

SEQUENCE LISTING

<110> EXELIXIS, INC.

<120> ANTI-ROR ANTIBODY CONSTRUCTS

<130> 14529-001-228

<140>

<141>

<150> US 62/659,635

<151> 2018-04-18

<160> 540

<170> PatentIn version 3.5

<210> 1

<211> 338

<212> PRT

<213> Artificial Sequence

<220>

<223> Example 1, bivalent monospecific construct CHAIN 1, VL

<400> 1

Val	Glu	Ile	Lys	Arg	Thr	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro
1				5					10					15	

Pro	Cys	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Trp	Cys	Leu
			20					25					30		

Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn
		35					40					45			

Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser
	50					55					60				

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

Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu
				85					90					95	

His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	Asp
			100					105					110		

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
115 120 125

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
145 150 155 160

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
165 170 175

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
180 185 190

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

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
210 215 220

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
225 230 235 240

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

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
260 265 270

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
275 280 285

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
290 295 300

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
305 310 315 320

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
325 330 335

Gly Lys

<210> 2
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Example 1, bivalent monospecific construct CHAIN 2, VH

<400> 2

Val Thr Val Ser Ser Ala Ser Pro Arg Glu Pro Gln Val Tyr Thr Leu
1 5 10 15

Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys
20 25 30

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
35 40 45

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
50 55 60

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
65 70 75 80

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
85 90 95

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105 110

<210> 3
<211> 338
<212> PRT
<213> Artificial Sequence

<220>
<223> Example 1, bivalent, bispecific construct CHAIN 1, VL

<400> 3

Val Glu Ile Lys Arg Thr Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
1 5 10 15

Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu
20 25 30

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
35 40 45

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
50 55 60

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

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
85 90 95

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Asp
100 105 110

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
115 120 125

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
145 150 155 160

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
165 170 175

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
180 185 190

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

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
210 215 220

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
225 230 235 240

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

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
260 265 270

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
275 280 285

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
290 295 300

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
305 310 315 320

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
325 330 335

Gly Lys

<210> 4
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Example 1, bivalent, bispecific construct CHAIN 2, VH

<400> 4

Val Thr Val Ser Ser Ala Ser Pro Arg Glu Pro Gln Val Tyr Thr Leu
1 5 10 15

Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys
20 25 30

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
35 40 45

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
50 55 60

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
65 70 75 80

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
85 90 95

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105 110

<210> 5
<211> 338
<212> PRT
<213> Artificial Sequence

<220>
<223> Example 1, bivalent, bispecific construct CHAIN 3, VL

<400> 5

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
1 5 10 15

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

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
35 40 45

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
50 55 60

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
65 70 75 80

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
85 90 95

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Asp
100 105 110

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
115 120 125

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
145 150 155 160

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
165 170 175

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
180 185 190

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

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
210 215 220

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys
225 230 235 240

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
245 250 255

Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
260 265 270

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
275 280 285

Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp
290 295 300

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
305 310 315 320

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
325 330 335

Gly Lys

<210> 6
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Example 1, bivalent, bispecific construct CHAIN 4, VH

<400> 6

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
1 5 10 15

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
20 25 30

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
35 40 45

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
50 55 60

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
65 70 75 80

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
85 90 95

Thr Lys Val Asp Lys Lys Val Glu Pro Pro Lys Ser Cys
100 105

<210> 7
<211> 105
<212> PRT
<213> Artificial Sequence

<220>

<223> Fc Fragment of Human IgG1

<400> 7

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

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

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro
100 105

<210> 8

<211> 441

<212> PRT

<213> Artificial Sequence

<220>

<223> BC1 chain 1

<400> 8

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
85 90 95

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

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
115 120 125

Gln Val Ser Leu Lys Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
130 135 140

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
145 150 155 160

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
165 170 175

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
180 185 190

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
195 200 205

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
225 230 235 240

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
245 250 255

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
260 265 270

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
275 280 285

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
290 295 300

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
305 310 315 320

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
325 330 335

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu
340 345 350

Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro
355 360 365

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
370 375 380

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
385 390 395 400

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
405 410 415

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
420 425 430

Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 9
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> BC1 chain 2

<400> 9

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

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

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

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

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

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

Ala Arg Leu Val Gly Glu Ile Ala Thr Gly Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Pro Arg Glu Pro Gln Val
115 120 125

Tyr Thr Asp Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205

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

Gly Glu Cys
225

<210> 10
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> BC1 chain 3 and BC28 bivalent chain 3

<400> 10

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

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

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

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

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Ser Asn Trp Pro Arg
85 90 95

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
210 215 220

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
225 230 235 240

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
245 250 255

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
260 265 270

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
275 280 285

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
290 295 300

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
305 310 315 320

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
325 330 335

Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Glu Glu Met
340 345 350

Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro
355 360 365

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
370 375 380

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
385 390 395 400

Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
405 410 415

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
420 425 430

Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 11
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> BC1 chain 4 and BC28 bivalent chain 4

<400> 11

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

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

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

Ala Val Ile Trp Tyr Asp Gly Ser Lys Arg Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

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

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

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
145 150 155 160

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

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

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
195 200 205

Lys Lys Val Glu Pro Pro Lys Ser Cys
210 215

<210> 12
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> BC1 Domain A

<400> 12

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105

<210> 13
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> BC1 Domain B

<400> 13

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
1 5 10 15

Thr Lys Asn Gln Val Ser Leu Lys Cys Leu Val Lys Gly Phe Tyr Pro
20 25 30

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
35 40 45

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
50 55 60

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
65 70 75 80

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
85 90 95

Lys Ser Leu Ser Leu Ser Lys Ser Cys
100 105

<210> 14
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> BC1 Domain D

<400> 14

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

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

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105 110

<210> 15
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> BC1 Domain E

<400> 15

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp
1 5 10 15

Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe
20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 16
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> BC1 Domain F

<400> 16

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

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

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

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

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

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

Ala Arg Leu Val Gly Glu Ile Ala Thr Gly Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser
115 120

<210> 17
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> BC1 Domain G

<400> 17

Pro Arg Glu Pro Gln Val Tyr Thr Asp Pro Pro Ser Arg Asp Glu Leu
1 5 10 15

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
20 25 30

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
35 40 45

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
50 55 60

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
65 70 75 80

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
85 90 95

Lys Ser Leu Ser Leu Ser Gly Glu Cys
100 105

<210> 18
<211> 107
<212> PRT
<213> Artificial Sequence

<220>

<223> BC1 Domain H

<400> 18

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

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

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

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

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Ser Asn Trp Pro Arg
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 19

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> BC1 Domain I

<400> 19

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

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

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 20
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> BC1 Domain J

<400> 20

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

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

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105 110

<210> 21
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> BC1 Domain K

<400> 21

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

Glu Met Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe
20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60

Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 22
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> BC1 Domain L

<400> 22

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

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

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

Ala Val Ile Trp Tyr Asp Gly Ser Lys Arg Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

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

Ser

<210> 23
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<223> BC1 Domain M

<400> 23

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Pro Lys Ser Cys
100

<210> 24
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> BC28 chain 1

<400> 24

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
85 90 95

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

Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
115 120 125

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
130 135 140

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
145 150 155 160

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
165 170 175

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
180 185 190

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
195 200 205

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
225 230 235 240

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
245 250 255

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
260 265 270

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
275 280 285

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
290 295 300

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
305 310 315 320

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
325 330 335

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu
340 345 350

Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro
355 360 365

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
370 375 380

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
385 390 395 400

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
405 410 415

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
420 425 430

Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 25
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> BC28 chain 2

<400> 25

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

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

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

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

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

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

Ala Arg Leu Val Gly Glu Ile Ala Thr Gly Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Pro Arg Glu Pro Gln Val
115 120 125

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

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205

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

Pro Gly Lys
225

<210> 26
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> BC28 domain A

<400> 26

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105

<210> 27
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> BC28 domain B

<400> 27

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

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
20 25 30

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
35 40 45

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
50 55 60

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
65 70 75 80

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
85 90 95

Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 28
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> BC28 domain D

<400> 28

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

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

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105 110

<210> 29
<211> 107
<212> PRT
<213> Artificial Sequence

<220>

<223> BC28 domain E

<400> 29

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp
1 5 10 15

Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe
20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 30

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> BC28 domain F

<400> 30

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

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

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

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

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

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

Ala Arg Leu Val Gly Glu Ile Ala Thr Gly Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser
115 120

<210> 31
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> BC28 domain G

<400> 31

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu
1 5 10 15

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
20 25 30

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
35 40 45

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
50 55 60

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
65 70 75 80

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
85 90 95

Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 32
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> BC44 chain 1

<400> 32

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Arg Glu
100 105 110

Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
115 120 125

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
130 135 140

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
145 150 155 160

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
165 170 175

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
180 185 190

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
195 200 205

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
225 230 235 240

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
245 250 255

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
260 265 270

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
275 280 285

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
290 295 300

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
305 310 315 320

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
325 330 335

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu
340 345 350

Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro
355 360 365

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
370 375 380

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
385 390 395 400

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
405 410 415

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
420 425 430

Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 33
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> BC44 Domain A

<400> 33

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105

<210> 34
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> BC44 Domain B

<400> 34

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

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
20 25 30

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
35 40 45

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
50 55 60

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
65 70 75 80

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
85 90 95

Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 35
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> BC44 Domain D

<400> 35

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

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

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105 110

<210> 36
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> BC44 Domain E

<400> 36

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp
1 5 10 15

Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe
20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 37
<211> 661
<212> PRT
<213> Artificial Sequence

<220>
<223> BC28 1x2 chain 3

<400> 37

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
85 90 95

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

Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
115 120 125

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
130 135 140

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
145 150 155 160

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
165 170 175

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
180 185 190

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
195 200 205

Ser Leu Ser Pro Gly Lys Gly Ser Gly Ser Gly Ser Glu Ile Val Leu
210 215 220

Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
225 230 235 240

Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala Trp Tyr
245 250 255

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser
260 265 270

Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
275 280 285

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala
290 295 300

Val Tyr Tyr Cys Gln Gln Ser Ser Asn Trp Pro Arg Thr Phe Gly Gln
305 310 315 320

Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
325 330 335

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
340 345 350

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
355 360 365

Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr
370 375 380

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
385 390 395 400

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
405 410 415

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
420 425 430

Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
435 440 445

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
450 455 460

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
465 470 475 480

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
485 490 495

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
500 505 510

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
515 520 525

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
530 535 540

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
545 550 555 560

Gln Val Cys Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
565 570 575

Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
580 585 590

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
595 600 605

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu
610 615 620

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
625 630 635 640

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
645 650 655

Leu Ser Pro Gly Lys
660

<210> 38
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> BC28 1x2 domain R

<400> 38

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105

<210> 39
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> BC28 1x2 domain S

<400> 39

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

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
20 25 30

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
35 40 45

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
50 55 60

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
65 70 75 80

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
85 90 95

Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 40
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> BC28 1x2 linker

<400> 40

Gly Ser Gly Ser Gly Ser
1 5

<210> 41

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> BC28 1x2 domain H

<400> 41

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

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

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

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

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Ser Asn Trp Pro Arg
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 42

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> BC28 1x2 domain I

<400> 42

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

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

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 43
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> BC28 1x2 domain J

<400> 43

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

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

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105 110

<210> 44
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> BC28 1x2 domain K

<400> 44

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

Glu Met Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe
20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60

Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 45
<211> 661
<212> PRT
<213> Artificial Sequence

<220>

<223> BC28-1x1x1a chain 3

<400> 45

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Ser Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Ser Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Arg Asp Ser Tyr Leu Trp
85 90 95

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

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
115 120 125

Gln Val Ser Leu Lys Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
130 135 140

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
145 150 155 160

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
165 170 175

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
180 185 190

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
195 200 205

Ser Leu Ser Lys Ser Cys Gly Ser Gly Ser Gly Ser Glu Ile Val Leu
210 215 220

Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
225 230 235 240

Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala Trp Tyr
245 250 255

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser
260 265 270

Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
275 280 285

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala
290 295 300

Val Tyr Tyr Cys Gln Gln Ser Ser Asn Trp Pro Arg Thr Phe Gly Gln
305 310 315 320

Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
325 330 335

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
340 345 350

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
355 360 365

Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr
370 375 380

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
385 390 395 400

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
405 410 415

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
420 425 430

Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
435 440 445

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
450 455 460

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
465 470 475 480

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
485 490 495

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
500 505 510

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
515 520 525

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
530 535 540

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
545 550 555 560

Gln Val Cys Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
565 570 575

Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
580 585 590

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
595 600 605

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu
610 615 620

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
625 630 635 640

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
645 650 655

Leu Ser Pro Gly Lys
660

<210> 46
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> BC28-1x1x1a domain R

<400> 46

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Ser Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Ser Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Arg Asp Ser Tyr Leu Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105

<210> 47
<211> 105
<212> PRT
<213> Artificial Sequence

<220>

<223> BC28-1x1x1a domain S

<400> 47

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
1 5 10 15

Thr Lys Asn Gln Val Ser Leu Lys Cys Leu Val Lys Gly Phe Tyr Pro
20 25 30

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
35 40 45

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
50 55 60

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
65 70 75 80

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
85 90 95

Lys Ser Leu Ser Leu Ser Lys Ser Cys
100 105

<210> 48

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> BC28-1x1x1a linker

<400> 48

Gly Ser Gly Ser Gly Ser
1 5

<210> 49

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> BC28-1x1x1a domain H

<400> 49

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

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

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

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

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Ser Asn Trp Pro Arg
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 50

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> BC28-1x1x1a domain I

<400> 50

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

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

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 51
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> BC28-1x1x1a domain J

<400> 51

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

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

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105 110

<210> 52
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> BC28-1x1x1a domain K

<400> 52

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

Glu Met Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe
20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60

Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 53
<211> 224
<212> PRT
<213> Artificial Sequence

<220>
<223> hCTLA4-4.chain 2

<400> 53

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

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

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

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

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

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

Val Thr Val Ser Ser Ala Ser Pro Arg Glu Pro Gln Val Tyr Thr Asp
115 120 125

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
130 135 140

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
145 150 155 160

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
165 170 175

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

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
195 200 205

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Gly Glu Cys
210 215 220

<210> 54
<211> 119
<212> PRT
<213> Artificial Sequence

<220>

<223> hCTLA4-4 domain F

<400> 54

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

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

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

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

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

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

Val Thr Val Ser Ser Ala Ser
115

<210> 55

<211> 105

<212> PRT

<213> Artificial Sequence

<220>

<223> hCTLA4-4 domain G

<400> 55

Pro Arg Glu Pro Gln Val Tyr Thr Asp Pro Pro Ser Arg Asp Glu Leu
1 5 10 15

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
20 25 30

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
35 40 45

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
50 55 60

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
65 70 75 80

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
85 90 95

Lys Ser Leu Ser Leu Ser Gly Glu Cys
100 105

<210> 56
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge

<400> 56

Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10

<210> 57
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> BC1, BC5, BC6, BC13, BC14, BC24, BC25, BC28, BC30, and BC45,
Polypeptide 1 Domain Junction

<400> 57

Ile Lys Arg Thr Pro Arg Glu Pro
1 5

<210> 58
<211> 8
<212> PRT

<213> Artificial Sequence

<220>

<223> BC15 and BC44 Polypeptide 1 Domain Junction

<400> 58

Ile Lys Arg Thr Val Arg Glu Pro
1 5

<210> 59

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> BC16-Polypeptide 1 Domain Junction

<400> 59

Ile Lys Arg Thr Arg Glu Pro
1 5

<210> 60

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> BC17-Polypeptide 1 Domain Junction

<400> 60

Ile Lys Arg Thr Val Pro Arg Glu Pro
1 5

<210> 61

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> BC26-Polypeptide 1 Domain Junction

<400> 61

Ile Lys Arg Thr Val Ala Glu Pro
1 5

<210> 62

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

<220>
<223> BC27-Polypeptide 1 Domain Junction

<400> 62

Ile Lys Arg Thr Val Ala Pro Arg Glu Pro
1 5 10

<210> 63
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> BC1, BC5, BC6, BC15, BC16, BC17, BC26, BC27, BC28, BC30, BC44,
and BC45, Polypeptide 2 Domain Junction

<400> 63

Ser Ser Ala Ser Pro Arg Glu Pro
1 5

<210> 64
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> BC13-Polypeptide 2 Domain Junction

<400> 64

Ser Ser Ala Ser Thr Arg Glu Pro
1 5

<210> 65
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> BC14-Polypeptide 2 Domain Junction

<400> 65

Ser Ser Ala Ser Thr Pro Arg Glu Pro
1 5

<210> 66
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> BC24-Polypeptide 2 Domain Junction

<400> 66

Ser Ser Ala Ser Thr Lys Gly Glu Pro
1 5

<210> 67
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> BC25-Polypeptide 2 Domain Junction

<400> 67

Ser Ser Ala Ser Thr Lys Gly Arg Glu Pro
1 5 10

<210> 68
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> SP34-89 VH

<400> 68

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

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

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

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

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

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
115 120

<210> 69

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> SP34-89 VL

<400> 69

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

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Trp Thr Pro Ala Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 70
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> SP34-89 VH-N30S VH, lower case denotes mutation

<400> 70

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

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

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

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

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
115 120

<210> 71
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> SP34-89 VH-G65D VH, lower case denotes mutation

<400> 71

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

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

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

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

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

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
115 120

<210> 72

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> SP34-89 VH-S68T VH, lower case denotes mutation

<400> 72

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

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

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

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

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

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
115 120

<210> 73
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> SP34-89 VL-W57G VL, lower case denotes mutation

<400> 73

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

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Thr Pro Ala Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 74
<211> 455
<212> PRT
<213> Artificial Sequence

<220>
<223> Phage display heavy chain

<220>
<221> misc_feature
<222> (30)..(33)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MISC_FEATURE
<222> (34)..(35)
<223> CDR sequences that were constant

<220>
<221> misc_feature
<222> (50)..(60)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MISC_FEATURE
<222> (61)..(67)
<223> CDR sequences that were constant

<220>
<221> misc_feature
<222> (100)..(112)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MISC_FEATURE
<222> (113)..(114)
<223> CDR sequences that were constant

<400> 74

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Xaa Xaa Xaa
20 25 30

Xaa Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Ala Asp Ser
 50 55 60

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

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

Cys Ala Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 100 105 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
 115 120 125

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Pro Gly Lys
450 455

<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Phage display light chain

<220>
<221> MISC_FEATURE
<222> (24)..(32)
<223> CDR sequences that were constant

<220>
<221> MISC_FEATURE
<222> (50)..(56)
<223> CDR sequences that were constant

<220>
<221> MISC_FEATURE
<222> (89)..(90)
<223> CDR sequences that were constant

<220>
<221> misc_feature
<222> (91)..(96)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MISC_FEATURE
<222> (97)..(98)
<223> CDR sequences that were constant

<400> 75

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Ser Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Ser Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
210

<210> 76
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> B-Body Domain A/H Scaffold

<220>
<221> MISC_FEATURE
<222> (24)..(32)
<223> CDR sequences that were constant

<220>
<221> MISC_FEATURE
<222> (50)..(56)

<223> CDR sequences that were constant

<220>

<221> MISC_FEATURE

<222> (89)..(90)

<223> CDR sequences that were constant

<220>

<221> misc_feature

<222> (91)..(96)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> MISC_FEATURE

<222> (97)..(98)

<223> CDR sequences that were constant

<400> 76

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Ser Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Ser Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105

<210> 77

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> B-Body Domain F/L Scaffold

<220>
<221> misc_feature
<222> (30)..(33)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MISC_FEATURE
<222> (34)..(35)
<223> CDR sequences that were constant

<220>
<221> misc_feature
<222> (50)..(60)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MISC_FEATURE
<222> (61)..(67)
<223> CDR sequences that were constant

<220>
<221> misc_feature
<222> (100)..(112)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MISC_FEATURE
<222> (113)..(114)
<223> CDR sequences that were constant

<400> 77

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Xaa Xaa Xaa
20 25 30

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

Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Ala Asp Ser
50 55 60

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

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

Cys Ala Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
115 120 125

<210> 78
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> BC1 Chain 1 Scaffold

<220>
<221> MISC_FEATURE
<222> (24)..(32)
<223> CDR sequences that were constant

<220>
<221> MISC_FEATURE
<222> (50)..(56)
<223> CDR sequences that were constant

<220>
<221> MISC_FEATURE
<222> (89)..(90)
<223> CDR sequences that were constant

<220>
<221> misc_feature
<222> (91)..(96)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MISC_FEATURE
<222> (97)..(98)
<223> CDR sequences that were constant

<400> 78

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Ser Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Ser Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95

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

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
115 120 125

Gln Val Ser Leu Lys Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
130 135 140

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
145 150 155 160

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
165 170 175

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
180 185 190

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
195 200 205

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
225 230 235 240

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
245 250 255

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
260 265 270

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
275 280 285

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
290 295 300

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
305 310 315 320

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
325 330 335

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu
340 345 350

Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro
355 360 365

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
370 375 380

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
385 390 395 400

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
405 410 415

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
420 425 430

Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 79

<211> 232

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

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

Cys Ala Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Pro
115 120 125

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

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

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

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

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

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

Ser Leu Ser Leu Ser Gly Glu Cys
225 230

<210> 80
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> BC1 Chain 3 Scaffold

<220>
<221> MISC_FEATURE
<222> (24)..(32)
<223> CDR sequences that were constant

<220>
<221> MISC_FEATURE
<222> (50)..(56)
<223> CDR sequences that were constant

<220>
<221> MISC_FEATURE
<222> (89)..(90)
<223> CDR sequences that were constant

<220>
<221> misc_feature
<222> (91)..(96)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MISC_FEATURE
<222> (97)..(98)
<223> CDR sequences that were constant

<400> 80

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Ser Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Ser Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
210 215 220

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
225 230 235 240

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
245 250 255

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
260 265 270

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
275 280 285

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
290 295 300

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
305 310 315 320

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

325

330

335

Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Glu Glu Met
340 345 350

Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro
355 360 365

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
370 375 380

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
385 390 395 400

Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
405 410 415

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
420 425 430

Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 81

<211> 229

<212> PRT

<213> Artificial Sequence

<220>

<223> BC1 Chain 4 Scaffold

<220>

<221> misc_feature

<222> (30)..(33)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> MISC_FEATURE

<222> (34)..(35)

<223> CDR sequences that were constant

<220>

<221> misc_feature

<222> (50)..(60)

<223> Xaa can be any naturally occurring amino acid

<220>
<221> MISC_FEATURE
<222> (61)..(67)
<223> CDR sequences that were constant

<220>
<221> misc_feature
<222> (100)..(112)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> MISC_FEATURE
<222> (113)..(114)
<223> CDR sequences that were constant

<400> 81

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Xaa Xaa Xaa
20 25 30

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

Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Ala Asp Ser
50 55 60

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

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

Cys Ala Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
115 120 125

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

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

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

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

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

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

Pro Pro Lys Ser Cys
225

<210> 82
<211> 668
<212> PRT
<213> Artificial Sequence

<220>
<223> BC1 Chain 3 1(A)x2(B-A) SP34-89 Scaffold

<220>
<221> MISC_FEATURE
<222> (24)..(32)
<223> CDR sequences that were constant

<220>
<221> MISC_FEATURE
<222> (50)..(56)
<223> CDR sequences that were constant

<220>
<221> MISC_FEATURE
<222> (89)..(90)
<223> CDR sequences that were constant

<220>
<221> misc_feature
<222> (91)..(96)
<223> Xaa can be any naturally occurring amino acid

<220>

<221> MISC_FEATURE

<222> (97)..(98)

<223> CDR sequences that were constant

<400> 82

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Ser Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Ser Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95

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

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
115 120 125

Gln Val Ser Leu Lys Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
130 135 140

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
145 150 155 160

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
165 170 175

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
180 185 190

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
195 200 205

Ser Leu Ser Lys Ser Cys Thr Ala Ser Ser Gly Gly Ser Ser Ser Gly
210 215 220

Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
225 230 235 240

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
245 250 255

Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
260 265 270

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Trp Thr Pro Ala Arg Phe
275 280 285

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Thr Gly Ala
290 295 300

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
305 310 315 320

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Arg Thr
325 330 335

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
340 345 350

Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
355 360 365

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
370 375 380

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
385 390 395 400

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
405 410 415

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
420 425 430

Thr Lys Ser Phe Asn Arg Gly Glu Cys Asp Lys Thr His Thr Cys Pro
435 440 445

Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe
450 455 460

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
465 470 475 480

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
485 490 495

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
500 505 510

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
515 520 525

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
530 535 540

Ser Asn Lys Ala Leu Lys Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
545 550 555 560

Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg
565 570 575

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly
580 585 590

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
595 600 605

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
610 615 620

Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
625 630 635 640

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
645 650 655

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
660 665

<210> 83
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> BC1 Chain 3 1(A)x2(B-A) SP34-89 S-H Junction

<400> 83

Thr Ala Ser Ser Gly Gly Ser Ser Ser Gly
1 5 10

<210> 84
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 Chain 1 BC1 1x1

<400> 84

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Ser Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Ser Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Tyr Tyr Pro Gly
85 90 95

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

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
115 120 125

Gln Val Ser Leu Lys Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
130 135 140

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
145 150 155 160

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
165 170 175

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
180 185 190

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
195 200 205

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

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
225 230 235 240

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
245 250 255

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
260 265 270

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
275 280 285

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
290 295 300

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
305 310 315 320

Ala Leu Lys Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
325 330 335

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu
340 345 350

Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro
355 360 365

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
370 375 380

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
385 390 395 400

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
405 410 415

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
420 425 430

Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 85
<211> 223
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 Chain 2 BC1 1x1

<400> 85

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ala Gly Ile Tyr Pro Ser Asp Gly Tyr Thr Ser Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Tyr Tyr Ser Gly Met Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser Ala Ser Pro Arg Glu Pro Gln Val Tyr Thr Asp Pro
115 120 125

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
130 135 140

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
145 150 155 160

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

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

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
195 200 205

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Gly Glu Cys
210 215 220

<210> 86
<211> 444

<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 Chain 3 BC1 1x1

<400> 86

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

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Trp Thr Pro Ala Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Arg Thr
100 105 110

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

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

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

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

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

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

Thr Lys Ser Phe Asn Arg Gly Glu Cys Asp Lys Thr His Thr Cys Pro
210 215 220

Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe
225 230 235 240

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

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
260 265 270

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

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
290 295 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305 310 315 320

Ser Asn Lys Ala Leu Lys Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
325 330 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg
340 345 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly
355 360 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
370 375 380

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

Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 87
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 Chain 4 BC1 1x1

<400> 87

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

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

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

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

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

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
115 120 125

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

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

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

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

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

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

Pro Pro Lys Ser Cys
225

<210> 88
<211> 668
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 Chain 3 BC1 1x2

<400> 88

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Ser Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Ser Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Tyr Tyr Pro Gly
85 90 95

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

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
115 120 125

Gln Val Ser Leu Lys Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
130 135 140

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
145 150 155 160

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
165 170 175

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
180 185 190

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
195 200 205

Ser Leu Ser Lys Ser Cys Thr Ala Ser Ser Gly Gly Ser Ser Ser Gly
210 215 220

Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
225 230 235 240

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
245 250 255

Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
260 265 270

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Trp Thr Pro Ala Arg Phe
275 280 285

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Thr Gly Ala
290 295 300

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
305 310 315 320

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Arg Thr
325 330 335

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
340 345 350

Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
355 360 365

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
370 375 380

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
385 390 395 400

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
405 410 415

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
420 425 430

Thr Lys Ser Phe Asn Arg Gly Glu Cys Asp Lys Thr His Thr Cys Pro
435 440 445

Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe
450 455 460

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
465 470 475 480

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
485 490 495

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
500 505 510

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
515 520 525

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
530 535 540

Ser Asn Lys Ala Leu Lys Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
545 550 555 560

Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg
565 570 575

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly
580 585 590

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
595 600 605

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
610 615 620

Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
625 630 635 640

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
645 650 655

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
660 665

<210> 89

<211> 441

<212> PRT

<213> Artificial Sequence

<220>

<223> I2A-27 Chain 1 BC1 1x1

<400> 89

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Ser Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Ser Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

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

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

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
115 120 125

Gln Val Ser Leu Lys Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
130 135 140

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
145 150 155 160

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
165 170 175

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
180 185 190

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
195 200 205

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

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
225 230 235 240

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
245 250 255

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
260 265 270

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
275 280 285

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
290 295 300

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
305 310 315 320

Ala Leu Lys Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
325 330 335

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu
340 345 350

Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro
355 360 365

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
370 375 380

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
385 390 395 400

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
405 410 415

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
420 425 430

Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 90
<211> 225
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-27 Chain 2 BC1 1x1

<400> 90

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

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

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

Ala Ala Ile Tyr Pro Tyr Gly Gly Ser Thr Asp Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Val Tyr Ile Tyr Gly Val Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Pro Arg Glu Pro Gln Val Tyr Thr
115 120 125

Asp Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
130 135 140

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

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
165 170 175

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

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
195 200 205

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Gly Glu
210 215 220

Cys
225

<210> 91
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-27 Chain 3 BC1 1x1

<400> 91

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

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Trp Thr Pro Ala Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Arg Thr
100 105 110

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

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

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

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

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

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

Thr Lys Ser Phe Asn Arg Gly Glu Cys Asp Lys Thr His Thr Cys Pro
210 215 220

Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe
225 230 235 240

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

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
260 265 270

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

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
290 295 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305 310 315 320

Ser Asn Lys Ala Leu Lys Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
325 330 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg
340 345 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly
355 360 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
370 375 380

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

Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 92
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-27 Chain 4 BC1 1x1

<400> 92

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

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

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

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

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

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
115 120 125

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

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

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

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

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

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

Pro Pro Lys Ser Cys
225

<210> 93
<211> 668
<212> PRT
<213> Artificial Sequence

<220>

<223> I2A-27 Chain 3 BC1 1x2

<400> 93

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Ser Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Ser Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

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

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

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
115 120 125

Gln Val Ser Leu Lys Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
130 135 140

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
145 150 155 160

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
165 170 175

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
180 185 190

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
195 200 205

Ser Leu Ser Lys Ser Cys Thr Ala Ser Ser Gly Gly Ser Ser Ser Gly
210 215 220

Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
225 230 235 240

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
245 250 255

Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
260 265 270

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Trp Thr Pro Ala Arg Phe
275 280 285

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Thr Gly Ala
290 295 300

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
305 310 315 320

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Arg Thr
325 330 335

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
340 345 350

Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
355 360 365

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
370 375 380

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
385 390 395 400

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
405 410 415

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
420 425 430

Thr Lys Ser Phe Asn Arg Gly Glu Cys Asp Lys Thr His Thr Cys Pro
435 440 445

Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe
450 455 460

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
465 470 475 480

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
485 490 495

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
500 505 510

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
515 520 525

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
530 535 540

Ser Asn Lys Ala Leu Lys Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
545 550 555 560

Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg
565 570 575

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly
580 585 590

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
595 600 605

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
610 615 620

Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
625 630 635 640

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
645 650 655

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
660 665

<210> 94

<211> 937

<212> PRT

<213> Homo sapiens

<220>

<223> Human ROR1 (UniProt accession #Q01973)

<400> 94

Met His Arg Pro Arg Arg Arg Gly Thr Arg Pro Pro Leu Leu Ala Leu
1 5 10 15

Leu Ala Ala Leu Leu Leu Ala Ala Arg Gly Ala Ala Ala Gln Glu Thr
20 25 30

Glu Leu Ser Val Ser Ala Glu Leu Val Pro Thr Ser Ser Trp Asn Ile
35 40 45

Ser Ser Glu Leu Asn Lys Asp Ser Tyr Leu Thr Leu Asp Glu Pro Met
50 55 60

Asn Asn Ile Thr Thr Ser Leu Gly Gln Thr Ala Glu Leu His Cys Lys
65 70 75 80

Val Ser Gly Asn Pro Pro Pro Thr Ile Arg Trp Phe Lys Asn Asp Ala
85 90 95

Pro Val Val Gln Glu Pro Arg Arg Leu Ser Phe Arg Ser Thr Ile Tyr
100 105 110

Gly Ser Arg Leu Arg Ile Arg Asn Leu Asp Thr Thr Asp Thr Gly Tyr
115 120 125

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

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

Ser Asp Glu Tyr Glu Glu Asp Gly Phe Cys Gln Pro Tyr Arg Gly Ile
165 170 175

Ala Cys Ala Arg Phe Ile Gly Asn Arg Thr Val Tyr Met Glu Ser Leu
180 185 190

His Met Gln Gly Glu Ile Glu Asn Gln Ile Thr Ala Ala Phe Thr Met
195 200 205

Ile Gly Thr Ser Ser His Leu Ser Asp Lys Cys Ser Gln Phe Ala Ile
210 215 220

Pro Ser Leu Cys His Tyr Ala Phe Pro Tyr Cys Asp Glu Thr Ser Ser
225 230 235 240

Val Pro Lys Pro Arg Asp Leu Cys Arg Asp Glu Cys Glu Ile Leu Glu
245 250 255

Asn Val Leu Cys Gln Thr Glu Tyr Ile Phe Ala Arg Ser Asn Pro Met
260 265 270

Ile Leu Met Arg Leu Lys Leu Pro Asn Cys Glu Asp Leu Pro Gln Pro
275 280 285

Glu Ser Pro Glu Ala Ala Asn Cys Ile Arg Ile Gly Ile Pro Met Ala
290 295 300

Asp Pro Ile Asn Lys Asn His Lys Cys Tyr Asn Ser Thr Gly Val Asp
305 310 315 320

Tyr Arg Gly Thr Val Ser Val Thr Lys Ser Gly Arg Gln Cys Gln Pro
325 330 335

Trp Asn Ser Gln Tyr Pro His Thr His Thr Phe Thr Ala Leu Arg Phe
340 345 350

Pro Glu Leu Asn Gly Gly His Ser Tyr Cys Arg Asn Pro Gly Asn Gln
355 360 365

Lys Glu Ala Pro Trp Cys Phe Thr Leu Asp Glu Asn Phe Lys Ser Asp
370 375 380

Leu Cys Asp Ile Pro Ala Cys Asp Ser Lys Asp Ser Lys Glu Lys Asn
385 390 395 400

Lys Met Glu Ile Leu Tyr Ile Leu Val Pro Ser Val Ala Ile Pro Leu
405 410 415

Ala Ile Ala Leu Leu Phe Phe Phe Ile Cys Val Cys Arg Asn Asn Gln
420 425 430

Lys Ser Ser Ser Ala Pro Val Gln Arg Gln Pro Lys His Val Arg Gly
435 440 445

Gln Asn Val Glu Met Ser Met Leu Asn Ala Tyr Lys Pro Lys Ser Lys
450 455 460

Ala Lys Glu Leu Pro Leu Ser Ala Val Arg Phe Met Glu Glu Leu Gly
465 470 475 480

Glu Cys Ala Phe Gly Lys Ile Tyr Lys Gly His Leu Tyr Leu Pro Gly
485 490 495

Met Asp His Ala Gln Leu Val Ala Ile Lys Thr Leu Lys Asp Tyr Asn
500 505 510

Asn Pro Gln Gln Trp Thr Glu Phe Gln Gln Glu Ala Ser Leu Met Ala
515 520 525

Glu Leu His His Pro Asn Ile Val Cys Leu Leu Gly Ala Val Thr Gln
530 535 540

Glu Gln Pro Val Cys Met Leu Phe Glu Tyr Ile Asn Gln Gly Asp Leu
545 550 555 560

His Glu Phe Leu Ile Met Arg Ser Pro His Ser Asp Val Gly Cys Ser
565 570 575

Ser Asp Glu Asp Gly Thr Val Lys Ser Ser Leu Asp His Gly Asp Phe
580 585 590

Leu His Ile Ala Ile Gln Ile Ala Ala Gly Met Glu Tyr Leu Ser Ser
595 600 605

His Phe Phe Val His Lys Asp Leu Ala Ala Arg Asn Ile Leu Ile Gly
610 615 620

Glu Gln Leu His Val Lys Ile Ser Asp Leu Gly Leu Ser Arg Glu Ile
625 630 635 640

Tyr Ser Ala Asp Tyr Tyr Arg Val Gln Ser Lys Ser Leu Leu Pro Ile
645 650 655

Arg Trp Met Pro Pro Glu Ala Ile Met Tyr Gly Lys Phe Ser Ser Asp
660 665 670

Ser Asp Ile Trp Ser Phe Gly Val Val Leu Trp Glu Ile Phe Ser Phe
675 680 685

Gly Leu Gln Pro Tyr Tyr Gly Phe Ser Asn Gln Glu Val Ile Glu Met
690 695 700

Val Arg Lys Arg Gln Leu Leu Pro Cys Ser Glu Asp Cys Pro Pro Arg
705 710 715 720

Met Tyr Ser Leu Met Thr Glu Cys Trp Asn Glu Ile Pro Ser Arg Arg
725 730 735

Pro Arg Phe Lys Asp Ile His Val Arg Leu Arg Ser Trp Glu Gly Leu
740 745 750

Ser Ser His Thr Ser Ser Thr Thr Pro Ser Gly Gly Asn Ala Thr Thr
755 760 765

Gln Thr Thr Ser Leu Ser Ala Ser Pro Val Ser Asn Leu Ser Asn Pro
770 775 780

Arg Tyr Pro Asn Tyr Met Phe Pro Ser Gln Gly Ile Thr Pro Gln Gly
785 790 795 800

Gln Ile Ala Gly Phe Ile Gly Pro Pro Ile Pro Gln Asn Gln Arg Phe
805 810 815

Ile Pro Ile Asn Gly Tyr Pro Ile Pro Pro Gly Tyr Ala Ala Phe Pro
820 825 830

Ala Ala His Tyr Gln Pro Thr Gly Pro Pro Arg Val Ile Gln His Cys
835 840 845

Pro Pro Pro Lys Ser Arg Ser Pro Ser Ser Ala Ser Gly Ser Thr Ser
850 855 860

Thr Gly His Val Thr Ser Leu Pro Ser Ser Gly Ser Asn Gln Glu Ala
865 870 875 880

Asn Ile Pro Leu Leu Pro His Met Ser Ile Pro Asn His Pro Gly Gly
885 890 895

Met Gly Ile Thr Val Phe Gly Asn Lys Ser Gln Lys Pro Tyr Lys Ile
900 905 910

Asp Ser Lys Gln Ala Ser Leu Leu Gly Asp Ala Asn Ile His Gly His
915 920 925

Thr Glu Ser Met Ile Ser Ala Glu Leu
930 935

<210> 95
<211> 943
<212> PRT
<213> Homo sapiens

<220>
<223> Human ROR2 (UniProt accession #Q01974)

<400> 95

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

Ala Val Trp Ala Ala Ala Ala Leu Leu Leu Ser Val Ser Arg Thr Ser
20 25 30

Gly Glu Val Glu Val Leu Asp Pro Asn Asp Pro Leu Gly Pro Leu Asp
35 40 45

Gly Gln Asp Gly Pro Ile Pro Thr Leu Lys Gly Tyr Phe Leu Asn Phe
50 55 60

Leu Glu Pro Val Asn Asn Ile Thr Ile Val Gln Gly Gln Thr Ala Ile
65 70 75 80

Leu His Cys Lys Val Ala Gly Asn Pro Pro Pro Asn Val Arg Trp Leu
85 90 95

Lys Asn Asp Ala Pro Val Val Gln Glu Pro Arg Arg Ile Ile Ile Arg
100 105 110

Lys Thr Glu Tyr Gly Ser Arg Leu Arg Ile Gln Asp Leu Asp Thr Thr
115 120 125

Asp Thr Gly Tyr Tyr Gln Cys Val Ala Thr Asn Gly Met Lys Thr Ile
130 135 140

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

Asn His Asn Phe Gln Asp Asp Tyr His Glu Asp Gly Phe Cys Gln Pro
165 170 175

Tyr Arg Gly Ile Ala Cys Ala Arg Phe Ile Gly Asn Arg Thr Ile Tyr
180 185 190

Val Asp Ser Leu Gln Met Gln Gly Glu Ile Glu Asn Arg Ile Thr Ala
195 200 205

Ala Phe Thr Met Ile Gly Thr Ser Thr His Leu Ser Asp Gln Cys Ser
210 215 220

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

Ala Arg Ser Arg Thr Pro Lys Pro Arg Glu Leu Cys Arg Asp Glu Cys
245 250 255

Glu Val Leu Glu Ser Asp Leu Cys Arg Gln Glu Tyr Thr Ile Ala Arg
260 265 270

Ser Asn Pro Leu Ile Leu Met Arg Leu Gln Leu Pro Lys Cys Glu Ala
275 280 285

Leu Pro Met Pro Glu Ser Pro Asp Ala Ala Asn Cys Met Arg Ile Gly
290 295 300

Ile Pro Ala Glu Arg Leu Gly Arg Tyr His Gln Cys Tyr Asn Gly Ser
305 310 315 320

Gly Met Asp Tyr Arg Gly Thr Ala Ser Thr Thr Lys Ser Gly His Gln
325 330 335

Cys Gln Pro Trp Ala Leu Gln His Pro His Ser His His Leu Ser Ser
340 345 350

Thr Asp Phe Pro Glu Leu Gly Gly Gly His Ala Tyr Cys Arg Asn Pro
355 360 365

Gly Gly Gln Met Glu Gly Pro Trp Cys Phe Thr Gln Asn Lys Asn Val
370 375 380

Arg Met Glu Leu Cys Asp Val Pro Ser Cys Ser Pro Arg Asp Ser Ser
385 390 395 400

Lys Met Gly Ile Leu Tyr Ile Leu Val Pro Ser Ile Ala Ile Pro Leu
405 410 415

Val Ile Ala Cys Leu Phe Phe Leu Val Cys Met Cys Arg Asn Lys Gln
420 425 430

Lys Ala Ser Ala Ser Thr Pro Gln Arg Arg Gln Leu Met Ala Ser Pro
435 440 445

Ser Gln Asp Met Glu Met Pro Leu Ile Asn Gln His Lys Gln Ala Lys
450 455 460

Leu Lys Glu Ile Ser Leu Ser Ala Val Arg Phe Met Glu Glu Leu Gly
465 470 475 480

Glu Asp Arg Phe Gly Lys Val Tyr Lys Gly His Leu Phe Gly Pro Ala
485 490 495

Pro Gly Glu Gln Thr Gln Ala Val Ala Ile Lys Thr Leu Lys Asp Lys
500 505 510

Ala Glu Gly Pro Leu Arg Glu Glu Phe Arg His Glu Ala Met Leu Arg
515 520 525

Ala Arg Leu Gln His Pro Asn Val Val Cys Leu Leu Gly Val Val Thr
530 535 540

Lys Asp Gln Pro Leu Ser Met Ile Phe Ser Tyr Cys Ser His Gly Asp
545 550 555 560

Leu His Glu Phe Leu Val Met Arg Ser Pro His Ser Asp Val Gly Ser
565 570 575

Thr Asp Asp Asp Arg Thr Val Lys Ser Ala Leu Glu Pro Pro Asp Phe
580 585 590

Val His Leu Val Ala Gln Ile Ala Ala Gly Met Glu Tyr Leu Ser Ser
595 600 605

His His Val Val His Lys Asp Leu Ala Thr Arg Asn Val Leu Val Tyr
610 615 620

Asp Lys Leu Asn Val Lys Ile Ser Asp Leu Gly Leu Phe Arg Glu Val
625 630 635 640

Tyr Ala Ala Asp Tyr Tyr Lys Leu Leu Gly Asn Ser Leu Leu Pro Ile
645 650 655

Arg Trp Met Ala Pro Glu Ala Ile Met Tyr Gly Lys Phe Ser Ile Asp
660 665 670

Ser Asp Ile Trp Ser Tyr Gly Val Val Leu Trp Glu Val Phe Ser Tyr
675 680 685

Gly Leu Gln Pro Tyr Cys Gly Tyr Ser Asn Gln Asp Val Val Glu Met
690 695 700

Ile Arg Asn Arg Gln Val Leu Pro Cys Pro Asp Asp Cys Pro Ala Trp
705 710 715 720

Val Tyr Ala Leu Met Ile Glu Cys Trp Asn Glu Phe Pro Ser Arg Arg
725 730 735

Pro Arg Phe Lys Asp Ile His Ser Arg Leu Arg Ala Trp Gly Asn Leu
740 745 750

Ser Asn Tyr Asn Ser Ser Ala Gln Thr Ser Gly Ala Ser Asn Thr Thr
755 760 765

Gln Thr Ser Ser Leu Ser Thr Ser Pro Val Ser Asn Val Ser Asn Ala
770 775 780

Arg Tyr Val Gly Pro Lys Gln Lys Ala Pro Pro Phe Pro Gln Pro Gln
785 790 795 800

Phe Ile Pro Met Lys Gly Gln Ile Arg Pro Met Val Pro Pro Pro Gln
805 810 815

Leu Tyr Val Pro Val Asn Gly Tyr Gln Pro Val Pro Ala Tyr Gly Ala
820 825 830

Tyr Leu Pro Asn Phe Tyr Pro Val Gln Ile Pro Met Gln Met Ala Pro
835 840 845

Gln Gln Val Pro Pro Gln Met Val Pro Lys Pro Ser Ser His His Ser
850 855 860

Gly Ser Gly Ser Thr Ser Thr Gly Tyr Val Thr Thr Ala Pro Ser Asn
865 870 875 880

Thr Ser Met Ala Asp Arg Ala Ala Leu Leu Ser Glu Gly Ala Asp Asp
885 890 895

Thr Gln Asn Ala Pro Glu Asp Gly Ala Gln Ser Thr Val Gln Glu Ala
900 905 910

Glu Glu Glu Glu Glu Gly Ser Val Pro Glu Thr Glu Leu Leu Gly Asp
915 920 925

Cys Asp Thr Leu Gln Val Asp Glu Ala Gln Val Gln Leu Glu Ala
930 935 940

<210> 96
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-27 Chain 1

<400> 96

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Ser Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Ser Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

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

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

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
115 120 125

Gln Val Ser Leu Lys Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
130 135 140

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
145 150 155 160

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
165 170 175

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
180 185 190

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
195 200 205

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

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
225 230 235 240

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
245 250 255

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
260 265 270

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
275 280 285

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
290 295 300

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
305 310 315 320

Ala Leu Lys Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
325 330 335

Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Glu Glu Met
340 345 350

Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro
355 360 365

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
370 375 380

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
385 390 395 400

Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
405 410 415

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
420 425 430

Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 97

<211> 225

<212> PRT

<213> Artificial Sequence

<220>

<223> I2A-27 Chain 2 or Chain 5

<400> 97

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

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

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

Ala Ala Ile Tyr Pro Tyr Gly Gly Ser Thr Asp Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Val Tyr Ile Tyr Gly Val Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Pro Arg Glu Pro Gln Val Tyr Thr
115 120 125

Asp Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
130 135 140

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

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
165 170 175

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

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
195 200 205

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Gly Glu
210 215 220

Cys
225

<210> 98
<211> 668
<212> PRT
<213> Artificial Sequence

<220>

<223> I2A-27 Chain 3

<400> 98

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Ser Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Ser Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

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

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

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
115 120 125

Gln Val Ser Leu Lys Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
130 135 140

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
145 150 155 160

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
165 170 175

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
180 185 190

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
195 200 205

Ser Leu Ser Lys Ser Cys Thr Ala Ser Ser Gly Gly Ser Ser Ser Gly
210 215 220

Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
225 230 235 240

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
245 250 255

Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
260 265 270

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Trp Thr Pro Ala Arg Phe
275 280 285

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Thr Gly Ala
290 295 300

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
305 310 315 320

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Arg Thr
325 330 335

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
340 345 350

Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
355 360 365

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
370 375 380

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
385 390 395 400

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
405 410 415

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
420 425 430

Thr Lys Ser Phe Asn Arg Gly Glu Cys Asp Lys Thr His Thr Cys Pro
435 440 445

Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe
450 455 460

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
465 470 475 480

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
485 490 495

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
500 505 510

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
515 520 525

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
530 535 540

Ser Asn Lys Ala Leu Lys Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
545 550 555 560

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg
565 570 575

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly
580 585 590

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
595 600 605

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
610 615 620

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
625 630 635 640

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
645 650 655

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
660 665

<210> 99
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-27 Chain 4

<400> 99

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

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

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

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

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

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
115 120 125

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

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

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

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

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

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

Pro Pro Lys Ser Cys
225

<210> 100
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-27 Domain A

<400> 100

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Ser Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Ser Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105

<210> 101
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-27 Domain B

<400> 101

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
1 5 10 15

Thr Lys Asn Gln Val Ser Leu Lys Cys Leu Val Lys Gly Phe Tyr Pro
20 25 30

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
35 40 45

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
50 55 60

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
65 70 75 80

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
85 90 95

Lys Ser Leu Ser Leu Ser Lys Ser Cys
100 105

<210> 102
<211> 110
<212> PRT
<213> Artificial Sequence

<220>

<223> I2A-27 Domain D

<400> 102

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

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

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Ala Leu Lys Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105 110

<210> 103

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> I2A-27 Domain E

<400> 103

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

Glu Met Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe
20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60

Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 104
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-27 Domain F or Domain T

<400> 104

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

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

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

Ala Ala Ile Tyr Pro Tyr Gly Gly Ser Thr Asp Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Val Tyr Ile Tyr Gly Val Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser
115 120

<210> 105
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-27 Domain G or Domain U

<400> 105

Pro Arg Glu Pro Gln Val Tyr Thr Asp Pro Pro Ser Arg Asp Glu Leu
1 5 10 15

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
20 25 30

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
35 40 45

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
50 55 60

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
65 70 75 80

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
85 90 95

Lys Ser Leu Ser Leu Ser Gly Glu Cys
100 105

<210> 106
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-27 Domain R

<400> 106

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Ser Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Ser Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105

<210> 107
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-27 Domain S

<400> 107

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
1 5 10 15

Thr Lys Asn Gln Val Ser Leu Lys Cys Leu Val Lys Gly Phe Tyr Pro
20 25 30

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
35 40 45

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
50 55 60

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
65 70 75 80

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
85 90 95

Lys Ser Leu Ser Leu Ser Lys Ser Cys
100 105

<210> 108
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-27 Domain H

<400> 108

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

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Trp Thr Pro Ala Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Arg Thr
100 105 110

Val

<210> 109
<211> 104

<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-27 Domain I

<400> 109

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
1 5 10 15

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

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
35 40 45

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
50 55 60

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
65 70 75 80

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
85 90 95

Lys Ser Phe Asn Arg Gly Glu Cys
100

<210> 110
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-27 Domain J

<400> 110

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

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

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Ala Leu Lys Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105 110

<210> 111
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-27 Domain K

<400> 111

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp
1 5 10 15

Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe
20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 112
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-27 Domain L

<400> 112

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

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

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

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

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

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
115 120 125

<210> 113
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-27 Domain M

<400> 113

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
1 5 10 15

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

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
35 40 45

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
50 55 60

Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
65 70 75 80

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
85 90 95

Glu Pro Pro Lys Ser Cys
100

<210> 114

<211> 441

<212> PRT

<213> Artificial Sequence

<220>

<223> I2A-10 Chain 1

<400> 114

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Ser Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Ser Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Tyr Tyr Pro Gly
85 90 95

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

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
115 120 125

Gln Val Ser Leu Lys Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
130 135 140

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
145 150 155 160

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
165 170 175

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
180 185 190

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
195 200 205

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

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
225 230 235 240

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
245 250 255

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
260 265 270

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
275 280 285

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
290 295 300

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
305 310 315 320

Ala Leu Lys Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
325 330 335

Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Glu Glu Met
340 345 350

Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro
355 360 365

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
370 375 380

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
385 390 395 400

Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
405 410 415

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
420 425 430

Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 115
<211> 224
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 Chain 2 or Chain 5

<400> 115

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ala Gly Ile Tyr Pro Ser Asp Gly Tyr Thr Ser Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Tyr Tyr Val Ser Gly Met Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser Ala Ser Pro Arg Glu Pro Gln Val Tyr Thr Asp
115 120 125

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
130 135 140

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
145 150 155 160

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
165 170 175

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

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
195 200 205

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Gly Glu Cys
210 215 220

<210> 116
<211> 668
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 Chain 3

<400> 116

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Ser Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Ser Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Tyr Tyr Pro Gly
85 90 95

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

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
115 120 125

Gln Val Ser Leu Lys Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
130 135 140

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
145 150 155 160

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
165 170 175

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
180 185 190

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
195 200 205

Ser Leu Ser Lys Ser Cys Thr Ala Ser Ser Gly Gly Ser Ser Ser Gly
210 215 220

Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
225 230 235 240

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
245 250 255

Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
260 265 270

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Trp Thr Pro Ala Arg Phe
275 280 285

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Thr Gly Ala
290 295 300

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
305 310 315 320

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Arg Thr
325 330 335

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
340 345 350

Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
355 360 365

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
370 375 380

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
385 390 395 400

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
405 410 415

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
420 425 430

Thr Lys Ser Phe Asn Arg Gly Glu Cys Asp Lys Thr His Thr Cys Pro
435 440 445

Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe
450 455 460

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
465 470 475 480

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
485 490 495

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
500 505 510

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
515 520 525

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
530 535 540

Ser Asn Lys Ala Leu Lys Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
545 550 555 560

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg
565 570 575

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly
580 585 590

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
595 600 605

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
610 615 620

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
625 630 635 640

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
645 650 655

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
660 665

<210> 117
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 Chain 4

<400> 117

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

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

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

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

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

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
115 120 125

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

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

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

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

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

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

Pro Pro Lys Ser Cys
225

<210> 118
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 Domain A

<400> 118

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Ser Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Ser Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Tyr Tyr Pro Gly
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105

<210> 119
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 Domain B

<400> 119

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
1 5 10 15

Thr Lys Asn Gln Val Ser Leu Lys Cys Leu Val Lys Gly Phe Tyr Pro
20 25 30

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
35 40 45

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
50 55 60

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
65 70 75 80

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
85 90 95

Lys Ser Leu Ser Leu Ser Lys Ser Cys
100 105

<210> 120
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 Domain D

<400> 120

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

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

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Ala Leu Lys Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105 110

<210> 121
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 Domain E

<400> 121

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

Glu Met Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe
20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60

Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 122
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 Domain F or Domain T

<400> 122

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ala Gly Ile Tyr Pro Ser Asp Gly Tyr Thr Ser Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Tyr Tyr Val Ser Gly Met Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser Ala Ser
115

<210> 123
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 Domain G or Domain U

<400> 123

Pro Arg Glu Pro Gln Val Tyr Thr Asp Pro Pro Ser Arg Asp Glu Leu
1 5 10 15

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
20 25 30

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
35 40 45

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
50 55 60

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
65 70 75 80

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
85 90 95

Lys Ser Leu Ser Leu Ser Gly Glu Cys
100 105

<210> 124
<211> 109
<212> PRT
<213> Artificial Sequence

<220>

<223> I2A-10 Domain R

<400> 124

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Ser Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Ser Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Tyr Tyr Pro Gly
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105

<210> 125

<211> 105

<212> PRT

<213> Artificial Sequence

<220>

<223> I2A-10 Domain S

<400> 125

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
1 5 10 15

Thr Lys Asn Gln Val Ser Leu Lys Cys Leu Val Lys Gly Phe Tyr Pro
20 25 30

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
35 40 45

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
50 55 60

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
65 70 75 80

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
85 90 95

Lys Ser Leu Ser Leu Ser Lys Ser Cys
100 105

<210> 126
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 Domain H

<400> 126

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

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Trp Thr Pro Ala Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Arg Thr
100 105 110

Val

<210> 127
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 Domain I

<400> 127

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
1 5 10 15

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

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
35 40 45

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
50 55 60

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
65 70 75 80

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
85 90 95

Lys Ser Phe Asn Arg Gly Glu Cys
100

<210> 128
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 Domain J

<400> 128

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

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

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Ala Leu Lys Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105 110

<210> 129
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 Domain K

<400> 129

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp
1 5 10 15

Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe
20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 130
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 Domain L

<400> 130

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

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

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

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

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

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
115 120 125

<210> 131
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 Domain M

<400> 131

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
1 5 10 15

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

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
35 40 45

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
50 55 60

Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
65 70 75 80

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
85 90 95

Glu Pro Pro Lys Ser Cys
100

<210> 132
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 D54E Y55Q Chain 1

<400> 132

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Ser Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Tyr Tyr Pro Gly
85 90 95

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

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
115 120 125

Gln Val Ser Leu Lys Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
130 135 140

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
145 150 155 160

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
165 170 175

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
180 185 190

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
195 200 205

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

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
225 230 235 240

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
245 250 255

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
260 265 270

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
275 280 285

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
290 295 300

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
305 310 315 320

Ala Leu Lys Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
325 330 335

Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Glu Glu Met
340 345 350

Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro
355 360 365

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
370 375 380

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
385 390 395 400

Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
405 410 415

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
420 425 430

Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 133

<211> 224

<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 D54E Y55Q Chain 2 or Chain 5

<400> 133

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ala Gly Ile Tyr Pro Ser Glu Gly Tyr Thr Ser Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Tyr Tyr Val Ser Gly Met Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser Ala Ser Pro Arg Glu Pro Gln Val Tyr Thr Asp
115 120 125

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
130 135 140

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
145 150 155 160

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
165 170 175

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

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
195 200 205

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Gly Glu Cys
210 215 220

<210> 134
<211> 668
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 D54E Y55Q Chain 3

<400> 134

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Ser Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Tyr Tyr Pro Gly
85 90 95

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

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
115 120 125

Gln Val Ser Leu Lys Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
130 135 140

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
145 150 155 160

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
165 170 175

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
180 185 190

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
195 200 205

Ser Leu Ser Lys Ser Cys Thr Ala Ser Ser Gly Gly Ser Ser Ser Gly
210 215 220

Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
225 230 235 240

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
245 250 255

Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
260 265 270

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Trp Thr Pro Ala Arg Phe
275 280 285

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Thr Gly Ala
290 295 300

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
305 310 315 320

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Arg Thr
325 330 335

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
340 345 350

Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
355 360 365

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
370 375 380

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
385 390 395 400

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
405 410 415

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
420 425 430

Thr Lys Ser Phe Asn Arg Gly Glu Cys Asp Lys Thr His Thr Cys Pro
435 440 445

Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe
450 455 460

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
465 470 475 480

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
485 490 495

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
500 505 510

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
515 520 525

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
530 535 540

Ser Asn Lys Ala Leu Lys Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
545 550 555 560

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg
565 570 575

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly
580 585 590

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
595 600 605

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
610 615 620

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
625 630 635 640

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
645 650 655

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
660 665

<210> 135

<211> 229

<212> PRT

<213> Artificial Sequence

<220>

<223> I2A-10 D54E Y55Q Chain 4

<400> 135

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

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

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

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

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

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
115 120 125

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

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

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

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

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

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

Pro Pro Lys Ser Cys
225

<210> 136
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 D54E Y55Q Domain A

<400> 136

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Ser Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Tyr Tyr Pro Gly
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105

<210> 137

<211> 105

<212> PRT

<213> Artificial Sequence

<220>

<223> I2A-10 D54E Y55Q Domain B

<400> 137

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
1 5 10 15

Thr Lys Asn Gln Val Ser Leu Lys Cys Leu Val Lys Gly Phe Tyr Pro
20 25 30

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
35 40 45

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
50 55 60

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
65 70 75 80

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
85 90 95

Lys Ser Leu Ser Leu Ser Lys Ser Cys
100 105

<210> 138
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 D54E Y55Q Domain D

<400> 138

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

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

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Ala Leu Lys Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105 110

<210> 139
<211> 107
<212> PRT
<213> Artificial Sequence

<220>

<223> I2A-10 D54E Y55Q Domain E

<400> 139

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

Glu Met Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe
20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60

Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 140

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> I2A-10 D54E Y55Q Domain F or Domain T

<400> 140

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ala Gly Ile Tyr Pro Ser Glu Gly Tyr Thr Ser Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Tyr Tyr Val Ser Gly Met Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser Ala Ser
115

<210> 141
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 D54E Y55Q Domain G or Domain U

<400> 141

Pro Arg Glu Pro Gln Val Tyr Thr Asp Pro Pro Ser Arg Asp Glu Leu
1 5 10 15

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
20 25 30

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
35 40 45

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
50 55 60

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
65 70 75 80

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
85 90 95

Lys Ser Leu Ser Leu Ser Gly Glu Cys
100 105

<210> 142
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 D54E Y55Q Domain R

<400> 142

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Ser Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Tyr Tyr Pro Gly
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105

<210> 143
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 D54E Y55Q Domain S

<400> 143

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
1 5 10 15

Thr Lys Asn Gln Val Ser Leu Lys Cys Leu Val Lys Gly Phe Tyr Pro
20 25 30

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
35 40 45

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
50 55 60

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
65 70 75 80

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
85 90 95

Lys Ser Leu Ser Leu Ser Lys Ser Cys
100 105

<210> 144
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 D54E Y55Q Domain H

<400> 144

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

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Trp Thr Pro Ala Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Arg Thr
100 105 110

Val

<210> 145
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 D54E Y55Q Domain I

<400> 145

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
1 5 10 15

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

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
35 40 45

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
50 55 60

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
65 70 75 80

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
85 90 95

Lys Ser Phe Asn Arg Gly Glu Cys
100

<210> 146
<211> 110

<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 D54E Y55Q Domain J

<400> 146

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

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

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Ala Leu Lys Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105 110

<210> 147
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 D54E Y55Q Domain K

<400> 147

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp
1 5 10 15

Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe
20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 148
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 D54E Y55Q Domain L

<400> 148

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

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

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

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

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

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
115 120 125

<210> 149
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> I2A-10 D54E Y55Q Domain M

<400> 149

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
1 5 10 15

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

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
35 40 45

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
50 55 60

Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
65 70 75 80

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
85 90 95

Glu Pro Pro Lys Ser Cys
100

<210> 150
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary signal sequence for I2A-27, I2A-10 and I2A-10 D54E
Y55Q, e.g., Chain 1

<400> 150

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

Val Leu Ser

<210> 151

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Exemplary signal sequence for I2A-27, I2A-10 and I2A-10 D54E Y55Q
, e.g., Chain 2, 3, 4 or 5

<400> 151

Met Asp Phe Gln Val Gln Ile Ile Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

Val Ile Met Ser Arg Gly
20

<210> 152

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Exemplary signal sequence for I2A-27, I2A-10 and I2A-10 D54E
Y55Q, e.g., Chain 3

<400> 152

Met Asp Phe Gln Val Gln Ile Ile Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

Val Ile Met Ser Arg Gly Ser
20

<210> 153

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 VH of I2A-1

<400> 153

Phe Ser Ser Tyr Phe Ile

1 5

<210> 154

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 VH of I2A-1

<400> 154

Ala Ile Tyr Pro Glu Gly Gly Tyr Thr Tyr

1 5 10

<210> 155

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 VH of I2A-1

<400> 155

Asp Tyr Lys Tyr Val Gly Ala Leu

1 5

<210> 156

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 VL of I2A-1

<400> 156

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala

1 5 10

<210> 157

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 VL of I2A-1

<400> 157

Ser Ala Ser Ser Leu Tyr Ser
1 5

<210> 158

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 VL of I2A-1

<400> 158

Tyr Tyr Tyr Phe Pro Gly
1 5

<210> 159

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 VH of I2A-2

<400> 159

Phe Ser Tyr Tyr Gly Ile
1 5

<210> 160

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 VH of I2A-2

<400> 160

Phe Ile Tyr Ser Arg Gly Gly Tyr Thr Ile
1 5 10

<210> 161

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

<220>
<223> CDR3 VH of I2A-2

<400> 161

Tyr Ile Gly Ala Gly Leu
1 5

<210> 162
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 VL of I2A-2

<400> 162

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

<210> 163
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 VL of I2A-2

<400> 163

Ser Ala Ser Ser Leu Tyr Ser
1 5

<210> 164
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 VL of I2A-2

<400> 164

Tyr Tyr Trp Asp Pro Ile
1 5

<210> 165
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 VH of I2A-3

<400> 165

Phe Thr Ser Tyr Glu Ile
1 5

<210> 166
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 VH of I2A-3

<400> 166

His Ile Asp Pro Tyr Gly Gly Tyr Thr Gln
1 5 10

<210> 167
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 VH of I2A-3

<400> 167

Arg Gly Val Ala Val Phe
1 5

<210> 168
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 VL of I2A-3

<400> 168

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala

1

5

10

<210> 169
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 VL of I2A-3

<400> 169

Ser Ala Ser Ser Leu Tyr Ser
1 5

<210> 170
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 VL of I2A-3

<400> 170

Trp Ala Tyr Ala Pro Val
1 5

<210> 171
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 VH of I2A-4

<400> 171

Phe Tyr Ser Tyr Asp Ile
1 5

<210> 172
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 VH of I2A-4

<400> 172

Tyr Ile Ser Pro Tyr Trp Gly Ile Thr Thr
1 5 10

<210> 173
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 VH of I2A-4

<400> 173

Tyr Ile Gly Ser Ser Tyr Trp Asp Ala Leu
1 5 10

<210> 174
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 VL of I2A-4

<400> 174

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

<210> 175
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 VL of I2A-4

<400> 175

Ser Ala Ser Ser Leu Tyr Ser
1 5

<210> 176
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 VL of I2A-4

<400> 176

Ser Asp Ser Ser Leu Val
1 5

<210> 177

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 VH of I2A-5

<400> 177

Phe Ser Ser Tyr Gly Ile
1 5

<210> 178

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 VH of I2A-5

<400> 178

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

<210> 179

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 VH of I2A-5

<400> 179

Ser Tyr Met Ile Tyr Gly Gly Leu
1 5

<210> 180

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 VL of I2A-5

<400> 180

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

<210> 181

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 VL of I2A-5

<400> 181

Ser Ala Ser Ser Leu Tyr Ser
1 5

<210> 182

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 VL of I2A-5

<400> 182

Arg Val Ser Ser Pro Trp
1 5

<210> 183

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 VH of I2A-6

<400> 183

Phe Ser Leu Tyr Ala Ile
1 5

<210> 184

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 VH of I2A-6

<400> 184

Glu	Ile	Asp	Ser	Trp	Leu	Gly	Tyr	Thr	Tyr
1				5					10

<210> 185

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 VH of I2A-6

<400> 185

Arg	Pro	Val	Thr	Glu	Val	Tyr	Tyr	Ser	Ala	Leu
1				5					10	

<210> 186

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 VL of I2A-6

<400> 186

Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ala	Val	Ala
1				5					10	

<210> 187

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 VL of I2A-6

<400> 187

Ser	Ala	Ser	Ser	Leu	Tyr	Ser
1				5		

<210> 188

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

<220>
<223> CDR3 VL of I2A-6

<400> 188

Tyr Asp Arg Ser Leu His
1 5

<210> 189
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 VH of I2A-7

<400> 189

Phe Ser Arg Tyr Tyr Ile
1 5

<210> 190
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 VH of I2A-7

<400> 190

Asp Ile Asp Ser Tyr Gly Gly Phe Thr Tyr
1 5 10

<210> 191
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 VH of I2A-7

<400> 191

Ala His Arg Phe Leu Gln Gly Gly Tyr Val Leu
1 5 10

<210> 192
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 VL of I2A-7

<400> 192

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

<210> 193
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 VL of I2A-7

<400> 193

Ser Ala Ser Ser Leu Tyr Ser
1 5

<210> 194
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 VL of I2A-7

<400> 194

Tyr Ser Trp Gly Leu Trp
1 5

<210> 195
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 VH of I2A-8

<400> 195

Phe Tyr Gly Tyr Tyr Ile

1 5

<210> 196
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 VH of I2A-8

<400> 196

Gly Ile Arg Pro Gly Gly Thr Tyr Thr Tyr
1 5 10

<210> 197
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 VH of I2A-8

<400> 197

Tyr Arg Tyr Pro Ala Phe
1 5

<210> 198
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 VL of I2A-8

<400> 198

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

<210> 199
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 VL of I2A-8

<400> 199

Ser Ala Ser Ser Leu Tyr Ser
1 5

<210> 200
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 VL of I2A-8

<400> 200

Arg Arg Gln His Leu Trp
1 5

<210> 201
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 VH of I2A-9

<400> 201

Phe Ser Ser Tyr Thr Ile
1 5

<210> 202
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 VH of I2A-9

<400> 202

Ala Ile Asp Ser Gly Trp Ser Tyr Thr Asp
1 5 10

<210> 203
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 VH of I2A-9

<400> 203

Ala Tyr Gly Gly Val Met
1 5

<210> 204

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 VL of I2A-9

<400> 204

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

<210> 205

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 VL of I2A-9

<400> 205

Ser Ala Ser Ser Leu Tyr Ser
1 5

<210> 206

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 VL of I2A-9

<400> 206

Tyr Trp Trp Pro Gly
1 5

<210> 207

<211> 6

<212> PRT

<213> Artificial Sequence

<220>
<223> CDR1 VH of I2A-10

<400> 207

Phe Ser Ser Tyr Phe Ile
1 5

<210> 208
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 VH of I2A-10

<400> 208

Gly Ile Tyr Pro Ser Asp Gly Tyr Thr Ser
1 5 10

<210> 209
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 VH of I2A-10

<400> 209

Tyr Tyr Val Ser Gly Met
1 5

<210> 210
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 VL of I2A-10

<400> 210

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

<210> 211
<211> 7
<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 VL of I2A-10

<400> 211

Ser Ala Ser Ser Leu Tyr Ser
1 5

<210> 212

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 VL of I2A-10

<400> 212

Tyr Tyr Tyr Tyr Pro Gly
1 5

<210> 213

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 VH of I2A-10 D54E Y55Q

<400> 213

Phe Ser Ser Tyr Phe Ile
1 5

<210> 214

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 VH of I2A-10 D54E Y55Q

<400> 214

Gly Ile Tyr Pro Ser Glu Gly Tyr Thr Ser
1 5 10

<210> 215

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

<220>
<223> CDR3 VH of I2A-10 D54E Y55Q

<400> 215

Tyr Tyr Val Ser Gly Met
1 5

<210> 216
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 VL of I2A-10 D54E Y55Q

<400> 216

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

<210> 217
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 VL of I2A-10 D54E Y55Q

<400> 217

Ser Ala Ser Ser Leu Gln Ser
1 5

<210> 218
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 VL of I2A-10 D54E Y55Q

<400> 218

Tyr Tyr Tyr Tyr Pro Gly
1 5

<210> 219
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 VH of I2A-11

<400> 219

Phe Ser Ser Tyr Val Ile
1 5

<210> 220
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 VH of I2A-11

<400> 220

Ala Ile Tyr Pro Tyr Thr Ser Ser Thr Gln
1 5 10

<210> 221
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 VH of I2A-11

<400> 221

Ser Tyr Gly Thr Gly Gly Phe
1 5

<210> 222
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 VL of I2A-11

<400> 222

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala

1

5

10

<210> 223
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 VL of I2A-11

<400> 223

Ser Ala Ser Ser Leu Tyr Ser
1 5

<210> 224
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 VL of I2A-11

<400> 224

Trp Tyr Ser Tyr Pro Leu
1 5

<210> 225
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 VH of I2A-12

<400> 225

Phe Thr Thr Tyr Tyr Ile
1 5

<210> 226
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 VH of I2A-12

<400> 226

Tyr Ile Ser Pro Glu Asp Gly Tyr Thr Ser
1 5 10

<210> 227
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 VH of I2A-12

<400> 227

Ala Tyr Tyr Ser Ala Val Met
1 5

<210> 228
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 VL of I2A-12

<400> 228

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

<210> 229
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 VL of I2A-12

<400> 229

Ser Ala Ser Ser Leu Tyr Ser
1 5

<210> 230
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 VL of I2A-12

<400> 230

Ser Trp Ser Pro Ala Thr
1 5

<210> 231

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 VH of I2A-13

<400> 231

Phe Ser Tyr Tyr Phe Ile
1 5

<210> 232

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 VH of I2A-13

<400> 232

Val Ile Tyr Pro Asp Gly Gly Tyr Thr Leu
1 5 10

<210> 233

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 VH of I2A-13

<400> 233

Ile Tyr Tyr Pro Ser Gly Ala Met
1 5

<210> 234

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 VL of I2A-13

<400> 234

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

<210> 235

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 VL of I2A-13

<400> 235

Ser Ala Ser Ser Leu Tyr Ser
1 5

<210> 236

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 VL of I2A-13

<400> 236

Thr Tyr Trp Tyr Pro Gly
1 5

<210> 237

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 VH of I2A-14

<400> 237

Phe Asp Ser Tyr Val Ile
1 5

<210> 238

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 VH of I2A-14

<400> 238

Tyr Ile Phe Ser Phe Gly Gly Tyr Thr Tyr
1 5 10

<210> 239

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 VH of I2A-14

<400> 239

Ser Pro Tyr Gly Thr Phe Ala Leu
1 5

<210> 240

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 VL of I2A-14

<400> 240

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

<210> 241

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 VL of I2A-14

<400> 241

Ser Ala Ser Ser Leu Tyr Ser
1 5

<210> 242

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

<220>
<223> CDR3 VL of I2A-14

<400> 242

Tyr Tyr Tyr Thr Pro Gly
1 5

<210> 243
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 VH of I2A-15

<400> 243

Phe Trp Gly Tyr Val Ile
1 5

<210> 244
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 VH of I2A-15

<400> 244

Ala Ile Asp Ser Trp Asp Gly Asp Thr Asp
1 5 10

<210> 245
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 VH of I2A-15

<400> 245

Ser Phe Tyr Tyr Ile Tyr Val Met
1 5

<210> 246
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
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<400> 246

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
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Ser Ala Ser Ser Leu Tyr Ser
1 5

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<211> 6
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Leu Tyr Ser Thr Leu Val
1 5

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<400> 249

Phe Ser Gly Tyr Phe Ile

1 5

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Ala Ile Phe Pro Tyr Arg Gly Gly Thr Ser
1 5 10

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Gly Gly Val Ser Pro Gly Gly Phe
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Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
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Ser Ala Ser Ser Leu Tyr Ser
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Tyr Tyr Leu Tyr Pro Gly
1 5

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Phe Glu Ser Tyr Asp Ile
1 5

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<400> 256

Ala Ile Phe Ser Tyr Gly Gly Tyr Thr Thr
1 5 10

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<400> 257

Gly Ser Tyr Gly Asp Gly Arg Gly Met
1 5

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<400> 258

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

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<400> 259

Ser Ala Ser Ser Leu Tyr Ser
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Tyr Tyr Tyr Trp Pro Gly
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<400> 261

Phe Ser Ser Tyr Phe Ile
1 5

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<400> 262

Ala Ile His Pro Ala Phe Ser Phe Thr Tyr
1 5 10

<210> 263
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<400> 263

Pro Arg Leu Ser Ser Ala Val Val Leu
1 5

<210> 264
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<400> 264

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

<210> 265
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Ser Ala Ser Ser Leu Tyr Ser
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<400> 266

Phe Ser Ser Tyr Phe Ile
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<400> 267

Trp Ile Tyr Pro Ser Gly Ser Tyr Thr Tyr
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<211> 10

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<400> 268

Glu Met Asp Arg Val Gly Tyr Ser Gly Met
1 5 10

<210> 269

<211> 11
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<220>
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<400> 269

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

<210> 270
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<400> 270

Ser Ala Ser Ser Leu Tyr Ser
1 5

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<400> 271

Tyr Arg Thr Pro Leu Gly
1 5

<210> 272
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<220>
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<400> 272

Phe Ser Asp Tyr Gly Ile
1 5

<210> 273
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<220>
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<400> 273

Glu	Ile	Asp	Ser	Trp	Leu	Gly	Tyr	Thr	Tyr
1				5					10

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<400> 274

Ser	Pro	Tyr	His	Tyr	Leu	Tyr	Tyr	Gly	Leu
1				5					10

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<400> 275

Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ala	Val	Ala
1				5					10	

<210> 276
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<400> 276

Ser Ala Ser Ser Leu Tyr Ser

1 5

<210> 277
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<220>
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<400> 277

Leu Ser Ser Ser Leu Gly
1 5

<210> 278
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<400> 278

Phe Ser Gly Tyr Phe Ile
1 5

<210> 279
<211> 10
<212> PRT
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<220>
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<400> 279

Gly Ile Ser Pro Trp Ala Gly Tyr Thr Ser
1 5 10

<210> 280
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<212> PRT
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<220>
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<400> 280

Gly Gly Gly Arg Ala Phe
1 5

<210> 281
<211> 11
<212> PRT
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<220>
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<400> 281

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

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<212> PRT
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<400> 282

Ser Ala Ser Ser Leu Tyr Ser
1 5

<210> 283
<211> 6
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<400> 283

Tyr Tyr Trp Tyr Pro Gly
1 5

<210> 284
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<212> PRT
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<400> 284

Phe Ser Ser Tyr Phe Ile
1 5

<210> 285

<211> 10

<212> PRT

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<223> CDR2 VH of I2A-22

<400> 285

Ala Ile Tyr Pro Ser Gly Trp Tyr Thr Ser
1 5 10

<210> 286

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<400> 286

Val Gln Ala Gly Val Phe
1 5

<210> 287

<211> 11

<212> PRT

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<400> 287

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

<210> 288

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<400> 288

Ser Ala Ser Ser Leu Tyr Ser
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<210> 289

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<212> PRT

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<400> 289

Tyr Tyr Tyr Tyr Pro Gly
1 5

<210> 290

<211> 6

<212> PRT

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<223> CDR1 VH of I2A-23

<400> 290

Phe Asp Asp Tyr Phe Ile
1 5

<210> 291

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 VH of I2A-23

<400> 291

Ala Ile Ser Ser Glu Gly Gly Tyr Thr Asp
1 5 10

<210> 292

<211> 6

<212> PRT

<213> Artificial Sequence

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<223> CDR3 VH of I2A-23

<400> 292

Ala Tyr Arg Gly Val Phe
1 5

<210> 293

<211> 11

<212> PRT

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<220>

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<400> 293

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

<210> 294

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 VL of I2A-23

<400> 294

Ser Ala Ser Ser Leu Tyr Ser
1 5

<210> 295

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 VL of I2A-23

<400> 295

Tyr Tyr Tyr Phe Pro Gly
1 5

<210> 296

<211> 6
<212> PRT
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<220>
<223> CDR1 VH of I2A-24

<400> 296

Phe Ser Thr Tyr Gly Ile
1 5

<210> 297
<211> 10
<212> PRT
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<220>
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<400> 297

Ala Ile Tyr Pro Gly Thr Ser Tyr Thr Gly
1 5 10

<210> 298
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<400> 298

Glu Tyr Phe Met Gly Met
1 5

<210> 299
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<400> 299

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

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<400> 300

Ser Ala Ser Ser Leu Tyr Ser
1 5

<210> 301
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<400> 301

Tyr Tyr Tyr Trp Pro Gly
1 5

<210> 302
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<400> 302

Phe Tyr Gly Tyr Thr Ile
1 5

<210> 303
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<400> 303

Ala Ile Tyr Pro Tyr Thr Asp Ser Thr Arg

1 5 10

<210> 304
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<400> 304

Asp Tyr Arg Arg Ala Leu
1 5

<210> 305
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<400> 305

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

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<400> 306

Ser Ala Ser Ser Leu Tyr Ser
1 5

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<400> 307

Tyr Thr Asp Phe Pro Trp
1 5

<210> 308
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<400> 308

Phe Gln Ser Tyr Asp Ile
1 5

<210> 309
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<400> 309

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

<210> 310
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<400> 310

Asp Tyr Gly Val Phe
1 5

<210> 311
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<400> 311

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

<210> 312

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<400> 312

Ser Ala Ser Ser Leu Tyr Ser
1 5

<210> 313

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<400> 313

Phe Tyr Arg Ser Pro Ala
1 5

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<400> 314

Phe Lys Gly Tyr Tyr Ile
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<400> 315

Ala	Ile	Tyr	Pro	Tyr	Gly	Gly	Ser	Thr	Asp
1				5					10

<210> 316

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<400> 316

Val	Tyr	Ile	Tyr	Gly	Val	Phe
1				5		

<210> 317

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<400> 317

Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ala	Val	Ala
1				5					10	

<210> 318

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<400> 318

Ser	Ala	Ser	Ser	Leu	Tyr	Ser
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<210> 319

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<220>

<223> CDR3 VL of I2A-27

<400> 319

Tyr Tyr Ser Ser Pro Arg
1 5

<210> 320

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<220>

<223> CDR1 VH of I2A-28

<400> 320

Phe Ser Ser Tyr Trp Ile
1 5

<210> 321

<211> 10

<212> PRT

<213> Artificial Sequence

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<223> CDR2 VH of I2A-28

<400> 321

Trp Ile Tyr Pro Gly Thr Arg Tyr Thr Glu
1 5 10

<210> 322

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<212> PRT

<213> Artificial Sequence

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<223> CDR3 VH of I2A-28

<400> 322

Asp Tyr Val Trp Pro Tyr Gly Phe
1 5

<210> 323

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<220>
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<400> 323

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

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<400> 324

Ser Ala Ser Ser Leu Tyr Ser
1 5

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<400> 325

Ala Ser Trp Ser Pro Val
1 5

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<400> 326

Phe Ser Ser Tyr Trp Ile
1 5

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<400> 327

Trp	Ile	Tyr	Ser	Ser	Gly	Gly	Tyr	Thr	Phe
1				5					10

<210> 328
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<220>
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<400> 328

Glu	Tyr	Phe	Leu	Tyr	Thr	Gly	Phe
1				5			

<210> 329
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<400> 329

Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ala	Val	Ala
1				5					10	

<210> 330
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<400> 330

Ser Ala Ser Ser Leu Tyr Ser

1 5

<210> 331
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<220>
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<400> 331

Tyr Ser Ser Gly Pro Val
1 5

<210> 332
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<220>
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<400> 332

Phe Asp Ser Tyr Phe Ile
1 5

<210> 333
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<400> 333

Tyr Ile Tyr Ser Trp Gly Ser Tyr Thr His
1 5 10

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<400> 334

Gly His Arg Arg Tyr Phe Ala Leu
1 5

<210> 335
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<400> 335

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

<210> 336
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<400> 336

Ser Ala Ser Ser Leu Tyr Ser
1 5

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<400> 337

Val Tyr Phe Thr Pro Gly
1 5

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<400> 338

Phe Ser Ser Tyr Trp Ile
1 5

<210> 339

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<400> 339

Phe Ile Gly Pro Ser Gly Gly Tyr Thr Tyr
1 5 10

<210> 340

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<212> PRT

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<400> 340

Glu Thr Asp Ser Tyr Thr Gly Phe
1 5

<210> 341

<211> 11

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<400> 341

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

<210> 342

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<400> 342

Ser Ala Ser Ser Leu Tyr Ser
1 5

<210> 343

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<400> 343

Tyr Tyr Ser Trp Leu Gly
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<210> 344

<211> 6

<212> PRT

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<400> 344

Phe Gln Ser Tyr Val Ile
1 5

<210> 345

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<400> 345

Ala Ile Tyr Pro Tyr Ser Ser Ser Thr Ile
1 5 10

<210> 346

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<212> PRT

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<400> 346

Ser Trp Ser Val Tyr Leu Gly Met
1 5

<210> 347

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<400> 347

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

<210> 348

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<223> CDR2 VL of I2A-32

<400> 348

Ser Ala Ser Ser Leu Tyr Ser
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<210> 349

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<400> 349

Ser Tyr Asp Ser Pro Arg
1 5

<210> 350

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<400> 350

Phe Asp Asp Tyr Tyr Ile
1 5

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<400> 351

Trp Ile Asp Ser Tyr Gly Gly Tyr Thr Ser
1 5 10

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<400> 352

Ser Ser Tyr Tyr Tyr Pro Gly Gly Phe
1 5

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<400> 353

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

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<400> 354

Ser Ala Ser Ser Leu Tyr Ser
1 5

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<400> 355

Trp Asp Ser Thr Leu Tyr
1 5

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Phe Ser Trp Tyr Val Ile
1 5

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<400> 357

Tyr Ile Ala Pro Tyr Thr Gly Ser Thr Tyr

1 5 10

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<400> 358

Ala Phe Phe Gly Ile Arg Leu Gly Leu
1 5

<210> 359
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<400> 359

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

<210> 360
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Ser Ala Ser Ser Leu Tyr Ser
1 5

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<400> 361

Ala Ile Ser Ser Pro Tyr
1 5

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Phe Ser Ala Tyr Asp Ile
1 5

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<400> 363

Trp Ile Asp Pro Tyr Gly Gly Asp Thr Asp
1 5 10

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<400> 364

Ser Pro Ser Tyr Met Gln Tyr Gly Gly Leu
1 5 10

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Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
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Ser Ala Ser Ser Leu Tyr Ser
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Tyr Tyr Ser Ser Leu Leu
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Phe Ser Gln Tyr Trp Ile
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Ala Ile Tyr Ser Ser Thr Lys Tyr Thr Ile
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Glu Ser Met Tyr Phe Tyr Ser Tyr Gly Leu
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Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
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Ser Ala Ser Ser Leu Tyr Ser
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Leu Pro Ser Thr Pro Leu
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Phe Ser Trp Tyr Gly Ile
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<400> 375

Tyr Ile Asp Ser Tyr Thr Ser Ser Thr Tyr
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<400> 376

Ser His Phe Gly His Tyr Asp Tyr Val Met
1 5 10

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Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

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<400> 378

Ser Ala Ser Ser Leu Tyr Ser
1 5

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<400> 379

Ala Tyr Asp Gln Leu Tyr
1 5

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Phe Asp Trp Tyr Arg Ile
1 5

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Trp	Ile	Asp	Ser	Tyr	Gly	Ser	Trp	Thr	Gly
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Ser	Tyr	Phe	Gly	Pro	Tyr	Gly	Tyr	Val	Leu
1				5					10

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<400> 383

Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ala	Val	Ala
1				5					10	

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<220>
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<400> 384

Ser Ala Ser Ser Leu Tyr Ser

1 5

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<220>
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<400> 385

Phe Thr Ser Tyr Gly Ile
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<220>
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<400> 386

Ala Ile Tyr Pro His Ser Gly Phe Thr Ser
1 5 10

<210> 387
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Thr Ser Tyr Arg Gly Phe
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<400> 388

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

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<400> 389

Ser Ala Ser Ser Leu Tyr Ser
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<400> 390

Tyr Tyr Trp Tyr Pro Gly
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Phe Ser Asp Tyr Phe Ile
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<400> 392

Gly Ile Tyr Pro Tyr Ser Gly Tyr Thr Lys
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<400> 393

Asp His Ser Pro Val Leu
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<400> 394

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

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<400> 395

Ser Ala Ser Ser Leu Tyr Ser
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<400> 396

Trp Tyr Tyr Trp Pro Gly
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<210> 397

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<212> PRT

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<223> CDR1 VH of I2C-3

<400> 397

Phe Ser His Tyr Trp Ile
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<211> 10

<212> PRT

<213> Artificial Sequence

<220>

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<400> 398

Leu Ile Ala Pro Gly Gly Asp Tyr Thr Ser
1 5 10

<210> 399

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<400> 399

Ser Gly Leu Pro Gly Phe
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Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
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Tyr Lys Ser Ser Pro Leu
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<210> 403

<211> 6

<212> PRT

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<223> CDR1 VH of I2C-4

<400> 403

Phe Trp Ser Tyr Phe Ile
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<400> 404

Tyr Ile His Pro Ser Ser Ser Tyr Thr Asp
1 5 10

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<400> 405

Thr Ser Arg Asp Gly Ala Met
1 5

<210> 406
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<400> 406

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

<210> 407
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<400> 407

Ser Ala Ser Ser Leu Tyr Ser
1 5

<210> 408
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<400> 408

Trp Tyr Ser Pro Pro Glu
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<210> 409
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<212> PRT
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<400> 409

Phe Ser Ser Tyr Asp Ile
1 5

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<400> 410

Trp Ile Tyr Pro Tyr Trp Gly Tyr Thr Ile
1 5 10

<210> 411
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<400> 411

Gly Thr Tyr Ala Pro Ala Leu

1 5

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Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

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Ser Ala Ser Ser Leu Tyr Ser
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Phe Tyr Ser Tyr Leu Ser
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<400> 415

Phe Ser Trp Tyr Phe Ile
1 5

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<400> 416

Arg Ile Tyr Ser Thr Gly Gly Tyr Thr Glu
1 5 10

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<400> 417

Ser Ala Phe Phe Gly Ala Leu
1 5

<210> 418
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<400> 418

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

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Ser Ala Ser Ser Leu Tyr Ser
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<400> 420

Tyr Pro Ser Gly Pro Glu
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<212> PRT

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<400> 421

Phe Asp Ser Tyr Tyr Ile
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Trp Ile Asp Pro Tyr Gly Leu Asp Thr Lys
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<400> 423

Glu Pro Gly Asp Tyr Gly Met
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<400> 424

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
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<400> 425

Ser Ala Ser Ser Leu Tyr Ser
1 5

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<400> 426

Ala Tyr Gly Ser Leu Leu
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<210> 427

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<223> CDR1 VH of I2C-8

<400> 427

Phe Ser Gly Tyr Phe Ile
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<210> 428

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<212> PRT

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<223> CDR2 VH of I2C-8

<400> 428

Ala Ile Phe Pro Tyr Arg Gly Gly Thr Ser
1 5 10

<210> 429

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<212> PRT

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<223> CDR3 VH of I2C-8

<400> 429

Gly Gly Val Ser Pro Gly Gly Phe
1 5

<210> 430

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<400> 430

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

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<400> 431

Ser Ala Ser Ser Leu Tyr Ser
1 5

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<400> 432

Tyr Tyr Leu Tyr Pro Gly
1 5

<210> 433
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<220>
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<400> 433

Phe Thr Asp Tyr Asp Ile
1 5

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<400> 434

Arg Ile Trp Pro His Gly Ser Tyr Thr Phe
1 5 10

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<400> 435

Ser Leu Thr His Ser Tyr Gly Phe
1 5

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<400> 436

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

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Ser Ala Ser Ser Leu Tyr Ser
1 5

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<400> 438

Tyr Tyr Thr Trp Leu Ile

1 5

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Phe Ser Ser Tyr Phe Ile
1 5

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Thr Ile His Ser Tyr Phe Asp Gly Thr Ser
1 5 10

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Thr Arg Pro Thr Gly Gly Ala Phe
1 5

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Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

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Ser Ala Ser Ser Leu Tyr Ser
1 5

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<400> 444

Ala Tyr Trp Ser Pro Ala
1 5

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Phe Gly Ser Tyr Phe Ile
1 5

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Ala Ile Phe Pro Ala Gly Gly Tyr Thr Tyr
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Tyr Gly Ser Met Gly Gly Ala Phe
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Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
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<400> 449

Ser Ala Ser Ser Leu Tyr Ser
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<212> PRT

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<400> 450

Tyr Tyr Trp Phe Pro Gly
1 5

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Phe Ser Ser Tyr Phe Ile
1 5

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Ala Ile His Pro Ala Phe Ser Phe Thr Tyr
1 5 10

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Pro Arg Leu Ser Ser Ala Val Val Leu
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Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
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<400> 455

Ser Ala Ser Ser Leu Tyr Ser
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Gly Tyr Tyr Phe Pro Gly
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<400> 457

Phe Ser Ser Tyr Gly Ile
1 5

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<400> 458

Tyr Ile His Ser Gly Ile Gly Tyr Thr Ile
1 5 10

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Thr Ser Ser Thr Ser Thr Ser Val Met
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Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
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Ser Ala Ser Ser Leu Tyr Ser
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Thr Tyr Trp Ser Pro Gly
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<400> 463

Phe Glu Ser Tyr Asp Ile
1 5

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Ala Ile Phe Ser Tyr Gly Gly Tyr Thr Thr
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<400> 465

Gly Ser Tyr Gly Asp Gly Arg Gly Met

1

5

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<400> 466

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

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Ser Ala Ser Ser Leu Tyr Ser
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Tyr Tyr Tyr Trp Pro Gly
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Phe Ser Ser Tyr Phe Ile
1 5

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Leu Ile Tyr Pro Asp Thr Asp Asp Thr Tyr
1 5 10

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Tyr Gly Tyr Leu Gly Val Gly Ala Phe
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Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

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Ser Ala Ser Ser Leu Tyr Ser
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<400> 474

Leu Tyr Trp Thr Pro Gly
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<210> 475

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<223> CDR1 VH of I2C-16

<400> 475

Phe Ser Ser Tyr Trp Ile
1 5

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<212> PRT

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<220>

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<400> 476

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

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<400> 478

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

<210> 479

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 VL of I2C-16

<400> 479

Ser Ala Ser Ser Leu Tyr Ser
1 5

<210> 480

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 VL of I2C-16

<400> 480

Tyr Tyr Tyr Phe Pro Gly
1 5

<210> 481

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 VH of I2C-17

<400> 481

Phe Ser Asp Tyr Phe Ile
1 5

<210> 482

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 VH of I2C-17

<400> 482

Tyr Ile Tyr Pro Ala Ser Gly Gly Thr Cys
1 5 10

<210> 483

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 VH of I2C-17

<400> 483

Gly Tyr Ile Pro His Met Ala Ala Leu
1 5

<210> 484

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 VL of I2C-17

<400> 484

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

<210> 485

<211> 7
<212> PRT
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<220>
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<400> 485

Ser Ala Ser Ser Leu Tyr Ser
1 5

<210> 486
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<400> 486

Tyr Tyr Trp Trp Pro Gly
1 5

<210> 487
<211> 6
<212> PRT
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<220>
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<400> 487

Phe Ala Gly Tyr Pro Ile
1 5

<210> 488
<211> 10
<212> PRT
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<220>
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<400> 488

Ala Ile Asp Pro Asp Gly Gly Tyr Thr Tyr
1 5 10

<210> 489
<211> 10
<212> PRT
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<220>
<223> CDR3 VH of I2C-18

<400> 489

His	Thr	Gly	Phe	His	Arg	Tyr	Arg	Gly	Met
1				5					10

<210> 490
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
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<400> 490

Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ala	Val	Ala
1				5						10

<210> 491
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<400> 491

Ser	Ala	Ser	Ser	Leu	Tyr	Ser
1				5		

<210> 492
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 VL of I2C-18

<400> 492

Tyr Tyr Trp Phe Pro Pro

1 5

<210> 493
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 VH of I2C-19

<400> 493

Phe Thr Ser Tyr Asp Ile
1 5

<210> 494
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 VH of I2C-19

<400> 494

Trp Ile Asp Pro Gly Leu Ser Tyr Thr Ser
1 5 10

<210> 495
<211> 10
<212> PRT
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<220>
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<400> 495

Ala Ser Ile Gly Gly Gly Val Pro Val Met
1 5 10

<210> 496
<211> 11
<212> PRT
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<220>
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<400> 496

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

<210> 497
<211> 7
<212> PRT
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<220>
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<400> 497

Ser Ala Ser Ser Leu Tyr Ser
1 5

<210> 498
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<400> 498

Tyr Val Thr Gly Pro Tyr
1 5

<210> 499
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 VH of I2C-20

<400> 499

Phe Ser Ser Tyr Tyr Ile
1 5

<210> 500
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 VH of I2C-20

<400> 500

Ile	Ile	Ile	Pro	Tyr	Ser	Gly	Tyr	Thr	Tyr
1				5					10

<210> 501

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 VH of I2C-20

<400> 501

Arg	Gly	Tyr	Phe	Ser	Leu	Gly	Thr	Ala	Met
1				5					10

<210> 502

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 VL of I2C-20

<400> 502

Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ala	Val	Ala
1				5					10	

<210> 503

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 VL of I2C-20

<400> 503

Ser	Ala	Ser	Ser	Leu	Tyr	Ser
1				5		

<210> 504

<211> 6

<212> PRT

<213> Artificial Sequence

<220>
<223> CDR3 VL of I2C-20

<400> 504

Val Tyr Trp Trp Pro Gly
1 5

<210> 505
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 VH of I2C-21

<400> 505

Phe Ser Ser Tyr Tyr Ile
1 5

<210> 506
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 VH of I2C-21

<400> 506

Trp Ile Asp Pro Tyr Ile Ser Tyr Thr Tyr
1 5 10

<210> 507
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 VH of I2C-21

<400> 507

Asp Ser Glu Leu Val Ser Gly Tyr Ala Met
1 5 10

<210> 508
<211> 11
<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 VL of I2C-21

<400> 508

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

<210> 509

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 VL of I2C-21

<400> 509

Ser Ala Ser Ser Leu Tyr Ser
1 5

<210> 510

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 VL of I2C-21

<400> 510

Gly Asp Ser Ser Leu Val
1 5

<210> 511

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 VH of I2C-22

<400> 511

Phe Ser Ser Tyr Ser Ile
1 5

<210> 512

<211> 10
<212> PRT
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<220>
<223> CDR2 VH of I2C-22

<400> 512

Ala	Ile	Tyr	Pro	Tyr	Trp	Gly	Thr	Thr	Glu
1				5					10

<210> 513
<211> 10
<212> PRT
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<220>
<223> CDR3 VH of I2C-22

<400> 513

Pro	Ser	Gly	Val	Thr	Tyr	Gly	Tyr	Ala	Leu
1				5					10

<210> 514
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 VL of I2C-22

<400> 514

Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ala	Val	Ala
1				5					10	

<210> 515
<211> 7
<212> PRT
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<220>
<223> CDR2 VL of I2C-22

<400> 515

Ser	Ala	Ser	Ser	Leu	Tyr	Ser
1				5		

<210> 516
<211> 6
<212> PRT
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<220>
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<400> 516

Tyr Tyr Tyr Ser Pro Trp
1 5

<210> 517
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 VH of I2C-23

<400> 517

Phe Ser Ser Tyr Glu Ile
1 5

<210> 518
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 VH of I2C-23

<400> 518

Ser Ile Tyr Pro Phe Ser Gly Asp Thr Tyr
1 5 10

<210> 519
<211> 10
<212> PRT
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<220>
<223> CDR3 VH of I2C-23

<400> 519

Pro Gly Arg Ala Ile Tyr Tyr Ala Val Met

1 5 10

<210> 520
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 VL of I2C-23

<400> 520

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

<210> 521
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 VL of I2C-23

<400> 521

Ser Ala Ser Ser Leu Tyr Ser
1 5

<210> 522
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<400> 522

Ala Gly Ser His Leu Phe
1 5

<210> 523
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 VH of I2C-24

<400> 523

Phe Ser Arg Tyr Tyr Ile
1 5

<210> 524
<211> 10
<212> PRT
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<220>
<223> CDR2 VH of I2C-24

<400> 524

Asp Ile Asp Ser Tyr Gly Gly Phe Thr Tyr
1 5 10

<210> 525
<211> 11
<212> PRT
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<220>
<223> CDR3 VH of I2C-24

<400> 525

Ala His Arg Phe Leu Gln Gly Gly Tyr Val Leu
1 5 10

<210> 526
<211> 11
<212> PRT
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<220>
<223> CDR1 VL of I2C-24

<400> 526

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

<210> 527
<211> 7
<212> PRT
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<220>
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<400> 527

Ser Ala Ser Ser Leu Tyr Ser
1 5

<210> 528

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 VL of I2C-24

<400> 528

Tyr Ser Trp Gly Leu Trp
1 5

<210> 529

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 VH of I2C-25

<400> 529

Phe Ser Asp Tyr Tyr Ile
1 5

<210> 530

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 VH of I2C-25

<400> 530

Tyr Ile Ala Pro Tyr Gly Gly Phe Thr Tyr
1 5 10

<210> 531

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 VH of I2C-25

<400> 531

Asp	Ser	Tyr	Arg	Arg	Gly	Tyr	Val	Ser	Gly	Phe
1				5					10	

<210> 532

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 VL of I2C-25

<400> 532

Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ala	Val	Ala
1				5					10	

<210> 533

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 VL of I2C-25

<400> 533

Ser	Ala	Ser	Ser	Leu	Tyr	Ser
1				5		

<210> 534

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 VL of I2C-25

<400> 534

Arg	Tyr	Ser	Ser	Pro	Ser
1				5	

<210> 535

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 VH of I2C-26

<400> 535

Phe Ser Asp Tyr Tyr Ile
1 5

<210> 536

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 VH of I2C-26

<400> 536

Asp Ile Asp Ser Tyr Gly Gly Phe Thr Tyr
1 5 10

<210> 537

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 VH of I2C-26

<400> 537

Asp Pro His Phe Leu Asp Asp Val Tyr Val Leu
1 5 10

<210> 538

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 VL of I2C-26

<400> 538

Arg Ala Ser Gln Ser Val Ser Ser Ala Val Ala
1 5 10

<210> 539

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

<220>
<223> CDR2 VL of I2C-26

<400> 539

Ser Ala Ser Ser Leu Tyr Ser
1 5

<210> 540
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 VL of I2C-26

<400> 540

Tyr Ser Trp Gly Leu Trp
1 5