

pctgb2016051576-seq1
SEQUENCE LISTING

<110> UCL Business PLC

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<130> P106294PCT

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<151> 2015-06-01

<160> 63

<170> PatentIn version 3.5

<210> 1

<211> 619

<212> PRT

<213> Homo sapiens

<400> 1

Met Pro Asp Pro Ala Ala His Leu Pro Phe Phe Tyr Gly Ser Ile Ser
1 5 10 15

Arg Ala Glu Ala Glu Glu His Leu Lys Leu Ala Gly Met Ala Asp Gly
20 25 30

Leu Phe Leu Leu Arg Gln Cys Leu Arg Ser Leu Gly Gly Tyr Val Leu
35 40 45

Ser Leu Val His Asp Val Arg Phe His His Phe Pro Ile Glu Arg Gln
50 55 60

Leu Asn Gly Thr Tyr Ala Ile Ala Gly Gly Lys Ala His Cys Gly Pro
65 70 75 80

Ala Glu Leu Cys Glu Phe Tyr Ser Arg Asp Pro Asp Gly Leu Pro Cys
85 90 95

Asn Leu Arg Lys Pro Cys Asn Arg Pro Ser Gly Leu Glu Pro Gln Pro
100 105 110

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Gly Val Phe Asp Cys Leu Arg Asp Ala Met Val Arg Asp Tyr Val Arg
115 120 125

Gln Thr Trp Lys Leu Glu Gly Glu Ala Leu Glu Gln Ala Ile Ile Ser
130 135 140

Gln Ala Pro Gln Val Glu Lys Leu Ile Ala Thr Thr Ala His Glu Arg
145 150 155 160

Met Pro Trp Tyr His Ser Ser Leu Thr Arg Glu Glu Ala Glu Arg Lys
165 170 175

Leu Tyr Ser Gly Ala Gln Thr Asp Gly Lys Phe Leu Leu Arg Pro Arg
180 185 190

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

Tyr His Tyr Leu Ile Ser Gln Asp Lys Ala Gly Lys Tyr Cys Ile Pro
210 215 220

Glu Gly Thr Lys Phe Asp Thr Leu Trp Gln Leu Val Glu Tyr Leu Lys
225 230 235 240

Leu Lys Ala Asp Gly Leu Ile Tyr Cys Leu Lys Glu Ala Cys Pro Asn
245 250 255

Ser Ser Ala Ser Asn Ala Ser Gly Ala Ala Ala Pro Thr Leu Pro Ala
260 265 270

His Pro Ser Thr Leu Thr His Pro Gln Arg Arg Ile Asp Thr Leu Asn
275 280 285

Ser Asp Gly Tyr Thr Pro Glu Pro Ala Arg Ile Thr Ser Pro Asp Lys
290 295 300

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Pro Arg Pro Met Pro Met Asp Thr Ser Val Tyr Glu Ser Pro Tyr Ser
305 310 315 320

Asp Pro Glu Glu Leu Lys Asp Lys Lys Leu Phe Leu Lys Arg Asp Asn
325 330 335

Leu Leu Ile Ala Asp Ile Glu Leu Gly Cys Gly Asn Phe Gly Ser Val
340 345 350

Arg Gln Gly Val Tyr Arg Met Arg Lys Lys Gln Ile Asp Val Ala Ile
355 360 365

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

Arg Glu Ala Gln Ile Met His Gln Leu Asp Asn Pro Tyr Ile Val Arg
385 390 395 400

Leu Ile Gly Val Cys Gln Ala Glu Ala Leu Met Leu Val Met Glu Met
405 410 415

Ala Gly Gly Gly Pro Leu His Lys Phe Leu Val Gly Lys Arg Glu Glu
420 425 430

Ile Pro Val Ser Asn Val Ala Glu Leu Leu His Gln Val Ser Met Gly
435 440 445

Met Lys Tyr Leu Glu Glu Lys Asn Phe Val His Arg Asp Leu Ala Ala
450 455 460

Arg Asn Val Leu Leu Val Asn Arg His Tyr Ala Lys Ile Ser Asp Phe
465 470 475 480

Gly Leu Ser Lys Ala Leu Gly Ala Asp Asp Ser Tyr Tyr Thr Ala Arg
485 490 495

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Ser Ala Gly Lys Trp Pro Leu Lys Trp Tyr Ala Pro Glu Cys Ile Asn
500 505 510

Phe Arg Lys Phe Ser Ser Arg Ser Asp Val Trp Ser Tyr Gly Val Thr
515 520 525

Met Trp Glu Ala Leu Ser Tyr Gly Gln Lys Pro Tyr Lys Lys Met Lys
530 535 540

Gly Pro Glu Val Met Ala Phe Ile Glu Gln Gly Lys Arg Met Glu Cys
545 550 555 560

Pro Pro Glu Cys Pro Pro Glu Leu Tyr Ala Leu Met Ser Asp Cys Trp
565 570 575

Ile Tyr Lys Trp Glu Asp Arg Pro Asp Phe Leu Thr Val Glu Gln Arg
580 585 590

Met Arg Ala Cys Tyr Tyr Ser Leu Ala Ser Lys Val Glu Gly Pro Pro
595 600 605

Gly Ser Thr Gln Lys Ala Glu Ala Ala Cys Ala
610 615

<210> 2
<211> 280
<212> PRT
<213> Artificial Sequence

<220>
<223> ZAP70 complete SH2 domain

<400> 2

Met Pro Asp Pro Ala Ala His Leu Pro Phe Phe Tyr Gly Ser Ile Ser
1 5 10 15

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Arg Ala Glu Ala Glu Glu His Leu Lys Leu Ala Gly Met Ala Asp Gly
20 25 30

Leu Phe Leu Leu Arg Gln Cys Leu Arg Ser Leu Gly Gly Tyr Val Leu
35 40 45

Ser Leu Val His Asp Val Arg Phe His His Phe Pro Ile Glu Arg Gln
50 55 60

Leu Asn Gly Thr Tyr Ala Ile Ala Gly Gly Lys Ala His Cys Gly Pro
65 70 75 80

Ala Glu Leu Cys Glu Phe Tyr Ser Arg Asp Pro Asp Gly Leu Pro Cys
85 90 95

Asn Leu Arg Lys Pro Cys Asn Arg Pro Ser Gly Leu Glu Pro Gln Pro
100 105 110

Gly Val Phe Asp Cys Leu Arg Asp Ala Met Val Arg Asp Tyr Val Arg
115 120 125

Gln Thr Trp Lys Leu Glu Gly Glu Ala Leu Glu Gln Ala Ile Ile Ser
130 135 140

Gln Ala Pro Gln Val Glu Lys Leu Ile Ala Thr Thr Ala His Glu Arg
145 150 155 160

Met Pro Trp Tyr His Ser Ser Leu Thr Arg Glu Glu Ala Glu Arg Lys
165 170 175

Leu Tyr Ser Gly Ala Gln Thr Asp Gly Lys Phe Leu Leu Arg Pro Arg
180 185 190

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

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Tyr His Tyr Leu Ile Ser Gln Asp Lys Ala Gly Lys Tyr Cys Ile Pro
210 215 220

Glu Gly Thr Lys Phe Asp Thr Leu Trp Gln Leu Val Glu Tyr Leu Lys
225 230 235 240

Leu Lys Ala Asp Gly Leu Ile Tyr Cys Leu Lys Glu Ala Cys Pro Asn
245 250 255

Ser Ser Ala Ser Asn Ala Ser Gly Ala Ala Ala Pro Thr Leu Pro Ala
260 265 270

His Pro Ser Thr Leu Thr His Pro
275 280

<210> 3
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> ZAP70 SH2 1

<400> 3

Phe Phe Tyr Gly Ser Ile Ser Arg Ala Glu Ala Glu Glu His Leu Lys
1 5 10 15

Leu Ala Gly Met Ala Asp Gly Leu Phe Leu Leu Arg Gln Cys Leu Arg
20 25 30

Ser Leu Gly Gly Tyr Val Leu Ser Leu Val His Asp Val Arg Phe His
35 40 45

His Phe Pro Ile Glu Arg Gln Leu Asn Gly Thr Tyr Ala Ile Ala Gly
50 55 60

Gly Lys Ala His Cys Gly Pro Ala Glu Leu Cys Glu Phe Tyr Ser Arg
65 70 75 80

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Asp Pro Asp Gly Leu Pro Cys Asn Leu Arg Lys Pro Cys
85 90

<210> 4
<211> 92
<212> PRT
<213> Artificial Sequence

<220>
<223> ZAP70 SH2 2

<400> 4

Trp Tyr His Ser Ser Leu Thr Arg Glu Glu Ala Glu Arg Lys Leu Tyr
1 5 10 15

Ser Gly Ala Gln Thr Asp Gly Lys Phe Leu Leu Arg Pro Arg Lys Glu
20 25 30

Gln Gly Thr Tyr Ala Leu Ser Leu Ile Tyr Gly Lys Thr Val Tyr His
35 40 45

Tyr Leu Ile Ser Gln Asp Lys Ala Gly Lys Tyr Cys Ile Pro Glu Gly
50 55 60

Thr Lys Phe Asp Thr Leu Trp Gln Leu Val Glu Tyr Leu Lys Leu Lys
65 70 75 80

Ala Asp Gly Leu Ile Tyr Cys Leu Lys Glu Ala Cys
85 90

<210> 5
<211> 595
<212> PRT
<213> Homo sapiens

<400> 5

Met Val Arg Trp Phe His Arg Asp Leu Ser Gly Leu Asp Ala Glu Thr

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

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195

200

205

Leu Arg Gln Pro Tyr Tyr Ala Thr Arg Val Asn Ala Ala Asp Ile Glu
 210 215 220

Asn Arg Val Leu Glu Leu Asn Lys Lys Gln Glu Ser Glu Asp Thr Ala
 225 230 235 240

Lys Ala Gly Phe Trp Glu Glu Phe Glu Ser Leu Gln Lys Gln Glu Val
 245 250 255

Lys Asn Leu His Gln Arg Leu Glu Gly Gln Arg Pro Glu Asn Lys Gly
 260 265 270

Lys Asn Arg Tyr Lys Asn Ile Leu Pro Phe Asp His Ser Arg Val Ile
 275 280 285

Leu Gln Gly Arg Asp Ser Asn Ile Pro Gly Ser Asp Tyr Ile Asn Ala
 290 295 300

Asn Tyr Ile Lys Asn Gln Leu Leu Gly Pro Asp Glu Asn Ala Lys Thr
 305 310 315 320

Tyr Ile Ala Ser Gln Gly Cys Leu Glu Ala Thr Val Asn Asp Phe Trp
 325 330 335

Gln Met Ala Trp Gln Glu Asn Ser Arg Val Ile Val Met Thr Thr Arg
 340 345 350

Glu Val Glu Lys Gly Arg Asn Lys Cys Val Pro Tyr Trp Pro Glu Val
 355 360 365

Gly Met Gln Arg Ala Tyr Gly Pro Tyr Ser Val Thr Asn Cys Gly Glu
 370 375 380

His Asp Thr Thr Glu Tyr Lys Leu Arg Thr Leu Gln Val Ser Pro Leu

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385		390		395		400									
Asp	Asn	Gly	Asp	Leu	Ile	Arg	Glu	Ile	Trp	His	Tyr	Gln	Tyr	Leu	Ser
				405					410					415	
Trp	Pro	Asp	His	Gly	Val	Pro	Ser	Glu	Pro	Gly	Gly	Val	Leu	Ser	Phe
			420					425					430		
Leu	Asp	Gln	Ile	Asn	Gln	Arg	Gln	Glu	Ser	Leu	Pro	His	Ala	Gly	Pro
		435					440					445			
Ile	Ile	Val	His	Cys	Ser	Ala	Gly	Ile	Gly	Arg	Thr	Gly	Thr	Ile	Ile
	450					455					460				
Val	Ile	Asp	Met	Leu	Met	Glu	Asn	Ile	Ser	Thr	Lys	Gly	Leu	Asp	Cys
465					470					475					480
Asp	Ile	Asp	Ile	Gln	Lys	Thr	Ile	Gln	Met	Val	Arg	Ala	Gln	Arg	Ser
				485					490					495	
Gly	Met	Val	Gln	Thr	Glu	Ala	Gln	Tyr	Lys	Phe	Ile	Tyr	Val	Ala	Ile
			500					505					510		
Ala	Gln	Phe	Ile	Glu	Thr	Thr	Lys	Lys	Lys	Leu	Glu	Val	Leu	Gln	Ser
		515					520					525			
Gln	Lys	Gly	Gln	Glu	Ser	Glu	Tyr	Gly	Asn	Ile	Thr	Tyr	Pro	Pro	Ala
	530					535					540				
Met	Lys	Asn	Ala	His	Ala	Lys	Ala	Ser	Arg	Thr	Ser	Ser	Lys	His	Lys
545					550					555					560
Glu	Asp	Val	Tyr	Glu	Asn	Leu	His	Thr	Lys	Asn	Lys	Arg	Glu	Glu	Lys
				565					570					575	
Val	Lys	Lys	Gln	Arg	Ser	Ala	Asp	Lys	Glu	Lys	Ser	Lys	Gly	Ser	Leu

580

585

590

Lys Arg Lys
595

<210> 6

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> PTPN6 SH2 complete domain

<400> 6

Met Val Arg Trp Phe His Arg Asp Leu Ser Gly Leu Asp Ala Glu Thr
1 5 10 15

Leu Leu Lys Gly Arg Gly Val His Gly Ser Phe Leu Ala Arg Pro Ser
20 25 30

Arg Lys Asn Gln Gly Asp Phe Ser Leu Ser Val Arg Val Gly Asp Gln
35 40 45

Val Thr His Ile Arg Ile Gln Asn Ser Gly Asp Phe Tyr Asp Leu Tyr
50 55 60

Gly Gly Glu Lys Phe Ala Thr Leu Thr Glu Leu Val Glu Tyr Tyr Thr
65 70 75 80

Gln Gln Gln Gly Val Leu Gln Asp Arg Asp Gly Thr Ile Ile His Leu
85 90 95

Lys Tyr Pro Leu Asn Cys Ser Asp Pro Thr Ser Glu Arg Trp Tyr His
100 105 110

Gly His Met Ser Gly Gly Gln Ala Glu Thr Leu Leu Gln Ala Lys Gly
115 120 125

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Glu Pro Trp Thr Phe Leu Val Arg Glu Ser Leu Ser Gln Pro Gly Asp
130 135 140

Phe Val Leu Ser Val Leu Ser Asp Gln Pro Lys Ala Gly Pro Gly Ser
145 150 155 160

Pro Leu Arg Val Thr His Ile Lys Val Met Cys Glu Gly Gly Arg Tyr
165 170 175

Thr Val Gly Gly Leu Glu Thr Phe Asp Ser Leu Thr Asp Leu Val Glu
180 185 190

His Phe Lys Lys Thr Gly Ile Glu Glu Ala Ser Gly Ala Phe Val Tyr
195 200 205

Leu Arg Gln Pro Tyr Tyr
210

<210> 7
<211> 97
<212> PRT
<213> Artificial Sequence

<220>
<223> PTPN6 SH2 1

<400> 7

Trp Phe His Arg Asp Leu Ser Gly Leu Asp Ala Glu Thr Leu Leu Lys
1 5 10 15

Gly Arg Gly Val His Gly Ser Phe Leu Ala Arg Pro Ser Arg Lys Asn
20 25 30

Gln Gly Asp Phe Ser Leu Ser Val Arg Val Gly Asp Gln Val Thr His
35 40 45

Ile Arg Ile Gln Asn Ser Gly Asp Phe Tyr Asp Leu Tyr Gly Gly Glu

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50

55

60

Lys Phe Ala Thr Leu Thr Glu Leu Val Glu Tyr Tyr Thr Gln Gln Gln
65 70 75 80

Gly Val Leu Gln Asp Arg Asp Gly Thr Ile Ile His Leu Lys Tyr Pro
85 90 95

Leu

<210> 8

<211> 104

<212> PRT

<213> Artificial Sequence

<220>

<223> PTPN6 SH2 2

<400> 8

Trp Tyr His Gly His Met Ser Gly Gly Gln Ala Glu Thr Leu Leu Gln
1 5 10 15

Ala Lys Gly Glu Pro Trp Thr Phe Leu Val Arg Glu Ser Leu Ser Gln
20 25 30

Pro Gly Asp Phe Val Leu Ser Val Leu Ser Asp Gln Pro Lys Ala Gly
35 40 45

Pro Gly Ser Pro Leu Arg Val Thr His Ile Lys Val Met Cys Glu Gly
50 55 60

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

Leu Val Glu His Phe Lys Lys Thr Gly Ile Glu Glu Ala Ser Gly Ala
85 90 95

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Phe Val Tyr Leu Arg Gln Pro Tyr
100

<210> 9
<211> 597
<212> PRT
<213> Homo sapiens

<400> 9

Met Thr Ser Arg Arg Trp Phe His Pro Asn Ile Thr Gly Val Glu Ala
1 5 10 15

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

Pro Ser Lys Ser Asn Pro Gly Asp Phe Thr Leu Ser Val Arg Arg Asn
35 40 45

Gly Ala Val Thr His Ile Lys Ile Gln Asn Thr Gly Asp Tyr Tyr Asp
50 55 60

Leu Tyr Gly Gly Glu Lys Phe Ala Thr Leu Ala Glu Leu Val Gln Tyr
65 70 75 80

Tyr Met Glu His His Gly Gln Leu Lys Glu Lys Asn Gly Asp Val Ile
85 90 95

Glu Leu Lys Tyr Pro Leu Asn Cys Ala Asp Pro Thr Ser Glu Arg Trp
100 105 110

Phe His Gly His Leu Ser Gly Lys Glu Ala Glu Lys Leu Leu Thr Glu
115 120 125

Lys Gly Lys His Gly Ser Phe Leu Val Arg Glu Ser Gln Ser His Pro
130 135 140

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Gly Asp Phe Val Leu Ser Val Arg Thr Gly Asp Asp Lys Gly Glu Ser
145 150 155 160

Asn Asp Gly Lys Ser Lys Val Thr His Val Met Ile Arg Cys Gln Glu
165 170 175

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

Leu Val Glu His Tyr Lys Lys Asn Pro Met Val Glu Thr Leu Gly Thr
195 200 205

Val Leu Gln Leu Lys Gln Pro Leu Asn Thr Thr Arg Ile Asn Ala Ala
210 215 220

Glu Ile Glu Ser Arg Val Arg Glu Leu Ser Lys Leu Ala Glu Thr Thr
225 230 235 240

Asp Lys Val Lys Gln Gly Phe Trp Glu Glu Phe Glu Thr Leu Gln Gln
245 250 255

Gln Glu Cys Lys Leu Leu Tyr Ser Arg Lys Glu Gly Gln Arg Gln Glu
260 265 270

Asn Lys Asn Lys Asn Arg Tyr Lys Asn Ile Leu Pro Phe Asp His Thr
275 280 285

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

Ile Asn Ala Asn Ile Ile Met Pro Glu Phe Glu Thr Lys Cys Asn Asn
305 310 315 320

Ser Lys Pro Lys Lys Ser Tyr Ile Ala Thr Gln Gly Cys Leu Gln Asn
325 330 335

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Thr Val Asn Asp Phe Trp Arg Met Val Phe Gln Glu Asn Ser Arg Val
340 345 350

Ile Val Met Thr Thr Lys Glu Val Glu Arg Gly Lys Ser Lys Cys Val
355 360 365

Lys Tyr Trp Pro Asp Glu Tyr Ala Leu Lys Glu Tyr Gly Val Met Arg
370 375 380

Val Arg Asn Val Lys Glu Ser Ala Ala His Asp Tyr Thr Leu Arg Glu
385 390 395 400

Leu Lys Leu Ser Lys Val Gly Gln Ala Leu Leu Gln Gly Asn Thr Glu
405 410 415

Arg Thr Val Trp Gln Tyr His Phe Arg Thr Trp Pro Asp His Gly Val
420 425 430

Pro Ser Asp Pro Gly Gly Val Leu Asp Phe Leu Glu Glu Val His His
435 440 445

Lys Gln Glu Ser Ile Val Asp Ala Gly Pro Val Val Val His Cys Ser
450 455 460

Ala Gly Ile Gly Arg Thr Gly Thr Phe Ile Val Ile Asp Ile Leu Ile
465 470 475 480

Asp Ile Ile Arg Glu Lys Gly Val Asp Cys Asp Ile Asp Val Pro Lys
485 490 495

Thr Ile Gln Met Val Arg Ser Gln Arg Ser Gly Met Val Gln Thr Glu
500 505 510

Ala Gln Tyr Arg Phe Ile Tyr Met Ala Val Gln His Tyr Ile Glu Thr
515 520 525

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Leu Gln Arg Arg Ile Glu Glu Glu Gln Lys Ser Lys Arg Lys Gly His
530 535 540

Glu Tyr Thr Asn Ile Lys Tyr Ser Leu Val Asp Gln Thr Ser Gly Asp
545 550 555 560

Gln Ser Pro Leu Pro Pro Cys Thr Pro Thr Pro Pro Cys Ala Glu Met
565 570 575

Arg Glu Asp Ser Ala Arg Val Tyr Glu Asn Val Gly Leu Met Gln Gln
580 585 590

Gln Arg Ser Phe Arg
595

<210> 10
<211> 97
<212> PRT
<213> Artificial Sequence

<220>
<223> SHP-2 first SH2 domain

<400> 10

Trp Phe His Pro Asn Ile Thr Gly Val Glu Ala Glu Asn Leu Leu Leu
1 5 10 15

Thr Arg Gly Val Asp Gly Ser Phe Leu Ala Arg Pro Ser Lys Ser Asn
20 25 30

Pro Gly Asp Phe Thr Leu Ser Val Arg Arg Asn Gly Ala Val Thr His
35 40 45

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

Lys Phe Ala Thr Leu Ala Glu Leu Val Gln Tyr Tyr Met Glu His His
65 70 75 80

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Gly Gln Leu Lys Glu Lys Asn Gly Asp Val Ile Glu Leu Lys Tyr Pro
85 90 95

Leu

<210> 11
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> SHP-2 second SH2 domain

<400> 11

Trp Phe His Gly His Leu Ser Gly Lys Glu Ala Glu Lys Leu Leu Thr
1 5 10 15

Glu Lys Gly Lys His Gly Ser Phe Leu Val Arg Glu Ser Gln Ser His
20 25 30

Pro Gly Asp Phe Val Leu Ser Val Arg Thr Gly Asp Asp Lys Gly Glu
35 40 45

Ser Asn Asp Gly Lys Ser Lys Val Thr His Val Met Ile Arg Cys Gln
50 55 60

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

Asp Leu Val Glu His Tyr Lys Lys Asn Pro Met Val Glu Thr Leu Gly
85 90 95

Thr Val Leu Gln Leu Lys Gln Pro Leu
100 105

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

<220>
 <223> SHP-2 both SH2 domains

<400> 12

Trp Phe His Pro Asn Ile Thr Gly Val Glu Ala Glu Asn Leu Leu Leu
 1 5 10 15

Thr Arg Gly Val Asp Gly Ser Phe Leu Ala Arg Pro Ser Lys Ser Asn
 20 25 30

Pro Gly Asp Phe Thr Leu Ser Val Arg Arg Asn Gly Ala Val Thr His
 35 40 45

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

Lys Phe Ala Thr Leu Ala Glu Leu Val Gln Tyr Tyr Met Glu His His
 65 70 75 80

Gly Gln Leu Lys Glu Lys Asn Gly Asp Val Ile Glu Leu Lys Tyr Pro
 85 90 95

Leu Asn Cys Ala Asp Pro Thr Ser Glu Arg Trp Phe His Gly His Leu
 100 105 110

Ser Gly Lys Glu Ala Glu Lys Leu Leu Thr Glu Lys Gly Lys His Gly
 115 120 125

Ser Phe Leu Val Arg Glu Ser Gln Ser His Pro Gly Asp Phe Val Leu
 130 135 140

Ser Val Arg Thr Gly Asp Asp Lys Gly Glu Ser Asn Asp Gly Lys Ser
 145 150 155 160

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Lys Val Thr His Val Met Ile Arg Cys Gln Glu Leu Lys Tyr Asp Val
165 170 175

Gly Gly Gly Glu Arg Phe Asp Ser Leu Thr Asp Leu Val Glu His Tyr
180 185 190

Lys Lys Asn Pro Met Val Glu Thr Leu Gly Thr Val Leu Gln Leu Lys
195 200 205

Gln Pro Leu
210

<210> 13
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3-zeta endodomain

<400> 13

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

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

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

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

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

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

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

<210> 14
<211> 754
<212> PRT
<213> Artificial Sequence

<220>
<223> ZAP70-SH2 domain fused to a CD3-zeta endodomain

<400> 14

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

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

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

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

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

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

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

Pro Arg Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

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Gly Ser Gly Gly Gly Gly Ser Met Pro Asp Pro Ala Ala His Leu Pro
130 135 140

Phe Phe Tyr Gly Ser Ile Ser Arg Ala Glu Ala Glu Glu His Leu Lys
145 150 155 160

Leu Ala Gly Met Ala Asp Gly Leu Phe Leu Leu Arg Gln Cys Leu Arg
165 170 175

Ser Leu Gly Gly Tyr Val Leu Ser Leu Val His Asp Val Arg Phe His
180 185 190

His Phe Pro Ile Glu Arg Gln Leu Asn Gly Thr Tyr Ala Ile Ala Gly
195 200 205

Gly Lys Ala His Cys Gly Pro Ala Glu Leu Cys Glu Phe Tyr Ser Arg
210 215 220

Asp Pro Asp Gly Leu Pro Cys Asn Leu Arg Lys Pro Cys Asn Arg Pro
225 230 235 240

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

Met Val Arg Asp Tyr Val Arg Gln Thr Trp Lys Leu Glu Gly Glu Ala
260 265 270

Leu Glu Gln Ala Ile Ile Ser Gln Ala Pro Gln Val Glu Lys Leu Ile
275 280 285

Ala Thr Thr Ala His Glu Arg Met Pro Trp Tyr His Ser Ser Leu Thr
290 295 300

Arg Glu Glu Ala Glu Arg Lys Leu Tyr Ser Gly Ala Gln Thr Asp Gly
305 310 315 320

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Lys Phe Leu Leu Arg Pro Arg Lys Glu Gln Gly Thr Tyr Ala Leu Ser
325 330 335

Leu Ile Tyr Gly Lys Thr Val Tyr His Tyr Leu Ile Ser Gln Asp Lys
340 345 350

Ala Gly Lys Tyr Cys Ile Pro Glu Gly Thr Lys Phe Asp Thr Leu Trp
355 360 365

Gln Leu Val Glu Tyr Leu Lys Leu Lys Ala Asp Gly Leu Ile Tyr Cys
370 375 380

Leu Lys Glu Ala Cys Pro Asn Ser Ser Ala Ser Asn Ala Ser Gly Ala
385 390 395 400

Ala Ala Pro Thr Leu Pro Ala His Pro Ser Thr Leu Thr His Pro Gln
405 410 415

Arg Arg Ile Asp Thr Leu Asn Ser Asp Gly Tyr Thr Pro Glu Pro Ala
420 425 430

Arg Ile Thr Ser Pro Asp Lys Pro Arg Pro Met Pro Met Asp Thr Ser
435 440 445

Val Tyr Glu Ser Pro Tyr Ser Asp Pro Glu Glu Leu Lys Asp Lys Lys
450 455 460

Leu Phe Leu Lys Arg Asp Asn Leu Leu Ile Ala Asp Ile Glu Leu Gly
465 470 475 480

Cys Gly Asn Phe Gly Ser Val Arg Gln Gly Val Tyr Arg Met Arg Lys
485 490 495

Lys Gln Ile Asp Val Ala Ile Lys Val Leu Lys Gln Gly Thr Glu Lys
500 505 510

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Ala Asp Thr Glu Glu Met Met Arg Glu Ala Gln Ile Met His Gln Leu
515 520 525

Asp Asn Pro Tyr Ile Val Arg Leu Ile Gly Val Cys Gln Ala Glu Ala
530 535 540

Leu Met Leu Val Met Glu Met Ala Gly Gly Gly Pro Leu His Lys Phe
545 550 555 560

Leu Val Gly Lys Arg Glu Glu Ile Pro Val Ser Asn Val Ala Glu Leu
565 570 575

Leu His Gln Val Ser Met Gly Met Lys Tyr Leu Glu Glu Lys Asn Phe
580 585 590

Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Leu Val Asn Arg His
595 600 605

Tyr Ala Lys Ile Ser Asp Phe Gly Leu Ser Lys Ala Leu Gly Ala Asp
610 615 620

Asp Ser Tyr Tyr Thr Ala Arg Ser Ala Gly Lys Trp Pro Leu Lys Trp
625 630 635 640

Tyr Ala Pro Glu Cys Ile Asn Phe Arg Lys Phe Ser Ser Arg Ser Asp
645 650 655

Val Trp Ser Tyr Gly Val Thr Met Trp Glu Ala Leu Ser Tyr Gly Gln
660 665 670

Lys Pro Tyr Lys Lys Met Lys Gly Pro Glu Val Met Ala Phe Ile Glu
675 680 685

Gln Gly Lys Arg Met Glu Cys Pro Pro Glu Cys Pro Pro Glu Leu Tyr
690 695 700

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Ala Leu Met Ser Asp Cys Trp Ile Tyr Lys Trp Glu Asp Arg Pro Asp
705 710 715 720

Phe Leu Thr Val Glu Gln Arg Met Arg Ala Cys Tyr Tyr Ser Leu Ala
725 730 735

Ser Lys Val Glu Gly Pro Pro Gly Ser Thr Gln Lys Ala Glu Ala Ala
740 745 750

Cys Ala

<210> 15
<211> 97
<212> PRT
<213> Artificial Sequence

<220>
<223> PDCD1 endodomain

<400> 15

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

Pro Leu Lys Glu Asp Pro Ser Ala Val Pro Val Phe Ser Val Asp Tyr
20 25 30

Gly Glu Leu Asp Phe Gln Trp Arg Glu Lys Thr Pro Glu Pro Pro Val
35 40 45

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

Gly Met Gly Thr Ser Ser Pro Ala Arg Arg Gly Ser Ala Asp Gly Pro
65 70 75 80

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Arg Ser Ala Gln Pro Leu Arg Pro Glu Asp Gly His Cys Ser Trp Pro
85 90 95

Leu

<210> 16
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> BTLA4 endodomain

<400> 16

Lys Leu Gln Arg Arg Trp Lys Arg Thr Gln Ser Gln Gln Gly Leu Gln
1 5 10 15

Glu Asn Ser Ser Gly Gln Ser Phe Phe Val Arg Asn Lys Lys Val Arg
20 25 30

Arg Ala Pro Leu Ser Glu Gly Pro His Ser Leu Gly Cys Tyr Asn Pro
35 40 45

Met Met Glu Asp Gly Ile Ser Tyr Thr Thr Leu Arg Phe Pro Glu Met
50 55 60

Asn Ile Pro Arg Thr Gly Asp Ala Glu Ser Ser Glu Met Gln Arg Pro
65 70 75 80

Pro Pro Asp Cys Asp Asp Thr Val Thr Tyr Ser Ala Leu His Lys Arg
85 90 95

Gln Val Gly Asp Tyr Glu Asn Val Ile Pro Asp Phe Pro Glu Asp Glu
100 105 110

Gly Ile His Tyr Ser Glu Leu Ile Gln Phe Gly Val Gly Glu Arg Pro
115 120 125

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Gln Ala Gln Glu Asn Val Asp Tyr Val Ile Leu Lys His
 130 135 140

<210> 17
 <211> 168
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> LILRB1 endodomain

<400> 17

Leu Arg His Arg Arg Gln Gly Lys His Trp Thr Ser Thr Gln Arg Lys
 1 5 10 15

Ala Asp Phe Gln His Pro Ala Gly Ala Val Gly Pro Glu Pro Thr Asp
 20 25 30

Arg Gly Leu Gln Trp Arg Ser Ser Pro Ala Ala Asp Ala Gln Glu Glu
 35 40 45

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

Met Asp Thr Arg Ser Pro His Asp Glu Asp Pro Gln Ala Val Thr Tyr
 65 70 75 80

Ala Glu Val Lys His Ser Arg Pro Arg Arg Glu Met Ala Ser Pro Pro
 85 90 95

Ser Pro Leu Ser Gly Glu Phe Leu Asp Thr Lys Asp Arg Gln Ala Glu
 100 105 110

Glu Asp Arg Gln Met Asp Thr Glu Ala Ala Ala Ser Glu Ala Pro Gln
 115 120 125

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Asp Val Thr Tyr Ala Gln Leu His Ser Leu Thr Leu Arg Arg Glu Ala
130 135 140

Thr Glu Pro Pro Pro Ser Gln Glu Gly Pro Ser Pro Ala Val Pro Ser
145 150 155 160

Ile Tyr Ala Thr Leu Ala Ile His
165

<210> 18
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> LAIR1 endodomain

<400> 18

His Arg Gln Asn Gln Ile Lys Gln Gly Pro Pro Arg Ser Lys Asp Glu
1 5 10 15

Glu Gln Lys Pro Gln Gln Arg Pro Asp Leu Ala Val Asp Val Leu Glu
20 25 30

Arg Thr Ala Asp Lys Ala Thr Val Asn Gly Leu Pro Glu Lys Asp Arg
35 40 45

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

Tyr Ala Gln Leu Asp His Trp Ala Leu Thr Gln Arg Thr Ala Arg Ala
65 70 75 80

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

Ala Val Ala Arg His
100

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<210> 19
 <211> 62
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CTLA4 endodomain

<400> 19

Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe Tyr
 1 5 10 15

Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys Arg
 20 25 30

Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu Pro
 35 40 45

Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
 50 55 60

<210> 20
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KIR2DL1 endodomain

<400> 20

Gly Asn Ser Arg His Leu His Val Leu Ile Gly Thr Ser Val Val Ile
 1 5 10 15

Ile Pro Phe Ala Ile Leu Leu Phe Phe Leu Leu His Arg Trp Cys Ala
 20 25 30

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

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Thr Val Asn Arg Glu Asp Ser Asp Glu Gln Asp Pro Gln Glu Val Thr
50 55 60

Tyr Thr Gln Leu Asn His Cys Val Phe Thr Gln Arg Lys Ile Thr Arg
65 70 75 80

Pro Ser Gln Arg Pro Lys Thr Pro Pro Thr Asp Ile Ile Val Tyr Thr
85 90 95

Glu Leu Pro Asn Ala Glu Ser Arg Ser Lys Val Val Ser Cys Pro
100 105 110

<210> 21
<211> 143
<212> PRT
<213> Artificial Sequence

<220>
<223> KIR2DL4 endodomain

<400> 21

Gly Ile Ala Arg His Leu His Ala Val Ile Arg Tyr Ser Val Ala Ile
1 5 10 15

Ile Leu Phe Thr Ile Leu Pro Phe Phe Leu Leu His Arg Trp Cys Ser
20 25 30

Lys Lys Lys Glu Asn Ala Ala Val Met Asn Gln Glu Pro Ala Gly His
35 40 45

Arg Thr Val Asn Arg Glu Asp Ser Asp Glu Gln Asp Pro Gln Glu Val
50 55 60

Thr Tyr Ala Gln Leu Asp His Cys Ile Phe Thr Gln Arg Lys Ile Thr
65 70 75 80

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

Ile Glu Leu Pro Asn Ala Glu Pro Arg Ala Leu Ser Pro Ala His Glu
100 105 110

His His Ser Gln Ala Leu Met Gly Ser Ser Arg Glu Thr Thr Ala Leu
115 120 125

Ser Gln Thr Gln Leu Ala Ser Ser Asn Val Pro Ala Ala Gly Ile
130 135 140

<210> 22
<211> 143
<212> PRT
<213> Artificial Sequence

<220>
<223> KIR2DL5 endodomain

<400> 22

Thr Gly Ile Arg Arg His Leu His Ile Leu Ile Gly Thr Ser Val Ala
1 5 10 15

Ile Ile Leu Phe Ile Ile Leu Phe Phe Phe Leu Leu His Cys Cys Cys
20 25 30

Ser Asn Lys Lys Asn Ala Ala Val Met Asp Gln Glu Pro Ala Gly Asp
35 40 45

Arg Thr Val Asn Arg Glu Asp Ser Asp Asp Gln Asp Pro Gln Glu Val
50 55 60

Thr Tyr Ala Gln Leu Asp His Cys Val Phe Thr Gln Thr Lys Ile Thr
65 70 75 80

Ser Pro Ser Gln Arg Pro Lys Thr Pro Pro Thr Asp Thr Thr Met Tyr
85 90 95

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Met Glu Leu Pro Asn Ala Lys Pro Arg Ser Leu Ser Pro Ala His Lys
100 105 110

His His Ser Gln Ala Leu Arg Gly Ser Ser Arg Glu Thr Thr Ala Leu
115 120 125

Ser Gln Asn Arg Val Ala Ser Ser His Val Pro Ala Ala Gly Ile
130 135 140

<210> 23
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> KIR3DL1 endodomain

<400> 23

Lys Asp Pro Arg His Leu His Ile Leu Ile Gly Thr Ser Val Val Ile
1 5 10 15

Ile Leu Phe Ile Leu Leu Leu Phe Phe Leu Leu His Leu Trp Cys Ser
20 25 30

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

Thr Ala Asn Ser Glu Asp Ser Asp Glu Gln Asp Pro Glu Glu Val Thr
50 55 60

Tyr Ala Gln Leu Asp His Cys Val Phe Thr Gln Arg Lys Ile Thr Arg
65 70 75 80

Pro Ser Gln Arg Pro Lys Thr Pro Pro Thr Asp Thr Ile Leu Tyr Thr
85 90 95

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Glu Leu Pro Asn Ala Lys Pro Arg Ser Lys Val Val Ser Cys Pro
 100 105 110

<210> 24
 <211> 97
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KIR3DL3 endodomain

<400> 24

Lys Asp Pro Gly Asn Ser Arg His Leu His Val Leu Ile Gly Thr Ser
 1 5 10 15

Val Val Ile Ile Pro Phe Ala Ile Leu Leu Phe Phe Leu Leu His Arg
 20 25 30

Trp Cys Ala Asn Lys Lys Asn Ala Val Val Met Asp Gln Glu Pro Ala
 35 40 45

Gly Asn Arg Thr Val Asn Arg Glu Asp Ser Asp Glu Gln Asp Pro Gln
 50 55 60

Glu Val Thr Tyr Ala Gln Leu Asn His Cys Val Phe Thr Gln Arg Lys
 65 70 75 80

Ile Thr Arg Pro Ser Gln Arg Pro Lys Thr Pro Pro Thr Asp Thr Ser
 85 90 95

Val

<210> 25
 <211> 701
 <212> PRT
 <213> Artificial Sequence

<220>

pctgb2016051576-seq1

<223> PTPN6-SH2 domain fused to a PD1 endodomain

<400> 25

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

Ser Val Asp Tyr Gly Glu Leu Asp Phe Gln Trp Arg Glu Lys Thr Pro
20 25 30

Glu Pro Pro Val Pro Cys Val Pro Glu Gln Thr Glu Tyr Ala Thr Ile
35 40 45

Val Phe Pro Ser Gly Met Gly Thr Ser Ser Pro Ala Arg Arg Gly Ser
50 55 60

Ala Asp Gly Pro Arg Ser Ala Gln Pro Leu Arg Pro Glu Asp Gly His
65 70 75 80

Cys Ser Trp Pro Leu Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
85 90 95

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Met Val Arg Trp Phe His
100 105 110

Arg Asp Leu Ser Gly Leu Asp Ala Glu Thr Leu Leu Lys Gly Arg Gly
115 120 125

Val His Gly Ser Phe Leu Ala Arg Pro Ser Arg Lys Asn Gln Gly Asp
130 135 140

Phe Ser Leu Ser Val Arg Val Gly Asp Gln Val Thr His Ile Arg Ile
145 150 155 160

Gln Asn Ser Gly Asp Phe Tyr Asp Leu Tyr Gly Gly Glu Lys Phe Ala
165 170 175

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Thr Leu Thr Glu Leu Val Glu Tyr Tyr Thr Gln Gln Gln Gly Val Leu
180 185 190

Gln Asp Arg Asp Gly Thr Ile Ile His Leu Lys Tyr Pro Leu Asn Cys
195 200 205

Ser Asp Pro Thr Ser Glu Arg Trp Tyr His Gly His Met Ser Gly Gly
210 215 220

Gln Ala Glu Thr Leu Leu Gln Ala Lys Gly Glu Pro Trp Thr Phe Leu
225 230 235 240

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

Ser Asp Gln Pro Lys Ala Gly Pro Gly Ser Pro Leu Arg Val Thr His
260 265 270

Ile Lys Val Met Cys Glu Gly Gly Arg Tyr Thr Val Gly Gly Leu Glu
275 280 285

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

Ile Glu Glu Ala Ser Gly Ala Phe Val Tyr Leu Arg Gln Pro Tyr Tyr
305 310 315 320

Ala Thr Arg Val Asn Ala Ala Asp Ile Glu Asn Arg Val Leu Glu Leu
325 330 335

Asn Lys Lys Gln Glu Ser Glu Asp Thr Ala Lys Ala Gly Phe Trp Glu
340 345 350

Glu Phe Glu Ser Leu Gln Lys Gln Glu Val Lys Asn Leu His Gln Arg
355 360 365

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Leu Glu Gly Gln Arg Pro Glu Asn Lys Gly Lys Asn Arg Tyr Lys Asn
370 375 380

Ile Leu Pro Phe Asp His Ser Arg Val Ile Leu Gln Gly Arg Asp Ser
385 390 395 400

Asn Ile Pro Gly Ser Asp Tyr Ile Asn Ala Asn Tyr Ile Lys Asn Gln
405 410 415

Leu Leu Gly Pro Asp Glu Asn Ala Lys Thr Tyr Ile Ala Ser Gln Gly
420 425 430

Cys Leu Glu Ala Thr Val Asn Asp Phe Trp Gln Met Ala Trp Gln Glu
435 440 445

Asn Ser Arg Val Ile Val Met Thr Thr Arg Glu Val Glu Lys Gly Arg
450 455 460

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

Gly Pro Tyr Ser Val Thr Asn Cys Gly Glu His Asp Thr Thr Glu Tyr
485 490 495

Lys Leu Arg Thr Leu Gln Val Ser Pro Leu Asp Asn Gly Asp Leu Ile
500 505 510

Arg Glu Ile Trp His Tyr Gln Tyr Leu Ser Trp Pro Asp His Gly Val
515 520 525

Pro Ser Glu Pro Gly Gly Val Leu Ser Phe Leu Asp Gln Ile Asn Gln
530 535 540

Arg Gln Glu Ser Leu Pro His Ala Gly Pro Ile Ile Val His Cys Ser
545 550 555 560

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Ala Gly Ile Gly Arg Thr Gly Thr Ile Ile Val Ile Asp Met Leu Met
565 570 575

Glu Asn Ile Ser Thr Lys Gly Leu Asp Cys Asp Ile Asp Ile Gln Lys
580 585 590

Thr Ile Gln Met Val Arg Ala Gln Arg Ser Gly Met Val Gln Thr Glu
595 600 605

Ala Gln Tyr Lys Phe Ile Tyr Val Ala Ile Ala Gln Phe Ile Glu Thr
610 615 620

Thr Lys Lys Lys Leu Glu Val Leu Gln Ser Gln Lys Gly Gln Glu Ser
625 630 635 640

Glu Tyr Gly Asn Ile Thr Tyr Pro Pro Ala Met Lys Asn Ala His Ala
645 650 655

Lys Ala Ser Arg Thr Ser Ser Lys His Lys Glu Asp Val Tyr Glu Asn
660 665 670

Leu His Thr Lys Asn Lys Arg Glu Glu Lys Val Lys Lys Gln Arg Ser
675 680 685

Ala Asp Lys Glu Lys Ser Lys Gly Ser Leu Lys Arg Lys
690 695 700

<210> 26
<211> 299
<212> PRT
<213> Artificial Sequence

<220>
<223> ZAP70 kinase domain

<400> 26

Asp Pro Glu Glu Leu Lys Asp Lys Lys Leu Phe Leu Lys Arg Asp Asn
1 5 10 15

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Leu Leu Ile Ala Asp Ile Glu Leu Gly Cys Gly Asn Phe Gly Ser Val
20 25 30

Arg Gln Gly Val Tyr Arg Met Arg Lys Lys Gln Ile Asp Val Ala Ile
35 40 45

Lys Val Leu Lys Gln Gly Thr Glu Lys Ala Asp Thr Glu Glu Met Met
50 55 60

Arg Glu Ala Gln Ile Met His Gln Leu Asp Asn Pro Tyr Ile Val Arg
65 70 75 80

Leu Ile Gly Val Cys Gln Ala Glu Ala Leu Met Leu Val Met Glu Met
85 90 95

Ala Gly Gly Gly Pro Leu His Lys Phe Leu Val Gly Lys Arg Glu Glu
100 105 110

Ile Pro Val Ser Asn Val Ala Glu Leu Leu His Gln Val Ser Met Gly
115 120 125

Met Lys Tyr Leu Glu Glu Lys Asn Phe Val His Arg Asp Leu Ala Ala
130 135 140

Arg Asn Val Leu Leu Val Asn Arg His Tyr Ala Lys Ile Ser Asp Phe
145 150 155 160

Gly Leu Ser Lys Ala Leu Gly Ala Asp Asp Ser Tyr Tyr Thr Ala Arg
165 170 175

Ser Ala Gly Lys Trp Pro Leu Lys Trp Tyr Ala Pro Glu Cys Ile Asn
180 185 190

Phe Arg Lys Phe Ser Ser Arg Ser Asp Val Trp Ser Tyr Gly Val Thr
195 200 205

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Met Trp Glu Ala Leu Ser Tyr Gly Gln Lys Pro Tyr Lys Lys Met Lys
210 215 220

Gly Pro Glu Val Met Ala Phe Ile Glu Gln Gly Lys Arg Met Glu Cys
225 230 235 240

Pro Pro Glu Cys Pro Pro Glu Leu Tyr Ala Leu Met Ser Asp Cys Trp
245 250 255

Ile Tyr Lys Trp Glu Asp Arg Pro Asp Phe Leu Thr Val Glu Gln Arg
260 265 270

Met Arg Ala Cys Tyr Tyr Ser Leu Ala Ser Lys Val Glu Gly Pro Pro
275 280 285

Gly Ser Thr Gln Lys Ala Glu Ala Ala Cys Ala
290 295

<210> 27
<211> 280
<212> PRT
<213> Artificial Sequence

<220>
<223> PTPN6 phosphatase domain

<400> 27

Phe Trp Glu Glu Phe Glu Ser Leu Gln Lys Gln Glu Val Lys Asn Leu
1 5 10 15

His Gln Arg Leu Glu Gly Gln Arg Pro Glu Asn Lys Gly Lys Asn Arg
20 25 30

Tyr Lys Asn Ile Leu Pro Phe Asp His Ser Arg Val Ile Leu Gln Gly
35 40 45

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

Lys Asn Gln Leu Leu Gly Pro Asp Glu Asn Ala Lys Thr Tyr Ile Ala
65 70 75 80

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

Trp Gln Glu Asn Ser Arg Val Ile Val Met Thr Thr Arg Glu Val Glu
100 105 110

Lys Gly Arg Asn Lys Cys Val Pro Tyr Trp Pro Glu Val Gly Met Gln
115 120 125

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

Thr Glu Tyr Lys Leu Arg Thr Leu Gln Val Ser Pro Leu Asp Asn Gly
145 150 155 160

Asp Leu Ile Arg Glu Ile Trp His Tyr Gln Tyr Leu Ser Trp Pro Asp
165 170 175

His Gly Val Pro Ser Glu Pro Gly Gly Val Leu Ser Phe Leu Asp Gln
180 185 190

Ile Asn Gln Arg Gln Glu Ser Leu Pro His Ala Gly Pro Ile Ile Val
195 200 205

His Cys Ser Ala Gly Ile Gly Arg Thr Gly Thr Ile Ile Val Ile Asp
210 215 220

Met Leu Met Glu Asn Ile Ser Thr Lys Gly Leu Asp Cys Asp Ile Asp
225 230 235 240

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Ile Gln Lys Thr Ile Gln Met Val Arg Ala Gln Arg Ser Gly Met Val
245 250 255

Gln Thr Glu Ala Gln Tyr Lys Phe Ile Tyr Val Ala Ile Ala Gln Phe
260 265 270

Ile Glu Thr Thr Lys Lys Lys Leu
275 280

<210> 28

<211> 274

<212> PRT

<213> Artificial Sequence

<220>

<223> SHP-2 phosphatase domain

<400> 28

Trp Glu Glu Phe Glu Thr Leu Gln Gln Gln Glu Cys Lys Leu Leu Tyr
1 5 10 15

Ser Arg Lys Glu Gly Gln Arg Gln Glu Asn Lys Asn Lys Asn Arg Tyr
20 25 30

Lys Asn Ile Leu Pro Phe Asp His Thr Arg Val Val Leu His Asp Gly
35 40 45

Asp Pro Asn Glu Pro Val Ser Asp Tyr Ile Asn Ala Asn Ile Ile Met
50 55 60

Pro Glu Phe Glu Thr Lys Cys Asn Asn Ser Lys Pro Lys Lys Ser Tyr
65 70 75 80

Ile Ala Thr Gln Gly Cys Leu Gln Asn Thr Val Asn Asp Phe Trp Arg
85 90 95

Met Val Phe Gln Glu Asn Ser Arg Val Ile Val Met Thr Thr Lys Glu
100 105 110

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Val Glu Arg Gly Lys Ser Lys Cys Val Lys Tyr Trp Pro Asp Glu Tyr
115 120 125

Ala Leu Lys Glu Tyr Gly Val Met Arg Val Arg Asn Val Lys Glu Ser
130 135 140

Ala Ala His Asp Tyr Thr Leu Arg Glu Leu Lys Leu Ser Lys Val Gly
145 150 155 160

Gln Ala Leu Leu Gln Gly Asn Thr Glu Arg Thr Val Trp Gln Tyr His
165 170 175

Phe Arg Thr Trp Pro Asp His Gly Val Pro Ser Asp Pro Gly Gly Val
180 185 190

Leu Asp Phe Leu Glu Glu Val His His Lys Gln Glu Ser Ile Met Asp
195 200 205

Ala Gly Pro Val Val Val His Cys Ser Ala Gly Ile Gly Arg Thr Gly
210 215 220

Thr Phe Ile Val Ile Asp Ile Leu Ile Asp Ile Ile Arg Glu Lys Gly
225 230 235 240

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

Gln Arg Ser Gly Met Val Gln Thr Glu Ala Gln Tyr Arg Phe Ile Tyr
260 265 270

Met Ala

<210> 29
<211> 519

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<212> PRT

<213> Artificial Sequence

<220>

<223> PTPN6 SH2 domain fusion: ZAP70 kinase domain

<400> 29

Met Val Arg Trp Phe His Arg Asp Leu Ser Gly Leu Asp Ala Glu Thr
1 5 10 15

Leu Leu Lys Gly Arg Gly Val His Gly Ser Phe Leu Ala Arg Pro Ser
20 25 30

Arg Lys Asn Gln Gly Asp Phe Ser Leu Ser Val Arg Val Gly Asp Gln
35 40 45

Val Thr His Ile Arg Ile Gln Asn Ser Gly Asp Phe Tyr Asp Leu Tyr
50 55 60

Gly Gly Glu Lys Phe Ala Thr Leu Thr Glu Leu Val Glu Tyr Tyr Thr
65 70 75 80

Gln Gln Gln Gly Val Leu Gln Asp Arg Asp Gly Thr Ile Ile His Leu
85 90 95

Lys Tyr Pro Leu Asn Cys Ser Asp Pro Thr Ser Glu Arg Trp Tyr His
100 105 110

Gly His Met Ser Gly Gly Gln Ala Glu Thr Leu Leu Gln Ala Lys Gly
115 120 125

Glu Pro Trp Thr Phe Leu Val Arg Glu Ser Leu Ser Gln Pro Gly Asp
130 135 140

Phe Val Leu Ser Val Leu Ser Asp Gln Pro Lys Ala Gly Pro Gly Ser
145 150 155 160

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Pro Leu Arg Val Thr His Ile Lys Val Met Cys Glu Gly Gly Arg Tyr
165 170 175

Thr Val Gly Gly Leu Glu Thr Phe Asp Ser Leu Thr Asp Leu Val Glu
180 185 190

His Phe Lys Lys Thr Gly Ile Glu Glu Ala Ser Gly Ala Phe Val Tyr
195 200 205

Leu Arg Gln Pro Tyr Tyr Ser Gly Gly Gly Gly Ser Asp Pro Glu Glu
210 215 220

Leu Lys Asp Lys Lys Leu Phe Leu Lys Arg Asp Asn Leu Leu Ile Ala
225 230 235 240

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

Tyr Arg Met Arg Lys Lys Gln Ile Asp Val Ala Ile Lys Val Leu Lys
260 265 270

Gln Gly Thr Glu Lys Ala Asp Thr Glu Glu Met Met Arg Glu Ala Gln
275 280 285

Ile Met His Gln Leu Asp Asn Pro Tyr Ile Val Arg Leu Ile Gly Val
290 295 300

Cys Gln Ala Glu Ala Leu Met Leu Val Met Glu Met Ala Gly Gly Gly
305 310 315 320

Pro Leu His Lys Phe Leu Val Gly Lys Arg Glu Glu Ile Pro Val Ser
325 330 335

Asn Val Ala Glu Leu Leu His Gln Val Ser Met Gly Met Lys Tyr Leu
340 345 350

pctgb2016051576-seq1

Glu Glu Lys Asn Phe Val His Arg Asp Leu Ala Ala Arg Asn Val Leu
 355 360 365

Leu Val Asn Arg His Tyr Ala Lys Ile Ser Asp Phe Gly Leu Ser Lys
 370 375 380

Ala Leu Gly Ala Asp Asp Ser Tyr Tyr Thr Ala Arg Ser Ala Gly Lys
 385 390 395 400

Trp Pro Leu Lys Trp Tyr Ala Pro Glu Cys Ile Asn Phe Arg Lys Phe
 405 410 415

Ser Ser Arg Ser Asp Val Trp Ser Tyr Gly Val Thr Met Trp Glu Ala
 420 425 430

Leu Ser Tyr Gly Gln Lys Pro Tyr Lys Lys Met Lys Gly Pro Glu Val
 435 440 445

Met Ala Phe Ile Glu Gln Gly Lys Arg Met Glu Cys Pro Pro Glu Cys
 450 455 460

Pro Pro Glu Leu Tyr Ala Leu Met Ser Asp Cys Trp Ile Tyr Lys Trp
 465 470 475 480

Glu Asp Arg Pro Asp Phe Leu Thr Val Glu Gln Arg Met Arg Ala Cys
 485 490 495

Tyr Tyr Ser Leu Ala Ser Lys Val Glu Gly Pro Pro Gly Ser Thr Gln
 500 505 510

Lys Ala Glu Ala Ala Cys Ala
 515

<210> 30

<211> 581

<212> PRT

<213> Artificial Sequence

pctgb2016051576-seq1

<220>

<223> ZAP70 SH2 domain fusion: PTPN6 phosphatase domain

<400> 30

Met Pro Asp Pro Ala Ala His Leu Pro Phe Phe Tyr Gly Ser Ile Ser
1 5 10 15

Arg Ala Glu Ala Glu Glu His Leu Lys Leu Ala Gly Met Ala Asp Gly
20 25 30

Leu Phe Leu Leu Arg Gln Cys Leu Arg Ser Leu Gly Gly Tyr Val Leu
35 40 45

Ser Leu Val His Asp Val Arg Phe His His Phe Pro Ile Glu Arg Gln
50 55 60

Leu Asn Gly Thr Tyr Ala Ile Ala Gly Gly Lys Ala His Cys Gly Pro
65 70 75 80

Ala Glu Leu Cys Glu Phe Tyr Ser Arg Asp Pro Asp Gly Leu Pro Cys
85 90 95

Asn Leu Arg Lys Pro Cys Asn Arg Pro Ser Gly Leu Glu Pro Gln Pro
100 105 110

Gly Val Phe Asp Cys Leu Arg Asp Ala Met Val Arg Asp Tyr Val Arg
115 120 125

Gln Thr Trp Lys Leu Glu Gly Glu Ala Leu Glu Gln Ala Ile Ile Ser
130 135 140

Gln Ala Pro Gln Val Glu Lys Leu Ile Ala Thr Thr Ala His Glu Arg
145 150 155 160

Met Pro Trp Tyr His Ser Ser Leu Thr Arg Glu Glu Ala Glu Arg Lys
165 170 175

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Leu Tyr Ser Gly Ala Gln Thr Asp Gly Lys Phe Leu Leu Arg Pro Arg
180 185 190

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

Tyr His Tyr Leu Ile Ser Gln Asp Lys Ala Gly Lys Tyr Cys Ile Pro
210 215 220

Glu Gly Thr Lys Phe Asp Thr Leu Trp Gln Leu Val Glu Tyr Leu Lys
225 230 235 240

Leu Lys Ala Asp Gly Leu Ile Tyr Cys Leu Lys Glu Ala Cys Pro Asn
245 250 255

Ser Ser Ala Ser Asn Ala Ser Gly Ala Ala Ala Pro Thr Leu Pro Ala
260 265 270

His Pro Ser Thr Leu Thr His Pro Ser Gly Gly Gly Gly Ser Gly Gly
275 280 285

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Phe Trp Glu
290 295 300

Glu Phe Glu Ser Leu Gln Lys Gln Glu Val Lys Asn Leu His Gln Arg
305 310 315 320

Leu Glu Gly Gln Arg Pro Glu Asn Lys Gly Lys Asn Arg Tyr Lys Asn
325 330 335

Ile Leu Pro Phe Asp His Ser Arg Val Ile Leu Gln Gly Arg Asp Ser
340 345 350

Asn Ile Pro Gly Ser Asp Tyr Ile Asn Ala Asn Tyr Ile Lys Asn Gln
355 360 365

pctgb2016051576-seq1

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

Cys Leu Glu Ala Thr Val Asn Asp Phe Trp Gln Met Ala Trp Gln Glu
385 390 395 400

Asn Ser Arg Val Ile Val Met Thr Thr Arg Glu Val Glu Lys Gly Arg
405 410 415

Asn Lys Cys Val Pro Tyr Trp Pro Glu Val Gly Met Gln Arg Ala Tyr
420 425 430

Gly Pro Tyr Ser Val Thr Asn Cys Gly Glu His Asp Thr Thr Glu Tyr
435 440 445

Lys Leu Arg Thr Leu Gln Val Ser Pro Leu Asp Asn Gly Asp Leu Ile
450 455 460

Arg Glu Ile Trp His Tyr Gln Tyr Leu Ser Trp Pro Asp His Gly Val
465 470 475 480

Pro Ser Glu Pro Gly Gly Val Leu Ser Phe Leu Asp Gln Ile Asn Gln
485 490 495

Arg Gln Glu Ser Leu Pro His Ala Gly Pro Ile Ile Val His Cys Ser
500 505 510

Ala Gly Ile Gly Arg Thr Gly Thr Ile Ile Val Ile Asp Met Leu Met
515 520 525

Glu Asn Ile Ser Thr Lys Gly Leu Asp Cys Asp Ile Asp Ile Gln Lys
530 535 540

Thr Ile Gln Met Val Arg Ala Gln Arg Ser Gly Met Val Gln Thr Glu
545 550 555 560

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Ala Gln Tyr Lys Phe Ile Tyr Val Ala Ile Ala Gln Phe Ile Glu Thr
565 570 575

Thr Lys Lys Lys Leu
580

<210> 31
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<223> CD28 endodomain

<400> 31

Met Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
1 5 10 15

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
20 25 30

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
35 40

<210> 32
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> 41BB endodomain

<400> 32

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

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

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Phe Pro Glu Glu Glu Gly Gly Cys Glu Leu
 35 40

<210> 33
 <211> 37
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> OX40 endodomain

<400> 33

Met Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly
 1 5 10 15

Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser
 20 25 30

Thr Leu Ala Lys Ile
 35

<210> 34
 <211> 38
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ICOS endodomain

<400> 34

Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro Asn
 1 5 10 15

Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser Arg
 20 25 30

Leu Thr Asp Val Thr Leu
 35

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<210> 35
 <211> 48
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD27 endodomain

<400> 35

Gln Arg Arg Lys Tyr Arg Ser Asn Lys Gly Glu Ser Pro Val Glu Pro
 1 5 10 15

Ala Glu Pro Cys His Tyr Ser Cys Pro Arg Glu Glu Glu Gly Ser Thr
 20 25 30

Ile Pro Ile Gln Glu Asp Tyr Arg Lys Pro Glu Pro Ala Cys Ser Pro
 35 40 45

<210> 36
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> BTLA endodomain

<400> 36

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

Glu Ile Asn Leu Val Asp Ala His Leu Lys Ser Glu Gln Thr Glu Ala
 20 25 30

Ser Thr Arg Gln Asn Ser Gln Val Leu Leu Ser Glu Thr Gly Ile Tyr
 35 40 45

Asp Asn Asp Pro Asp Leu Cys Phe Arg Met Gln Glu Gly Ser Glu Val
 50 55 60

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Tyr Ser Asn Pro Cys Leu Glu Glu Asn Lys Pro Gly Ile Val Tyr Ala
65 70 75 80

Ser Leu Asn His Ser Val Ile Gly Pro Asn Ser Arg Leu Ala Arg Asn
85 90 95

Val Lys Glu Ala Pro Thr Glu Tyr Ala Ser Ile Cys Val Arg Ser
100 105 110

<210> 37
<211> 188
<212> PRT
<213> Artificial Sequence

<220>
<223> CD30 endodomain

<400> 37

His Arg Arg Ala Cys Arg Lys Arg Ile Arg Gln Lys Leu His Leu Cys
1 5 10 15

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

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

Pro Val Ala Glu Glu Arg Gly Leu Met Ser Gln Pro Leu Met Glu Thr
50 55 60

Cys His Ser Val Gly Ala Ala Tyr Leu Glu Ser Leu Pro Leu Gln Asp
65 70 75 80

Ala Ser Pro Ala Gly Gly Pro Ser Ser Pro Arg Asp Leu Pro Glu Pro
85 90 95

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Arg Val Ser Thr Glu His Thr Asn Asn Lys Ile Glu Lys Ile Tyr Ile
100 105 110

Met Lys Ala Asp Thr Val Ile Val Gly Thr Val Lys Ala Glu Leu Pro
115 120 125

Glu Gly Arg Gly Leu Ala Gly Pro Ala Glu Pro Glu Leu Glu Glu Glu
130 135 140

Leu Glu Ala Asp His Thr Pro His Tyr Pro Glu Gln Glu Thr Glu Pro
145 150 155 160

Pro Leu Gly Ser Cys Ser Asp Val Met Leu Ser Val Glu Glu Glu Gly
165 170 175

Lys Glu Asp Pro Leu Pro Thr Ala Ala Ser Gly Lys
180 185

<210> 38
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> GITR endodomain

<400> 38

Gln Leu Gly Leu His Ile Trp Gln Leu Arg Ser Gln Cys Met Trp Pro
1 5 10 15

Arg Glu Thr Gln Leu Leu Leu Glu Val Pro Pro Ser Thr Glu Asp Ala
20 25 30

Arg Ser Cys Gln Phe Pro Glu Glu Glu Arg Gly Glu Arg Ser Ala Glu
35 40 45

Glu Lys Gly Arg Leu Gly Asp Leu Trp Val
50 55

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<210> 39
 <211> 60
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HVEM endodomain

<400> 39

Cys Val Lys Arg Arg Lys Pro Arg Gly Asp Val Val Lys Val Ile Val
 1 5 10 15

Ser Val Gln Arg Lys Arg Gln Glu Ala Glu Gly Glu Ala Thr Val Ile
 20 25 30

Glu Ala Leu Gln Ala Pro Pro Asp Val Thr Thr Val Ala Val Glu Glu
 35 40 45

Thr Ile Pro Ser Phe Thr Gly Arg Ser Pro Asn His
 50 55 60

<210> 40
 <211> 682
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD28 endodomain fused to amino-terminus of full-length ZAP

<400> 40

Met Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
 1 5 10 15

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
 20 25 30

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Ser Gly Gly Gly Gly Ser
 35 40 45

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Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Met
50 55 60

Pro Asp Pro Ala Ala His Leu Pro Phe Phe Tyr Gly Ser Ile Ser Arg
65 70 75 80

Ala Glu Ala Glu Glu His Leu Lys Leu Ala Gly Met Ala Asp Gly Leu
85 90 95

Phe Leu Leu Arg Gln Cys Leu Arg Ser Leu Gly Gly Tyr Val Leu Ser
100 105 110

Leu Val His Asp Val Arg Phe His His Phe Pro Ile Glu Arg Gln Leu
115 120 125

Asn Gly Thr Tyr Ala Ile Ala Gly Gly Lys Ala His Cys Gly Pro Ala
130 135 140

Glu Leu Cys Glu Phe Tyr Ser Arg Asp Pro Asp Gly Leu Pro Cys Asn
145 150 155 160

Leu Arg Lys Pro Cys Asn Arg Pro Ser Gly Leu Glu Pro Gln Pro Gly
165 170 175

Val Phe Asp Cys Leu Arg Asp Ala Met Val Arg Asp Tyr Val Arg Gln
180 185 190

Thr Trp Lys Leu Glu Gly Glu Ala Leu Glu Gln Ala Ile Ile Ser Gln
195 200 205

Ala Pro Gln Val Glu Lys Leu Ile Ala Thr Thr Ala His Glu Arg Met
210 215 220

Pro Trp Tyr His Ser Ser Leu Thr Arg Glu Glu Ala Glu Arg Lys Leu
225 230 235 240

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Tyr Ser Gly Ala Gln Thr Asp Gly Lys Phe Leu Leu Arg Pro Arg Lys
245 250 255

Glu Gln Gly Thr Tyr Ala Leu Ser Leu Ile Tyr Gly Lys Thr Val Tyr
260 265 270

His Tyr Leu Ile Ser Gln Asp Lys Ala Gly Lys Tyr Cys Ile Pro Glu
275 280 285

Gly Thr Lys Phe Asp Thr Leu Trp Gln Leu Val Glu Tyr Leu Lys Leu
290 295 300

Lys Ala Asp Gly Leu Ile Tyr Cys Leu Lys Glu Ala Cys Pro Asn Ser
305 310 315 320

Ser Ala Ser Asn Ala Ser Gly Ala Ala Ala Pro Thr Leu Pro Ala His
325 330 335

Pro Ser Thr Leu Thr His Pro Gln Arg Arg Ile Asp Thr Leu Asn Ser
340 345 350

Asp Gly Tyr Thr Pro Glu Pro Ala Arg Ile Thr Ser Pro Asp Lys Pro
355 360 365

Arg Pro Met Pro Met Asp Thr Ser Val Tyr Glu Ser Pro Tyr Ser Asp
370 375 380

Pro Glu Glu Leu Lys Asp Lys Lys Leu Phe Leu Lys Arg Asp Asn Leu
385 390 395 400

Leu Ile Ala Asp Ile Glu Leu Gly Cys Gly Asn Phe Gly Ser Val Arg
405 410 415

Gln Gly Val Tyr Arg Met Arg Lys Lys Gln Ile Asp Val Ala Ile Lys
420 425 430

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Val Leu Lys Gln Gly Thr Glu Lys Ala Asp Thr Glu Glu Met Met Arg
435 440 445

Glu Ala Gln Ile Met His Gln Leu Asp Asn Pro Tyr Ile Val Arg Leu
450 455 460

Ile Gly Val Cys Gln Ala Glu Ala Leu Met Leu Val Met Glu Met Ala
465 470 475 480

Gly Gly Gly Pro Leu His Lys Phe Leu Val Gly Lys Arg Glu Glu Ile
485 490 495

Pro Val Ser Asn Val Ala Glu Leu Leu His Gln Val Ser Met Gly Met
500 505 510

Lys Tyr Leu Glu Glu Lys Asn Phe Val His Arg Asp Leu Ala Ala Arg
515 520 525

Asn Val Leu Leu Val Asn Arg His Tyr Ala Lys Ile Ser Asp Phe Gly
530 535 540

Leu Ser Lys Ala Leu Gly Ala Asp Asp Ser Tyr Tyr Thr Ala Arg Ser
545 550 555 560

Ala Gly Lys Trp Pro Leu Lys Trp Tyr Ala Pro Glu Cys Ile Asn Phe
565 570 575

Arg Lys Phe Ser Ser Arg Ser Asp Val Trp Ser Tyr Gly Val Thr Met
580 585 590

Trp Glu Ala Leu Ser Tyr Gly Gln Lys Pro Tyr Lys Lys Met Lys Gly
595 600 605

Pro Glu Val Met Ala Phe Ile Glu Gln Gly Lys Arg Met Glu Cys Pro
610 615 620

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Pro Glu Cys Pro Pro Glu Leu Tyr Ala Leu Met Ser Asp Cys Trp Ile
625 630 635 640

Tyr Lys Trp Glu Asp Arg Pro Asp Phe Leu Thr Val Glu Gln Arg Met
645 650 655

Arg Ala Cys Tyr Tyr Ser Leu Ala Ser Lys Val Glu Gly Pro Pro Gly
660 665 670

Ser Thr Gln Lys Ala Glu Ala Ala Cys Ala
675 680

<210> 41
<211> 683
<212> PRT
<213> Artificial Sequence

<220>
<223> 41BB endodomain fused to amino-terminus of full-length ZAP

<400> 41

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

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

Phe Pro Glu Glu Glu Gly Gly Cys Glu Leu Ser Gly Gly Gly Gly
35 40 45

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
50 55 60

Met Pro Asp Pro Ala Ala His Leu Pro Phe Phe Tyr Gly Ser Ile Ser
65 70 75 80

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Arg Ala Glu Ala Glu Glu His Leu Lys Leu Ala Gly Met Ala Asp Gly
85 90 95

Leu Phe Leu Leu Arg Gln Cys Leu Arg Ser Leu Gly Gly Tyr Val Leu
100 105 110

Ser Leu Val His Asp Val Arg Phe His His Phe Pro Ile Glu Arg Gln
115 120 125

Leu Asn Gly Thr Tyr Ala Ile Ala Gly Gly Lys Ala His Cys Gly Pro
130 135 140

Ala Glu Leu Cys Glu Phe Tyr Ser Arg Asp Pro Asp Gly Leu Pro Cys
145 150 155 160

Asn Leu Arg Lys Pro Cys Asn Arg Pro Ser Gly Leu Glu Pro Gln Pro
165 170 175

Gly Val Phe Asp Cys Leu Arg Asp Ala Met Val Arg Asp Tyr Val Arg
180 185 190

Gln Thr Trp Lys Leu Glu Gly Glu Ala Leu Glu Gln Ala Ile Ile Ser
195 200 205

Gln Ala Pro Gln Val Glu Lys Leu Ile Ala Thr Thr Ala His Glu Arg
210 215 220

Met Pro Trp Tyr His Ser Ser Leu Thr Arg Glu Glu Ala Glu Arg Lys
225 230 235 240

Leu Tyr Ser Gly Ala Gln Thr Asp Gly Lys Phe Leu Leu Arg Pro Arg
245 250 255

Lys Glu Gln Gly Thr Tyr Ala Leu Ser Leu Ile Tyr Gly Lys Thr Val
260 265 270

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Tyr His Tyr Leu Ile Ser Gln Asp Lys Ala Gly Lys Tyr Cys Ile Pro
 275 280 285

Glu Gly Thr Lys Phe Asp Thr Leu Trp Gln Leu Val Glu Tyr Leu Lys
 290 295 300

Leu Lys Ala Asp Gly Leu Ile Tyr Cys Leu Lys Glu Ala Cys Pro Asn
 305 310 315 320

Ser Ser Ala Ser Asn Ala Ser Gly Ala Ala Ala Pro Thr Leu Pro Ala
 325 330 335

His Pro Ser Thr Leu Thr His Pro Gln Arg Arg Ile Asp Thr Leu Asn
 340 345 350

Ser Asp Gly Tyr Thr Pro Glu Pro Ala Arg Ile Thr Ser Pro Asp Lys
 355 360 365

Pro Arg Pro Met Pro Met Asp Thr Ser Val Tyr Glu Ser Pro Tyr Ser
 370 375 380

Asp Pro Glu Glu Leu Lys Asp Lys Lys Leu Phe Leu Lys Arg Asp Asn
 385 390 395 400

Leu Leu Ile Ala Asp Ile Glu Leu Gly Cys Gly Asn Phe Gly Ser Val
 405 410 415

Arg Gln Gly Val Tyr Arg Met Arg Lys Lys Gln Ile Asp Val Ala Ile
 420 425 430

Lys Val Leu Lys Gln Gly Thr Glu Lys Ala Asp Thr Glu Glu Met Met
 435 440 445

Arg Glu Ala Gln Ile Met His Gln Leu Asp Asn Pro Tyr Ile Val Arg
 450 455 460

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Leu Ile Gly Val Cys Gln Ala Glu Ala Leu Met Leu Val Met Glu Met
465 470 475 480

Ala Gly Gly Gly Pro Leu His Lys Phe Leu Val Gly Lys Arg Glu Glu
485 490 495

Ile Pro Val Ser Asn Val Ala Glu Leu Leu His Gln Val Ser Met Gly
500 505 510

Met Lys Tyr Leu Glu Glu Lys Asn Phe Val His Arg Asp Leu Ala Ala
515 520 525

Arg Asn Val Leu Leu Val Asn Arg His Tyr Ala Lys Ile Ser Asp Phe
530 535 540

Gly Leu Ser Lys Ala Leu Gly Ala Asp Asp Ser Tyr Tyr Thr Ala Arg
545 550 555 560

Ser Ala Gly Lys Trp Pro Leu Lys Trp Tyr Ala Pro Glu Cys Ile Asn
565 570 575

Phe Arg Lys Phe Ser Ser Arg Ser Asp Val Trp Ser Tyr Gly Val Thr
580 585 590

Met Trp Glu Ala Leu Ser Tyr Gly Gln Lys Pro Tyr Lys Lys Met Lys
595 600 605

Gly Pro Glu Val Met Ala Phe Ile Glu Gln Gly Lys Arg Met Glu Cys
610 615 620

Pro Pro Glu Cys Pro Pro Glu Leu Tyr Ala Leu Met Ser Asp Cys Trp
625 630 635 640

Ile Tyr Lys Trp Glu Asp Arg Pro Asp Phe Leu Thr Val Glu Gln Arg
645 650 655

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Met Arg Ala Cys Tyr Tyr Ser Leu Ala Ser Lys Val Glu Gly Pro Pro
660 665 670

Gly Ser Thr Gln Lys Ala Glu Ala Ala Cys Ala
675 680

<210> 42
<211> 677
<212> PRT
<213> Artificial Sequence

<220>
<223> OX40 endodomain fused to amino-terminus of full-length ZAP

<400> 42

Met Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly
1 5 10 15

Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser
20 25 30

Thr Leu Ala Lys Ile Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
35 40 45

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Met Pro Asp Pro Ala Ala
50 55 60

His Leu Pro Phe Phe Tyr Gly Ser Ile Ser Arg Ala Glu Ala Glu Glu
65 70 75 80

His Leu Lys Leu Ala Gly Met Ala Asp Gly Leu Phe Leu Leu Arg Gln
85 90 95

Cys Leu Arg Ser Leu Gly Gly Tyr Val Leu Ser Leu Val His Asp Val
100 105 110

Arg Phe His His Phe Pro Ile Glu Arg Gln Leu Asn Gly Thr Tyr Ala
115 120 125

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Ile Ala Gly Gly Lys Ala His Cys Gly Pro Ala Glu Leu Cys Glu Phe
130 135 140

Tyr Ser Arg Asp Pro Asp Gly Leu Pro Cys Asn Leu Arg Lys Pro Cys
145 150 155 160

Asn Arg Pro Ser Gly Leu Glu Pro Gln Pro Gly Val Phe Asp Cys Leu
165 170 175

Arg Asp Ala Met Val Arg Asp Tyr Val Arg Gln Thr Trp Lys Leu Glu
180 185 190

Gly Glu Ala Leu Glu Gln Ala Ile Ile Ser Gln Ala Pro Gln Val Glu
195 200 205

Lys Leu Ile Ala Thr Thr Ala His Glu Arg Met Pro Trp Tyr His Ser
210 215 220

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

Thr Asp Gly Lys Phe Leu Leu Arg Pro Arg Lys Glu Gln Gly Thr Tyr
245 250 255

Ala Leu Ser Leu Ile Tyr Gly Lys Thr Val Tyr His Tyr Leu Ile Ser
260 265 270

Gln Asp Lys Ala Gly Lys Tyr Cys Ile Pro Glu Gly Thr Lys Phe Asp
275 280 285

Thr Leu Trp Gln Leu Val Glu Tyr Leu Lys Leu Lys Ala Asp Gly Leu
290 295 300

Ile Tyr Cys Leu Lys Glu Ala Cys Pro Asn Ser Ser Ala Ser Asn Ala
305 310 315 320

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Ser Gly Ala Ala Ala Pro Thr Leu Pro Ala His Pro Ser Thr Leu Thr
325 330 335

His Pro Gln Arg Arg Ile Asp Thr Leu Asn Ser Asp Gly Tyr Thr Pro
340 345 350

Glu Pro Ala Arg Ile Thr Ser Pro Asp Lys Pro Arg Pro Met Pro Met
355 360 365

Asp Thr Ser Val Tyr Glu Ser Pro Tyr Ser Asp Pro Glu Glu Leu Lys
370 375 380

Asp Lys Lys Leu Phe Leu Lys Arg Asp Asn Leu Leu Ile Ala Asp Ile
385 390 395 400

Glu Leu Gly Cys Gly Asn Phe Gly Ser Val Arg Gln Gly Val Tyr Arg
405 410 415

Met Arg Lys Lys Gln Ile Asp Val Ala Ile Lys Val Leu Lys Gln Gly
420 425 430

Thr Glu Lys Ala Asp Thr Glu Glu Met Met Arg Glu Ala Gln Ile Met
435 440 445

His Gln Leu Asp Asn Pro Tyr Ile Val Arg Leu Ile Gly Val Cys Gln
450 455 460

Ala Glu Ala Leu Met Leu Val Met Glu Met Ala Gly Gly Gly Pro Leu
465 470 475 480

His Lys Phe Leu Val Gly Lys Arg Glu Glu Ile Pro Val Ser Asn Val
485 490 495

Ala Glu Leu Leu His Gln Val Ser Met Gly Met Lys Tyr Leu Glu Glu
500 505 510

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Lys Asn Phe Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Leu Val
515 520 525

Asn Arg His Tyr Ala Lys Ile Ser Asp Phe Gly Leu Ser Lys Ala Leu
530 535 540

Gly Ala Asp Asp Ser Tyr Tyr Thr Ala Arg Ser Ala Gly Lys Trp Pro
545 550 555 560

Leu Lys Trp Tyr Ala Pro Glu Cys Ile Asn Phe Arg Lys Phe Ser Ser
565 570 575

Arg Ser Asp Val Trp Ser Tyr Gly Val Thr Met Trp Glu Ala Leu Ser
580 585 590

Tyr Gly Gln Lys Pro Tyr Lys Lys Met Lys Gly Pro Glu Val Met Ala
595 600 605

Phe Ile Glu Gln Gly Lys Arg Met Glu Cys Pro Pro Glu Cys Pro Pro
610 615 620

Glu Leu Tyr Ala Leu Met Ser Asp Cys Trp Ile Tyr Lys Trp Glu Asp
625 630 635 640

Arg Pro Asp Phe Leu Thr Val Glu Gln Arg Met Arg Ala Cys Tyr Tyr
645 650 655

Ser Leu Ala Ser Lys Val Glu Gly Pro Pro Gly Ser Thr Gln Lys Ala
660 665 670

Glu Ala Ala Cys Ala
675

<210> 43
<211> 276

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<212> PRT

<213> Artificial Sequence

<220>

<223> CD28 endodomain fused to the amino-terminus of PTPN6 SH2 domain

<400> 43

Met Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
1 5 10 15

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
20 25 30

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Ser Gly Gly Gly Gly Ser
35 40 45

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Met
50 55 60

Val Arg Trp Phe His Arg Asp Leu Ser Gly Leu Asp Ala Glu Thr Leu
65 70 75 80

Leu Lys Gly Arg Gly Val His Gly Ser Phe Leu Ala Arg Pro Ser Arg
85 90 95

Lys Asn Gln Gly Asp Phe Ser Leu Ser Val Arg Val Gly Asp Gln Val
100 105 110

Thr His Ile Arg Ile Gln Asn Ser Gly Asp Phe Tyr Asp Leu Tyr Gly
115 120 125

Gly Glu Lys Phe Ala Thr Leu Thr Glu Leu Val Glu Tyr Tyr Thr Gln
130 135 140

Gln Gln Gly Val Leu Gln Asp Arg Asp Gly Thr Ile Ile His Leu Lys
145 150 155 160

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Tyr Pro Leu Asn Cys Ser Asp Pro Thr Ser Glu Arg Trp Tyr His Gly
165 170 175

His Met Ser Gly Gly Gln Ala Glu Thr Leu Leu Gln Ala Lys Gly Glu
180 185 190

Pro Trp Thr Phe Leu Val Arg Glu Ser Leu Ser Gln Pro Gly Asp Phe
195 200 205

Val Leu Ser Val Leu Ser Asp Gln Pro Lys Ala Gly Pro Gly Ser Pro
210 215 220

Leu Arg Val Thr His Ile Lys Val Met Cys Glu Gly Gly Arg Tyr Thr
225 230 235 240

Val Gly Gly Leu Glu Thr Phe Asp Ser Leu Thr Asp Leu Val Glu His
245 250 255

Phe Lys Lys Thr Gly Ile Glu Glu Ala Ser Gly Ala Phe Val Tyr Leu
260 265 270

Arg Gln Pro Tyr
275

<210> 44

<211> 277

<212> PRT

<213> Artificial Sequence

<220>

<223> 41BB endodomain fused to the amino-terminus of PTPN6 SH2 domain

<400> 44

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

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

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Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Ser Gly Gly Gly Gly
35 40 45

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
50 55 60

Met Val Arg Trp Phe His Arg Asp Leu Ser Gly Leu Asp Ala Glu Thr
65 70 75 80

Leu Leu Lys Gly Arg Gly Val His Gly Ser Phe Leu Ala Arg Pro Ser
85 90 95

Arg Lys Asn Gln Gly Asp Phe Ser Leu Ser Val Arg Val Gly Asp Gln
100 105 110

Val Thr His Ile Arg Ile Gln Asn Ser Gly Asp Phe Tyr Asp Leu Tyr
115 120 125

Gly Gly Glu Lys Phe Ala Thr Leu Thr Glu Leu Val Glu Tyr Tyr Thr
130 135 140

Gln Gln Gln Gly Val Leu Gln Asp Arg Asp Gly Thr Ile Ile His Leu
145 150 155 160

Lys Tyr Pro Leu Asn Cys Ser Asp Pro Thr Ser Glu Arg Trp Tyr His
165 170 175

Gly His Met Ser Gly Gly Gln Ala Glu Thr Leu Leu Gln Ala Lys Gly
180 185 190

Glu Pro Trp Thr Phe Leu Val Arg Glu Ser Leu Ser Gln Pro Gly Asp
195 200 205

Phe Val Leu Ser Val Leu Ser Asp Gln Pro Lys Ala Gly Pro Gly Ser
210 215 220

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Pro Leu Arg Val Thr His Ile Lys Val Met Cys Glu Gly Gly Arg Tyr
225 230 235 240

Thr Val Gly Gly Leu Glu Thr Phe Asp Ser Leu Thr Asp Leu Val Glu
245 250 255

His Phe Lys Lys Thr Gly Ile Glu Glu Ala Ser Gly Ala Phe Val Tyr
260 265 270

Leu Arg Gln Pro Tyr
275

<210> 45
<211> 271
<212> PRT
<213> Artificial Sequence

<220>
<223> OX40 endodomain fused to the amino-terminus of PTPN6 SH2 domain

<400> 45

Met Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly
1 5 10 15

Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser
20 25 30

Thr Leu Ala Lys Ile Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
35 40 45

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Met Val Arg Trp Phe His
50 55 60

Arg Asp Leu Ser Gly Leu Asp Ala Glu Thr Leu Leu Lys Gly Arg Gly
65 70 75 80

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Val His Gly Ser Phe Leu Ala Arg Pro Ser Arg Lys Asn Gln Gly Asp
85 90 95

Phe Ser Leu Ser Val Arg Val Gly Asp Gln Val Thr His Ile Arg Ile
100 105 110

Gln Asn Ser Gly Asp Phe Tyr Asp Leu Tyr Gly Gly Glu Lys Phe Ala
115 120 125

Thr Leu Thr Glu Leu Val Glu Tyr Tyr Thr Gln Gln Gln Gly Val Leu
130 135 140

Gln Asp Arg Asp Gly Thr Ile Ile His Leu Lys Tyr Pro Leu Asn Cys
145 150 155 160

Ser Asp Pro Thr Ser Glu Arg Trp Tyr His Gly His Met Ser Gly Gly
165 170 175

Gln Ala Glu Thr Leu Leu Gln Ala Lys Gly Glu Pro Trp Thr Phe Leu
180 185 190

Val Arg Glu Ser Leu Ser Gln Pro Gly Asp Phe Val Leu Ser Val Leu
195 200 205

Ser Asp Gln Pro Lys Ala Gly Pro Gly Ser Pro Leu Arg Val Thr His
210 215 220

Ile Lys Val Met Cys Glu Gly Gly Arg Tyr Thr Val Gly Gly Leu Glu
225 230 235 240

Thr Phe Asp Ser Leu Thr Asp Leu Val Glu His Phe Lys Lys Thr Gly
245 250 255

Ile Glu Glu Ala Ser Gly Ala Phe Val Tyr Leu Arg Gln Pro Tyr
260 265 270

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<210> 46
 <211> 350
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Akt kinase domain

<400> 46

Ala Glu Glu Met Glu Val Ser Leu Ala Lys Pro Lys His Arg Val Thr
 1 5 10 15

Met Asn Glu Phe Glu Tyr Leu Lys Leu Leu Gly Lys Gly Thr Phe Gly
 20 25 30

Lys Val Ile Leu Val Lys Glu Lys Ala Thr Gly Arg Tyr Tyr Ala Met
 35 40 45

Lys Ile Leu Lys Lys Glu Val Ile Val Ala Lys Asp Glu Val Ala His
 50 55 60

Thr Leu Thr Glu Asn Arg Val Leu Gln Asn Ser Arg His Pro Phe Leu
 65 70 75 80

Thr Ala Leu Lys Tyr Ser Phe Gln Thr His Asp Arg Leu Cys Phe Val
 85 90 95

Met Glu Tyr Ala Asn Gly Gly Glu Leu Phe Phe His Leu Ser Arg Glu
 100 105 110

Arg Val Phe Ser Glu Asp Arg Ala Arg Phe Tyr Gly Ala Glu Ile Val
 115 120 125

Ser Ala Leu Asp Tyr Leu His Ser Glu Lys Asn Val Val Tyr Arg Asp
 130 135 140

Leu Lys Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile Lys Ile
 145 150 155 160

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Thr Asp Phe Gly Leu Cys Lys Glu Gly Ile Lys Asp Gly Ala Thr Met
165 170 175

Lys Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Glu
180 185 190

Asp Asn Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly Val Val
195 200 205

Met Tyr Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln Asp His
210 215 220

Glu Lys Leu Phe Glu Leu Ile Leu Met Glu Glu Ile Arg Phe Pro Arg
225 230 235 240

Thr Leu Gly Pro Glu Ala Lys Ser Leu Leu Ser Gly Leu Leu Lys Lys
245 250 255

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

Met Gln His Arg Phe Phe Ala Gly Ile Val Trp Gln His Val Tyr Glu
275 280 285

Lys Lys Leu Ser Pro Pro Phe Lys Pro Gln Val Thr Ser Glu Thr Asp
290 295 300

Thr Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Met Ile Thr Ile Thr
305 310 315 320

Pro Pro Asp Gln Asp Asp Ser Met Glu Cys Val Asp Ser Glu Arg Arg
325 330 335

Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Gly Thr Ala
340 345 350

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<210> 47
 <211> 630
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ZAP70-SH2 domain fused directly to an Akt kinase domain

<400> 47

Met Pro Asp Pro Ala Ala His Leu Pro Phe Phe Tyr Gly Ser Ile Ser
 1 5 10 15

Arg Ala Glu Ala Glu Glu His Leu Lys Leu Ala Gly Met Ala Asp Gly
 20 25 30

Leu Phe Leu Leu Arg Gln Cys Leu Arg Ser Leu Gly Gly Tyr Val Leu
 35 40 45

Ser Leu Val His Asp Val Arg Phe His His Phe Pro Ile Glu Arg Gln
 50 55 60

Leu Asn Gly Thr Tyr Ala Ile Ala Gly Gly Lys Ala His Cys Gly Pro
 65 70 75 80

Ala Glu Leu Cys Glu Phe Tyr Ser Arg Asp Pro Asp Gly Leu Pro Cys
 85 90 95

Asn Leu Arg Lys Pro Cys Asn Arg Pro Ser Gly Leu Glu Pro Gln Pro
 100 105 110

Gly Val Phe Asp Cys Leu Arg Asp Ala Met Val Arg Asp Tyr Val Arg
 115 120 125

Gln Thr Trp Lys Leu Glu Gly Glu Ala Leu Glu Gln Ala Ile Ile Ser
 130 135 140

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Gln Ala Pro Gln Val Glu Lys Leu Ile Ala Thr Thr Ala His Glu Arg
145 150 155 160

Met Pro Trp Tyr His Ser Ser Leu Thr Arg Glu Glu Ala Glu Arg Lys
165 170 175

Leu Tyr Ser Gly Ala Gln Thr Asp Gly Lys Phe Leu Leu Arg Pro Arg
180 185 190

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

Tyr His Tyr Leu Ile Ser Gln Asp Lys Ala Gly Lys Tyr Cys Ile Pro
210 215 220

Glu Gly Thr Lys Phe Asp Thr Leu Trp Gln Leu Val Glu Tyr Leu Lys
225 230 235 240

Leu Lys Ala Asp Gly Leu Ile Tyr Cys Leu Lys Glu Ala Cys Pro Asn
245 250 255

Ser Ser Ala Ser Asn Ala Ser Gly Ala Ala Ala Pro Thr Leu Pro Ala
260 265 270

His Pro Ser Thr Leu Thr His Pro Ala Glu Glu Met Glu Val Ser Leu
275 280 285

Ala Lys Pro Lys His Arg Val Thr Met Asn Glu Phe Glu Tyr Leu Lys
290 295 300

Leu Leu Gly Lys Gly Thr Phe Gly Lys Val Ile Leu Val Lys Glu Lys
305 310 315 320

Ala Thr Gly Arg Tyr Tyr Ala Met Lys Ile Leu Lys Lys Glu Val Ile
325 330 335

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Val Ala Lys Asp Glu Val Ala His Thr Leu Thr Glu Asn Arg Val Leu
340 345 350

Gln Asn Ser Arg His Pro Phe Leu Thr Ala Leu Lys Tyr Ser Phe Gln
355 360 365

Thr His Asp Arg Leu Cys Phe Val Met Glu Tyr Ala Asn Gly Gly Glu
370 375 380

Leu Phe Phe His Leu Ser Arg Glu Arg Val Phe Ser Glu Asp Arg Ala
385 390 395 400

Arg Phe Tyr Gly Ala Glu Ile Val Ser Ala Leu Asp Tyr Leu His Ser
405 410 415

Glu Lys Asn Val Val Tyr Arg Asp Leu Lys Leu Glu Asn Leu Met Leu
420 425 430

Asp Lys Asp Gly His Ile Lys Ile Thr Asp Phe Gly Leu Cys Lys Glu
435 440 445

Gly Ile Lys Asp Gly Ala Thr Met Lys Thr Phe Cys Gly Thr Pro Glu
450 455 460

Tyr Leu Ala Pro Glu Val Leu Glu Asp Asn Asp Tyr Gly Arg Ala Val
465 470 475 480

Asp Trp Trp Gly Leu Gly Val Val Met Tyr Glu Met Met Cys Gly Arg
485 490 495

Leu Pro Phe Tyr Asn Gln Asp His Glu Lys Leu Phe Glu Leu Ile Leu
500 505 510

Met Glu Glu Ile Arg Phe Pro Arg Thr Leu Gly Pro Glu Ala Lys Ser
515 520 525

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Leu Leu Ser Gly Leu Leu Lys Lys Asp Pro Lys Gln Arg Leu Gly Gly
530 535 540

Gly Ser Glu Asp Ala Lys Glu Ile Met Gln His Arg Phe Phe Ala Gly
545 550 555 560

Ile Val Trp Gln His Val Tyr Glu Lys Lys Leu Ser Pro Pro Phe Lys
565 570 575

Pro Gln Val Thr Ser Glu Thr Asp Thr Arg Tyr Phe Asp Glu Glu Phe
580 585 590

Thr Ala Gln Met Ile Thr Ile Thr Pro Pro Asp Gln Asp Asp Ser Met
595 600 605

Glu Cys Val Asp Ser Glu Arg Arg Pro His Phe Pro Gln Phe Ser Tyr
610 615 620

Ser Ala Ser Gly Thr Ala
625 630

<210> 48
<211> 651
<212> PRT
<213> Artificial Sequence

<220>
<223> ZAP70-SH2 domain fused to an Akt kinase domain via a linker

<400> 48

Met Pro Asp Pro Ala Ala His Leu Pro Phe Phe Tyr Gly Ser Ile Ser
1 5 10 15

Arg Ala Glu Ala Glu Glu His Leu Lys Leu Ala Gly Met Ala Asp Gly
20 25 30

Leu Phe Leu Leu Arg Gln Cys Leu Arg Ser Leu Gly Gly Tyr Val Leu
35 40 45

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Ser Leu Val His Asp Val Arg Phe His His Phe Pro Ile Glu Arg Gln
50 55 60

Leu Asn Gly Thr Tyr Ala Ile Ala Gly Gly Lys Ala His Cys Gly Pro
65 70 75 80

Ala Glu Leu Cys Glu Phe Tyr Ser Arg Asp Pro Asp Gly Leu Pro Cys
85 90 95

Asn Leu Arg Lys Pro Cys Asn Arg Pro Ser Gly Leu Glu Pro Gln Pro
100 105 110

Gly Val Phe Asp Cys Leu Arg Asp Ala Met Val Arg Asp Tyr Val Arg
115 120 125

Gln Thr Trp Lys Leu Glu Gly Glu Ala Leu Glu Gln Ala Ile Ile Ser
130 135 140

Gln Ala Pro Gln Val Glu Lys Leu Ile Ala Thr Thr Ala His Glu Arg
145 150 155 160

Met Pro Trp Tyr His Ser Ser Leu Thr Arg Glu Glu Ala Glu Arg Lys
165 170 175

Leu Tyr Ser Gly Ala Gln Thr Asp Gly Lys Phe Leu Leu Arg Pro Arg
180 185 190

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

Tyr His Tyr Leu Ile Ser Gln Asp Lys Ala Gly Lys Tyr Cys Ile Pro
210 215 220

Glu Gly Thr Lys Phe Asp Thr Leu Trp Gln Leu Val Glu Tyr Leu Lys
225 230 235 240

pctgb2016051576-seq1

Leu Lys Ala Asp Gly Leu Ile Tyr Cys Leu Lys Glu Ala Cys Pro Asn
245 250 255

Ser Ser Ala Ser Asn Ala Ser Gly Ala Ala Ala Pro Thr Leu Pro Ala
260 265 270

His Pro Ser Thr Leu Thr His Pro Ser Gly Gly Gly Gly Ser Gly Gly
275 280 285

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Glu Glu
290 295 300

Met Glu Val Ser Leu Ala Lys Pro Lys His Arg Val Thr Met Asn Glu
305 310 315 320

Phe Glu Tyr Leu Lys Leu Leu Gly Lys Gly Thr Phe Gly Lys Val Ile
325 330 335

Leu Val Lys Glu Lys Ala Thr Gly Arg Tyr Tyr Ala Met Lys Ile Leu
340 345 350

Lys Lys Glu Val Ile Val Ala Lys Asp Glu Val Ala His Thr Leu Thr
355 360 365

Glu Asn Arg Val Leu Gln Asn Ser Arg His Pro Phe Leu Thr Ala Leu
370 375 380

Lys Tyr Ser Phe Gln Thr His Asp Arg Leu Cys Phe Val Met Glu Tyr
385 390 395 400

Ala Asn Gly Gly Glu Leu Phe Phe His Leu Ser Arg Glu Arg Val Phe
405 410 415

Ser Glu Asp Arg Ala Arg Phe Tyr Gly Ala Glu Ile Val Ser Ala Leu
420 425 430

pctgb2016051576-seq1

Asp Tyr Leu His Ser Glu Lys Asn Val Val Tyr Arg Asp Leu Lys Leu
435 440 445

Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile Lys Ile Thr Asp Phe
450 455 460

Gly Leu Cys Lys Glu Gly Ile Lys Asp Gly Ala Thr Met Lys Thr Phe
465 470 475 480

Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp Asn Asp
485 490 495

Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly Val Val Met Tyr Glu
500 505 510

Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln Asp His Glu Lys Leu
515 520 525

Phe Glu Leu Ile Leu Met Glu Glu Ile Arg Phe Pro Arg Thr Leu Gly
530 535 540

Pro Glu Ala Lys Ser Leu Leu Ser Gly Leu Leu Lys Lys Asp Pro Lys
545 550 555 560

Gln Arg Leu Gly Gly Gly Ser Glu Asp Ala Lys Glu Ile Met Gln His
565 570 575

Arg Phe Phe Ala Gly Ile Val Trp Gln His Val Tyr Glu Lys Lys Leu
580 585 590

Ser Pro Pro Phe Lys Pro Gln Val Thr Ser Glu Thr Asp Thr Arg Tyr
595 600 605

Phe Asp Glu Glu Phe Thr Ala Gln Met Ile Thr Ile Thr Pro Pro Asp
610 615 620

pctgb2016051576-seq1

Gln Asp Asp Ser Met Glu Cys Val Asp Ser Glu Arg Arg Pro His Phe
625 630 635 640

Pro Gln Phe Ser Tyr Ser Ala Ser Gly Thr Ala
645 650

<210> 49
<211> 630
<212> PRT
<213> Artificial Sequence

<220>
<223> ZAP70 mutated to be non-functional and fused to an Akt kinase domain

<400> 49

Met Pro Asp Pro Ala Ala His Leu Pro Phe Phe Tyr Gly Ser Ile Ser
1 5 10 15

Arg Ala Glu Ala Glu Glu His Leu Lys Leu Ala Gly Met Ala Asp Gly
20 25 30

Leu Phe Leu Leu Arg Gln Cys Leu Arg Ser Leu Gly Gly Tyr Val Leu
35 40 45

Ser Leu Val His Asp Val Arg Phe His His Phe Pro Ile Glu Arg Gln
50 55 60

Leu Asn Gly Thr Tyr Ala Ile Ala Gly Gly Lys Ala His Cys Gly Pro
65 70 75 80

Ala Glu Leu Cys Glu Phe Tyr Ser Arg Asp Pro Asp Gly Leu Pro Cys
85 90 95

Asn Leu Arg Lys Pro Cys Asn Arg Pro Ser Gly Leu Glu Pro Gln Pro
100 105 110

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Gly Val Phe Asp Cys Leu Arg Asp Ala Met Val Arg Asp Tyr Val Arg
115 120 125

Gln Thr Trp Lys Leu Glu Gly Glu Ala Leu Glu Gln Ala Ile Ile Ser
130 135 140

Gln Ala Pro Gln Val Glu Lys Leu Ile Ala Thr Thr Ala His Glu Arg
145 150 155 160

Met Pro Trp Tyr His Ser Ser Leu Thr Arg Glu Glu Ala Glu Arg Lys
165 170 175

Leu Tyr Ser Gly Ala Gln Thr Asp Gly Lys Phe Leu Leu Lys Pro Arg
180 185 190

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

Tyr His Tyr Leu Ile Ser Gln Asp Lys Ala Gly Lys Tyr Cys Ile Pro
210 215 220

Glu Gly Thr Lys Phe Asp Thr Leu Trp Gln Leu Val Glu Tyr Leu Lys
225 230 235 240

Leu Lys Ala Asp Gly Leu Ile Tyr Cys Leu Lys Glu Ala Cys Pro Asn
245 250 255

Ser Ser Ala Ser Asn Ala Ser Gly Ala Ala Ala Pro Thr Leu Pro Ala
260 265 270

His Pro Ser Thr Leu Thr His Pro Ala Glu Glu Met Glu Val Ser Leu
275 280 285

Ala Lys Pro Lys His Arg Val Thr Met Asn Glu Phe Glu Tyr Leu Lys
290 295 300

pctgb2016051576-seq1

Leu Leu Gly Lys Gly Thr Phe Gly Lys Val Ile Leu Val Lys Glu Lys
305 310 315 320

Ala Thr Gly Arg Tyr Tyr Ala Met Lys Ile Leu Lys Lys Glu Val Ile
325 330 335

Val Ala Lys Asp Glu Val Ala His Thr Leu Thr Glu Asn Arg Val Leu
340 345 350

Gln Asn Ser Arg His Pro Phe Leu Thr Ala Leu Lys Tyr Ser Phe Gln
355 360 365

Thr His Asp Arg Leu Cys Phe Val Met Glu Tyr Ala Asn Gly Gly Glu
370 375 380

Leu Phe Phe His Leu Ser Arg Glu Arg Val Phe Ser Glu Asp Arg Ala
385 390 395 400

Arg Phe Tyr Gly Ala Glu Ile Val Ser Ala Leu Asp Tyr Leu His Ser
405 410 415

Glu Lys Asn Val Val Tyr Arg Asp Leu Lys Leu Glu Asn Leu Met Leu
420 425 430

Asp Lys Asp Gly His Ile Lys Ile Thr Asp Phe Gly Leu Cys Lys Glu
435 440 445

Gly Ile Lys Asp Gly Ala Thr Met Lys Thr Phe Cys Gly Thr Pro Glu
450 455 460

Tyr Leu Ala Pro Glu Val Leu Glu Asp Asn Asp Tyr Gly Arg Ala Val
465 470 475 480

Asp Trp Trp Gly Leu Gly Val Val Met Tyr Glu Met Met Cys Gly Arg
485 490 495

pctgb2016051576-seq1

Leu Pro Phe Tyr Asn Gln Asp His Glu Lys Leu Phe Glu Leu Ile Leu
500 505 510

Met Glu Glu Ile Arg Phe Pro Arg Thr Leu Gly Pro Glu Ala Lys Ser
515 520 525

Leu Leu Ser Gly Leu Leu Lys Lys Asp Pro Lys Gln Arg Leu Gly Gly
530 535 540

Gly Ser Glu Asp Ala Lys Glu Ile Met Gln His Arg Phe Phe Ala Gly
545 550 555 560

Ile Val Trp Gln His Val Tyr Glu Lys Lys Leu Ser Pro Pro Phe Lys
565 570 575

Pro Gln Val Thr Ser Glu Thr Asp Thr Arg Tyr Phe Asp Glu Glu Phe
580 585 590

Thr Ala Gln Met Ile Thr Ile Thr Pro Pro Asp Gln Asp Asp Ser Met
595 600 605

Glu Cys Val Asp Ser Glu Arg Arg Pro His Phe Pro Gln Phe Ser Tyr
610 615 620

Ser Ala Ser Gly Thr Ala
625 630

<210> 50
<211> 590
<212> PRT
<213> Artificial Sequence

<220>
<223> Kinase containing domain of JAK2

<400> 50

Arg Asn Glu Asp Leu Ile Phe Asn Glu Ser Leu Gly Gln Gly Thr Phe

pctgb2016051576-seq1

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

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195

200

205

Gly Gly Asp Lys Pro Leu Ser Ala Leu Asp Ser Gln Arg Lys Leu Gln
 210 215 220

Phe Tyr Glu Asp Arg His Gln Leu Pro Ala Pro Lys Trp Ala Glu Leu
 225 230 235 240

Ala Asn Leu Ile Asn Asn Cys Met Asp Tyr Glu Pro Asp Phe Arg Pro
 245 250 255

Ser Phe Arg Ala Ile Ile Arg Asp Leu Asn Ser Leu Phe Thr Pro Asp
 260 265 270

Tyr Glu Leu Leu Thr Glu Asn Asp Met Leu Pro Asn Met Arg Ile Gly
 275 280 285

Ala Leu Gly Phe Ser Gly Ala Phe Glu Asp Arg Asp Pro Thr Gln Phe
 290 295 300

Glu Glu Arg His Leu Lys Phe Leu Gln Gln Leu Gly Lys Gly Asn Phe
 305 310 315 320

Gly Ser Val Glu Met Cys Arg Tyr Asp Pro Leu Gln Asp Asn Thr Gly
 325 330 335

Glu Val Val Ala Val Lys Lys Leu Gln His Ser Thr Glu Glu His Leu
 340 345 350

Arg Asp Phe Glu Arg Glu Ile Glu Ile Leu Lys Ser Leu Gln His Asp
 355 360 365

Asn Ile Val Lys Tyr Lys Gly Val Cys Tyr Ser Ala Gly Arg Arg Asn
 370 375 380

Leu Lys Leu Ile Met Glu Tyr Leu Pro Tyr Gly Ser Leu Arg Asp Tyr

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385 390 395 400
 Leu Gln Lys His Lys Glu Arg Ile Asp His Ile Lys Leu Leu Gln Tyr
 405 410 415
 Thr Ser Gln Ile Cys Lys Gly Met Glu Tyr Leu Gly Thr Lys Arg Tyr
 420 425 430
 Ile His Arg Asp Leu Ala Thr Arg Asn Ile Leu Val Glu Asn Glu Asn
 435 440 445
 Arg Val Lys Ile Gly Asp Phe Gly Leu Thr Lys Val Leu Pro Gln Asp
 450 455 460
 Lys Glu Tyr Tyr Lys Val Lys Glu Pro Gly Glu Ser Pro Ile Phe Trp
 465 470 475 480
 Tyr Ala Pro Glu Ser Leu Thr Glu Ser Lys Phe Ser Val Ala Ser Asp
 485 490 495
 Val Trp Ser Phe Gly Val Val Leu Tyr Glu Leu Phe Thr Tyr Ile Glu
 500 505 510
 Lys Ser Lys Ser Pro Pro Ala Glu Phe Met Arg Met Ile Gly Asn Asp
 515 520 525
 Lys Gln Gly Gln Met Ile Val Phe His Leu Ile Glu Leu Leu Lys Asn
 530 535 540
 Asn Gly Arg Leu Pro Arg Pro Asp Gly Cys Pro Asp Glu Ile Tyr Met
 545 550 555 560
 Ile Met Thr Glu Cys Trp Asn Asn Asn Val Asn Gln Arg Pro Ser Phe
 565 570 575
 Arg Asp Leu Ala Leu Arg Val Asp Gln Ile Arg Asp Asn Met

580

<210> 51
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus Tobacco Etch Virus (TEV) cleavage site

<400> 51

Glu Asn Leu Tyr Phe Gln Ser
1 5

<210> 52
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> TeV protease domain

<400> 52

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

Cys His Leu Thr Asn Glu Ser Asp Gly His Thr Thr Ser Leu Tyr Gly
20 25 30

Ile Gly Phe Gly Pro Phe Ile Ile Thr Asn Lys His Leu Phe Arg Arg
35 40 45

Asn Asn Gly Thr Leu Leu Val Gln Ser Leu His Gly Val Phe Lys Val
50 55 60

Lys Asn Thr Thr Thr Leu Gln Gln His Leu Ile Asp Gly Arg Asp Met
65 70 75 80

Ile Ile Ile Arg Met Pro Lys Asp Phe Pro Pro Phe Pro Gln Lys Leu

pctgb2016051576-seq1

85

90

95

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

Asn Phe Gln Thr Lys Ser Met Ser Ser Met Val Ser Asp Thr Ser Cys
 115 120 125

Thr Phe Pro Ser Ser Asp Gly Ile Phe Trp Lys His Trp Ile Gln Thr
 130 135 140

Lys Asp Gly Gln Cys Gly Ser Pro Leu Val Ser Thr Arg Asp Gly Phe
 145 150 155 160

Ile Val Gly Ile His Ser Ala Ser Asn Phe Thr Asn Thr Asn Asn Tyr
 165 170 175

Phe Thr Ser Val Pro Lys Asn Phe Met Glu Leu Leu Thr Asn Gln Glu
 180 185 190

Ala Gln Gln Trp Val Ser Gly Trp Arg Leu Asn Ala Asp Ser Val Leu
 195 200 205

Trp Gly Gly His Lys Val Phe Met Ser Lys Pro Glu Glu Pro Phe Gln
 210 215 220

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

<210> 53

<211> 541

<212> PRT

<213> Artificial Sequence

<220>

<223> ZAP70-SH2 domain fused to a TEV protease sequence

<400> 53

pctgb2016051576-seq1

Met Pro Asp Pro Ala Ala His Leu Pro Phe Phe Tyr Gly Ser Ile Ser
1 5 10 15

Arg Ala Glu Ala Glu Glu His Leu Lys Leu Ala Gly Met Ala Asp Gly
20 25 30

Leu Phe Leu Leu Arg Gln Cys Leu Arg Ser Leu Gly Gly Tyr Val Leu
35 40 45

Ser Leu Val His Asp Val Arg Phe His His Phe Pro Ile Glu Arg Gln
50 55 60

Leu Asn Gly Thr Tyr Ala Ile Ala Gly Gly Lys Ala His Cys Gly Pro
65 70 75 80

Ala Glu Leu Cys Glu Phe Tyr Ser Arg Asp Pro Asp Gly Leu Pro Cys
85 90 95

Asn Leu Arg Lys Pro Cys Asn Arg Pro Ser Gly Leu Glu Pro Gln Pro
100 105 110

Gly Val Phe Asp Cys Leu Arg Asp Ala Met Val Arg Asp Tyr Val Arg
115 120 125

Gln Thr Trp Lys Leu Glu Gly Glu Ala Leu Glu Gln Ala Ile Ile Ser
130 135 140

Gln Ala Pro Gln Val Glu Lys Leu Ile Ala Thr Thr Ala His Glu Arg
145 150 155 160

Met Pro Trp Tyr His Ser Ser Leu Thr Arg Glu Glu Ala Glu Arg Lys
165 170 175

Leu Tyr Ser Gly Ala Gln Thr Asp Gly Lys Phe Leu Leu Arg Pro Arg
180 185 190

pctgb2016051576-seq1

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

Tyr His Tyr Leu Ile Ser Gln Asp Lys Ala Gly Lys Tyr Cys Ile Pro
210 215 220

Glu Gly Thr Lys Phe Asp Thr Leu Trp Gln Leu Val Glu Tyr Leu Lys
225 230 235 240

Leu Lys Ala Asp Gly Leu Ile Tyr Cys Leu Lys Glu Ala Cys Pro Asn
245 250 255

Ser Ser Ala Ser Asn Ala Ser Gly Ala Ala Ala Pro Thr Leu Pro Ala
260 265 270

His Pro Ser Thr Leu Thr His Pro Ser Gly Gly Gly Gly Ser Gly Gly
275 280 285

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Leu Phe
290 295 300

Lys Gly Pro Arg Asp Tyr Asn Pro Ile Ser Ser Thr Ile Cys His Leu
305 310 315 320

Thr Asn Glu Ser Asp Gly His Thr Thr Ser Leu Tyr Gly Ile Gly Phe
325 330 335

Gly Pro Phe Ile Ile Thr Asn Lys His Leu Phe Arg Arg Asn Asn Gly
340 345 350

Thr Leu Leu Val Gln Ser Leu His Gly Val Phe Lys Val Lys Asn Thr
355 360 365

Thr Thr Leu Gln Gln His Leu Ile Asp Gly Arg Asp Met Ile Ile Ile
370 375 380

pctgb2016051576-seq1

Arg Met Pro Lys Asp Phe Pro Pro Phe Pro Gln Lys Leu Lys Phe Arg
385 390 395 400

Glu Pro Gln Arg Glu Glu Arg Ile Cys Leu Val Thr Thr Asn Phe Gln
405 410 415

Thr Lys Ser Met Ser Ser Met Val Ser Asp Thr Ser Cys Thr Phe Pro
420 425 430

Ser Ser Asp Gly Ile Phe Trp Lys His Trp Ile Gln Thr Lys Asp Gly
435 440 445

Gln Cys Gly Ser Pro Leu Val Ser Thr Arg Asp Gly Phe Ile Val Gly
450 455 460

Ile His Ser Ala Ser Asn Phe Thr Asn Thr Asn Asn Tyr Phe Thr Ser
465 470 475 480

Val Pro Lys Asn Phe Met Glu Leu Leu Thr Asn Gln Glu Ala Gln Gln
485 490 495

Trp Val Ser Gly Trp Arg Leu Asn Ala Asp Ser Val Leu Trp Gly Gly
500 505 510

His Lys Val Phe Met Ser Lys Pro Glu Glu Pro Phe Gln Pro Val Lys
515 520 525

Glu Ala Thr Gln Leu Met Asn Glu Leu Val Tyr Ser Gln
530 535 540

<210> 54

<211> 460

<212> PRT

<213> Artificial Sequence

<220>

<223> PTPN6-SH2 domain fused to a TEV protease sequence

pctgb2016051576-seq1

<400> 54

Met Val Arg Trp Phe His Arg Asp Leu Ser Gly Leu Asp Ala Glu Thr
1 5 10 15

Leu Leu Lys Gly Arg Gly Val His Gly Ser Phe Leu Ala Arg Pro Ser
20 25 30

Arg Lys Asn Gln Gly Asp Phe Ser Leu Ser Val Arg Val Gly Asp Gln
35 40 45

Val Thr His Ile Arg Ile Gln Asn Ser Gly Asp Phe Tyr Asp Leu Tyr
50 55 60

Gly Gly Glu Lys Phe Ala Thr Leu Thr Glu Leu Val Glu Tyr Tyr Thr
65 70 75 80

Gln Gln Gln Gly Val Leu Gln Asp Arg Asp Gly Thr Ile Ile His Leu
85 90 95

Lys Tyr Pro Leu Asn Cys Ser Asp Pro Thr Ser Glu Arg Trp Tyr His
100 105 110

Gly His Met Ser Gly Gly Gln Ala Glu Thr Leu Leu Gln Ala Lys Gly
115 120 125

Glu Pro Trp Thr Phe Leu Val Arg Glu Ser Leu Ser Gln Pro Gly Asp
130 135 140

Phe Val Leu Ser Val Leu Ser Asp Gln Pro Lys Ala Gly Pro Gly Ser
145 150 155 160

Pro Leu Arg Val Thr His Ile Lys Val Met Cys Glu Gly Gly Arg Tyr
165 170 175

Thr Val Gly Gly Leu Glu Thr Phe Asp Ser Leu Thr Asp Leu Val Glu

pctgb2016051576-seq1

180

185

190

His Phe Lys Lys Thr Gly Ile Glu Glu Ala Ser Gly Ala Phe Val Tyr
 195 200 205

Leu Arg Gln Pro Tyr Tyr Ser Gly Gly Gly Gly Ser Ser Leu Phe Lys
 210 215 220

Gly Pro Arg Asp Tyr Asn Pro Ile Ser Ser Thr Ile Cys His Leu Thr
 225 230 235 240

Asn Glu Ser Asp Gly His Thr Thr Ser Leu Tyr Gly Ile Gly Phe Gly
 245 250 255

Pro Phe Ile Ile Thr Asn Lys His Leu Phe Arg Arg Asn Asn Gly Thr
 260 265 270

Leu Leu Val Gln Ser Leu His Gly Val Phe Lys Val Lys Asn Thr Thr
 275 280 285

Thr Leu Gln Gln His Leu Ile Asp Gly Arg Asp Met Ile Ile Ile Arg
 290 295 300

Met Pro Lys Asp Phe Pro Pro Phe Pro Gln Lys Leu Lys Phe Arg Glu
 305 310 315 320

Pro Gln Arg Glu Glu Arg Ile Cys Leu Val Thr Thr Asn Phe Gln Thr
 325 330 335

Lys Ser Met Ser Ser Met Val Ser Asp Thr Ser Cys Thr Phe Pro Ser
 340 345 350

Ser Asp Gly Ile Phe Trp Lys His Trp Ile Gln Thr Lys Asp Gly Gln
 355 360 365

Cys Gly Ser Pro Leu Val Ser Thr Arg Asp Gly Phe Ile Val Gly Ile

pctgb2016051576-seq1

370

375

380

His Ser Ala Ser Asn Phe Thr Asn Thr Asn Asn Tyr Phe Thr Ser Val
385 390 395 400

Pro Lys Asn Phe Met Glu Leu Leu Thr Asn Gln Glu Ala Gln Gln Trp
405 410 415

Val Ser Gly Trp Arg Leu Asn Ala Asp Ser Val Leu Trp Gly Gly His
420 425 430

Lys Val Phe Met Ser Lys Pro Glu Glu Pro Phe Gln Pro Val Lys Glu
435 440 445

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

<210> 55
<211> 438
<212> PRT
<213> Artificial Sequence

<220>
<223> membrane tethered transcription factor

<400> 55

Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
1 5 10 15

Asp His Ala Asp Ala Cys Pro Tyr Ser Asn Pro Ser Leu Cys Ser Gly
20 25 30

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

Thr Asn Val Ser Pro Ala Lys Pro Thr Thr Thr Ala Cys Pro Tyr Ser
50 55 60

pctgb2016051576-seq1

Asn Pro Ser Leu Cys Ser Gly Gly Gly Gly Ser Pro Ala Pro Arg Pro
65 70 75 80

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
85 90 95

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
100 105 110

Asp Phe Ala Cys Asp Met Ala Leu Ile Val Leu Gly Gly Val Ala Gly
115 120 125

Leu Leu Leu Phe Ile Gly Leu Gly Ile Phe Phe Cys Val Arg Cys Arg
130 135 140

His Arg Arg Arg Gln Ala Glu Arg Met Ala Gln Ile Lys Arg Val Val
145 150 155 160

Ser Glu Lys Lys Thr Ala Gln Ala Pro His Arg Phe Gln Lys Thr Cys
165 170 175

Ser Pro Ile Ser Gly Gly Gly Gly Ser Glu Asn Leu Tyr Phe Gln Met
180 185 190

Pro Lys Lys Lys Arg Lys Val Ala Pro Pro Thr Asp Val Ser Leu Gly
195 200 205

Asp Glu Leu His Leu Asp Gly Glu Asp Val Ala Met Ala His Ala Asp
210 215 220

Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Asp Gly Asp Ser Pro
225 230 235 240

Gly Pro Gly Phe Thr Pro His Asp Ser Ala Pro Tyr Gly Ala Leu Asp
245 250 255

pctgb2016051576-seq1

Met Ala Asp Phe Glu Phe Glu Gln Met Phe Thr Asp Ala Leu Gly Ile
260 265 270

Asp Glu Tyr Gly Gly Ser Gly Gly Gly Ser Met Gln Ile Leu Val Ala
275 280 285

Ser Asp Ala Thr Met Lys Leu Leu Ser Ser Ile Glu Gln Ala Cys Asp
290 295 300

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

Ala Lys Cys Leu Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr
325 330 335

Lys Arg Ser Pro Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg
340 345 350

Leu Glu Arg Leu Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp
355 360 365

Leu Asp Met Ile Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu
370 375 380

Leu Thr Gly Leu Phe Val Gln Asp Asn Val Asn Lys Asp Ala Val Thr
385 390 395 400

Asp Arg Leu Ala Ser Val Glu Thr Asp Met Pro Leu Thr Leu Arg Gln
405 410 415

His Arg Ile Ser Ala Thr Ser Ser Ser Glu Glu Ser Ser Asn Lys Gly
420 425 430

Gln Arg Gln Leu Thr Val
435

pctgb2016051576-seq1

<210> 56
 <211> 438
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> target receptor

<400> 56

Met Ala Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr
 1 5 10 15

Asp Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
 20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp
 35 40 45

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

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

Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser
 85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Lys
 100 105 110

Asn Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
 115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 130 135 140

Gly Gly Gly Gly Ser Arg Ser Glu Val Gln Leu Val Glu Ser Gly Gly

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

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340

345

350

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

Phe Ser Val Asp Tyr Gly Glu Leu Asp Phe Gln Trp Arg Glu Lys Thr
370 375 380

Pro Glu Pro Pro Val Pro Cys Val Pro Glu Gln Thr Glu Tyr Ala Thr
385 390 395 400

Ile Val Phe Pro Ser Gly Met Gly Thr Ser Ser Pro Ala Arg Arg Gly
405 410 415

Ser Ala Asp Gly Pro Arg Ser Ala Gln Pro Leu Arg Pro Glu Asp Gly
420 425 430

His Cys Ser Trp Pro Leu
435

<210> 57

<211> 509

<212> PRT

<213> Artificial Sequence

<220>

<223> receptor containing a CAR against CD19 with a cleavable CD3-zeta
endodomain

<400> 57

Met Ser Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu
20 25 30

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

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Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
50 55 60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65 70 75 80

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

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
115 120 125

Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

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

Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys Thr Val Ser Gly
165 170 175

Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg
180 185 190

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr
195 200 205

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

Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr
225 230 235 240

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Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala
245 250 255

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp Pro
260 265 270

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

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

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

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
325 330 335

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Cys Arg His Arg Arg Arg
340 345 350

Gln Ala Glu Arg Met Ala Gln Ile Lys Arg Val Val Ser Glu Lys Lys
355 360 365

Thr Ala Gln Ala Pro His Arg Phe Gln Lys Thr Cys Ser Pro Ile Ser
370 375 380

Gly Gly Gly Gly Ser Glu Asn Leu Tyr Phe Gln Met Arg Arg Val Lys
385 390 395 400

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
405 410 415

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
420 425 430

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Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
435 440 445

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
450 455 460

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
465 470 475 480

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
485 490 495

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
500 505

<210> 58
<211> 827
<212> PRT
<213> Artificial Sequence

<220>
<223> receptor containing a CAR against CD19 with a CD3-zeta endodomain
and a cleavable CD148 endodomain

<400> 58

Met Ser Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu
20 25 30

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

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
50 55 60

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Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65 70 75 80

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

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
115 120 125

Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

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

Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys Thr Val Ser Gly
165 170 175

Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg
180 185 190

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr
195 200 205

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

Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr
225 230 235 240

Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala
245 250 255

pctgb2016051576-seq1

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp Pro
260 265 270

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

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

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

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
325 330 335

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Arg Val Lys Phe Ser Arg
340 345 350

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
355 360 365

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
370 375 380

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
385 390 395 400

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
405 410 415

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
420 425 430

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
435 440 445

pctgb2016051576-seq1

Ala Leu His Met Gln Ala Leu Pro Pro Arg Glu Asn Leu Tyr Phe Gln
450 455 460

Met Ala Val Phe Gly Cys Ile Phe Gly Ala Leu Val Ile Val Thr Val
465 470 475 480

Gly Gly Phe Ile Phe Trp Arg Lys Lys Arg Lys Asp Ala Lys Asn Asn
485 490 495

Glu Val Ser Phe Ser Gln Ile Lys Pro Lys Lys Ser Lys Leu Ile Arg
500 505 510

Val Glu Asn Phe Glu Ala Tyr Phe Lys Lys Gln Gln Ala Asp Ser Asn
515 520 525

Cys Gly Phe Ala Glu Glu Tyr Glu Asp Leu Lys Leu Val Gly Ile Ser
530 535 540

Gln Pro Lys Tyr Ala Ala Glu Leu Ala Glu Asn Arg Gly Lys Asn Arg
545 550 555 560

Tyr Asn Asn Val Leu Pro Tyr Asp Ile Ser Arg Val Lys Leu Ser Val
565 570 575

Gln Thr His Ser Thr Asp Asp Tyr Ile Asn Ala Asn Tyr Met Pro Gly
580 585 590

Tyr His Ser Lys Lys Asp Phe Ile Ala Thr Gln Gly Pro Leu Pro Asn
595 600 605

Thr Leu Lys Asp Phe Trp Arg Met Val Trp Glu Lys Asn Val Tyr Ala
610 615 620

Ile Ile Met Leu Thr Lys Cys Val Glu Gln Gly Arg Thr Lys Cys Glu
625 630 635 640

pctgb2016051576-seq1

Glu Tyr Trp Pro Ser Lys Gln Ala Gln Asp Tyr Gly Asp Ile Thr Val
645 650 655

Ala Met Thr Ser Glu Ile Val Leu Pro Glu Trp Thr Ile Arg Asp Phe
660 665 670

Thr Val Lys Asn Ile Gln Thr Ser Glu Ser His Pro Leu Arg Gln Phe
675 680 685

His Phe Thr Ser Trp Pro Asp His Gly Val Pro Asp Thr Thr Asp Leu
690 695 700

Leu Ile Asn Phe Arg Tyr Leu Val Arg Asp Tyr Met Lys Gln Ser Pro
705 710 715 720

Pro Glu Ser Pro Ile Leu Val His Cys Ser Ala Gly Val Gly Arg Thr
725 730 735

Gly Thr Phe Ile Ala Ile Asp Arg Leu Ile Tyr Gln Ile Glu Asn Glu
740 745 750

Asn Thr Val Asp Val Tyr Gly Ile Val Tyr Asp Leu Arg Met His Arg
755 760 765

Pro Leu Met Val Gln Thr Glu Asp Gln Tyr Val Phe Leu Asn Gln Cys
770 775 780

Val Leu Asp Ile Val Arg Ser Gln Lys Asp Ser Lys Val Asp Leu Ile
785 790 795 800

Tyr Gln Asn Thr Thr Ala Met Thr Ile Tyr Glu Asn Leu Ala Pro Val
805 810 815

Thr Thr Phe Gly Lys Thr Asn Gly Tyr Ile Ala
820 825

pctgb2016051576-seq1

<210> 59
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> 2a self-cleaving peptide

<400> 59

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

Asn Pro Gly Pro
20

<210> 60
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> 2a self-cleaving peptide

<400> 60

Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly Asp Val Glu Ser
1 5 10 15

Asn Pro Gly Pro
20

<210> 61
<211> 563
<212> PRT
<213> Artificial Sequence

<220>
<223> dual SH2 domains from SHP-2 fused to ZAP70 kinase domain

<400> 61

Trp Phe His Pro Asn Ile Thr Gly Val Glu Ala Glu Asn Leu Leu Leu

pctgb2016051576-seq1

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

pctgb2016051576-seq1

195

200

205

Gln Pro Leu Asn Thr Thr Arg Ile Asn Pro Asn Ser Ser Ala Ser Asn
 210 215 220

Ala Ser Gly Ala Ala Ala Pro Thr Leu Pro Ala His Pro Ser Thr Leu
 225 230 235 240

Thr His Pro Gln Arg Arg Ile Asp Thr Leu Asn Ser Asp Gly Tyr Thr
 245 250 255

Pro Glu Pro Ala Arg Ile Thr Ser Pro Asp Lys Pro Arg Pro Met Pro
 260 265 270

Met Asp Thr Ser Val Tyr Glu Ser Pro Tyr Ser Asp Pro Glu Glu Leu
 275 280 285

Lys Asp Lys Lys Leu Phe Leu Lys Arg Asp Asn Leu Leu Ile Ala Asp
 290 295 300

Ile Glu Leu Gly Cys Gly Asn Phe Gly Ser Val Arg Gln Gly Val Tyr
 305 310 315 320

Arg Met Arg Lys Lys Gln Ile Asp Val Ala Ile Lys Val Leu Lys Gln
 325 330 335

Gly Thr Glu Lys Ala Asp Thr Glu Glu Met Met Arg Glu Ala Gln Ile
 340 345 350

Met His Gln Leu Asp Asn Pro Tyr Ile Val Arg Leu Ile Gly Val Cys
 355 360 365

Gln Ala Glu Ala Leu Met Leu Val Met Glu Met Ala Gly Gly Gly Pro
 370 375 380

Leu His Lys Phe Leu Val Gly Lys Arg Glu Glu Ile Pro Val Ser Asn

385 390 395 400

Glu Lys Asn Phe Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Leu
420 425 430

Val Asn Arg His Tyr Ala Lys Ile Ser Asp Phe Gly Leu Ser Lys Ala
435 440 445

Leu Gly Ala Asp Asp Ser Tyr Tyr Thr Ala Arg Ser Ala Gly Lys Trp
450 455 460

Pro Leu Lys Trp Tyr Ala Pro Glu Cys Ile Asn Phe Arg Lys Phe Ser
465 470 475 480

Ser Arg Ser Asp Val Trp Ser Tyr Gly Val Thr Met Trp Glu Ala Leu
485 490 495

Ser Tyr Gly Gln Lys Pro Tyr Lys Lys Met Lys Gly Pro Glu Val Met
500 505 510

Ala Phe Ile Glu Gln Gly Lys Arg Met Glu Cys Pro Pro Glu Cys Pro
515 520 525

Pro Glu Leu Tyr Ala Leu Met Ser Asp Cys Trp Ile Tyr Lys Trp Glu
530 535 540

Asp Arg Pro Asp Phe Leu Thr Val Glu Gln Arg Met Arg Ala Cys Tyr
545 550 555 560

Tyr Ser Leu

pctgb2016051576-seq1

<211> 567

<212> PRT

<213> Artificial Sequence

<220>

<223> dual SHP-2 SH2 domain fused to an Akt kinase domain

<400> 62

Trp Phe His Pro Asn Ile Thr Gly Val Glu Ala Glu Asn Leu Leu Leu
1 5 10 15

Thr Arg Gly Val Asp Gly Ser Phe Leu Ala Arg Pro Ser Lys Ser Asn
20 25 30

Pro Gly Asp Phe Thr Leu Ser Val Arg Arg Asn Gly Ala Val Thr His
35 40 45

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

Lys Phe Ala Thr Leu Ala Glu Leu Val Gln Tyr Tyr Met Glu His His
65 70 75 80

Gly Gln Leu Lys Glu Lys Asn Gly Asp Val Ile Glu Leu Lys Tyr Pro
85 90 95

Leu Asn Cys Ala Asp Pro Thr Ser Glu Arg Trp Phe His Gly His Leu
100 105 110

Ser Gly Lys Glu Ala Glu Lys Leu Leu Thr Glu Lys Gly Lys His Gly
115 120 125

Ser Phe Leu Val Arg Glu Ser Gln Ser His Pro Gly Asp Phe Val Leu
130 135 140

Ser Val Arg Thr Gly Asp Asp Lys Gly Glu Ser Asn Asp Gly Lys Ser
145 150 155 160

pctgb2016051576-seq1

Lys Val Thr His Val Met Ile Arg Cys Gln Glu Leu Lys Tyr Asp Val
165 170 175

Gly Gly Gly Glu Arg Phe Asp Ser Leu Thr Asp Leu Val Glu His Tyr
180 185 190

Lys Lys Asn Pro Met Val Glu Thr Leu Gly Thr Val Leu Gln Leu Lys
195 200 205

Gln Pro Leu Asn Thr Thr Arg Ile Asn Ala Glu Glu Met Glu Val Ser
210 215 220

Leu Ala Lys Pro Lys His Arg Val Thr Met Asn Glu Phe Glu Tyr Leu
225 230 235 240

Lys Leu Leu Gly Lys Gly Thr Phe Gly Lys Val Ile Leu Val Lys Glu
245 250 255

Lys Ala Thr Gly Arg Tyr Tyr Ala Met Lys Ile Leu Lys Lys Glu Val
260 265 270

Ile Val Ala Lys Asp Glu Val Ala His Thr Leu Thr Glu Asn Arg Val
275 280 285

Leu Gln Asn Ser Arg His Pro Phe Leu Thr Ala Leu Lys Tyr Ser Phe
290 295 300

Gln Thr His Asp Arg Leu Cys Phe Val Met Glu Tyr Ala Asn Gly Gly
305 310 315 320

Glu Leu Phe Phe His Leu Ser Arg Glu Arg Val Phe Ser Glu Asp Arg
325 330 335

Ala Arg Phe Tyr Gly Ala Glu Ile Val Ser Ala Leu Asp Tyr Leu His
340 345 350

pctgb2016051576-seq1

Ser Glu Lys Asn Val Val Tyr Arg Asp Leu Lys Leu Glu Asn Leu Met
355 360 365

Leu Asp Lys Asp Gly His Ile Lys Ile Thr Asp Phe Gly Leu Cys Lys
370 375 380

Glu Gly Ile Lys Asp Gly Ala Thr Met Lys Thr Phe Cys Gly Thr Pro
385 390 395 400

Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp Asn Asp Tyr Gly Arg Ala
405 410 415

Val Asp Trp Trp Gly Leu Gly Val Val Met Tyr Glu Met Met Cys Gly
420 425 430

Arg Leu Pro Phe Tyr Asn Gln Asp His Glu Lys Leu Phe Glu Leu Ile
435 440 445

Leu Met Glu Glu Ile Arg Phe Pro Arg Thr Leu Gly Pro Glu Ala Lys
450 455 460

Ser Leu Leu Ser Gly Leu Leu Lys Lys Asp Pro Lys Gln Arg Leu Gly
465 470 475 480

Gly Gly Ser Glu Asp Ala Lys Glu Ile Met Gln His Arg Phe Phe Ala
485 490 495

Gly Ile Val Trp Gln His Val Tyr Glu Lys Lys Leu Ser Pro Pro Phe
500 505 510

Lys Pro Gln Val Thr Ser Glu Thr Asp Thr Arg Tyr Phe Asp Glu Glu
515 520 525

Phe Thr Ala Gln Met Ile Thr Ile Thr Pro Pro Asp Gln Asp Asp Ser
530 535 540

pctgb2016051576-seq1

Met Glu Cys Val Asp Ser Glu Arg Arg Pro His Phe Pro Gln Phe Ser
 545 550 555 560

Tyr Ser Ala Ser Gly Thr Ala
 565

<210> 63
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ITIM conserved sequence

<220>
 <221> MISC_FEATURE
 <222> (1)..(1)
 <223> Xaa may be Ser, Ile, Val or Leu

<220>
 <221> misc_feature
 <222> (2)..(2)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> misc_feature
 <222> (4)..(5)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> MISC_FEATURE
 <222> (6)..(6)
 <223> Xaa may be Ile, Val or Leu

<400> 63

Xaa Xaa Tyr Xaa Xaa Xaa
 1 5