Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His Arg Gly Pro Ala
 290 295 300
 Glu Ser Val Cys Lys Met Thr His Gly Lys Thr Arg Trp Thr Gln Pro
 305 310 315 320
 Gln Leu Ile Cys Thr Gly Glu Met Glu Thr Ser Gln Phe Pro Gly Glu
 325 330 335
 Glu Lys Pro Gln Ala Ser Pro Glu Gly Arg Pro Glu Ser Glu Thr Ser
 340 345 350
 Cys Leu Val Thr Thr Thr Asp Phe Gln Ile Gln Thr Glu Met Ala Ala
 355 360 365
 Thr Met Glu Thr Ser Ile Phe Thr Thr Glu Tyr Gln Gly Gly His His
 370 375 380
 His His His His
 385

<210> 59

<211> 392

<212> PRT

<213> Artificial Sequence

<220>

464173SEQLIST

<223> Synthesized unprocessed form of IL-2 (Gly3Ser)3-
extracellular domain of IL-2 R + glycine spacer
and poly-histidine region

<400> 59

Met	Asp	Arg	Met	Gln	Leu	Leu	Ser	Cys	Ile	Ala	Leu	Ser	Leu	Ala	Leu
1				5					10					15	
Val	Thr	Asn	Ser	Ala	Pro	Thr	Ser	Ser	Ser	Thr	Lys	Lys	Thr	Gln	Leu
		20					25					30			
Gln	Leu	Glu	His	Leu	Leu	Leu	Asp	Leu	Gln	Met	Ile	Leu	Asn	Gly	Ile
		35					40					45			
Asn	Asn	Tyr	Lys	Asn	Pro	Lys	Leu	Thr	Arg	Met	Leu	Thr	Phe	Lys	Phe
	50					55				60					
Tyr	Met	Pro	Lys	Lys	Ala	Thr	Glu	Leu	Lys	His	Leu	Gln	Cys	Leu	Glu
65					70				75					80	
Glu	Glu	Leu	Lys	Pro	Leu	Glu	Glu	Val	Leu	Asn	Leu	Ala	Gln	Ser	Lys
				85				90					95		
Asn	Phe	His	Leu	Arg	Pro	Arg	Asp	Leu	Ile	Ser	Asn	Ile	Asn	Val	Ile
			100				105						110		
Val	Leu	Glu	Leu	Lys	Gly	Ser	Glu	Thr	Thr	Phe	Met	Cys	Glu	Tyr	Ala
		115					120					125			
Asp	Glu	Thr	Ala	Thr	Ile	Val	Glu	Phe	Leu	Asn	Arg	Trp	Ile	Thr	Phe
	130					135					140				
Cys	Gln	Ser	Ile	Ile	Ser	Thr	Leu	Thr	Gly	Gly	Gly	Ser	Gly	Gly	Gly
145					150					155					160
Ser	Gly	Gly	Gly	Ser	Glu	Leu	Cys	Asp	Asp	Asp	Pro	Pro	Glu	Ile	Pro
				165					170					175	
His	Ala	Thr	Phe	Lys	Ala	Met	Ala	Tyr	Lys	Glu	Gly	Thr	Met	Leu	Asn
			180					185					190		
Cys	Glu	Cys	Lys	Arg	Gly	Phe	Arg	Arg	Ile	Lys	Ser	Gly	Ser	Leu	Tyr
		195					200					205			
Met	Leu	Cys	Thr	Gly	Asn	Ser	Ser	His	Ser	Ser	Trp	Asp	Asn	Gln	Cys
	210					215						220			
Gln	Cys	Thr	Ser	Ser	Ala	Thr	Arg	Asn	Thr	Thr	Lys	Gln	Val	Thr	Pro
225					230						235				240
Gln	Pro	Glu	Glu	Gln	Lys	Glu	Arg	Lys	Thr	Thr	Glu	Met	Gln	Ser	Pro
				245					250					255	
Met	Gln	Pro	Val	Asp	Gln	Ala	Ser	Leu	Pro	Gly	His	Cys	Arg	Glu	Pro
			260					265					270		
Pro	Pro	Trp	Glu	Asn	Glu	Ala	Thr	Glu	Arg	Ile	Tyr	His	Phe	Val	Val
			275				280						285		
Gly	Gln	Met	Val	Tyr	Tyr	Gln	Cys	Val	Gln	Gly	Tyr	Arg	Ala	Leu	His
	290					295					300				
Arg	Gly	Pro	Ala	Glu	Ser	Val	Cys	Lys	Met	Thr	His	Gly	Lys	Thr	Arg
305					310					315					320
Trp	Thr	Gln	Pro	Gln	Leu	Ile	Cys	Thr	Gly	Glu	Met	Glu	Thr	Ser	Gln
				325					330					335	
Phe	Pro	Gly	Glu	Glu	Lys	Pro	Gln	Ala	Ser	Pro	Glu	Gly	Arg	Pro	Glu

464173SEQLIST

```

          340          345          350
Ser Glu Thr Ser Cys Leu Val Thr Thr Thr Asp Phe Gln Ile Gln Thr
          355          360          365
Glu Met Ala Ala Thr Met Glu Thr Ser Ile Phe Thr Thr Glu Tyr Gln
          370          375          380
Gly Gly His His His His His His
385          390

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<210> 60

<211> 396

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized unprocessed form IL-2 (Gly3Ser)4-
extracellular domain of IL-2 R + glycine spacer
and poly-histidine region

<400> 60

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Met Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
1          5          10          15
Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu
          20          25          30
Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile
          35          40          45
Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe
          50          55          60
Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu
65          70          75          80
Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys
          85          90          95
Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile
          100          105          110
Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala
          115          120          125
Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe
          130          135          140
Cys Gln Ser Ile Ile Ser Thr Leu Thr Gly Gly Gly Ser Gly Gly Gly
145          150          155          160
Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Leu Cys Asp Asp Asp Pro
          165          170          175
Pro Glu Ile Pro His Ala Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly
          180          185          190
Thr Met Leu Asn Cys Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser
          195          200          205
Gly Ser Leu Tyr Met Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp
210          215          220

```

464173SEQLIST

```

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

```

<210> 61

<211> 400

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized unprocessed form IL-2 (Gly4Ser)4-
extracellular domain of IL-2 R + glycine spacer
and poly-histidine region

<400> 61

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Met Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
1          5          10          15
Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu
                20          25          30
Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile
                35          40          45
Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe
50          55          60
Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu
65          70          75          80
Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys
                85          90          95
Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile

```

464173SEQLIST

[illegible]

<210> 62

<211> 364

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthesized mature form IL-2 (Gly3Ser)3-extracellular domain of mutIL-2 R

464173SEQLIST

<400> 62

Ala	Pro	Thr	Ser	Ser	Ser	Thr	Lys	Lys	Thr	Gln	Leu	Gln	Leu	Glu	His
1				5					10					15	
Leu	Leu	Leu	Asp	Leu	Gln	Met	Ile	Leu	Asn	Gly	Ile	Asn	Asn	Tyr	Lys
			20					25					30		
Asn	Pro	Lys	Leu	Thr	Arg	Met	Leu	Thr	Phe	Lys	Phe	Tyr	Met	Pro	Lys
		35					40					45			
Lys	Ala	Thr	Glu	Leu	Lys	His	Leu	Gln	Cys	Leu	Glu	Glu	Glu	Leu	Lys
	50					55					60				
Pro	Leu	Glu	Glu	Val	Leu	Asn	Leu	Ala	Gln	Ser	Lys	Asn	Phe	His	Leu
65					70					75					80
Arg	Pro	Arg	Asp	Leu	Ile	Ser	Asn	Ile	Asn	Val	Ile	Val	Leu	Glu	Leu
			85						90					95	
Lys	Gly	Ser	Glu	Thr	Thr	Phe	Met	Cys	Glu	Tyr	Ala	Asp	Glu	Thr	Ala
			100					105					110		
Thr	Ile	Val	Glu	Phe	Leu	Asn	Arg	Trp	Ile	Thr	Phe	Cys	Gln	Ser	Ile
		115					120					125			
Ile	Ser	Thr	Leu	Thr	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly
		130				135						140			
Ser	Glu	Leu	Cys	Asp	Asp	Asp	Pro	Pro	Glu	Ile	Pro	His	Ala	Thr	Phe
145					150					155					160
Lys	Ala	Met	Ala	Tyr	Lys	Glu	Gly	Thr	Met	Leu	Asn	Cys	Glu	Cys	Lys
			165						170					175	
Arg	Gly	Phe	Thr	Ser	Ile	Lys	Ser	Gly	Ser	Leu	Tyr	Met	Leu	Cys	Thr
			180					185					190		
Gly	Asn	Ser	Ser	His	Ser	Ser	Trp	Asp	Asn	Gln	Cys	Gln	Cys	Thr	Ser
		195					200					205			
Ser	Ala	Thr	Arg	Asn	Thr	Thr	Lys	Gln	Val	Thr	Pro	Gln	Pro	Glu	Glu
	210					215					220				
Gln	Lys	Glu	Arg	Lys	Thr	Thr	Glu	Met	Gln	Ser	Pro	Met	Gln	Pro	Val
225					230					235					240
Asp	Gln	Ala	Ser	Leu	Pro	Gly	His	Cys	Arg	Glu	Pro	Pro	Pro	Trp	Glu
			245						250					255	
Asn	Glu	Ala	Thr	Glu	Arg	Ile	Tyr	His	Phe	Val	Val	Gly	Gln	Met	Val
			260					265					270		
Tyr	Tyr	Gln	Cys	Val	Gln	Gly	Tyr	Arg	Ala	Leu	His	Arg	Gly	Pro	Ala
		275					280					285			
Glu	Ser	Val	Cys	Lys	Met	Thr	His	Gly	Lys	Thr	Arg	Trp	Thr	Gln	Pro
		290				295					300				
Gln	Leu	Ile	Cys	Thr	Gly	Glu	Met	Glu	Thr	Ser	Gln	Phe	Pro	Gly	Glu
305					310					315					320
Glu	Lys	Pro	Gln	Ala	Ser	Pro	Glu	Gly	Arg	Pro	Glu	Ser	Glu	Thr	Ser
			325						330					335	
Cys	Leu	Val	Thr	Thr	Thr	Asp	Phe	Gln	Ile	Gln	Thr	Glu	Met	Ala	Ala
			340					345					350		
Thr	Met	Glu	Thr	Ser	Ile	Phe	Thr	Thr	Glu	Tyr	Gln				
		355					360								

464173SEQLIST

<210> 63
 <211> 1182
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthesized unprocessed form IL-2 (Gly3Ser)3-
 extracellular domain of mutIL-2 R Mut

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<400> 63
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gcacctactt caagttctac aaagaaaaca cagctacaac tggagcattt actgctggat 120
ttacagatga ttttgaatgg aattaataat tacaagaatc ccaaactcac caggatgctc 180
acattttaagt tttacatgcc caagaaggcc acagaactga aacatcttca gtgtctagaa 240
gaagaactca aacctctgga ggaagtgcta aatttagctc aaagcaaaaa ctttacttta 300
agaccagggg acttaatcag caatatcaac gtaatatgtt tggaactaaa gggatctgaa 360
acaacattca tgtgtgaata tgctgatgag acagcaacca ttgtagaatt tctgaacaga 420
tggattacct tttgtcaaag catcatctca acactgactg gtggagggtt tgggtggagg 480
tcagggtggag gttcggagct ctgtgacgat gaccgccag agatcccaca cgccacattc 540
aaagccatgg cctacaagga aggaaccatg ttgaactgtg aatgcaagag aggtttcacc 600
tcaataaaaa gcgggtcact ctatatgctc tgtacaggaa actctagcca ctcgtcctgg 660
gacaaccaat gtcaatgcac aagctctgcc actcggaaaca caacgaaaca agtgacacct 720
caacctgaag aacagaaaaga aaggaaaacc acagaaatgc aaagtccaat gcagccagt 780
gaccaagcga gccttccagg tcaactgcagg gaacctccac catgggaaaa tgaagccaca 840
gagagaattt atcatttcgt ggtggggcag atggtttatt atcagtgcgt ccagggatac 900
agggtcttac acagagggtc tgctgagagc gtctgcaaaa tgaccacagg gaagacaagg 960
tggaccagc cccagctcat atgcacaggt gaaatggaga ccagtcagtt tccaggtgaa 1020
gagaagcctc aggcaagccc cgaaggccgt cctgagagtg agacttcctg cctcgtcaca 1080
acaacagatt ttcaaataca gacagaaatg gctgcaacca tggagacgtc catatttaca 1140
acagagtacc aggggtggaca tcaccatcac catcactaat aa 1182
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<210> 64
 <211> 372
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthesized mature form IL-2 (Gly4Ser)4-
 extracellular domain of mutIL-2 R

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<400> 64
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
1           5           10          15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
20          25          30
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
35          40          45
```

464173SEQLIST

Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
 50 55 60
 Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
 65 70 75 80
 Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
 85 90 95
 Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
 100 105 110
 Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
 115 120 125
 Ile Ser Thr Leu Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 130 135 140
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu Cys Asp Asp Asp Pro
 145 150 155 160
 Pro Glu Ile Pro His Ala Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly
 165 170 175
 Thr Met Leu Asn Cys Glu Cys Lys Arg Gly Phe Thr Ser Ile Lys Ser
 180 185 190
 Gly Ser Leu Tyr Met Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp
 195 200 205
 Asp Asn Gln Cys Gln Cys Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys
 210 215 220
 Gln Val Thr Pro Gln Pro Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu
 225 230 235 240
 Met Gln Ser Pro Met Gln Pro Val Asp Gln Ala Ser Leu Pro Gly His
 245 250 255
 Cys Arg Glu Pro Pro Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr
 260 265 270
 His Phe Val Val Gly Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr
 275 280 285
 Arg Ala Leu His Arg Gly Pro Ala Glu Ser Val Cys Lys Met Thr His
 290 295 300
 Gly Lys Thr Arg Trp Thr Gln Pro Gln Leu Ile Cys Thr Gly Glu Met
 305 310 315 320
 Glu Thr Ser Gln Phe Pro Gly Glu Glu Lys Pro Gln Ala Ser Pro Glu
 325 330 335
 Gly Arg Pro Glu Ser Glu Thr Ser Cys Leu Val Thr Thr Thr Asp Phe
 340 345 350
 Gln Ile Gln Thr Glu Met Ala Ala Thr Met Glu Thr Ser Ile Phe Thr
 355 360 365
 Thr Glu Tyr Gln
 370

<210> 65

<211> 1206

<212> DNA

<213> Artificial Sequence

464173SEQLIST

<220>

<223> Synthesized unprocessed form IL-2 (Gly4Ser)4-extracellular domain of mutIL-2 R

<400> 65

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atggacagga tgcaactcct gtcttgcat gcactaagtc ttgcacttgt cacaacagct 60
gcacctactt caagttctac aaagaaaaca cagctacaac tggagcattt actgctggat 120
ttacagatga ttttgaatgg aattaataat tacaagaatc ccaaactcac caggatgctc 180
acatttaagt ttacatgcc caagaaggcc acagaactga aacatcttca gtgtctagaa 240
gaagaactca aacctctgga ggaagtgcta aatttagctc aaagcaaaaa ctttcaactta 300
agaccagggg acttaatcag caatatcaac gtaatagttc tggaactaaa gggatctgaa 360
acaacattca tgtgtgaata tgctgatgag acagcaacca ttgtagaatt tctgaacaga 420
tggattacct tttgtcaaag catcatctca acactgactg gtggagggtg atctggtgga 480
ggtggatcag gtggagggtg atccggtgga ggtggatctg agctctgtga cgatgacccg 540
ccagagatcc cacacgccac attcaaagcc atggcctaca aggaagggaac catgttgaac 600
tgtgaatgca agagagggtt cacctcaata aaaagcgggt cactctatat gctctgtaca 660
ggaaactcta gccactcgtc ctgggacaac caatgtcaat gcacaagctc tgccactcgg 720
aacacaacga aacaagtgac acctcaacct gaagaacaga aagaaaggaa aaccacagaa 780
atgcaaagtc caatgcagcc agtggacca gcgagccttc caggtcactg cagggaacct 840
ccaccatggg aaaatgaagc cacagagaga atttatcatt tcgtggtggg gcagatggtt 900
tattatcagt gcgtccaggg atacagggt ctacacagag gtcctgctga gagcgtctgc 960
aaaatgaccc acgggaagac aagggtggacc cagccccagc tcatatgcac aggtgaaatg 1020
gagaccagtc agtttccagg tgaagagaag cctcaggcaa gccccgaagg ccgtcctgag 1080
agtgagactt cctgcctcgt cacaacaaca gattttcaaa tacagacaga aatggctgca 1140
accatggaga cgtccatatt tacaacagag taccagggtg gacatcacca tcaccatcac 1200
taataa                                           1206

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