

SEQUENCE LISTING

<110> Immetacyte Ltd

<120> RECEPTORS PROVIDING TARGETED COSTIMULATION FOR ADOPTIVE CELL THERAPY

<130> P37029W01

<150> US62/951,770

<151> 2019-12-20

<150> GB1900858.0

<151> 2019-01-22

<160> 14

<170> PatentIn version 3.5

<210> 1

<211> 4900

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (223)..(885)

<223> Acession No. NM_006139

<220>

<221> sig_peptide

<222> (223)..(276)

<220>

<221> transmembrane

<222> (456)..(537)

<400> 1

taaagtcatc aaaacaacgt tatatcctgt gtgaaatgct gcagtcagga tgccttgtgg	60
tttgagtgcc ttgatcatgt gccctaaggg gatgggtggcg gtgggtgggtgg ccgtggatga	120
cggagactct caggccttgg caggtgcgtc tttcagttcc cctcacactt cgggttcctc	180
ggggaggagg ggctggaacc ctagcccatc gtcaggacaa ag atg ctc agg ctg	234
	Met Leu Arg Leu
	1
ctc ttg gct ctc aac tta ttc cct tca att caa gta aca gga aac aag	282

Leu	Leu	Ala	Leu	Asn	Leu	Phe	Pro	Ser	Ile	Gln	Val	Thr	Gly	Asn	Lys	
5				10					15					20		
att	ttg	gtg	aag	cag	tcg	ccc	atg	ctt	gta	gcg	tac	gac	aat	gcg	gtc	330
Ile	Leu	Val	Lys	Gln	Ser	Pro	Met	Leu	Val	Ala	Tyr	Asp	Asn	Ala	Val	
			25					30					35			
aac	ctt	agc	tgc	aag	tat	tcc	tac	aat	ctc	ttc	tca	agg	gag	ttc	cgg	378
Asn	Leu	Ser	Cys	Lys	Tyr	Ser	Tyr	Asn	Leu	Phe	Ser	Arg	Glu	Phe	Arg	
		40						45				50				
gca	tcc	ctt	cac	aaa	gga	ctg	gat	agt	gct	gtg	gaa	gtc	tgt	gtt	gta	426
Ala	Ser	Leu	His	Lys	Gly	Leu	Asp	Ser	Ala	Val	Glu	Val	Cys	Val	Val	
		55					60					65				
tat	ggg	aat	tac	tcc	cag	cag	ctt	cag	gtt	tac	tca	aaa	acg	ggg	ttc	474
Tyr	Gly	Asn	Tyr	Ser	Gln	Gln	Leu	Gln	Val	Tyr	Ser	Lys	Thr	Gly	Phe	
	70					75				80						
aac	tgt	gat	ggg	aaa	ttg	ggc	aat	gaa	tca	gtg	aca	ttc	tac	ctc	cag	522
Asn	Cys	Asp	Gly	Lys	Leu	Gly	Asn	Glu	Ser	Val	Thr	Phe	Tyr	Leu	Gln	
85					90				95						100	
aat	ttg	tat	gtt	aac	caa	aca	gat	att	tac	ttc	tgc	aaa	att	gaa	gtt	570
Asn	Leu	Tyr	Val	Asn	Gln	Thr	Asp	Ile	Tyr	Phe	Cys	Lys	Ile	Glu	Val	
				105				110						115		
atg	tat	cct	cct	cct	tac	cta	gac	aat	gag	aag	agc	aat	gga	acc	att	618
Met	Tyr	Pro	Pro	Pro	Tyr	Leu	Asp	Asn	Glu	Lys	Ser	Asn	Gly	Thr	Ile	
			120					125					130			
atc	cat	gtg	aaa	ggg	aaa	cac	ctt	tgt	cca	agt	ccc	cta	ttt	ccc	gga	666
Ile	His	Val	Lys	Gly	Lys	His	Leu	Cys	Pro	Ser	Pro	Leu	Phe	Pro	Gly	
		135					140					145				
cct	tct	aag	ccc	ttt	tgg	gtg	ctg	gtg	gtg	gtt	ggt	gga	gtc	ctg	gct	714
Pro	Ser	Lys	Pro	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	
		150				155					160					
tgc	tat	agc	ttg	cta	gta	aca	gtg	gcc	ttt	att	att	ttc	tgg	gtg	agg	762
Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Phe	Trp	Val	Arg	
165					170				175						180	
agt	aag	agg	agc	agg	ctc	ctg	cac	agt	gac	tac	atg	aac	atg	act	ccc	810
Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro	
				185					190					195		
cgc	cgc	ccc	ggg	ccc	acc	cgc	aag	cat	tac	cag	ccc	tat	gcc	cca	cca	858
Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	
			200					205					210			

cgc gac ttc gca gcc tat cgc tcc tga cacggacgcc tatccagaag	905
Arg Asp Phe Ala Ala Tyr Arg Ser	
215 220	
ccagccggct ggcagccccc atctgctcaa tatcactgct ctggatagga aatgaccgcc	965
atctccagcc ggccacctca ggcccctgtt gggccaccaa tgccaatttt tctcgagtga	1025
ctagaccaaaa tatcaagatc attttgagac tctgaaatga agtaaaagag atttcctgtg	1085
acaggccaag tcttacagtg ccatggccca cattccaact taccatgtac ttagtgactt	1145
gactgagaag ttagggtaga aaacaaaaag ggagtggatt ctgggagcct cttccctttc	1205
tcactcacct gcacatctca gtcaagcaaa gtgtggtatc cacagacatt ttagttgcag	1265
aagaaaggct aggaaatcat tccttttggg taaatgggtg tttaatcttt tggttagtgg	1325
gttaaacggg gtaagttaga gtagggggag ggataggaag acatatttaa aaaccattaa	1385
aacactgtct ccactcatg aaatgagcca cgtagttcct atttaatgct gttttccttt	1445
agtttagaaa tacatagaca ttgtctttta tgaattctga tcatatttag tcattttgac	1505
caaatgaggg atttgggtcaa atgagggatt ccctcaaagc aatatcaggt aaaccaagtt	1565
gctttcctca ctccctgtca tgagacttca gtgttaatgt tcacaatata ctttcgaaag	1625
aataaaatag ttctcttaca tgaagaaaga atatgtcagg aaataaggtc actttatgtc	1685
aaaattatth gagtactatg ggacctggcg cagtggctca tgcttgtaat ccagcactt	1745
tgggaggccg aggtgggcag atcacttgag atcaggacca gcctgggtcaa gatgggtgaaa	1805
ctccgtctgt actaaaaata caaaatttag cttggcctgg tggcaggcac ctgtaatccc	1865
agctgcccga gaggctgagg catgagaatc gcttgaacct ggcaggcgga ggttgcagtg	1925
agccgagata gtgccacagc tctccagcct gggcgacaga gtgagactcc atctcaaaca	1985
acaacaacaa caacaacaac aacaacaac caaaaatta tttgagtact gtgaaggatt	2045
atttgtctaa cagttcattc caatcagacc aggtaggagc tttcctgttt catatgtttc	2105
agggttgac agttggtctc tttaatgtcg gtgtggagat ccaaagtggg ttgtggaaag	2165
agcgtccata ggagaagtga gaatactgtg aaaaagggat gttagcattc attagagtat	2225
gaggatgagt cccaagaagg ttctttggaa ggaggacgaa tagaatggag taatgaaatt	2285

cttgccatgt gctgaggaga tagccagcat taggtgacaa tcttccagaa gtggtcaggc	2345
agaagggtgcc ctggtgagag ctcctttaca gggactttat gtggtttagg gctcagagct	2405
ccaaaactct gggctcagct gctcctgtac cttggagggtc cattcacatg ggaaagtatt	2465
ttggaatgtg tcttttgaag agagcatcag agttcttaag ggactgggta aggcctgacc	2525
ctgaaatgac catggatatt tttctaccta cagtttgagt caactagaat atgcctgggg	2585
accttgaaga atggcccttc agtggccctc accatttggt catgcttcag ttaattcagg	2645
tgttgaagga gcttaggttt tagaggcacg tagacttggt tcaagtctcg ttagtagttg	2705
aatagcctca ggcaagtcac tgcccaccta agatgatggt tcttcaacta taaaatggag	2765
ataatggtta caaatgtctc ttcctatagt ataactctca taagggcagtg gcccagctc	2825
gtctttgact ctgcctatcc ctgacattta gtagcatgcc cgacatacaa tgtagctat	2885
tggtattatt gccatataga taaattatgt ataaaaatta aactgggcaa tagcctaaga	2945
aggggggaat attgtaacac aaatttaaac ccactacgca gggatgaggt gctataatat	3005
gaggaccttt taacttccat cattttcctg tttcttgaaa tagtttatct tgtaatgaaa	3065
tataaggcac ctcccacttt tatgtataga aagaggctctt ttaatttttt tttaatgtga	3125
gaaggaaggg aggagtagga atcttgagat tccagatcga aaatactgta ctttggttga	3185
tttttaagtg ggcttccatt ccatggattt aatcagttcc aagaagatca aactcagcag	3245
tacttgggtg ctgaagaact gttggattta ccctggcacg tgtgccactt gccagcttct	3305
tgggcacaca gagttcttca atccaagtta tcagattgta tttgaaaatg acagagctgg	3365
agagtttttt gaaatggcag tggcaaataa ataaatactt ttttttaaat ggaaagactt	3425
gatctatggt aataaatgat tttgttttct gactggaaaa ataggcctac taaagatgaa	3485
tcacacttga gatgtttctt actcactctg cacagaaaca aagaagaaat gttatacagg	3545
gaagtccgtt ttcactatta gtatgaacca agaaatgggt caaaaacagt ggtaggagca	3605
atgctttcat agtttcagat atggtagtta tgaagaaaac aatgtcattt gctgctatta	3665
ttgtaagagt cttataatta atgggtactcc tataattttt gattgtgagc tcacctattt	3725
gggttaagca tgccaattta aagagaccaa gtgtatgtac attatgttct acatattcag	3785

tgataaaaatt actaaactac tatatgtctg ctttaaattt gtactttaat attgtctttt	3845
ggtattaaga aagatatgct ttcagaatag atatgcttcg ctttggcaag gaatttggat	3905
agaacttgct atttaaaaga ggtgtgggggt aaatccttgt ataaatctcc agtttagcct	3965
tttttgaaaa agctagactt tcaaatacta atttcacttc aagcagggtta cgtttctggt	4025
ttgtttgctt gacttcagtc acaatttctt atcagaccaa tggctgacct ctttgagatg	4085
tcaggctagg cttacctatg tgttctgtgt catgtgaatg ctgagaagtt tgacagagat	4145
ccaacttcag ccttgacccc atcagtcctt cgggttaact aactgagcca ccggtcctca	4205
tggctatttt aatgagggtta ttgatggtta aatgcatgtc tgatccctta tcccagccat	4265
ttgcactgcc agctgggaac tataccagac ctggatactg atcccaaagt gttaaattca	4325
actacatgct ggagattaga gatggtgcca ataaaggacc cagaaccagg atcttgattg	4385
ctatagactt attaataatc cagggtcaaag agagtgcac acactctctc aagacctggg	4445
gtgaggggagt ctgtgttatc tgcaaggcca tttgaggctc agaaagtctc tctttcctat	4505
agatatatgc atactttctg acatatagga atgtatcagg aatactcaac catcacaggc	4565
atgttcctac ctcagggcct ttacatgtcc tgtttactct gtctagaatg tccttctgta	4625
gatgacctgg cttgcctcgt cacccttcag gtccttgctc aagtgtcatc ttctccccta	4685
gttaaactac cccacaccct gtctgctttc cttgcttatt tttctccata gcattttacc	4745
atctcttaca ttagacattt ttcttattta tttgtagttt ataagcttca tgaggcaagt	4805
aactttgctt tgtttcttgc tgtatctcca gtgcccagag cagtgcctgg tatataataa	4865
atattttattg actgagtga aaaaaaaaaa aaaaa	4900

<210> 2
 <211> 220
 <212> PRT
 <213> Homo sapiens

<400> 2

Met	Leu	Arg	Leu	Leu	Leu	Ala	Leu	Asn	Leu	Phe	Pro	Ser	Ile	Gln	Val
1			5					10						15	

Thr Gly Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr
20 25 30

Asp Asn Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser
35 40 45

Arg Glu Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu
50 55 60

Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser
65 70 75 80

Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr
85 90 95

Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys
100 105 110

Lys Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser
115 120 125

Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
130 135 140

Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
145 150 155 160

Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
165 170 175

Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
180 185 190

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
195 200 205

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser

210

215

220

<210> 3

<211> 165

<212> PRT

<213> Homo sapiens

<400> 3

Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr Asp Asn
 1 5 10 15

Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser Arg Glu
 20 25 30

Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu Val Cys
 35 40 45

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

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

Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys Lys Ile
 85 90 95

Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly
 100 105 110

Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe
 115 120 125

Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val
 130 135 140

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

Val Arg Ser Lys Arg
165

<210> 4
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein

<220>
<221> DOMAIN
<222> (1)..(166)
<223> CD28

<220>
<221> DOMAIN
<222> (167)..(248)
<223> CD137

<400> 4

Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr Asp Asn
1 5 10 15

Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser Arg Glu
20 25 30

Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu Val Cys
35 40 45

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

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

Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys Lys Ile
85 90 95

Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly

100

105

110

Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe
 115 120 125

Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val
 130 135 140

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

Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
 165 170 175

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
 180 185 190

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Phe Ser Val Val Lys
 195 200 205

Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg
 210 215 220

Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro
 225 230 235 240

Glu Glu Glu Glu Gly Gly Cys Glu
 245

<210> 5
 <211> 239
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fusion protein

<220>
 <221> DOMAIN

<222> (1)..(202)

<223> CD28

<220>

<221> DOMAIN

<222> (203)..(239)

<223> CD134

<400> 5

Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr Asp Asn
1 5 10 15

Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser Arg Glu
20 25 30

Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu Val Cys
35 40 45

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

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

Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys Lys Ile
85 90 95

Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly
100 105 110

Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe
115 120 125

Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val
130 135 140

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

Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
165 170 175

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
180 185 190

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Arg Asp Gln Arg Leu
195 200 205

Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro
210 215 220

Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile
225 230 235

<210> 6
<211> 318
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein

<220>
<221> DOMAIN
<222> (1)..(202)
<223> CD28

<220>
<221> DOMAIN
<222> (203)..(318)
<223> CD2

<400> 6

Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr Asp Asn
1 5 10 15

Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser Arg Glu
20 25 30

Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu Val Cys

35

40

45

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

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

Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys Lys Ile
 85 90 95

Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly
 100 105 110

Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe
 115 120 125

Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val
 130 135 140

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

Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
 165 170 175

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
 180 185 190

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg Lys Lys Gln Arg
 195 200 205

Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His Arg Val Ala
 210 215 220

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

Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Pro Gly His Arg
245 250 255

Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His Arg Val Gln
260 265 270

His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr Gln Val His
275 280 285

Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln Pro Lys Pro
290 295 300

Pro His Gly Ala Ala Glu Asn Ser Leu Ser Pro Ser Ser Asn
305 310 315

<210> 7
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein

<220>
<221> DOMAIN
<222> (1)..(202)
<223> CD28

<220>
<221> DOMAIN
<222> (202)..(249)
<223> CD29

<400> 7

Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr Asp Asn
1 5 10 15

Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser Arg Glu
20 25 30

Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu Val Cys
35 40 45

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

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

Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys Lys Ile
85 90 95

Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly
100 105 110

Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe
115 120 125

Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val
130 135 140

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

Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
165 170 175

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
180 185 190

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys Leu Leu Met Ile Ile
195 200 205

His Asp Arg Arg Glu Phe Ala Lys Phe Glu Lys Glu Lys Met Asn Ala
210 215 220

Lys Trp Asp Thr Gly Glu Asn Pro Ile Tyr Lys Ser Ala Val Thr Thr
225 230 235 240

Val Val Asn Pro Lys Tyr Glu Gly Lys
245

<210> 8
<211> 260
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein

<220>
<221> DOMAIN
<222> (1)..(202)
<223> CD28

<220>
<221> DOMAIN
<222> (203)..(260)
<223> GITR

<400> 8

Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr Asp Asn
1 5 10 15

Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser Arg Glu
20 25 30

Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu Val Cys
35 40 45

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

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

Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys Lys Ile
85 90 95

Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly
100 105 110

Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe
115 120 125

Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val
130 135 140

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

Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
165 170 175

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
180 185 190

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Gln Leu Gly Leu His Ile
195 200 205

Trp Gln Leu Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu
210 215 220

Leu Glu Val Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro
225 230 235 240

Glu Glu Glu Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly
245 250 255

Asp Leu Trp Val
260

<210> 9
<211> 288
<212> PRT
<213> Artificial Sequence

<220>

<223> Fusion protein

<220>

<221> DOMAIN

<222> (1)..(202)

<223> CD28

<220>

<221> DOMAIN

<222> (203)..(288)

<223> IL2Rg

<400> 9

Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr Asp Asn
1 5 10 15

Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser Arg Glu
20 25 30

Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu Val Cys
35 40 45

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

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

Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys Lys Ile
85 90 95

Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly
100 105 110

Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe
115 120 125

Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val
130 135 140

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

Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
165 170 175

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
180 185 190

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Glu Arg Thr Met Pro Arg
195 200 205

Ile Pro Thr Leu Lys Asn Leu Glu Asp Leu Val Thr Glu Tyr His Gly
210 215 220

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

Gln Pro Asp Tyr Ser Glu Arg Leu Cys Leu Val Ser Glu Ile Pro Pro
245 250 255

Lys Gly Gly Ala Leu Gly Glu Gly Pro Gly Ala Ser Pro Cys Asn Gln
260 265 270

His Ser Pro Tyr Trp Ala Pro Pro Cys Tyr Thr Leu Lys Pro Glu Thr
275 280 285

<210> 10
<211> 264
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein

<220>
<221> DOMAIN
<222> (1)..(202)

<223> CD28

<220>

<221> DOMAIN

<222> (203)..(264)

<223> CD40

<400> 10

Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr Asp Asn
1 5 10 15

Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser Arg Glu
20 25 30

Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu Val Cys
35 40 45

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

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

Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys Lys Ile
85 90 95

Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly
100 105 110

Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe
115 120 125

Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val
130 135 140

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

Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met

165

170

175

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
 180 185 190

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys Lys Val Ala Lys Lys
 195 200 205

Pro Thr Asn Lys Ala Pro His Pro Lys Gln Glu Pro Gln Glu Ile Asn
 210 215 220

Phe Pro Asp Asp Leu Pro Gly Ser Asn Thr Ala Ala Pro Val Gln Glu
 225 230 235 240

Thr Leu His Gly Cys Gln Pro Val Thr Gln Glu Asp Gly Lys Glu Ser
 245 250 255

Arg Ile Ser Val Gln Glu Arg Gln
 260

<210> 11
 <211> 277
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein fusion

<220>
 <221> DOMAIN
 <222> (1)..(202)
 <223> CD28

<220>
 <221> DOMAIN
 <222> (203)..(277)
 <223> CD150

<400> 11

Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr Asp Asn
 1 5 10 15

Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser Arg Glu
20 25 30

Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu Val Cys
35 40 45

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

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

Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys Lys Ile
85 90 95

Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly
100 105 110

Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe
115 120 125

Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val
130 135 140

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

Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
165 170 175

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
180 185 190

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Arg Arg Gly Lys Thr
195 200 205

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

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

Ala Gln Asp Pro Cys Thr Thr Ile Tyr Val Ala Ala Thr Glu Pro Val
245 250 255

Pro Glu Ser Val Gln Glu Thr Asn Ser Ile Thr Val Tyr Ala Ser Val
260 265 270

Thr Leu Pro Glu Ser
275

<210> 12
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein fusion

<220>
<221> DOMAIN
<222> (1)..(202)
<223> CD28

<220>
<221> DOMAIN
<222> (203)..(318)
<223> CD2

<220>
<221> DOMAIN
<222> (319)..(350)
<223> CD40

<220>
<221> DOMAIN
<222> (319)..(380)
<223> CD40

<400> 12

Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr Asp Asn
1 5 10 15

Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser Arg Glu
20 25 30

Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu Val Cys
35 40 45

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

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

Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys Lys Ile
85 90 95

Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly
100 105 110

Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe
115 120 125

Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val
130 135 140

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

Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
165 170 175

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
180 185 190

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg Lys Lys Gln Arg

195

200

205

Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His Arg Val Ala
 210 215 220

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

Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Pro Gly His Arg
 245 250 255

Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His Arg Val Gln
 260 265 270

His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr Gln Val His
 275 280 285

Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln Pro Lys Pro
 290 295 300

Pro His Gly Ala Ala Glu Asn Ser Leu Ser Pro Ser Ser Asn Lys Lys
 305 310 315 320

Val Ala Lys Lys Pro Thr Asn Lys Ala Pro His Pro Lys Gln Glu Pro
 325 330 335

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

Pro Val Gln Glu Thr Leu His Gly Cys Gln Pro Val Thr Gln Glu Asp
 355 360 365

Gly Lys Glu Ser Arg Ile Ser Val Gln Glu Arg Gln
 370 375 380

<210> 13

<211> 98

<212> PRT

<213> Homo sapiens

<220>

<221> DOMAIN

<222> (1)..(98)

<223> CD28 Extracellular truncation

<400> 13

Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr Asp Asn
1 5 10 15

Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser Arg Glu
20 25 30

Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu Val Cys
35 40 45

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

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

Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys Lys Ile
85 90 95

Glu Val

<210> 14

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein Tag

<400> 14

Asp Tyr Lys Asp Asp Asp Asp His
1 5