

SEQUENCE LISTING

<110> KAHR Medical Ltd.
Thomas Jefferson University
TYKOCINSKY, Mark L.
TAMIR, Ami
BREMER, Edwin

<120> HETERODIMERS AND METHODS OF USE THEREOF

<130> 82913

<150> US 62/872,741

<151> 2019-07-11

<160> 166

<170> PatentIn version 3.5

<210> 1

<211> 288

<212> PRT

<213> Artificial sequence

<220>

<223> aa sequence of full length PD1

<400> 1

Met	Gln	Ile	Pro	Gln	Ala	Pro	Trp	Pro	Val	Val	Trp	Ala	Val	Leu	Gln
1				5					10					15	

Leu	Gly	Trp	Arg	Pro	Gly	Trp	Phe	Leu	Asp	Ser	Pro	Asp	Arg	Pro	Trp
			20					25					30		

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

Asn	Ala	Thr	Phe	Thr	Cys	Ser	Phe	Ser	Asn	Thr	Ser	Glu	Ser	Phe	Val
	50					55					60				

Leu	Asn	Trp	Tyr	Arg	Met	Ser	Pro	Ser	Asn	Gln	Thr	Asp	Lys	Leu	Ala
65					70					75				80	

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

Val	Thr	Gln	Leu	Pro	Asn	Gly	Arg	Asp	Phe	His	Met	Ser	Val	Val	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

100

105

110

Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu
 115 120 125

Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val
 130 135 140

Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro
 145 150 155 160

Arg Pro Ala Gly Gln Phe Gln Thr Leu Val Val Gly Val Val Gly Gly
 165 170 175

Leu Leu Gly Ser Leu Val Leu Leu Val Trp Val Leu Ala Val Ile Cys
 180 185 190

Ser Arg Ala Ala Arg Gly Thr Ile Gly Ala Arg Arg Thr Gly Gln Pro
 195 200 205

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

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

Cys Val Pro Glu Gln Thr Glu Tyr Ala Thr Ile Val Phe Pro Ser Gly
 245 250 255

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

Ser Ala Gln Pro Leu Arg Pro Glu Asp Gly His Cys Ser Trp Pro Leu
 275 280 285

<210> 2

<211> 867

<212> DNA

<213> Artificial sequence

<220>

<223> na sequence of full length PD1

<400> 2

atgcagatcc cacaggcgcc ctggccagtc gtctgggcgg tgctacaact gggctggcgg	60
ccaggatggg tcttagactc cccagacagg ccctggaacc ccccccacctt ctccccagcc	120
ctgctcgtgg tgaccgaagg ggacaacgcc accttcacct gcagcttctc caacacatcg	180
gagagcttcg tgctaaactg gtaccgcatg agccccagca accagacgga caagctggcc	240
gccttccccg aggaccgcag ccagcccggc caggactgcc gcttccgtgt cacacaactg	300
cccaacgggc gtgacttcca catgagcgtg gtcagggccc ggcgcaatga cagcggcacc	360
tacctctgtg gggccatctc cctggccccc aaggcgcaga tcaaagagag cctgcgggca	420
gagctcaggg tgacagagag aagggcagaa gtgcccacag cccaccccag cccctcacc	480
aggccagccg gccagttcca aaccctgggtg gttgggtgtcg tgggcggcct gctgggcagc	540
ctggtgctgc tagtctgggt cctggccgtc atctgctccc gggccgcacg agggacaata	600
ggagccaggc gcaccggcca gcccctgaag gaggaccct cagccgtgcc tgtgtttctt	660
gtggactatg gggagctgga tttccagtgg cgagagaaga ccccgagcc ccccggtccc	720
tgtgtccctg agcagacgga gtatgccacc attgtctttc ctagcggaat gggcacctca	780
tccccgccc gcaggggctc agctgacggc cctcggagtg cccagccact gaggcctgag	840
gatggacact gctcttggcc cctctga	867

<210> 3
 <211> 150
 <212> PRT
 <213> Artificial sequence

<220>
 <223> sequence of PD1 ECD Full with CYS93>Ser substitution

<400> 3

Pro	Gly	Trp	Phe	Leu	Asp	Ser	Pro	Asp	Arg	Pro	Trp	Asn	Pro	Pro	Thr
1				5					10					15	

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

Thr	Cys	Ser	Phe	Ser	Asn	Thr	Ser	Glu	Ser	Phe	Val	Leu	Asn	Trp	Tyr
	35						40					45			

Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu
50 55 60

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

Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn
85 90 95

Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala
100 105 110

Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg
115 120 125

Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly
130 135 140

Gln Phe Gln Thr Leu Val
145 150

<210> 4
<211> 450
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO 3

<400> 4
cccggctggt ttctggactc tccagacaga ctttgaacc ctccaacctt ctctcccgt 60
ctgctggtgg ttaccgaggg cgacaatgcc accttcacct gttccttcag caacacctcc 120
gagtccttcg tgctgaactg gtacagaatg tcccctagca accagaccga caagctggcc 180
gcctttcctg aggacagatc tcagccaggc caggactctc ggttcagagt taccagctg 240
cctaacggcc gggacttcca catgtctgtt gtgcgggccca gacggaacga ctctggcaca 300
tatctgtgcg gcgccatctc tctggctccc aaggctcaga tcaaagagtc tctgcgggcc 360
gagctgagag tgacagaaag acgagctgag gtgcccaccg ctcatccctc accttctcca 420
agacctgctg gccagtttca gacactcgtg 450

<210> 5
<211> 167
<212> PRT
<213> Artificial sequence

<220>
<223> PD1 ECM KNOWN FRAGMENT

<400> 5

Met Gln Ile Pro Gln Ala Pro Trp Pro Val Val Trp Ala Val Leu Gln
1 5 10 15

Leu Gly Trp Arg Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp
20 25 30

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

Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val
50 55 60

Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala
65 70 75 80

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

Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg
100 105 110

Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu
115 120 125

Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val
130 135 140

Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro
145 150 155 160

Arg Pro Ala Gly Gln Phe Gln
165

<210> 6
<211> 122
<212> PRT
<213> Artificial sequence

<220>
<223> PD1 ECM KNOWN FRAGMENT

<400> 6

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
1 5 10 15

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

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
50 55 60

Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp
65 70 75 80

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg
115 120

<210> 7
<211> 150
<212> PRT
<213> Artificial sequence

<220>
<223> 150 aa ORIGINAL PD1 DOMAIN

<400> 7

Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr

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

<210> 8
 <211> 450
 <212> DNA
 <213> Artificial sequence

<220>
 <223> na pf SEQ ID NO 7

<400> 8	
ccaggatggt tcttagactc tccagatagg ccttggaatc cccctacctt tagccccgcc	60
ctgctggtgg tgacagaggg cgataacgcc accttcacat gctcttttag caacacctcc	120
gagtctttcg tgctgaattg gtacaggatg agcccttcca accagacaga caagctggca	180

gcatttcctg aggaccgctc ccagccaggc caggattgcc ggttcagagt gaccagctg 240
 ccaaattggca gggactttca catgagcgtg gtgcgcgccc ggagaaacga ttccggcaca 300
 tacctgtgcg gagcaatctc tctggcacca aaggcacaga tcaaggagtc cctgagggca 360
 gagctgaggg tgaccgagag gagggccgag gtgccaacag cacacccatc tcctagccca 420
 aggccagcag gacagttcca aaccctggtg 450

<210> 9
 <211> 150
 <212> PRT
 <213> Artificial sequence

<220>
 <223> 150 aa ORIGINAL PD1 DOMAIN with CYS93>Ser substitution

<400> 9

Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr
 1 5 10 15

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

Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr
 35 40 45

Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu
 50 55 60

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

Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn
 85 90 95

Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala
 100 105 110

Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg
 115 120 125

Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly

130

135

140

Gln Phe Gln Thr Leu Val
145 150

<210> 10
<211> 450
<212> DNA
<213> Artificial sequence

<220>
<223> na of SEQ ID NO 9

<400> 10
ccaggatggg tcttagactc tccagatagg ccttggaatc cccctacctt tagccccgcc 60
ctgctggtgg tgacagaggg cgataacgcc accttcacat gctcttttag caacacctcc 120
gagtccttcg tgctgaattg gtacaggatg agcccttcca accagacaga caagctggca 180
gcatttcctg aggaccgctc ccagccaggc caggattctc ggttcagagt gaccagctg 240
ccaaatggca gggactttca catgagcgtg gtgcgcgccc ggagaaacga ttccggcaca 300
tacctgtgcg gagcaatctc tctggcacca aaggcacaga tcaaggagtc cctgagggca 360
gagctgaggg tgaccgagag gagggccgag gtgccaacag cacacccatc tcctagccca 420
aggccagcag gacagttcca aaccctggtg 450

<210> 11
<211> 140
<212> PRT
<213> Artificial sequence

<220>
<223> 140 aa -5-5 in PD1 DOMAIN

<400> 11

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
1 5 10 15

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

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
50 55 60

Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp
65 70 75 80

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
115 120 125

Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly Gln
130 135 140

<210> 12
<211> 419
<212> DNA
<213> Artificial sequence

<220>
<223> na of SEQ ID NO 11

<400> 12
gactctccag ataggccttg gaatccccct accttttagcc ccgccctgct ggtggtgaca 60
gagggcgata acgccacctt cacatgctct tttagcaaca cctccgagtc tttcgtgctg 120
aattggtaca ggatgagccc ttccaaccag acagacaagc tggcagcatt tcctgaggac 180
cgctcccagc caggccagga ttgccggttc agagtgaccc agctgccaaa tggcagggac 240
tttcacatga gcgtggtgcg cgcccggaga aacgattccg gcacatacct gtgcggagca 300
atctctctgg caccaaaggc acagatcaag gagtccctga gggcagagct gagggtgacc 360
gagaggaggg ccgaggtgcc aacagcacac ccatctccta gcccaaggcc agcaggaca 419

<210> 13
<211> 140
<212> PRT
<213> Artificial sequence

<220>

<223> 140 aa -5-5 in PD1 DOMAIN with CYS93>Ser substitution

<400> 13

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
1 5 10 15

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

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
50 55 60

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

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
115 120 125

Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly Gln
130 135 140

<210> 14

<211> 419

<212> DNA

<213> Artificial sequence

<220>

<223> na of SEQ ID NO 13

<400> 14

gactctccag ataggccttg gaatccccct acctttagcc ccgccctgct ggtggtgaca 60

gagggcgata acgccacctt cacatgctct tttagcaaca cctccgagtc tttcgtgctg 120

aattggtaca	ggatgagccc	ttccaaccag	acagacaagc	tggcagcatt	tcctgaggac	180
cgctcccagc	caggccagga	tctccggttc	agagtgaccc	agctgccaaa	tggcagggac	240
tttcacatga	gcgtggtgcg	cgcccggaga	aacgattccg	gcacatacct	gtgcggagca	300
atctctctgg	caccaaaggc	acagatcaag	gagtccctga	gggcagagct	gagggtgacc	360
gagaggaggg	ccgaggtgcc	aacagcacac	ccatctccta	gccaaggcc	agcaggaca	419

$\langle 210 \rangle$	15
$\langle 211 \rangle$	140
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	Artificial sequence

<220>
<223> 140 aa PD1 segment

<400> 15

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
1 5 10 15

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

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
50 55 60

Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp
65 70 75 80

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
115 120 125

Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly Gln

130

135

140

<210> 16

<211> 420

<212> DNA

<213> Artificial sequence

<220>

<223> na sequence encoding SEQ ID NO 15

<400> 16

gactccccctg acagaccttg gaaccctcca accttctctc ccgctctgct ggtggttacc 60

gagggcgaca atgccacctt cacctgttcc ttcagcaaca cctccgagtc cttcgtgctg 120

aactggtaca gaatgtcccc tagcaaccag accgacaagc tggccgcctt tcctgaggac 180

agatctcagc caggccagga ctgccggttc agagttaccc agctgcctaa cggccgggac 240

ttccacatgt ctgttggtgcg ggccagacgg aacgactctg gcacatatct gtgcggcgcc 300

atctctctgg ctcccaaggc tcagatcaaa gagtctctgc gggccgagct gagagtgaca 360

gaaagacgag ctgaggtgcc caccgctcat ccctcacctt ctccaagacc tgccggccag 420

<210> 17

<211> 128

<212> PRT

<213> Artificial sequence

<220>

<223> 128 aa PD1 segment

<400> 17

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

Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val

65		70		75		80									
Val	Arg	Ala	Arg	Arg	Asn	Asp	Ser	Gly	Thr	Tyr	Leu	Cys	Gly	Ala	Ile
			85						90					95	
Ser	Leu	Ala	Pro	Lys	Ala	Gln	Ile	Lys	Glu	Ser	Leu	Arg	Ala	Glu	Leu
			100					105					110		
Arg	Val	Thr	Glu	Arg	Arg	Ala	Glu	Val	Pro	Thr	Ala	His	Pro	Ser	Pro
		115					120					125			

<210> 18
 <211> 384
 <212> DNA
 <213> Artificial sequence

<220>
 <223> na sequence encoding SEQ ID NO 17

<400> 18	
ccttggaacc ctccaacctt ctctcccgct ctgctggtgg ttaccgaggg cgacaatgcc	60
accttcacct gttccttcag caacacctcc gagtccttcg tgctgaactg gtacagaatg	120
tcccctagca accagaccga caagctggcc gcctttcctg aggacagatc tcagccaggc	180
caggactgcc ggttcagagt taccagctg cctaacggcc gggacttcca catgtctgtt	240
gtgcggggcca gacggaacga ctctggcaca tatctgtgcg gcgccatctc tctggctccc	300
aaggctcaga tcaaagagtc tctgcggggc gagctgagag tgacagaaag acgagctgag	360
gtgcccaccg ctcatccctc acct	384

<210> 19
 <211> 135
 <212> PRT
 <213> Artificial sequence

<220>
 <223> 135 aa PD1 segment

<400> 19

Pro	Trp	Asn	Pro	Pro	Thr	Phe	Ser	Pro	Ala	Leu	Leu	Val	Val	Thr	Glu
1				5					10					15	

Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser

20

25

30

Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys
 35 40 45

Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg
 50 55 60

Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val
 65 70 75 80

Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile
 85 90 95

Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu
 100 105 110

Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro
 115 120 125

Ser Pro Arg Pro Ala Gly Gln
 130 135

<210> 20
 <211> 405
 <212> DNA
 <213> Artificial sequence

<220>
 <223> na sequence encoding SEQ ID NO 19

<400> 20
 ccttggaacc ctccaacctt ctctcccgct ctgctggtgg ttaccgaggg cgacaatgcc 60
 accttcacct gttccttcag caacacctcc gagtccttcg tgctgaactg gtacagaatg 120
 tcccctagca accagaccga caagctggcc gcctttcctg aggacagatc tcagccaggc 180
 caggactgcc ggttcagagt taccagctg cctaacggcc gggacttcca catgtctgtt 240
 gtgcggggcca gacggaacga ctctggcaca tatctgtgcg gcgccatctc tctggctccc 300
 aaggctcaga tcaaagagtc tctgcgggcc gagctgagag tgacagaaaag acgagctgag 360
 gtgcccaccg ctcatccctc accttctcca agacctgccg gccag 405

<210> 21
<211> 133
<212> PRT
<213> Artificial sequence

<220>
<223> 133 aa PD1 segment

<400> 21

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
1 5 10 15

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

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
50 55 60

Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp
65 70 75 80

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
115 120 125

Ala His Pro Ser Pro
130

<210> 22
<211> 399
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO 21

<400> 22
gactcccctg acagaccttg gaaccctcca accttctctc ccgctctgct ggtggttacc 60
gagggcgaca atgccacctt cacctgttcc ttcagcaaca cctccgagtc cttcgtgctg 120
aactggtaca gaatgtcccc tagcaaccag accgacaagc tggccgcctt tcctgaggac 180
agatctcagc caggccagga ctgccggttc agagttaccc agctgcctaa cggccgggac 240
ttccacatgt ctgttgtgcg ggccagacgg aacgactctg gcacatatct gtgcggcgcc 300
atctctctgg ctcccaaggc tcagatcaaa gagtctctgc gggccgagct gagagtgaca 360
gaaagacgag ctgaggtgcc caccgctcat ccctcacct 399

<210> 23
<211> 135
<212> PRT
<213> Artificial sequence

<220>
<223> PD1 -10-5 (with CYS93>Ser substitution)

<400> 23

Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu
1 5 10 15

Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser
20 25 30

Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys
35 40 45

Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Ser Arg
50 55 60

Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val
65 70 75 80

Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile
85 90 95

Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu
100 105 110

Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro
115 120 125

Ser Pro Arg Pro Ala Gly Gln
130 135

<210> 24
<211> 405
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO 23

<400> 24
ccttgggaacc ctccaacctt ctctcccgct ctgctggtgg ttaccgaggg cgacaatgcc 60
accttcacct gttccttcag caacacctcc gagtccttcg tgctgaactg gtacagaatg 120
tcccctagca accagaccga caagctggcc gcctttcctg aggacagatc tcagccaggc 180
caggactctc ggttcagagt taccagctg cctaacggcc gggacttcca catgtctgtt 240
gtgcggggcca gacggaacga ctctggcaca tatctgtgcg gcgccatctc tctggctccc 300
aaggctcaga tcaaagagtc tctgcggggc gagctgagag tgacagaaag acgagctgag 360
gtgcccaccg ctcatccctc accttctcca agacctgctg gccag 405

<210> 25
<211> 128
<212> PRT
<213> Artificial sequence

<220>
<223> PD1 -10-12 (with CYS93>Ser substitution)

<400> 25

Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu
1 5 10 15

Gly Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser
20 25 30

Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys
35 40 45

Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Ser Arg
50 55 60

Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val
65 70 75 80

Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile
85 90 95

Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu
100 105 110

Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro
115 120 125

<210> 26
<211> 384
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO 25

<400> 26
ccttggacc ctccaacctt ctctcccgct ctgctggtgg ttaccgaggg cgacaatgcc 60
accttcacct gttccttcag caacacctcc gagtccttcg tgctgaactg gtacagaatg 120
tcccctagca accagaccga caagctggcc gcctttcctg aggacagatc tcagccaggc 180
caggactctc ggttcagagt taccagctg cctaacggcc gggacttcca catgtctgtt 240
gtgcggggcca gacggaacga ctctggcaca tatctgtgcg gcgccatctc tctggctccc 300
aaggctcaga tcaaagagtc tctgcggggc gagctgagag tgacagaaaag acgagctgag 360
gtgcccaccg ctcatccctc acct 384

<210> 27
<211> 133
<212> PRT
<213> Artificial sequence

<220>
<223> PD1 -5-12 (New, from V20) (with CYS93>Ser substitution)

<400> 27

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
1 5 10 15

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

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
50 55 60

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

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
115 120 125

Ala His Pro Ser Pro
130

<210> 28
<211> 399
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO 27

<400> 28
gactctccag acagaccttg gaaccctcca accttctctc ccgctctgct ggtggttacc 60
gagggcgaca atgccacctt cacctgttcc ttcagcaaca cctccgagtc cttcgtgctg 120
aactggtaca gaatgtcccc tagcaaccag accgacaagc tggccgcctt tcctgaggac 180
agatctcagc caggccagga ctctcggttc agagttaccc agctgcctaa cggccgggac 240

ttccacatgt ctgttgtgcg ggccagacgg aacgactctg gcacatatct gtgcggcgcc 300
atctctctgg ctccaaggc tcagatcaaa gagtctctgc gggccgagct gagagtgaca 360
gaaagacgag ctgaggtgcc caccgctcat ccctcacct 399

<210> 29
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> PD1 -11-12

<400> 29

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

Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe
20 25 30

Val Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu
35 40 45

Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe
50 55 60

Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val
65 70 75 80

Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser
85 90 95

Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg
100 105 110

Val Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro
115 120 125

<210> 30
<211> 381
<212> DNA
<213> Artificial sequence

<220>

<223> na sequence encoding SEQ ID NO 29

<400> 30

```
tggaaccctc caaccttctc tcccgtctctg ctggtgggta ccgagggcga caatgccacc      60
ttcacctgtt ccttcagcaa cacctccgag tccttcgtgc tgaactggta cagaatgtcc      120
cctagcaacc agaccgacaa gctggccgcc tttcctgagg acagatctca gccaggccag      180
gactgtcggg tcagagtgc ccagctgcct aacggcagag acttccacat gtccgtcgtg      240
cgggccagaa gaaacgactc tggcacctat ctgtgcggcg ccatctctct ggctcccaag      300
gctcagatca aagagtctct gcgggccgag ctgagagtga cagaaagacg agctgaggtg      360
cccaccgctc atccctcacc t                                              381
```

<210> 31

<211> 127

<212> PRT

<213> Artificial sequence

<220>

<223> PD1 -11-12 (New, from V18) (with CYS93>Ser substitution)

<400> 31

```
Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly
1              5              10              15
```

```
Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe
      20              25              30
```

```
Val Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu
      35              40              45
```

```
Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Ser Arg Phe
      50              55              60
```

```
Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val
      65              70              75              80
```

```
Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser
      85              90              95
```

```
Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg
```

100

105

110

Val Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro
 115 120 125

<210> 32
 <211> 381
 <212> DNA
 <213> Artificial sequence

<220>
 <223> na sequence encoding SEQ ID NO 31

<400> 32
 tggaaccctc caaccttctc tcccgtctg ctggtggtta ccgagggcga caatgccacc 60
 ttcacctgtt ccttcagcaa cacctccgag tccttcgtgc tgaactggta cagaatgtcc 120
 cctagcaacc agaccgacaa gctggccgcc tttcctgagg acagatctca gccaggccag 180
 gactctcggg tcagagtac ccagctgcct aacggcagag acttccacat gtccgtcgtg 240
 cgggccagaa gaaacgactc tggcacctat ctgtgcggcg ccatctctct ggctcccaag 300
 gctcagatca aagagtctct gcgggcccag ctgagagtga cagaaagacg agctgaggtg 360
 cccaccgctc atccctcacc t 381

<210> 33
 <211> 134
 <212> PRT
 <213> Artificial sequence

<220>
 <223> PD1 -11-5

<400> 33

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

Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe
 20 25 30

Val Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu
 35 40 45

Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe

50

55

60

Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val
65 70 75 80

Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser
85 90 95

Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg
100 105 110

Val Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser
115 120 125

Pro Arg Pro Ala Gly Gln
130

<210> 34
<211> 402
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO 33

<400> 34
tggaaccctc caaccttctc tcccgtctctg ctggtgggta cggagggcga caatgccacc 60
ttcacctgtt ccttcagcaa cacctccgag tccttcgtgc tgaactggta cagaatgtcc 120
cctagcaacc agaccgacaa gctggccgcc tttcctgagg acagatctca gccaggccag 180
gactgtcggg tcagagtgac ccagctgcct aacggcagag acttccacat gtccgtcgtg 240
cgggccagaa gaaacgactc tggcacctat ctgtgcggcg ccatctctct ggctcccaag 300
gctcagatca aagagtctct gcgggcccag ctgagagtga cagaaagacg agctgaggtg 360
cccaccgctc atccctcacc ttctccaaga cctgctggcc ag 402

<210> 35
<211> 134
<212> PRT
<213> Artificial sequence

<220>
<223> PD1 -11-5 (New, from V19) (with CYS93>Ser substitution)

<400> 35

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

Asp Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe
20 25 30

Val Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu
35 40 45

Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Ser Arg Phe
50 55 60

Arg Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val
65 70 75 80

Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser
85 90 95

Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg
100 105 110

Val Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser
115 120 125

Pro Arg Pro Ala Gly Gln
130

<210> 36

<211> 402

<212> DNA

<213> Artificial sequence

<220>

<223> na sequence encoding SEQ ID NO 35

<400> 36

tggaaccctc caaccttctc tcccgtctctg ctggtggtta ccgagggcga caatgccacc 60

ttcacctgtt ccttcagcaa cacctccgag tccttcgtgc tgaactggta cagaatgtcc 120

cctagcaacc agaccgacaa gctggccgcc tttcctgagg acagatctca gccaggccag 180

gactctcggt tcagagtgc ccagctgcct aacggcagag acttccacat gtccgtcgtg 240
 cgggccagaa gaaacgactc tggcacctat ctgtgcggcg ccattctctt ggctcccaag 300
 gctcagatca aagagtctct gcgggcccag ctgagagtga cagaaagacg agctgaggtg 360
 cccaccgctc atccctcacc ttctccaaga cctgctggcc ag 402

<210> 37
 <211> 138
 <212> PRT
 <213> Artificial sequence

<220>
 <223> PD1 -5-7

<400> 37

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
 1 5 10 15

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

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
 35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
 50 55 60

Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp
 65 70 75 80

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
 85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
 100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
 115 120 125

Ala His Pro Ser Pro Ser Pro Arg Pro Ala
 130 135

<210> 38
<211> 414
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO 37

<400> 38
gactctccag acagaccttg gaaccctcca accttctctc ccgctctgct ggtggttacc 60
gagggcgaca atgccacctt cacctgttcc ttcagcaaca cctccgagtc cttcgtgctg 120
aactggtaca gaatgtcccc tagcaaccag accgacaagc tggccgcctt tcctgaggac 180
agatctcagc caggccagga ctgtcggttc agagtgacct agctgcctaa cggcagagac 240
ttccacatgt ccgtcgtgcg ggccagaaga aacgactctg gcacctatct gtgcggcgcc 300
atctctctgg ctccaaggc tcagatcaaa gagtctctgc gggccgagct gagagtgaca 360
gaaagacgag ctgaggtgcc caccgctcat ccctcacctt ctccaagacc tgct 414

<210> 39
<211> 138
<212> PRT
<213> Artificial sequence

<220>
<223> PD1 -5-7 (New, from V21) (with CYS93>Ser substitution)

<400> 39

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
1 5 10 15

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

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
50 55 60

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

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
115 120 125

Ala His Pro Ser Pro Ser Pro Arg Pro Ala
130 135

<210> 40
<211> 414
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO 39

<400> 40
gactctccag acagaccttg gaaccctcca accttctctc ccgctctgct ggtggttacc 60
gagggcgaca atgccacctt cacctgttcc ttcagcaaca cctccgagtc cttcgtgctg 120
aactggtaca gaatgtcccc tagcaaccag accgacaagc tggccgcctt tcctgaggac 180
agatctcagc caggccagga ctctcggttc agagtgacct agctgcctaa cggcagagac 240
ttccacatgt ccgtcgtgcg ggccagaaga aacgactctg gcacctatct gtgcggcgcc 300
atctctctgg ctccaaggc tcagatcaaa gagtctctgc gggccgagct gagagtgaca 360
gaaagacgag ctgaggtgcc caccgctcat ccctcacctt ctccaagacc tgct 414

<210> 41
<211> 136
<212> PRT
<213> Artificial sequence

<220>
<223> PD1 -5-9 from (with out CYS93>Ser substitution)136 aa

<400> 41

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
1 5 10 15

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

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
50 55 60

Gly Gln Asp Cys Arg Phe Arg Val Thr Gln Leu Pro Asn Gly Arg Asp
65 70 75 80

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
115 120 125

Ala His Pro Ser Pro Ser Pro Arg
130 135

<210> 42

<211> 408

<212> DNA

<213> Artificial sequence

<220>

<223> na sequence encoding SEQ ID NO 41

<400> 42

gactctccag acagaccttg gaaccctcca accttctctc ccgctctgct ggtggttacc 60

gagggcgaca atgccacctt cacctgttcc ttcagcaaca cctccgagtc cttcgtgctg 120

aactggtaca gaatgtcccc tagcaaccag accgacaagc tggccgcctt tcctgaggac 180

agatctcagc caggccagga ctgtcggttc agagttaccc agctgcctaa cggccgggac 240

ttccacatgt ctgttgtgcg ggccagacgg aacgactctg gcacatatct gtgcggcgcc 300

atctctctgg ctcccaaggc tcagatcaaa gagtctctgc gggccgagct gagagtgaca 360

gaaagacgag ctgaggtgcc caccgctcat ccctcacctt ctccaaga

408

<210> 43

<211> 145

<212> PRT

<213> Artificial sequence

<220>

<223> PD1 -0-5 from (with out CYS93>Ser substitution)145 aa

<400> 43

Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr
1 5 10 15

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

Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr
35 40 45

Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu
50 55 60

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

Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn
85 90 95

Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala
100 105 110

Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg
115 120 125

Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly
130 135 140

Gln

145

<210> 44

<211> 435
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO 43

<400> 44
cccggctggt ttctggactc tccagacaga ccttgaacc ctccaacctt ctctcccgct 60
ctgctggtgg ttaccgaggg cgacaatgcc accttcacct gttccttcag caacacctcc 120
gagtccttcg tgctgaactg gtacagaatg tcccctagca accagaccga caagctggcc 180
gcctttcctg aggacagatc tcagccaggc caggactgtc ggttcagagt taccagctg 240
cctaacggcc gggacttcca catgtctgtt gtgcggggcca gacggaacga ctctggcaca 300
tatctgtgcg gcgccatctc tctggctccc aaggctcaga tcaaagagtc tctgcggggc 360
gagctgagag tgacagaaag acgagctgag gtgcccaccg ctcacccctc accttctcca 420
agacctgctg gccag 435

<210> 45
<211> 143
<212> PRT
<213> Artificial sequence

<220>
<223> PD1 -0-7 from (with out CYS93>Ser substitution) 143 aa

<400> 45

Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr
1 5 10 15

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

Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr
35 40 45

Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu
50 55 60

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

Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn
85 90 95

Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala
100 105 110

Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg
115 120 125

Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala
130 135 140

<210> 46
<211> 429
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO 45

<400> 46
cccggctggt ttctggactc tccagacaga ctttgggaacc ctccaacctt ctctcccgct 60
ctgctggtgg ttaccgaggg cgacaatgcc accttcacct gttccttcag caacacctcc 120
gagtccttcg tgctgaactg gtacagaatg tcccctagca accagaccga caagctggcc 180
gcctttcctg aggacagatc tcagccaggc caggactgtc gggttcagagt taccagctg 240
cctaacggcc gggacttcca catgtctgtt gtgcgggcca gacggaacga ctctggcaca 300
tatctgtgcg gcgccatctc tctggctccc aaggctcaga tcaaagagtc tctgcgggcc 360
gagctgagag tgacagaaag acgagctgag gtgcccaccg ctcacccctc accttctcca 420
agacctgct 429

<210> 47
<211> 254
<212> PRT
<213> Artificial sequence

<220>
<223> aa sequence of full length 41BBL

<400> 47

Met Glu Tyr Ala Ser Asp Ala Ser Leu Asp Pro Glu Ala Pro Trp Pro

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

Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val
 225 230 235 240

Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
 245 250

<210> 48
 <211> 765
 <212> DNA
 <213> Artificial sequence

<220>
 <223> na sequence of full length 41BBL

<400> 48
 atggaatacg cctctgacgc ttacttggac cccgaagccc cgtggcctcc cgcccccgcc 60
 gctcgcgcct gccgcgtact gccttggggc ctggtcgcgg ggctgctgct gctgctgctg 120
 ctcgctgccg cctgcgccgt cttcctcgcc tgcccctggg ccgtgtccgg ggctcgcgcc 180
 tcgcccggct ccgcggccag cccgagactc cgcgagggtc ccgagctttc gcccagcgat 240
 cccgccggcc tcttggacct gcggcagggc atgtttgcgc agctgggtggc ccaaaatgtt 300
 ctgctgatcg atggggccct gagctggtac agtgaccag gcctggcagg cgtgtccctg 360
 acggggggcc tgagctacaa agaggacacg aaggagctgg tgggtggccaa ggctggagtc 420
 tactatgtct tctttcaact agagctgcgg cgcgtggtgg ccggcgaggg ctcaggctcc 480
 gtttcacttg cgctgcacct gcagccactg cgctctgctg ctggggccgc cgccctggct 540
 ttgaccgtgg acctgccacc cgcctcctcc gaggtcggga actcggcctt cggtttccag 600
 ggccgcttgc tgcacctgag tgccggccag cgcctgggcg tccatcttca cactgaggcc 660
 agggcacgcc atgcctggca gcttaccag ggccgacag tcttgggact cttccgggtg 720
 acccccgaat tcccagccgg actcccttca ccgaggtcgg aataa 765

<210> 49
 <211> 205
 <212> PRT
 <213> Artificial sequence

<220>
 <223> ORIGINAL 41BBL DOMAIN

<400> 49

Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala
1 5 10 15

Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro
20 25 30

Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala
35 40 45

Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro
50 55 60

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

Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe
85 90 95

Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val
100 105 110

Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala
115 120 125

Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg
130 135 140

Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly
145 150 155 160

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

Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr
180 185 190

Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
195 200 205

<210> 50

<211> 615
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO: 49

<400> 50
gcctgccccct gggccgtgtc cggggctcgc gcctcgcccg gctccgcggc cagcccgaga 60
ctccgcgagg gtcccagact ttcgcccagc gatcccgccg gcctcttgga cctgcggcag 120
ggcatgtttg cgcagctggt ggcccaaaat gttctgtga tcgatgggcc cctgagctgg 180
tacagtgacc caggcctggc aggcgtgtcc ctgacggggg gcctgagcta caaagaggac 240
acgaaggagc tgggtggtggc caaggctgga gtctactatg tcttctttca actagagctg 300
cggcgcgtgg tggccggcga gggctcaggc tccgtttcac ttgcgtgca cctgcagcca 360
ctgcgctctg ctgctggggc cgccgccctg gctttgaccg tggacctgcc acccgctcc 420
tccgaggctc ggaactcggc cttcggtttc cagggccgct tgctgcacct gaggccggc 480
cagcgcttgg gcgtccatct tcacactgag gccagggcac gccatgcctg gcagcttacc 540
cagggcgcca cagtcttggg actcttccgg gtgacccccg aaatcccagc cggactccct 600
tcaccgaggt cgaa 615

<210> 51
<211> 191
<212> PRT
<213> Artificial sequence

<220>
<223> 191 aa 14-0 in 4-1BBL DOMAIN

<400> 51

Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp
1 5 10 15

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

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

Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys

50

55

60

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

Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly
85 90 95

Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
100 105 110

Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu
115 120 125

Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
130 135 140

Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
145 150 155 160

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
165 170 175

Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
180 185 190

<210> 52

<211> 573

<212> DNA

<213> Artificial sequence

<220>

<223> na of SEQ ID NO 51

<400> 52

agcgccgcct cccccaggct gcgcgaggga cctgagctgt cccagacga tcctgccggc 60

ctgctggacc tgagacaggg aatgtttgcc cagctggtcg ctcagaacgt gctgctgatt 120

gacggccccc tgtcctggta tagcgatcct ggactggcag gcgtgtctct gacaggcgga 180

ctgagttaca aagaagacac taaagaactg gtcgtcgcca aagccggcgt gtactacgtg 240

ttcttccaac tggagctgag gagggtcgtc gccggcgaag gcagcggtc tgtgagcctg 300

gccctgcacc tgcaaccact gaggagcgcc gccggcgccg ccgccctggc cctgactgtg 360
 gacctgccac cagcatcctc tgaggcaagg aattccgcct tcggcttcca gggccggctg 420
 ctgcacctgt ctgccggaca gagactgggc gtccacctgc ataccgaagc cagagccagg 480
 catgcctggc agctgacca gggcgccacc gtgctgggcc tgttcagagt gacccagaa 540
 attccagcag gactgccttc cccaaggtct gag 573

<210> 53
 <211> 197
 <212> PRT
 <213> Artificial sequence

<220>
 <223> 197 aa 41BBL segment

<400> 53

Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly
 1 5 10 15

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

Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly
 35 40 45

Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr
 50 55 60

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

Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val
 85 90 95

Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro
 100 105 110

Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu
 115 120 125

Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly

130

135

140

Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His
 145 150 155 160

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

Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro
 180 185 190

Ser Pro Arg Ser Glu
 195

<210> 54
 <211> 591
 <212> DNA
 <213> Artificial sequence

<220>
 <223> na sequence encoding SEQ ID NO 53

<400> 54
 gctagagctt ctctggctc tgccgcttct cccagactga gagaaggacc tgagctgagc 60
 cctgatgatc ctgctggact gctggatctg cggcagggca tgtttgctca gttggtggcc 120
 cagaacgtgc tgctgatcga tggccctctg tcctggtact ctgatccagg attggctggc 180
 gtgtccctga ctggcggcct gtcttacaaa gaggacacca aagaactggt ggtggccaag 240
 gccggcgtgt actacgtgtt ctttcagctg gaactgcgga gagtggtggc tggcgaagga 300
 tctggatctg tgtctctggc cctgcatctg cagcctctga gaagtgctgc aggcgctgct 360
 gcactggctc tgacagttga tctgcctcct gcctcctccg aggccagaaa ctccgccttt 420
 ggcttccaag gcagactgct gcacctgtcc gctggacaga gactgggagt ccatctgcac 480
 acagaggcca gagctagaca cgcttggcag ttgacacagg gcgctacagt gctgggcctg 540
 tttagagtga cccctgagat tccagccggc ctgccatctc ctagatctga g 591

<210> 55
 <211> 185
 <212> PRT
 <213> Artificial sequence

<220>

<223> 185 aa 41BBL segment

<400> 55

Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu
1 5 10 15

Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu
20 25 30

Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly
35 40 45

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

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

Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu
85 90 95

His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu
100 105 110

Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe
115 120 125

Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly
130 135 140

Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr
145 150 155 160

Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro
165 170 175

Ala Gly Leu Pro Ser Pro Arg Ser Glu
180 185

<210> 56

<211> 555
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO 55

<400> 56
ctgagagaag gacctgagct gagccctgat gatcctgctg gactgctgga tctgcggcag 60
ggcatgtttg ctgagttggt ggcccagaac gtgctgctga tcgatggccc tctgtcctgg 120
tactctgatac caggattggc tggcgtgtcc ctgactggcg gcctgtctta caaagaggac 180
accaaagaac tgggtggtggc caaggccggc gtgtactacg tgttctttca gctggaactg 240
cggagagtgg tggctggcga aggatctgga tctgtgtctc tggccctgca tctgcagcct 300
ctgagaagtg ctgcaggcgc tgctgcactg gctctgacag ttgatctgcc tcctgcctcc 360
tccgaggcca gaaactccgc ctttggcttc caaggcagac tgctgcacct gtccgctgga 420
cagagactgg gagtccatct gcacacagag gccagagcta gacacgcttg gcagttgaca 480
cagggcgcta cagtgtctggg cctgtttaga gtgaccctg agattccagc cggcctgcc 540
tctcctagat ctgag 555

<210> 57
<211> 199
<212> PRT
<213> Artificial sequence

<220>
<223> 199 aa 41BBL segment

<400> 57

Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser Pro Arg Leu Arg
1 5 10 15

Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu
20 25 30

Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile
35 40 45

Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser
50 55 60

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

Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg
85 90 95

Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu
100 105 110

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

Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe
130 135 140

Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His
145 150 155 160

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

Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly
180 185 190

Leu Pro Ser Pro Arg Ser Glu
195

<210> 58
<211> 597
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO 57

<400> 58
tctggcgcta gagcttctcc tggctctgcc gcttctccca gactgagaga aggacctgag 60
ctgagccctg atgacctgc tggactgctg gatctgcggc agggcatgtt tgctcagttg 120
gtggcccaga acgtgctgct gatcgatggc cctctgtcct ggtactctga tccaggattg 180
gctggcgtgt ccctgactgg cggcctgtct taaaaagagg acaccaaaga actggtggtg 240

gccaaagccg gcgtgtacta cgtgttcttt cagctggaac tgcggagagt ggtggctggc 300
 gaaggatctg gatctgtgtc tctggccctg catctgcagc ctctgagaag tgctgcaggc 360
 gctgctgcac tggctctgac agttgatctg cctcctgcct cctccgaggc cagaaactcc 420
 gcctttggct tccaaggcag actgctgcac ctgtccgctg gacagagact gggagtccat 480
 ctgcacacag aggccagagc tagacacgct tggcagttga cacagggcgc tacagtgtg 540
 ggcctgttta gaggtagcccc tgagattcca gccggcctgc catctcctag atctgag 597

<210> 59
 <211> 184
 <212> PRT
 <213> Artificial sequence

<220>
 <223> 4-1BBL -21-0 184 aa

<400> 59

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
 1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
 20 25 30

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

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

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

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
 85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
 100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
 115 120 125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala
165 170 175

Gly Leu Pro Ser Pro Arg Ser Glu
180

<210> 60
<211> 552
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO 59

<400> 60
agagaggggcc ctgagctgtc tcctgatgat cctgctggac tgctggacct gagacagggc 60
atgtttgctc agctggtggc ccagaacgtg ctgctgattg atggccctct gtcctggtac 120
tctgatcctg gattggctgg cgtgtccctg actggcggcc tgtcttaca agaggacacc 180
aaagaactgg tggtcgcaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 240
agagtgggtgg ctggcgaagg atctggatct gtgtctctgg ccctgcatct gcagcctctg 300
agaagtgtg caggcgtgc tgcactggct ctgacagttg atctgcctcc tgcctcctcc 360
gaggccagaa actccgcctt tggcttcaa ggcagactgc tgcattctgtc tgccggacag 420
agactgggag tgcacctcca tacagaggcc agagctagac acgcttggca gttgacacag 480
ggcgctacag tgctgggcct gtttagagt acacctgaga tcccagccgg cctgccatct 540
ccaagatctg aa 552

<210> 61
<211> 182
<212> PRT
<213> Artificial sequence

<220>
<223> 4-1BBL -23-0 182 aa

<400> 61

Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg
1 5 10 15

Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp
20 25 30

Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu
35 40 45

Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala
50 55 60

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

Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln
85 90 95

Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp
100 105 110

Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln
115 120 125

Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu
130 135 140

His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala
145 150 155 160

Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu
165 170 175

Pro Ser Pro Arg Ser Glu
180

<210> 62

<211> 546

<212> DNA

<213> Artificial sequence

<220>

<223> na sequence encoding SEQ ID NO 61

<400> 62

```
ggccctgagc tgtctcctga tgatcctgct ggactgctgg acctgagaca gggcatgttt      60
gctcagctgg tggcccagaa cgtgctgctg attgatggcc ctctgtcctg gtactctgat      120
cctggattgg ctggcgtgtc cctgactggc ggcctgtctt acaaagagga caccaaagaa      180
ctggtggtcg ccaaggccgg cgtgtactac gtgttctttc agctggaact gcggagagtg      240
gtggctggcg aaggatctgg atctgtgtct ctggccctgc atctgcagcc tctgagaagt      300
gctgcaggcg ctgctgcact ggctctgaca gttgatctgc ctctgcctc ctccgaggcc      360
agaaactccg cttttggctt ccaaggcaga ctgctgcatc tgtctgccgg acagagactg      420
ggagtgcacc tccatacaga ggccagagct agacacgctt ggcagttgac acagggcgct      480
acagtgctgg gcctgtttag agtgacacct gagatcccag ccggcctgcc atctccaaga      540
tctgaa                                          546
```

<210> 63

<211> 183

<212> PRT

<213> Artificial sequence

<220>

<223> 4-1BBL -14-8 183 aa

<400> 63

```
Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp
1              5              10              15
```

```
Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu
20              25              30
```

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

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

```
Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val
```

65		70		75		80									
Phe	Phe	Gln	Leu	Glu	Leu	Arg	Arg	Val	Val	Ala	Gly	Glu	Gly	Ser	Gly
			85					90						95	
Ser	Val	Ser	Leu	Ala	Leu	His	Leu	Gln	Pro	Leu	Arg	Ser	Ala	Ala	Gly
			100					105					110		
Ala	Ala	Ala	Leu	Ala	Leu	Thr	Val	Asp	Leu	Pro	Pro	Ala	Ser	Ser	Glu
		115					120					125			
Ala	Arg	Asn	Ser	Ala	Phe	Gly	Phe	Gln	Gly	Arg	Leu	Leu	His	Leu	Ser
	130					135					140				
Ala	Gly	Gln	Arg	Leu	Gly	Val	His	Leu	His	Thr	Glu	Ala	Arg	Ala	Arg
145					150					155					160
His	Ala	Trp	Gln	Leu	Thr	Gln	Gly	Ala	Thr	Val	Leu	Gly	Leu	Phe	Arg
			165						170					175	
Val	Thr	Pro	Glu	Ile	Pro	Ala									
			180												

<210> 64
 <211> 551
 <212> DNA
 <213> Artificial sequence

<220>
 <223> na sequence encoding SEQ ID NO 63

<400> 64	
gatctgccgc ttctcctaga ctgagagagg gccctgagct gtctcctgat gatcctgctg	60
gactgctgga cctgagacag ggcatgtttg ctcagctggt ggcccagaac gtgctgctga	120
ttgatggccc tctgtcctgg tactctgata ctggattggc tggcgtgtcc ctgactggcg	180
gcctgtctta caaagaggac accaaagaac tgggtggctgc caaggccggc gtgtactacg	240
tgttctttca gctggaactg cggagagtgg tggctggcga aggatctgga tctgtgtctc	300
tggccctgca tctgcagcct ctgagaagtg ctgcaggcgc tgctgcactg gctctgacag	360
ttgatctgcc tcctgcctcc tccgaggcca gaaactccgc ctttggcttc caaggcagac	420

tgctgcatct gtctgccgga cagagactgg gagtgcacct ccatacagag gccagagcta	480
gacacgcttg gcagttgaca cagggcgcta cagtgcctggg cctgtttaga gtgacacctg	540
agatcccagc c	551

<210> 65
 <211> 176
 <212> PRT
 <213> Artificial sequence

<220>
 <223> 4-1BBL -21-8 176 aa

<400> 65

Arg	Glu	Gly	Pro	Glu	Leu	Ser	Pro	Asp	Asp	Pro	Ala	Gly	Leu	Leu	Asp
1				5				10					15		

Leu	Arg	Gln	Gly	Met	Phe	Ala	Gln	Leu	Val	Ala	Gln	Asn	Val	Leu	Leu
		20					25					30			

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

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

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

Arg	Val	Val	Ala	Gly	Glu	Gly	Ser	Gly	Ser	Val	Ser	Leu	Ala	Leu	His
			85					90						95	

Leu	Gln	Pro	Leu	Arg	Ser	Ala	Ala	Gly	Ala	Ala	Ala	Leu	Ala	Leu	Thr
		100						105					110		

Val	Asp	Leu	Pro	Pro	Ala	Ser	Ser	Glu	Ala	Arg	Asn	Ser	Ala	Phe	Gly
	115						120					125			

Phe	Gln	Gly	Arg	Leu	Leu	His	Leu	Ser	Ala	Gly	Gln	Arg	Leu	Gly	Val
130						135					140				

His	Leu	His	Thr	Glu	Ala	Arg	Ala	Arg	His	Ala	Trp	Gln	Leu	Thr	Gln
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

145 150 155 160

Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala
165 170 175

<210>	66
<211>	528
<212>	DNA
<213>	Artificial sequence

```
<220>
<223> na sequence encoding SEQ ID NO 65
```

[illegible]

<210>	67
<211>	601
<212>	PRT
<213>	Artificial sequence

```
<220>
<223> 601 aa sc3x4-1BBL (-14-0) internal linker (GGGGS)x2+GGGG
```

<400> 67

Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp
1 5 10 15

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

Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser

35

40

45

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

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

Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly
 85 90 95

Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
 100 105 110

Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu
 115 120 125

Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
 130 135 140

Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
 145 150 155 160

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
 165 170 175

Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu Gly
 180 185 190

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Ala
 195 200 205

Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala
 210 215 220

Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln
 225 230 235 240

Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly
 245 250 255

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

Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln
275 280 285

Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser
290 295 300

Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala
305 310 315 320

Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn
325 330 335

Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln
340 345 350

Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp
355 360 365

Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro
370 375 380

Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly
385 390 395 400

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Ala Ser Pro Arg
405 410 415

Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu
420 425 430

Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu
435 440 445

Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly
450 455 460

Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu

465 470 475 480

Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu
485 490 495

Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu
500 505 510

His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu
515 520 525

Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe
530 535 540

Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly
545 550 555 560

Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr
565 570 575

Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro
580 585 590

Ala Gly Leu Pro Ser Pro Arg Ser Glu
595 600

<210> 68
<211> 1803
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO 67

<400> 68
agcgccgcct cccctaggct gcgcgaggga ccagagctga gccagacga tccagcagga 60
ctgctggacc tgaggcaggg aatgttcgca cagctggtgg ccagaacgt gctgctgac 120
gacggccctc tgtcttggtg cagcgatcca ggactggcag gcgtgagcct gacaggcgga 180
ctgtcctata aggaggatac caaggagctg gtggtggcaa aggcaggcgt gtactacgtg 240
ttcttccagc tggagctgag gagagtgggtg gcaggagagg gatccggatc tgtgagcctg 300

gccctgcacc tgcagccact gcggagcgcc gcaggagcag ccgccctggc cctgaccgtg	360
gacctgccac ctgcatctag cgaggcacgg aattctgcct tcggctttca gggcagactg	420
ctgcacctga gcgccggaca gaggctggga gtgcacctgc acacagaggc aagggaaga	480
cacgcatggc agctgacaca gggagcaacc gtgctgggac tgttccgcgt gacccctgag	540
atcccagcag gactgccatc cccccggtct gagggcggcg gcgggtccgg aggaggagga	600
tctggcggcg gcggcagcgc cgcctcccc aggctgcgcg agggacctga gctgtcccca	660
gacgatcctg ccggcctgct ggacctgaga cagggaatgt ttgccagct ggtcgctcag	720
aacgtgctgc tgattgacgg ccccctgtcc tggtatagcg atcctggact ggcaggcgtg	780
tctctgacag gcggactgag ttacaaagaa gacactaaag aactggtcgt cgccaaagcc	840
ggcgtgtact acgtgttctt ccaactggag ctgaggaggg tcgtcgccgg cgaaggcagc	900
ggctctgtga gcctggccct gcacctgcaa cactgagga gcgccgccgg cgccgccgcc	960
ctggccctga ctgtggacct gccaccagca tcctctgagg caaggaattc cgccttcggc	1020
ttccagggcc ggctgctgca cctgtctgcc ggacagagac tgggcgtcca cctgcatacc	1080
gaagccagag ccaggcatgc ctggcagctg acccagggcg ccaccgtgct gggcctgttc	1140
agagtgacct cagaaattcc agcaggactg ctttcccaa ggtctgaggg aggaggagga	1200
agtggcggag gaggatccgg agggggaggg agcgccgcct cccaagact gagagaggga	1260
ccagagctgt cccctgatga ccctgccggg ctgctggacc tgagacaagg catgttcgcc	1320
cagctggctg caaaaacgt gctgttaatt gacggccac tgtcctggta ttccgacctt	1380
ggcctggccg gcgtgtccct gacaggcggc ctgtcttaca aagaagacac aaaagaactg	1440
gtcgtcgcta aagctggcgt gtactacgtg ttcttccaat tagaactgag aagggtcgtc	1500
gccggcgagg gcagcgggtc tgtgagcctg gccctgcacc tgcaaccgct gcggagcgcc	1560
gccggcgctg ccgccctggc cctgacagtg gacctgcctc cagcaagctc cgaggcaagg	1620
aatagcgctt tcggctttca aggccgcctg ctgcacctgt ccgccggaca gcggctgggc	1680
gtccacctgc acaccgaagc cagagccgcg catgcctggc agctgactca gggcgctacc	1740
gtgctgggcc tgttccgcgt gacccagag atccctgccg gcctgcctc ccctcggtct	1800
gag	1803

<211> 504
<212> PRT
<213> Artificial sequence

<220>

<223> aa sequence of full length SIRP

<400> 69

Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
1 5 10 15

Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
20 25 30

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro Val Gly
50 55 60

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu Ile Tyr
65 70 75 80

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

Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn Ile Thr
100 105 110

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
115 120 125

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

Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala
145 150 155 160

Thr Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser
165 170 175

Pro Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser

180

185

190

Asp Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser
 195 200 205

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

Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu
 225 230 235 240

Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu
 245 250 255

Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr
 260 265 270

Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu
 275 280 285

Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu
 290 295 300

Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val
 305 310 315 320

Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp
 325 330 335

Gly Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His
 340 345 350

Pro Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Ser Asn
 355 360 365

Glu Arg Asn Ile Tyr Ile Val Val Gly Val Val Cys Thr Leu Leu Val
 370 375 380

Ala Leu Leu Met Ala Ala Leu Tyr Leu Val Arg Ile Arg Gln Lys Lys
 385 390 395 400

Ala Gln Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu Lys Asn
405 410 415

Ala Arg Glu Ile Thr Gln Asp Thr Asn Asp Ile Thr Tyr Ala Asp Leu
420 425 430

Asn Leu Pro Lys Gly Lys Lys Pro Ala Pro Gln Ala Ala Glu Pro Asn
435 440 445

Asn His Thr Glu Tyr Ala Ser Ile Gln Thr Ser Pro Gln Pro Ala Ser
450 455 460

Glu Asp Thr Leu Thr Tyr Ala Asp Leu Asp Met Val His Leu Asn Arg
465 470 475 480

Thr Pro Lys Gln Pro Ala Pro Lys Pro Glu Pro Ser Phe Ser Glu Tyr
485 490 495

Ala Ser Val Gln Val Pro Arg Lys
500

<210> 70

<211> 1512

<212> DNA

<213> Artificial sequence

<220>

<223> na sequence of full length SIRP

<400> 70

atggagcccc	ccggcccggc	ccccggccgc	ctcgggccgc	tgctctgcct	gctgctcgcc	60
gcgtcctgcg	cctggtcagg	agtggcgggt	gaggaggagc	tgacagtgat	tcagcctgac	120
aagtccgtat	cagttgcagc	tggagagtcg	gccattctgc	actgcactgt	gacctccctg	180
atccctgtgg	ggcccatcca	gtggttcaga	ggagctggac	cagcccggga	attaatctac	240
aatcaaaaag	aaggccactt	cccccggtta	acaactgttt	cagagtccac	aaagagagaa	300
aacatggact	tttccatcag	catcagtaac	atcaccccag	cagatgccgg	cacctactac	360
tgtgtgaagt	tccggaaagg	gagccctgac	acggagttta	agtctggagc	aggcactgag	420
ctgtctgtgc	gtgccaaacc	ctctgcccc	gtggtatcgg	gccctgcggc	gagggccaca	480

cctcagcaca cagtga	cctt	cgag	tccc	acggct	tctc	accag	agac	atcacc	540
ctgaaatggt tcaaaa	atgg	gaat	gagctc	tcag	acttcc	agacca	acgt	ggacccccgta	600
ggagagagcg tgtcct	acag	catcc	acagc	acagcca	agg	tggtgctgac	ccgcgaggac	660	
gttcactctc aagtc	atctg	cgaggtggcc	cacgtcacct	tgca	ggggga	ccctcttcgt	720		
gggactgcca actt	gtctga	gaccatccga	gttccacca	ccttggaggt	tactcaacag	780			
cccgtgaggg cagaga	acca	ggtgaatgtc	acctgccagg	tgaggaagtt	ctacccccag	840			
agactacagc tgac	ctgggt	ggagaatgga	aacgtgtccc	ggacagaaac	ggcctcaacc	900			
gttacagaga acaag	gatgg	tacctacaac	tgga	tgagct	ggctcctgggt	gaatgtatct	960		
gcccacaggg atga	tgtgaa	gctcacctgc	caggtggagc	atgacgggca	gccagcggtc	1020			
agcaaaagcc atga	ctgaa	ggtctcagcc	cacccgaagg	agcagggctc	aaataccgcc	1080			
gctgagaaca ctgg	atctaa	tgaacggaac	atctatattg	tggtgggtgt	ggtgtgcacc	1140			
ttgctgggtg ccct	actgat	ggcggccctc	tacctcgtcc	gaatcagaca	gaagaaagcc	1200			
cagggctcca cttct	tctac	aaggttgc	atgagccgaga	agaatgccag	agaaataaca	1260			
caggacacaa atga	tatcac	atatgcagac	ctgaacctgc	ccaaggggaa	gaagcctgct	1320			
ccccaggctg cggag	cccaa	caaccacacg	gagtatgcc	gcattcagac	cagcccgag	1380			
cccgcgtcgg agg	acacct	cacctatgct	gacctggaca	tggtccacct	caaccggacc	1440			
cccaagcagc cggcc	cccaa	gcctgagccg	tccttctcag	agtacgccag	cgtccaggtc	1500			
ccgaggaagt ga						1512			

<210> 71
 <211> 343
 <212> PRT
 <213> Artificial sequence

<220>
 <223> ORIGINAL SIRPa DOMAIN (343AA)

<400> 71

Glu	Glu	Glu	Leu	Gln	Val	Ile	Gln	Pro	Asp	Lys	Ser	Val	Leu	Val	Ala
1				5					10					15	

Ala	Gly	Glu	Thr	Ala	Thr	Leu	Arg	Cys	Thr	Ala	Thr	Ser	Leu	Ile	Pro
			20					25					30		

Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu
35 40 45

Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser
50 55 60

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

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

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

Ser Val Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala
115 120 125

Arg Ala Thr Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly
130 135 140

Phe Ser Pro Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu
145 150 155 160

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

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

His Ser Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp
195 200 205

Pro Leu Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro
210 215 220

Thr Leu Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn
225 230 235 240

Val Thr Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr

245

250

255

Trp Leu Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val
 260 265 270

Thr Glu Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val
 275 280 285

Asn Val Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu
 290 295 300

His Asp Gly Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser
 305 310 315 320

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

Ser Asn Glu Arg Asn Ile Tyr
 340

<210> 72

<211> 1029

<212> DNA

<213> Artificial sequence

<220>

<223> na sequence encoding SEQ ID NO 71

<400> 72

gaggaggagc tgcaggtgat tcagcctgac aagtccgtat cagttgcagc tggagagtcg 60

gccattctgc actgcactgt gacctccctg atccctgtgg ggcccatcca gtggttcaga 120

ggagctggac cagcccggga attaattctac aatcaaaaag aaggccactt cccccgggta 180

acaactgttt cagagtccac aaagagagaa aacatggact tttccatcag catcagtaac 240

atcaccccag cagatgccgg cacctactac tgtgtgaagt tccggaagg gagccctgac 300

acggagttta agtctggagc aggcactgag ctgtctgtgc gtgccaaacc ctctgcccc 360

gtggtatcgg gccctgcggc gagggccaca cctcagcaca cagtgagctt cacctgcgag 420

tcccacggct tctcaccag agacatcacc ctgaaatggt tcaaaaatgg gaatgagctc 480

tcagacttcc agaccaacgt ggaccccgta ggagagagcg tgtcctacag catccacagc 540

acagccaagg tgggtgctgac ccgcgaggac gttcactctc aagtcactctg cgaggtggcc 600
cacgtcacct tgcaggggga ccctcttcgt gggactgcca acttgtctga gaccatccga 660
gttccacca ccttggaggt tactcaacag cccgtgaggg cagagaacca ggtgaatgtc 720
acctgccagg tgaggaagtt ctacccccag agactacagc tgacctggtt ggagaatgga 780
aacgtgtccc ggacagaaac ggcctcaacc gttacagaga acaaggatgg tacctacaac 840
tggatgagct ggctcctggt gaatgtatct gcccacaggg atgatgtgaa gctcacctgc 900
caggtggagc atgacgggca gccagcggtc agcaaaagcc atgacctgaa ggtctcagcc 960
caccgaagg agcagggtc aaataccgcc gctgagaaca ctggatctaa tgaacggaac 1020
atctatatt 1029

<210> 73
<211> 116
<212> PRT
<213> Artificial sequence

<220>
<223> 116 aa SIRPa segment

<400> 73

Glu Glu Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala
1 5 10 15

Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro
20 25 30

Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu
35 40 45

Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser
50 55 60

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

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

Gly Ser Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu

100

105

110

Ser Val Arg Ala
115

<210> 74
<211> 348
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO 73

<400> 74
gaagaggaac tgcaagtgat ccagcctgac aagtccgtgc tgggtggctgc tggcgaaacc 60
gccacactga gatgtaccgc cacctctctg atccctgtgg gccctatcca gtggttttaga 120
ggcgtctggac ctggcagaga gctgatctac aaccagaaag agggccactt tcctagagtg 180
accaccgtgt ccgacctgac caagcggaaac aacatggact tctccatccg gatcggcaac 240
atcacccctg ctgatgccgg cacctactac tgcgtgaagt tccggaaggg ctcccctgac 300
gacgtcgagt ttaaattccgg cgctggcacc gaactgtccg tgcgagct 348

<210> 75
<211> 343
<212> PRT
<213> Artificial sequence

<220>
<223> 343 amino acids sequence of SIRPa with 4 point mutations

<400> 75

Glu Glu Glu Ile Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala
1 5 10 15

Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ile Thr Ser Leu Ile Pro
20 25 30

Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Val Leu
35 40 45

Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser
50 55 60

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

Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Ile Lys Phe Arg Lys
85 90 95

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

Ser Val Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala
115 120 125

Arg Ala Thr Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly
130 135 140

Phe Ser Pro Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu
145 150 155 160

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

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

His Ser Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp
195 200 205

Pro Leu Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro
210 215 220

Thr Leu Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn
225 230 235 240

Val Thr Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr
245 250 255

Trp Leu Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val
260 265 270

Thr Glu Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val

275

280

285

Asn Val Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu
 290 295 300

His Asp Gly Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser
 305 310 315 320

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

Ser Asn Glu Arg Asn Ile Tyr
 340

<210> 76

<211> 1029

<212> DNA

<213> Artificial sequence

<220>

<223> na sequence encoding SEQ ID NO 75

<400> 76

gaagaggaaa tccaagtgat ccagcctgac aagtccgtgc tgggtggctgc tggcgaaacc 60

gccacactga gatgtacat cacctctctg atccctgtgg gccctatcca gtggttttaga 120

ggcgcctggac ctggcagagt gctgatctac aaccagaaag agggccactt tcctagagtg 180

accaccgtgt ccgacctgac caagcggaac aacatggact tctccatccg gatcggcaac 240

atcacccctg ctgatgccgg cacctactac tgcatacaagt tccggaaggg ctcccctgac 300

gacgtcgagt ttaaataccgg cgctggcacc gaactgtccg tgcgagctaa accttctgct 360

cccgtgggtgt ctggccctgc cgctagagct acacctcagc acaccgtgtc ttttacctgc 420

gagtcccacg gcttcagccc tagagacatc accctgaagt ggttcaagaa cggcaacgag 480

ctgtccgact tccagaccaa cgtggaccct gtgggagagt ccgtgtccta ctccatccac 540

tctaccgcca aggtgggtgct gacccgagag gacgtgcaca gccaagtgat ctgtgaagtg 600

gcccacgtga ccctccaggg cgatcctttg agaggcaccg ccaacctgtc cgagacaatc 660

agagtgcctc ctacactgga agtgaccag cagcctgtgc gggccgagaa tcaagtgaac 720

gtgacctgcc aagtgcggaa gttctaccct cagagactgc agctgacctg gctggaaaac 780

ggcaatgtgt ccagaaccga gacagcctcc accgtgaccg agaacaagga tggcacctac 840
aattggatgt cctggctgct cgtgaacgtg tccgctcaca gagatgacgt gaagctgaca 900
tgccaggtgg aacacgatgg ccagcctgcc gtgtctaagt cccacgacct gaaagtgtct 960
gctcacccca aagagcaggg ctccaatacc gccgctgaga acaccggctc caacgagaga 1020
aacatctac 1029

<210> 77
<211> 116
<212> PRT
<213> Artificial sequence

<220>
<223> 116 amino acids sequence of SIRPa with 4 point mutations

<400> 77

Glu Glu Glu Ile Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala
1 5 10 15

Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ile Thr Ser Leu Ile Pro
20 25 30

Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Val Leu
35 40 45

Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser
50 55 60

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

Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Ile Lys Phe Arg Lys
85 90 95

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

Ser Val Arg Ala
115

<210> 78

<211> 348
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO 77

<400> 78
gaagaggaaa tccaagtgat ccagcctgac aagtccgtgc tgggtggctgc tggcgaaacc 60
gccacactga gatgtacat cacctctctg atccctgtgg gccctatcca gtggtttaga 120
ggcgctggac ctggcagagt gctgatctac aaccagaaag agggccactt tcctagagtg 180
accaccgtgt ccgacctgac caagcggaac aacatggact tctccatccg gatcggcaac 240
atcacccctg ctgatgccgg cacctactac tgcataaagt tccggaaggg ctcccctgac 300
gacgtcgagt ttaaattccgg cgctggcacc gaactgtccg tgcgagct 348

<210> 79
<211> 989
<212> PRT
<213> Artificial sequence

<220>
<223> 989 aa hole chain of DSP305 and DSP105_V1

<400> 79

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
1 5 10 15

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

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
50 55 60

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

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
115 120 125

Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly Gln Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
145 150 155 160

Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro
165 170 175

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
180 185 190

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

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
210 215 220

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
225 230 235 240

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
245 250 255

Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
260 265 270

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Cys
275 280 285

Glu Met Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe
290 295 300

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

305		310		315		320									
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe
				325					330					335	
Phe	Leu	Val	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly
			340					345					350		
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
		355					360					365			
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Gly	Gly	Gly	Gly	Ser
	370					375					380				
Gly	Gly	Gly	Gly	Ser	Ala	Ala	Ser	Pro	Arg	Leu	Arg	Glu	Gly	Pro	Glu
385					390					395					400
Leu	Ser	Pro	Asp	Asp	Pro	Ala	Gly	Leu	Leu	Asp	Leu	Arg	Gln	Gly	Met
				405					410					415	
Phe	Ala	Gln	Leu	Val	Ala	Gln	Asn	Val	Leu	Leu	Ile	Asp	Gly	Pro	Leu
			420					425					430		
Ser	Trp	Tyr	Ser	Asp	Pro	Gly	Leu	Ala	Gly	Val	Ser	Leu	Thr	Gly	Gly
		435					440					445			
Leu	Ser	Tyr	Lys	Glu	Asp	Thr	Lys	Glu	Leu	Val	Val	Ala	Lys	Ala	Gly
	450					455					460				
Val	Tyr	Tyr	Val	Phe	Phe	Gln	Leu	Glu	Leu	Arg	Arg	Val	Val	Ala	Gly
465					470					475					480
Glu	Gly	Ser	Gly	Ser	Val	Ser	Leu	Ala	Leu	His	Leu	Gln	Pro	Leu	Arg
				485					490					495	
Ser	Ala	Ala	Gly	Ala	Ala	Ala	Leu	Ala	Leu	Thr	Val	Asp	Leu	Pro	Pro
			500					505					510		
Ala	Ser	Ser	Glu	Ala	Arg	Asn	Ser	Ala	Phe	Gly	Phe	Gln	Gly	Arg	Leu
		515					520					525			

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

Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu
545 550 555 560

Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro
565 570 575

Arg Ser Glu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
580 585 590

Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro
595 600 605

Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln
610 615 620

Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr
625 630 635 640

Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr
645 650 655

Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr
660 665 670

Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser
675 680 685

Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala
690 695 700

Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser
705 710 715 720

Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu
725 730 735

Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala

740

745

750

Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe
 755 760 765

Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
 770 775 780

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala
 785 790 795 800

Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro
 805 810 815

Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala
 820 825 830

Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro
 835 840 845

Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp
 850 855 860

Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe
 865 870 875 880

Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val
 885 890 895

Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala
 900 905 910

Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg
 915 920 925

Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly
 930 935 940

Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala
 945 950 955 960

Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr
965 970 975

Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
980 985

<210> 80
<211> 2967
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO 79

<400> 80
gactctccag ataggccttg gaatccccct accttttagcc ccgccctgct ggtggtgaca 60
gagggcgata acgccacctt cacatgctct tttagcaaca cctccgagtc tttcgtgctg 120
aattggtaca ggatgagccc ttccaaccag acagacaagc tggcagcatt tcctgaggac 180
cgctcccagc caggccagga ttctcggttc agagtgaccc agctgccaaa tggcagggac 240
tttcacatga gcgtgggtgcg cgcccggaga aacgattccg gcacatacct gtgcggagca 300
atctctcttg caccaaaggc acagatcaag gagtccctga gggcagagct gagggtgacc 360
gagaggaggg ccgaggtgcc aacagcacac ccatctccta gcccaggcc agcaggacag 420
ggaggaggag gatccggagg aggaggatcc gagtctaagt atggaccacc atgccctcca 480
tgtccagcac ctgagtttga gggaggacct tccgtgttcc tgtttccccc taagccaaag 540
gacacactga tgatctccag gacaccagag gtgacctgcg tgggtggtgga cgtgtctcag 600
gaggatcccc aggtgcagtt caactggtac gtggatggcg tggaggtgca caatgccaaag 660
accaagccta gggaggagca gtttaactcc acataccgcg tgggtgtctgt gctgaccgtg 720
ctgcaccagg attggctgaa cggcaaggag tataagtgtg aggtgagcaa taagggcctg 780
ccaagctcca tcgagaagac catctccaag gcaaagggac agccaaggga gcctcaggtg 840
tatacactgc caccagcca gtgcgagatg accaagaacc aggtgagcct gtcctgtgccc 900
gtgaagggct tctacccatc tgacatcgcc gtggagtggg agagcaatgg ccagcccagag 960
aacaattata agaccacacc tccagtgtcg gactccgatg gctctttctt tctggtgtcc 1020
aggctgacag tggataagtc tcgctggcag gagggcaacg tgttttcttg tagcgtgatg 1080

cacgaggccc tgcacaatca ctacaccag aagtcctgt ctctgagcct gggcaagggc	1140
ggcggcggct ccggaggagg aggaagcgcc gcctccccta ggctgcgca gggaccagag	1200
ctgagcccag acgatccagc aggactgctg gacctgaggc agggaatgtt cgcacagctg	1260
gtggcccaga acgtgctgct gatcgacggc cctctgtctt ggtacagcga tccaggactg	1320
gcaggcgtga gcctgacagg cggactgtcc tataaggagg ataccaagga gctggtggtg	1380
gcaaaggcag gcgtgtacta cgtgttcttc cagctggagc tgaggagagt ggtggcagga	1440
gagggatccg gatctgtgag cctggccctg cacctgcagc cactgcggag cgccgcagga	1500
gcagccgccc tggccctgac cgtggacctg ccacctgcat ctagcgaggc acggaattct	1560
gccttcggct ttgaggcag actgctgcac ctgagcgccg gacagaggct gggagtgcac	1620
ctgcacacag aggcaagggc aagacacgca tggcagctga cacagggagc aaccgtgctg	1680
ggactgttcc gcgtgacccc tgagatcca gcaggactgc catcccccg gtctgagggc	1740
ggcggcgggt ccggaggagg aggatctggc ggcggcggca gcgccgctc cccagggctg	1800
cgcgagggac ctgagctgtc cccagacgat cctgccggcc tgctggacct gagacaggga	1860
atgtttgccc agctggctgc tcagaacgtg ctgctgattg acggccccct gtcctggtat	1920
agcgatcctg gactggcagg cgtgtctctg acaggcggac tgagttacaa agaagacact	1980
aaagaactgg tcgtcgccaa agccggcgtg tactacgtgt tcttccaact ggagctgagg	2040
agggtcgtcg ccggcgaagg cagcggctct gtgagcctgg ccctgcacct gcaaccactg	2100
aggagcgccg ccggcgccgc cgccctggcc ctgactgtgg acctgccacc agcatcctct	2160
gaggcaagga attccgcctt cggcttccag ggccggctgc tgcacctgtc tgccggacag	2220
agactgggcg tccacctgca taccgaagcc agagccaggc atgcctggca gctgaccag	2280
ggcgccaccg tgctgggcct gttcagagt accccagaaa ttccagcagg actgccttcc	2340
ccaaggctctg agggaggagg aggaagtggc ggaggaggat ccggaggggg agggagcgcc	2400
gcctcccaa gactgagaga gggaccagag ctgtcccctg atgacctgc cgggctgctg	2460
gacctgagac aaggcatgtt cgcccagctg gtcgcacaaa acgtgctgtt aattgacggc	2520
ccactgtcct ggtattccga ccctggcctg gccggcgtgt ccctgacagg cggcctgtct	2580
tacaaagaag acacaaaaga actggctgtc gctaaagctg gcgtgtacta cgtgttcttc	2640
caattagaac tgagaagggt cgtcgccggc gagggcagcg ggtctgtgag cctggccctg	2700

cacctgcaac cgctgcggag cgccgccggc gctgccgccc tggccctgac agtggacctg 2760
 cctccagcaa gctccgaggc aaggaatagc gccttcggct ttcaaggccg cctgctgcac 2820
 ctgtccgccg gacagcggct gggcgtccac ctgcacaccg aagccagagc ccgccatgcc 2880
 tggcagctga ctcagggcgc taccgtgctg ggcctgttcc gcgtgacccc agagatccct 2940
 gccggcctgc cctcccctcg gtctgag 2967

<210> 81

<211> 379

<212> PRT

<213> Artificial sequence

<220>

<223> 379 aa knob chain of DSP305

<400> 81

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
 1 5 10 15

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

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
 35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
 50 55 60

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

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
 85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
 100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
 115 120 125

Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly Gln Gly Gly Gly Gly

130

135

140

Ser Gly Gly Gly Gly Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
 145 150 155 160

Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro
 165 170 175

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 180 185 190

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

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 210 215 220

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 225 230 235 240

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 245 250 255

Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
 260 265 270

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

Glu Met Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe
 290 295 300

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 305 310 315 320

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 325 330 335

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
 340 345 350

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
355 360 365

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
370 375

<210> 82
<211> 1137
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO 81

<400> 82
gactctccag ataggccttg gaatccccct accttttagcc ccgccctgct ggtggtgaca 60
gagggcgata acgccacctt cacatgctct tttagcaaca cctccgagtc tttcgtgctg 120
aattggtaca ggatgagccc ttccaaccag acagacaagc tggcagcatt tcctgaggac 180
cgctcccagc caggccagga ttctcggttc agagtgacct agctgccaaa tggcagggac 240
tttcacatga gcgtgggtgcg cgcccggaga aacgattccg gcacatacct gtgcggagca 300
atctctcttg caccaaaggc acagatcaag gagtccctga gggcagagct gagggtgacc 360
gagaggaggg ccgaggtgcc aacagcacac ccattctccta gcccaggcc agcaggacag 420
ggcggaggag gcagcggagg aggaggatcc gagtctaagt acggaccacc atgccctcca 480
tgtcctgcac cagagttcga gggaggacca tccgtgttcc tgtttccacc taagcctaag 540
gacaccctga tgatctccag aacccccgag gtgacatgcg tgggtggtgga cgtgtctcag 600
gaggatcctg aggtgcagtt caattggtac gtggatggcg tggaggtgca caacgccaaag 660
acaaagcccc gggaggagca gtttaatagc acctacagag tgggtgtccgt gctgacagtg 720
ctgcaccagg attggctgaa tggcaaggag tataagtgtg aggtgagcaa caagggcctg 780
cctagctcca tcgagaagac catctccaag gccaaaggcc agccaagaga gccacaggtg 840
tgacacctgc caccaagcca ggaggagatg acaaagaatc aggtgtccct gtggtgtctg 900
gtgaagggct tctacccttc cgacatcgcc gtggagtggg agtctaacgg ccagccagag 960
aacaattaca agaccacacc tccagtgtg gactctgatg gcagcttctt tctgtattct 1020
cggctgaccg tggataagag cagatggcag gagggcaacg tgttcagctg ctccgtgatg 1080

cacgaggccc tgcacaacca ctatacacag aagtctctga gcctgtccct gggcaag

1137

<210> 83

<211> 389

<212> PRT

<213> Artificial sequence

<220>

<223> 389 aa knob chain of DSP305_V1

<400> 83

Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr
1 5 10 15

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

Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr
35 40 45

Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu
50 55 60

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

Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala Arg Arg Asn
85 90 95

Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala
100 105 110

Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg
115 120 125

Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly
130 135 140

Gln Phe Gln Thr Leu Val Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145 150 155 160

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe

165

170

175

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

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 195 200 205

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
 210 215 220

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
 225 230 235 240

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 245 250 255

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
 260 265 270

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 275 280 285

Gln Val Cys Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
 290 295 300

Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 305 310 315 320

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 325 330 335

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
 340 345 350

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
 355 360 365

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 370 375 380

Leu Ser Leu Gly Lys
385

<210> 84
<211> 1167
<212> DNA
<213> Artificial sequence

<220>
<223> na sequence encoding SEQ ID NO 83

<400> 84
ccaggatggg tcctggacag ccccgatagg ccttggaatc cccctacctt ttcccctgcc 60
ctgctgggtg tgacagaggg cgacaacgcc accttcacat gctcttttag caacacctcc 120
gagtctttcg tgctgaattg gtacaggatg agcccttcca accagacaga taagctggca 180
gcatttccag aggaccgcag ccagcctgga caggattgcc gggttcagagt gaccagctg 240
ccaaatggca gggactttca catgtccgtg gtgcgcgccc ggagaaacga ttctggcaca 300
tacctgtgcg gagcaatcag cctggcacca aaggcacaga tcaaggagtc cctgagggca 360
gagctgaggg tgaccgagag gagggccgag gtgccaacag cacacccatc tcctagccca 420
cggcccgcg gccagttcca gaccctgggtg ggaggaggag gaagcggagg aggaggatcc 480
gagtctaagt acggaccacc atgccctcca tgtcctgcac cagagtttga gggcggccca 540
tccgtgttcc tgtttcccc taagcccaag gacaccctga tgatcagccg gacccagag 600
gtgacatgcg tgggtgggtgga cgtgagccag gaggatcctg aggtgcagtt caattggtac 660
gtggatggcg tggaggtgca caacgccaag acaaagcccc gggaggagca gtttaattcc 720
acctacagag tgggtgtctgt gctgacagtg ctgcaccagg attggctgaa tggcaaggag 780
tataagtgtg aggtgtccaa caagggcctg cccagctcca tcgagaagac catctctaag 840
gccaagggcc agccaagaga gccacaggtg tgcaccctgc caccatcca ggaggagatg 900
acaaagaatc aggtgtctct gtggtgtctg gtgaagggtc tctacccttc tgacatcgca 960
gtggagtggg agagcaacgg acagccagag aacaattaca agaccacacc tccagtgtctg 1020
gactctgatg gcagcttctt tctgtatagc cggctgaccg tggataagtc cagatggcag 1080
gagggaacg tgttcagctg ttccgtgatg cagaggccc tgcacaacca ctatacacag 1140
aagtctctga gcctgtccct gggcaag 1167

<210> 85
<211> 1192
<212> PRT
<213> Artificial sequence

<220>
<223> 1192 aa TSP111 and TSP111_V2 "hole" chain

<400> 85

Glu Glu Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala
1 5 10 15

Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro
20 25 30

Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu
35 40 45

Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser
50 55 60

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

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

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

Ser Val Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala
115 120 125

Arg Ala Thr Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly
130 135 140

Phe Ser Pro Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu
145 150 155 160

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

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

His Ser Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp
195 200 205

Pro Leu Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro
210 215 220

Thr Leu Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn
225 230 235 240

Val Thr Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr
245 250 255

Trp Leu Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val
260 265 270

Thr Glu Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val
275 280 285

Asn Val Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu
290 295 300

His Asp Gly Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser
305 310 315 320

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

Ser Asn Glu Arg Asn Ile Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly
340 345 350

Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu
355 360 365

Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
370 375 380

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp

385		390		395		400
Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly						
		405		410		415
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn						
		420		425		430
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp						
		435		440		445
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro						
		450		455		460
Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu						
465		470		475		480
Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Cys Glu Met Thr Lys Asn						
		485		490		495
Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile						
		500		505		510
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr						
		515		520		525
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Arg						
		530		535		540
Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys						
545		550		555		560
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu						
		565		570		575
Ser Leu Ser Leu Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser						
		580		585		590
Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp						
		595		600		605

Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val
610 615 620

Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp
625 630 635 640

Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu
645 650 655

Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe
660 665 670

Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser
675 680 685

Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala
690 695 700

Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala
705 710 715 720

Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala
725 730 735

Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His
740 745 750

Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val
755 760 765

Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly
770 775 780

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Ala Ser
785 790 795 800

Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly
805 810 815

Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn

820

825

830

Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu
835 840 845

Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys
850 855 860

Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu
865 870 875 880

Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu
885 890 895

Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu
900 905 910

Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser
915 920 925

Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg
930 935 940

Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln
945 950 955 960

Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu
965 970 975

Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser
980 985 990

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Ala Ser Pro Arg Leu
995 1000 1005

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu
1010 1015 1020

Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val
1025 1030 1035

Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu
1040 1045 1050

Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr
1055 1060 1065

Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe
1070 1075 1080

Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser
1085 1090 1095

Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
1100 1105 1110

Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser
1115 1120 1125

Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His
1130 1135 1140

Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala
1145 1150 1155

Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu
1160 1165 1170

Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser
1175 1180 1185

Pro Arg Ser Glu
1190

<210> 86
<211> 3577
<212> DNA
<213> Artificial sequence

<220>
<223> na of SEQ ID NO 85

<400> 86

gaggaggagc tgcaggtcat ccagcccgat aagtctgtgc tggtaggcagc aggagagacc	60
gccacactga gatgcaccgc cacaagcctg atcccagtg gaccaatcca gtggttttagg	120
ggagcaggac ctggaaggga gctgatctac aaccagaagg agggccactt cccaagggtg	180
accacagtgt ccgacctgac caagcggaac aatatggatt tttctatcag aatcggcaat	240
atcacacctg ccgacgccgg cacctactat tgcgtgaagt tcagaaaggg cagcccagac	300
gatgtggagt ttaagagcgg agcaggaacc gagctgtccg tgagagccaa gccttctgcc	360
ccagtgggtga gcggaccagc agcaaggga accccacagc acacagtgtc cttcacctgt	420
gagagccacg gcttttcccc acgcgatatc aactgaagt ggttcaagaa cggcaatgag	480
ctgagcgact ttacagacaa cgtggatccc gtgggagagt ctgtgagcta ctccatccac	540
tctacagcca aggtgggtgt gacccgggag gacgtgcaca gccaggtcat ctgagaggtg	600
gcacacgtga ccctgcaggg cgatcctctg agaggcacag ccaatctgag cgagaccatc	660
agggtgcccc ctacactgga ggtgaccag cagcccgtga gggcagagaa ccaagtgaat	720
gtgacatgtc aggtgcggaa gttctaccct cagagactgc agctgacctg gctggagaac	780
ggcaacgtga gccggaccga gacagccagc accgtgacag agaacaagga cggcacatat	840
aattggatgt cttggctgct ggtgaacgtg agcgcccaca gggacgatgt gaagctgacc	900
tgccaggtgg agcacgacgg acagccagcc gtgtctaaga gccacgatct gaaggtgagc	960
gcccacccta aggagcaggg ctccaacaca gccgccgaga ataccggcag caacgagaga	1020
aatatctacg gaggaggagg atccggagga ggaggatccg agtctaagta tggaccacca	1080
tgccctccat gtccagcacc tgagtttgag ggaggacctt ccgtgttcct gtttccccct	1140
aagccaaagg acacactgat gatctccagg acaccagagg tgacctgcgt ggtggtggac	1200
gtgtctcagg aggatcccga ggtgcagttc aactggtacg tggatggcgt ggaggtgcac	1260
aatgccaaaga ccaagcctag ggaggagcag tttaactcca cataccgcgt ggtgtctgtg	1320
ctgaccgtgc tgcaccagga ttggctgaac ggcaaggagt ataagtgtaa ggtgagcaat	1380
aagggcctgc caagctccat cgagaagacc atctccaagg caaagggaca gccaaaggag	1440
cctcaggtgt atacactgcc acccagccag tgcgagatga ccaagaacca ggtgagcctg	1500
tcctgtgccg tgaagggtt ctacccatct gacatcgccg tggagtggga gagcaatggc	1560
cagcccagaga acaattataa gaccacacct ccagtgtgg actccgatgg ctctttcttt	1620

ctggtgtcca ggctgacagt ggataagtct cgctggcagg agggcaacgt gttttcttgt	1680
agcgtgatgc acgaggccct gcacaatcac tacaccaga agtccctgtc tctgagcctg	1740
ggcaagggcg gcggcggctc cggaggagga ggaagcgccg cctcccctag gctgcgcgag	1800
ggaccagagc tgagcccaga cgatccagca ggactgctgg acctgaggca gggaatgttc	1860
gcacagctgg tggcccagaa cgtgctgctg atcgacggcc ctctgtcttg gtacagcgat	1920
ccaggactgg caggcgtgag cctgacaggc ggactgtcct ataaggagga taccaaggag	1980
ctggtggtgg caaaggcagg cgtgtactac gtgttcttcc agctggagct gaggagagt	2040
gtggcaggag agggatccgg atctgtgagc ctggccctgc acctgcagcc actgcggagc	2100
gccgcaggag cagccgccct ggccctgacc gtggacctgc cacctgcata tagcgaggca	2160
cggaattctg ctttcggctt tcagggcaga ctgctgcacc tgagcgccgg acagaggctg	2220
ggagtgcacc tgcacacaga ggcaaggga agacacgcata ggagctgac acaggagca	2280
accgtgctgg gactgttccg cgtgaccct gagatcccag caggactgcc atcccccg	2340
tctgagggcg gcggcgggtc cggaggagga ggatctggcg gcggcggcag cgccgcctcc	2400
cccaggctgc gcgagggacc tgagctgtcc ccagacgata ctgccggcct gctggacctg	2460
agacaggga tgtttgccca gctggctgct cagaacgtgc tgctgattga cggccccctg	2520
tcctggtata gcgatactgg actggcaggc gtgtctctga caggcggact gagttacaaa	2580
gaagacacta aagaactggt cgtcgccaaa gccggcgtgt actacgtgtt cttccaactg	2640
gagctgagga gggctgtcgc cggcgaaggc agcggctctg tgagcctggc cctgcacctg	2700
caaccactga ggagcgccgc cggcgccgcc gccctggccc tgactgtgga cctgccacca	2760
gcatactctg aggcaaggaa ttccgccttc ggcttccagg gccggctgct gcacctgtct	2820
gccggacaga gactgggcgt ccacctgcata accgaagcca gagccaggca tgcctggcag	2880
ctgaccagg gcgccaccgt gctgggcctg ttcagagtga cccagaaat tccagcagga	2940
ctgccttccc caaggtctga gggaggagga ggaagtggcg gaggaggatc cggaggggga	3000
gggagcgccg cctccccaag actgagagag ggaccagagc tgtcccctga tgacctgcc	3060
gggctgctgg acctgagaca aggcattgtt gccagctgg tcgcacaaaa cgtgctgtta	3120
attgacggcc cactgtcctg gtattccgac cctggcctgg ccggcgtgtc cctgacaggc	3180
ggcctgtctt acaaagaaga cacaaaagaa ctggctgtcg ctaaagctgg cgtgtactac	3240

gtgttcttcc aattagaact gagaagggtc gtcgccggcg agggcagcgg gtctgtgagc 3300
ctggccctgc acctgcaacc gctgcgggagc gccgccggcg ctgccgccct ggccctgaca 3360
gtggacctgc ctccagcaag ctccgaggca aggaatagcg ccttcggctt tcaaggccgc 3420
ctgctgcacc tgtccgccgg acagcggctg ggcgtccacc tgcacaccga agccagagcc 3480
cgccatgcct ggcagctgac tcagggcgct accgtgctgg gcctgttccg cgtgacccca 3540
gagatccctg ccggcctgcc ctcccctcgg tctgagt 3577

<210> 87

<400> 87
000

<210> 88

<400> 88
000

<210> 89

<211> 379

<212> PRT

<213> Artificial sequence

<220>

<223> 379 aa TSP111_V1 "hole" chain

<400> 89

Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
1 5 10 15

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

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
50 55 60

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

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr

85

90

95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
 100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
 115 120 125

Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly Gln Gly Gly Gly Gly
 130 135 140

Ser Gly Gly Gly Gly Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
 145 150 155 160

Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro
 165 170 175

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 180 185 190

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

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 210 215 220

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 225 230 235 240

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 245 250 255

Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
 260 265 270

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Cys
 275 280 285

Glu Met Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe
 290 295 300

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
305 310 315 320

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
325 330 335

Phe Leu Val Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
340 345 350

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
355 360 365

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
370 375

<210> 90
<211> 1137
<212> DNA
<213> Artificial sequence

<220>
<223> na of SEQ ID NO 89

<400> 90
gactctccag ataggccttg gaatccccct acctttagcc ccgccctgct ggtggtgaca 60
gagggcgata acgccacctt cacatgctct tttagcaaca cctccgagtc tttcgtgctg 120
aattggtaca ggatgagccc ttccaaccag acagacaagc tggcagcatt tcctgaggac 180
cgcagccagc caggacagga ttccccggtt agagtgaccc agctgccaaa tggcagggac 240
tttcacatgt ctgtggtgcg cgccccggaga aacgatagcg gcacatacct gtgcggagca 300
atctcccctgg caccaaaggc acagatcaag gagtccctga gggcagagct gagggtgacc 360
gagaggaggg ccgaggtgcc aacagcacac ccatctccta gccaaggcc agcaggacag 420
ggaggaggag gctctggagg aggaggatcc gagtctaagt acggaccacc atgccctcca 480
tgtcctgcac cagagttcga gggaggacca tccgtgttcc tgtttccacc taagcctaag 540
gacaccctga tgatctccag aacccccgag gtgacatgcg tgggtggtgga cgtgtctcag 600
gaggatcctg aggtgcagtt caattggtac gtggatggcg tggaggtgca caacgccaaag 660
acaaagcccc gggaggagca gtttaattct acctacagag tgggtgagcgt gctgacagtg 720

ctgcaccagg attggctgaa tggcaaggag tataagtgtata aggtgagcaa caagggcctg 780
 cctagctcca tcgagaagac catctccaag gccaaagggcc agccaagaga gccccaggtg 840
 tacaccctgc caccagcca gtgcgagatg acaaagaatc aggtgagcct gtcctgtgcc 900
 gtgaagggct tctaccctag cgacatcgca gtggagtggg agtccaacgg acagccagag 960
 aacaattata agaccacacc tccagtgtg gactccgatg gctctttctt tctggtgtcc 1020
 cggctgaccg tggataagag ccggtggcag gagggaacg tgttcagctg cagcgtgatg 1080
 cacgaggccc tgcacaacca ctatacacag aagtcctgt ctctgagcct gggcaag 1137

<210> 91
 <211> 1192
 <212> PRT
 <213> Artificial sequence

<220>
 <223> 1192 aa TSP111_V1 "knob" chain

<400> 91

Glu Glu Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala
 1 5 10 15

Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro
 20 25 30

Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu
 35 40 45

Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser
 50 55 60

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

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

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

Ser Val Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala

115

120

125

Arg Ala Thr Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly
 130 135 140

Phe Ser Pro Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu
 145 150 155 160

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

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

His Ser Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp
 195 200 205

Pro Leu Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro
 210 215 220

Thr Leu Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn
 225 230 235 240

Val Thr Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr
 245 250 255

Trp Leu Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val
 260 265 270

Thr Glu Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val
 275 280 285

Asn Val Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu
 290 295 300

His Asp Gly Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser
 305 310 315 320

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

Ser Asn Glu Arg Asn Ile Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly
340 345 350

Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu
355 360 365

Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
370 375 380

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
385 390 395 400

Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
405 410 415

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
420 425 430

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
435 440 445

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
450 455 460

Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
465 470 475 480

Pro Gln Val Cys Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn
485 490 495

Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
500 505 510

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
515 520 525

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg
530 535 540

Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys

545		550		555		560									
Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu
				565					570					575	
Ser	Leu	Ser	Leu	Gly	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
			580					585					590		
Ala	Ala	Ser	Pro	Arg	Leu	Arg	Glu	Gly	Pro	Glu	Leu	Ser	Pro	Asp	Asp
		595					600					605			
Pro	Ala	Gly	Leu	Leu	Asp	Leu	Arg	Gln	Gly	Met	Phe	Ala	Gln	Leu	Val
	610						615				620				
Ala	Gln	Asn	Val	Leu	Leu	Ile	Asp	Gly	Pro	Leu	Ser	Trp	Tyr	Ser	Asp
625						630				635					640
Pro	Gly	Leu	Ala	Gly	Val	Ser	Leu	Thr	Gly	Gly	Leu	Ser	Tyr	Lys	Glu
				645					650					655	
Asp	Thr	Lys	Glu	Leu	Val	Val	Ala	Lys	Ala	Gly	Val	Tyr	Tyr	Val	Phe
			660					665					670		
Phe	Gln	Leu	Glu	Leu	Arg	Arg	Val	Val	Ala	Gly	Glu	Gly	Ser	Gly	Ser
		675					680					685			
Val	Ser	Leu	Ala	Leu	His	Leu	Gln	Pro	Leu	Arg	Ser	Ala	Ala	Gly	Ala
	690						695				700				
Ala	Ala	Leu	Ala	Leu	Thr	Val	Asp	Leu	Pro	Pro	Ala	Ser	Ser	Glu	Ala
705						710				715					720
Arg	Asn	Ser	Ala	Phe	Gly	Phe	Gln	Gly	Arg	Leu	Leu	His	Leu	Ser	Ala
				725					730					735	
Gly	Gln	Arg	Leu	Gly	Val	His	Leu	His	Thr	Glu	Ala	Arg	Ala	Arg	His
			740					745					750		
Ala	Trp	Gln	Leu	Thr	Gln	Gly	Ala	Thr	Val	Leu	Gly	Leu	Phe	Arg	Val
		755					760					765			

Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly
770 775 780

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Ala Ser
785 790 795 800

Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly
805 810 815

Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn
820 825 830

Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu
835 840 845

Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys
850 855 860

Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu
865 870 875 880

Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu
885 890 895

Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu
900 905 910

Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser
915 920 925

Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg
930 935 940

Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln
945 950 955 960

Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu
965 970 975

Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser

980

985

990

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Ala Ser Pro Arg Leu
 995 1000 1005

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu
 1010 1015 1020

Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val
 1025 1030 1035

Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu
 1040 1045 1050

Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr
 1055 1060 1065

Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe
 1070 1075 1080

Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser
 1085 1090 1095

Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
 1100 1105 1110

Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser
 1115 1120 1125

Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His
 1130 1135 1140

Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala
 1145 1150 1155

Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu
 1160 1165 1170

Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser
 1175 1180 1185

Pro Arg Ser Glu
1190

<210> 92
<211> 3576
<212> DNA
<213> Artificial sequence

<220>
<223> na of SEQ ID NO 91

<400> 92
gaggaggagc tgcaggtcat ccagcccgat aagtctgtgc tggtaggcagc aggagagacc 60
gccacactga gatgcaccgc cacaagcctg atcccagtgg gaccaatcca gtggtttagg 120
ggagcaggac ctggaaggga gctgatctac aaccagaagg agggccactt cccaagggtg 180
accacagtgt ccgacctgac caagcggaac aatatggatt tttctatcag aatcggcaat 240
atcacacctg ccgacgccgg cacctactat tgcgtgaagt tcagaaaggg cagcccagac 300
gatgtggagt ttaagtccgg agcaggaacc gagctgtctg tgagagcaaa gcctagcgcc 360
ccagtgggtg ccggaccagc agcaagggca accccacagc acacagtgtc cttcacctgt 420
gagtcccacg gcttttctcc acgcgatatc aactgaagt ggttcaagaa cggcaatgag 480
ctgagcgact ttcagaccaa cgtggatccc gtgggcgagt ctgtgagcta ctccatccac 540
tctacagcca aggtgggtgct gacccgggag gacgtgcaca gccaggtcat ctgcgagggtg 600
gcacacgtga ccctgcaggg cgatcctctg agaggcacag ccaatctgtc cgagaccatc 660
agggtgcccc ctacactgga ggtgaccag cagcccgtga gggcagagaa ccaagtgaat 720
gtgacatgtc aggtgcggaa gttctaccct cagagactgc agctgacctg gctggagaac 780
ggcaatgtga gccgcaccga gacagcctcc accgtgacag agaacaagga cggcacatat 840
aattggatga gctggctgct ggtgaacgtg tccgcccaca gggacgatgt gaagctgacc 900
tgccagggtg agcacgacgg acagccagcc gtgtctaaga gccacgatct gaaggtgtcc 960
gcccacccta aggagcaggg ctctaacaca gccgccgaga ataccggcag caacgagaga 1020
aatatctacg gaggaggagg atccggagga ggaggatccg agtctaagta tggaccacca 1080
tgccctccat gtccagcacc tgagtttgag ggaggaccta gcgtgttcct gtttccccct 1140
aagccaaagg acacactgat gatctccagg acaccagagg tgacctgcgt ggtggtggac 1200

gtgtctcagg	aggatccccga	ggtgcagttc	aactggtacg	tggatggcgt	ggaggtgcac	1260
aatgccaaaga	ccaagcctag	ggaggagcag	tttaactcta	cataccgcgt	ggtgagcgtg	1320
ctgaccgtgc	tgaccagga	ttggctgaac	ggcaaggagt	ataagtgtaa	ggtgagcaat	1380
aagggcctgc	caagctccat	cgagaagacc	atctccaagg	caaagggaca	gccaaaggag	1440
cctcaggtgt	gcacactgcc	accctctcag	gaggagatga	ccaagaacca	ggtgagcctg	1500
tggtgtctgg	tgaagggtt	ctaccaagc	gacatcgccg	tggagtggga	gtccaatggc	1560
cagcccgaga	acaattacaa	gaccacacct	ccagtgtctg	actctgatgg	cagcttcttt	1620
ctgtattcta	ggctgacagt	ggataagagc	cgctggcagg	agggcaacgt	gtttagctgt	1680
tccgtgatgc	acgaggccct	gcacaatcac	tatacccaga	agtctctgag	cctgtccctg	1740
ggcaagggcg	gcggcggcag	cggcggagga	ggatccgccg	cctctcctag	gctgaggggag	1800
ggaccagagc	tgagcccaga	cgatccagca	ggactgtctg	acctgaggca	gggaatgttc	1860
gcacagctgg	tggcccagaa	cgtgctgctg	atcgacggcc	ctctgagctg	gtactccgat	1920
ccaggactgg	caggcgtgtc	cctgacaggc	ggactgtctt	ataaggagga	taccaaggag	1980
ctggtgggtg	caaaggcagg	cgtgtactac	gtgttcttcc	agctggagct	gaggagagtg	2040
gtggcaggag	agggtctctg	aagcgtgtcc	ctggccctgc	acctgcagcc	actgcggagc	2100
gccgcaggag	cagccgccct	ggccctgacc	gtggacctgc	cacctgcata	tagcgaggca	2160
cggaattctg	ccttcggctt	tcagggcaga	ctgctgcacc	tgagcgccgg	acagaggctg	2220
ggagtgcacc	tgcacacaga	ggcaagggca	agacacgcata	ggcagctgac	acagggagca	2280
accgtgctgg	gactgttccg	cgtgaccctt	gagatcccag	caggactgcc	atctccacgg	2340
agcgagggcg	gcggcggctc	tggaggagga	ggaagcggag	gcggcggctc	cgccgcttct	2400
cccaggctgc	gcgagggacc	tgagctgtcc	ccagacgata	ctgccggcct	gctggacctg	2460
agacagggaa	tgtttgccca	gctggctcgt	cagaacgtgc	tgctgattga	cggccccctg	2520
tcctggtatt	ccgatcctgg	actggcaggc	gtgagcctga	caggcggcct	gagctacaaa	2580
gaagacacta	aagaactggt	cgtcgccaaa	gccggcgtgt	actacgtgtt	cttccaactg	2640
gagctgagga	gggtcgtcgc	cggcgaagga	tccggcagcg	tgtccctggc	cctgcacctg	2700
caaccactga	ggagcgccgc	cggcgccgcc	gccctggccc	tgactgtgga	cctgccacca	2760
gcacctctg	aggcaaggaa	ttccgccttc	ggcttccagg	gccggctgct	gcacctgtct	2820

gccggacaga gactgggcgt ccacctgcat accgaagcca gagccaggca tgcctggcag	2880
ctgacccagg gcgccaccgt gctgggcctg ttcagagtga cccagaaat tccagcagga	2940
ctgccttctc caaggagcga gggcggcggg ggctccggcg gaggaggctc tggcggcggc	3000
ggctccgccg cctctccaag gctgcgcgag ggaccagagc tgtcccctga tgaccctgcc	3060
gggctgctgg acctgagaca aggcattgtt gccagctgg tcgcacaaaa cgtgctgtta	3120
attgacggcc cactgtcctg gtatagcgac cctggcctgg ccggcgtgtc tctgacaggc	3180
ggactgagct acaaagaaga tactaaagaa ctggctgtgg ccaaagctgg cgtgtactac	3240
gtgttcttcc aattagaact gagaagggtc gtcgccggcg agggatccgg gagcgtgtcc	3300
ctggccctgc acctgcaacc gctgcggagc gccgccggcg ctgccgccct ggccctgaca	3360
gtggacctgc ctccagcaag ctccgaggca aggaatagcg ccttcggctt tcaaggccgc	3420
ctgctgcacc tgtccgccgg acagcggctg ggcgtccacc tgcacaccga agccagagcc	3480
cgccatgcct ggcagctgac tcagggcgct accgtgctgg gcctgttccg cgtgacccca	3540
gagatccctg caggactgcc ctctcctcgg agcgag	3576

<210> 93

<400> 93
000

<210> 94

<400> 94
000

<210> 95
<211> 21
<212> PRT
<213> Artificial sequence

<220>
<223> artificial signal peptide

<400> 95

Met	Glu	Ser	Pro	Ala	Gln	Leu	Leu	Phe	Leu	Leu	Leu	Leu	Trp	Leu	Pro
1				5				10					15		

Asp	Gly	Val	His	Ala
			20	

<210> 96
<211> 14
<212> PRT
<213> Artificial sequence

<220>
<223> linker peptide sequence

<400> 96

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

<210> 97
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> linker peptide sequence

<400> 97

Gly Gly Gly Gly Ser Gly Gly Gly Gly
1 5

<210> 98
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> linker peptide sequence

<220>
<221> REPEAT
<222> (1)..(5)
<223> may repeat 1-4 times

<400> 98

Gly Gly Gly Gly Ser
1 5

<210> 99
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> linker peptide sequence

<400> 99

Gly Gly Gly Gly Ser
1 5

<210> 100
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> linker peptide sequence

<400> 100

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

<210> 101
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> linker peptide sequence

<220>
<221> REPEAT
<222> (1)..(5)
<223> may repeat 1-3 times

<400> 101

Glu Ala Ala Ala Lys
1 5

<210> 102
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> linker peptide sequence

<220>
<221> REPEAT

<222> (2)..(6)
<223> repeat 2-5 times

<400> 102

Ala Glu Ala Ala Ala Lys Ala
1 5

<210> 103
<211> 12
<212> PRT
<213> Artificial sequence

<220>
<223> linker peptide sequence

<400> 103

Ala Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Ala
1 5 10

<210> 104
<211> 46
<212> PRT
<213> Artificial sequence

<220>
<223> linker peptide sequence

<400> 104

Ala Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
1 5 10 15

Glu Ala Ala Ala Lys Ala Leu Glu Ala Glu Ala Ala Ala Lys Glu Ala
20 25 30

Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Ala
35 40 45

<210> 105
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> linker peptide sequence

<400> 105

Pro Ala Pro Ala Pro
1 5

<210> 106
<211> 18
<212> PRT
<213> Artificial sequence

<220>
<223> linker peptide sequence

<400> 106

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

Leu Asp

<210> 107
<211> 14
<212> PRT
<213> Artificial sequence

<220>
<223> linker peptide sequence

<400> 107

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

<210> 108
<211> 12
<212> PRT
<213> Artificial sequence

<220>
<223> linker peptide sequence

<400> 108

Gly Ser Ala Gly Ser Ala Ala Gly Ser Gly Glu Phe
1 5 10

<210> 109
<211> 229
<212> PRT

<213> Artificial sequence

<220>

<223> linker peptide sequence

<400> 109

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
1 5 10 15

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

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

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

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95

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

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
115 120 125

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

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

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

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

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

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

Leu Ser Leu Gly Lys
225

<210> 110
<211> 229
<212> PRT
<213> Artificial sequence

<220>
<223> linker peptide sequence

<400> 110

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
1 5 10 15

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

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

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

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95

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

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
115 120 125

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

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

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

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

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

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

Leu Ser Leu Gly Lys
225

<210> 111
<211> 229
<212> PRT
<213> Artificial sequence

<220>
<223> linker peptide sequence

<400> 111

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
1 5 10 15

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

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

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

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95

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

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
115 120 125

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

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

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

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Arg Leu
180 185 190

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

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

Leu Ser Leu Gly Lys
225

<210> 112
<211> 232
<212> PRT
<213> Artificial sequence

<220>
<223> linker peptide sequence

<400> 112

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

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

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

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

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

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

210

215

220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 113

<211> 232

<212> PRT

<213> Artificial sequence

<220>

<223> linker peptide sequence

<400> 113

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

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

Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser

145		150		155		160									
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr
				165					170					175	
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr
			180					185					190		
Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe
		195					200					205			
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys
	210					215					220				
Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys								
225					230										
<210> 114															
<211> 232															
<212> PRT															
<213> Artificial sequence															
<220>															
<223> linker peptide sequence															
<400> 114															
Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala
1				5					10					15	
Pro	Glu	Ala	Ala	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
			20					25					30		
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val
		35					40					45			
Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val
	50					55					60				
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln
65					70					75					80
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln

85

90

95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125

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

Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys
 225 230

<210> 115

<211> 398

<212> PRT

<213> Artificial sequence

<220>

<223> LILRB2 D1-4, AA 22-419 (Q8N423-1 UniParc) AA SEQUENCE

<400> 115

Gln Thr Gly Thr Ile Pro Lys Pro Thr Leu Trp Ala Glu Pro Asp Ser
 1 5 10 15

Val Ile Thr Gln Gly Ser Pro Val Thr Leu Ser Cys Gln Gly Ser Leu

20

25

30

Glu Ala Gln Glu Tyr Arg Leu Tyr Arg Glu Lys Lys Ser Ala Ser Trp
 35 40 45

Ile Thr Arg Ile Arg Pro Glu Leu Val Lys Asn Gly Gln Phe His Ile
 50 55 60

Pro Ser Ile Thr Trp Glu His Thr Gly Arg Tyr Gly Cys Gln Tyr Tyr
 65 70 75 80

Ser Arg Ala Arg Trp Ser Glu Leu Ser Asp Pro Leu Val Leu Val Met
 85 90 95

Thr Gly Ala Tyr Pro Lys Pro Thr Leu Ser Ala Gln Pro Ser Pro Val
 100 105 110

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

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

Cys Leu Asn Ser Gln Pro His Ala Arg Gly Ser Ser Arg Ala Ile Phe
 145 150 155 160

Ser Val Gly Pro Val Ser Pro Asn Arg Arg Trp Ser His Arg Cys Tyr
 165 170 175

Gly Tyr Asp Leu Asn Ser Pro Tyr Val Trp Ser Ser Pro Ser Asp Leu
 180 185 190

Leu Glu Leu Leu Val Pro Gly Val Ser Lys Lys Pro Ser Leu Ser Val
 195 200 205

Gln Pro Gly Pro Val Val Ala Pro Gly Glu Ser Leu Thr Leu Gln Cys
 210 215 220

Val Ser Asp Val Gly Tyr Asp Arg Phe Val Leu Tyr Lys Glu Gly Glu
 225 230 235 240

Arg Asp Leu Arg Gln Leu Pro Gly Arg Gln Pro Gln Ala Gly Leu Ser
245 250 255

Gln Ala Asn Phe Thr Leu Gly Pro Val Ser Arg Ser Tyr Gly Gly Gln
260 265 270

Tyr Arg Cys Tyr Gly Ala His Asn Leu Ser Ser Glu Cys Ser Ala Pro
275 280 285

Ser Asp Pro Leu Asp Ile Leu Ile Thr Gly Gln Ile Arg Gly Thr Pro
290 295 300

Phe Ile Ser Val Gln Pro Gly Pro Thr Val Ala Ser Gly Glu Asn Val
305 310 315 320

Thr Leu Leu Cys Gln Ser Trp Arg Gln Phe His Thr Phe Leu Leu Thr
325 330 335

Lys Ala Gly Ala Ala Asp Ala Pro Leu Arg Leu Arg Ser Ile His Glu
340 345 350

Tyr Pro Lys Tyr Gln Ala Glu Phe Pro Met Ser Pro Val Thr Ser Ala
355 360 365

His Ala Gly Thr Tyr Arg Cys Tyr Gly Ser Leu Asn Ser Asp Pro Tyr
370 375 380

Leu Leu Ser His Pro Ser Glu Pro Leu Glu Leu Val Val Ser
385 390 395

<210> 116
<211> 1194
<212> DNA
<213> Artificial sequence

<220>
<223> LILRB2 D1-4, AA 22-419 (Q8N423-1 UniParc) NA SEQUENCE

<400> 116
cagaccggca caatcccaa gcctaccctg tgggccgagc cagatagcgt gatcaccag 60
ggctcccccg tgacactgtc ttgccagggc agcctggagg cacaggagta ccggctgtat 120

```

agagagaaga agagcgcctc ctggatcacc cggatcagac ccgagctggt gaagaacggc      180
cagtttcaca tcccttccat cacctgggag cacacaggcc ggtacggatg ccagtactat      240
tctcggggcca gatggagcga gctgtccgac cccctgggtgc tggtcatgac cggcgcctat      300
ccaaagccca cactgtccgc ccagccttct ccagtgggtga cctctggcgg cagagtgaca      360
ctgcagtgtg agagccaggt ggccttcggc ggctttatcc tgtgcaagga gggcgaggag      420
gagcaccccc agtgtctgaa tagccagcct cacgcccggg gcagctccag agccatcttc      480
tctgtggggc ctgtgagccc aaaccggaga tgggtcccaca ggtgctacgg ctatgacctg      540
aacagcccat acgtgtggtc tagcccctct gatctgctgg agctgctggt gcctggcgtg      600
agcaagaagc catctctgag cgtgcagcca ggccctgtgg tggcacctgg cgagtctctg      660
accctgcagt gcgtgagcga cgtgggctac gatcggttcg tgctgtataa ggaggagag      720
agggatctga ggcagctgcc aggcagacag cctcaggcag gactgtcca ggcaaacttt      780
acactgggcc ccgtgagccg gagctacggc ggacagtacc gctgctatgg agcacacaat      840
ctgtcctctg agtgttctgc ccccagcgac cccctggaca tcctgatcac cggccagatc      900
aggggcacac cattcatcag cgtgcagcca ggaccaaccg tggcctccgg cgagaacgtg      960
acactgctgt gccagagctg gcgccagttc cacacctttc tgctgacaaa ggcaggagca     1020
gcagacgcac ctctgaggct gcgctccatc cacgagtacc caaagtatca ggccgagttt     1080
ccaatgagcc ccgtgacctc cgcccacgca ggcacataca gatgctatgg cagcctgaac     1140
agcgaccctt acctgctgag ccacccttcc gagccactgg agctggtggt gtcc           1194

```

```

<210> 117
<211> 198
<212> PRT
<213> Artificial sequence

```

```

<220>
<223> LILRB2 D1-2, AA 22-219 (Q8N423-1 UniParc) AA SEQUENCE

```

```

<400> 117

```

```

Gln Thr Gly Thr Ile Pro Lys Pro Thr Leu Trp Ala Glu Pro Asp Ser
1           5           10          15

```

```

Val Ile Thr Gln Gly Ser Pro Val Thr Leu Ser Cys Gln Gly Ser Leu
          20          25          30

```

Glu Ala Gln Glu Tyr Arg Leu Tyr Arg Glu Lys Lys Ser Ala Ser Trp
35 40 45

Ile Thr Arg Ile Arg Pro Glu Leu Val Lys Asn Gly Gln Phe His Ile
50 55 60

Pro Ser Ile Thr Trp Glu His Thr Gly Arg Tyr Gly Cys Gln Tyr Tyr
65 70 75 80

Ser Arg Ala Arg Trp Ser Glu Leu Ser Asp Pro Leu Val Leu Val Met
85 90 95

Thr Gly Ala Tyr Pro Lys Pro Thr Leu Ser Ala Gln Pro Ser Pro Val
100 105 110

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

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

Cys Leu Asn Ser Gln Pro His Ala Arg Gly Ser Ser Arg Ala Ile Phe
145 150 155 160

Ser Val Gly Pro Val Ser Pro Asn Arg Arg Trp Ser His Arg Cys Tyr
165 170 175

Gly Tyr Asp Leu Asn Ser Pro Tyr Val Trp Ser Ser Pro Ser Asp Leu
180 185 190

Leu Glu Leu Leu Val Pro
195

<210> 118
<211> 594
<212> DNA
<213> Artificial sequence

<220>
<223> LILRB2 D1-2, AA 22-219 (Q8N423-1 UniParc) NA SEQUENCE

<400> 118

```

cagaccggca caatcccca gcctaccctg tgggccgagc cagatagcgt gatcaccag      60
ggctcccccg tgacactgtc ttgccagggc agcctggagg cacaggagta ccggctgtat      120
agagagaaga agagcgcctc ctggatcacc cggatcagac ccgagctggt gaagaacggc      180
cagtttcaca tcccttccat cacctgggag cacacaggcc ggtacggatg ccagtactat      240
tctcggggcca gatggagcga gctgtccgac cccctgggtgc tggtcatgac cggcgcctat      300
ccaaagccca cactgtccgc ccagccttct ccagtgggtga cctctggcgg cagagtgaca      360
ctgcagtgtg agagccaggt ggccttcggc ggctttatcc tgtgcaagga gggcgaggag      420
gagcaccccc agtgtctgaa tagccagcct cacgcccggg gcagctccag agccatcttc      480
tctgtggggc ctgtgagccc aaaccggaga tgggtcccaca ggtgctacgg ctatgacctg      540
aacagcccat acgtgtgggtc tagcccctct gatctgctgg agctgctggt gcct          594

```

```

<210> 119
<211> 148
<212> PRT
<213> Artificial sequence

```

```

<220>
<223> CD40L, AA 114-261 C194S (P29965 Uniprot) AA SEQUENCE

```

```

<400> 119

```

```

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

```

```

Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr
          20          25          30

```

```

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

```

```

Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe
          50          55          60

```

```

Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu
65           70           75          80

```

```

Ser Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala
          85          90          95

```

Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His Leu
100 105 110

Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn Val
115 120 125

Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly
130 135 140

Leu Leu Lys Leu
145

<210> 120
<211> 444
<212> DNA
<213> Artificial sequence

<220>
<223> CD40L, AA 114-261 C194S (P29965 Uniprot) NA SEQUENCE

<400> 120
cagaagggcg atcagaatcc tcagattgcc gccacgtga tctctgaggc ctctagcaag 60
accacaagcg tgctgcagtg ggcagaaaaa gggtactata caatgtctaa caatctggtg 120
accctggaga acggcaagca actgaccgtc aaaagacagg gcctgtacta catctacgct 180
caggtgacct tctgcagcaa tagggaggcc tcctctcagg caccttttat cgcctctctg 240
agcctgaagt cccagggcgg gttcgagaga atcctgttaa gggcagcaaa cactcacagc 300
tccgcaaacc catgtggaca gcagagcata cacctgggcg gcgtgttcga gctgcaaccg 360
ggagcctccg tgtttgtcaa tgtgaccgac ccatcccagg tgtctcacgg caccggcttc 420
accagcttcg gcctgctgaa gctg 444

<210> 121
<211> 474
<212> PRT
<213> Artificial sequence

<220>
<223> sc3xCD40L, AA 114-261 C194S (P29965 Uniprot) internal linker
3x(GGGGS) AA SEQUENCE

<400> 121

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

Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr
20 25 30

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

Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe
50 55 60

Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu
65 70 75 80

Ser Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala
85 90 95

Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His Leu
100 105 110

Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn Val
115 120 125

Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly
130 135 140

Leu Leu Lys Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145 150 155 160

Gly Gly Ser Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val
165 170 175

Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu
180 185 190

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

Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln
210 215 220

Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile
225 230 235 240

Ala Ser Leu Ser Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu
245 250 255

Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser
260 265 270

Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe
275 280 285

Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr
290 295 300

Ser Phe Gly Leu Leu Lys Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly
305 310 315 320

Ser Gly Gly Gly Gly Ser Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala
325 330 335

Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln
340 345 350

Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu
355 360 365

Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile
370 375 380

Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala
385 390 395 400

Pro Phe Ile Ala Ser Leu Ser Leu Lys Ser Pro Gly Arg Phe Glu Arg
405 410 415

Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly
420 425 430

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

Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr
450 455 460

Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu
465 470

<210> 122
<211> 215
<212> PRT
<213> Artificial sequence

<220>
<223> CD40L full ECD, AA 47-261 (P29965 Uniprot) AA SEQUENCE

<400> 122

His Arg Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp
1 5 10 15

Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser
20 25 30

Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe
35 40 45

Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser
50 55 60

Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val
65 70 75 80

Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu
85 90 95

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

Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln
115 120 125

Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile
130 135 140

Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu
145 150 155 160

Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser
165 170 175

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

Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr
195 200 205

Ser Phe Gly Leu Leu Lys Leu
210 215

<210> 123
<211> 148
<212> PRT
<213> Artificial sequence

<220>
<223> CD40L, AA 114-261 NO MUTATION (P29965 Uniprot) AA SEQUENCE

<400> 123

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

Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr
20 25 30

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

Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe
50 55 60

Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu
65 70 75 80

Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala
85 90 95

Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His Leu
100 105 110

Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn Val
115 120 125

Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly
130 135 140

Leu Leu Lys Leu
145

<210> 124
<211> 444
<212> DNA
<213> Artificial sequence

<220>
<223> CD40L, AA 114-261 NO MUTATION (P29965 Uniprot) NA SEQUENCE

<400> 124
cagaagggcg atcagaatcc tcagattgcc gccacgtga tctctgaggc ctctagcaag 60
accacaagcg tgctgcagtg ggcagaaaaa gggactata caatgtctaa caatctgggtg 120
accctggaga acggcaagca actgaccgtc aaaagacagg gcctgtacta catctacgct 180
caggtgacct tctgcagcaa tagggaggcc tcctctcagg caccttttat cgcctctctg 240
tgctgaagt cccagggcg gttcgagaga atcctgttaa gggcagcaaa cactcacagc 300
tccgccaac catgtggaca gcagagcata cacctgggcg gcgtgttcga gctgcaaccg 360
ggagcctccg tgtttgtcaa tgtgaccgac ccatcccagg tgtctcacgg caccggcttc 420
accagcttcg gcctgctgaa gctg 444

<210> 125
<211> 128
<212> PRT
<213> Artificial sequence

<220>
<223> Siglec 10, AA 18-145 NO MUTATION (Q96LC7-1 Uniprot) AA SEQUENCE

<400> 125

Asp Gly Arg Phe Trp Ile Arg Val Gln Glu Ser Val Met Val Pro Glu
1 5 10 15

Gly Leu Cys Ile Ser Val Pro Cys Ser Phe Ser Tyr Pro Arg Gln Asp
20 25 30

Trp Thr Gly Ser Thr Pro Ala Tyr Gly Tyr Trp Phe Lys Ala Val Thr
35 40 45

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

Val Glu Met Ser Thr Arg Gly Arg Phe Gln Leu Thr Gly Asp Pro Ala
65 70 75 80

Lys Gly Asn Cys Ser Leu Val Ile Arg Asp Ala Gln Met Gln Asp Glu
85 90 95

Ser Gln Tyr Phe Phe Arg Val Glu Arg Gly Ser Tyr Val Arg Tyr Asn
100 105 110

Phe Met Asn Asp Gly Phe Phe Leu Lys Val Thr Ala Leu Thr Gln Lys
115 120 125

<210> 126

<211> 186

<212> DNA

<213> Artificial sequence

<220>

<223> Siglec 10, AA 18-145 NO MUTATION (Q96LC7-1 Uniprot) AA SEQUENCE

<400> 126

gatggccggt tttggatcag agtgcaggag tccgtgatgg tgcctgaggg cctgtgcatc 60

agcgtgccat gtccttctc ttaccccaga caggactgga ccggctctac acccgcttac 120

ggctattggt ttaaggccgt gaccgagaca acaaagggcg cccctgtggc cacaaaccac 180

cagagc 186

<210> 127

<211> 128

<212> PRT
<213> Artificial sequence

<220>
<223> Siglec 10, AA 18-145 plus C36S (Q96LC7-1 Uniprot) AA SEQUENCE

<400> 127

Asp Gly Arg Phe Trp Ile Arg Val Gln Glu Ser Val Met Val Pro Glu
1 5 10 15

Gly Leu Ser Ile Ser Val Pro Cys Ser Phe Ser Tyr Pro Arg Gln Asp
20 25 30

Trp Thr Gly Ser Thr Pro Ala Tyr Gly Tyr Trp Phe Lys Ala Val Thr
35 40 45

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

Val Glu Met Ser Thr Arg Gly Arg Phe Gln Leu Thr Gly Asp Pro Ala
65 70 75 80

Lys Gly Asn Cys Ser Leu Val Ile Arg Asp Ala Gln Met Gln Asp Glu
85 90 95

Ser Gln Tyr Phe Phe Arg Val Glu Arg Gly Ser Tyr Val Arg Tyr Asn
100 105 110

Phe Met Asn Asp Gly Phe Phe Leu Lys Val Thr Ala Leu Thr Gln Lys
115 120 125

<210> 128
<211> 384
<212> DNA
<213> Artificial sequence

<220>
<223> Siglec 10, AA 18-145 plus C36S (Q96LC7-1 Uniprot) NA SEQUENCE

<400> 128

gatggccggt tttggatcag agtgcaggag tccgtgatgg tgcctgaggg cctgtctatc 60

agcgtgccat gtccttctc ttaccccaga caggactgga ccggctctac accgcctac 120

ggctattggt ttaaggccgt gaccgagaca acaaaggcg cccctgtggc cacaaccac 180

cagagcagag aggtggagat gtccacccgg ggcagattcc agctgacagg cgaccccgcc 240
aagggcaatt gtagcctggt catcagggac gccagatgc aggatgagtc tcagtacttc 300
tttagggtgg agcgcggcag ctacgtgcmc tataacttta tgaatgatgg cttctttctg 360
aaggtgaccg ccctgacaca gaag 384

<210> 129
<211> 534
<212> PRT
<213> Artificial sequence

<220>
<223> Siglec 10 full ECD, AA 17-550 (Q96LC7-1 Uniprot) AA SEQUENCE

<400> 129

Met Asp Gly Arg Phe Trp Ile Arg Val Gln Glu Ser Val Met Val Pro
1 5 10 15

Glu Gly Leu Cys Ile Ser Val Pro Cys Ser Phe Ser Tyr Pro Arg Gln
20 25 30

Asp Trp Thr Gly Ser Thr Pro Ala Tyr Gly Tyr Trp Phe Lys Ala Val
35 40 45

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

Glu Val Glu Met Ser Thr Arg Gly Arg Phe Gln Leu Thr Gly Asp Pro
65 70 75 80

Ala Lys Gly Asn Cys Ser Leu Val Ile Arg Asp Ala Gln Met Gln Asp
85 90 95

Glu Ser Gln Tyr Phe Phe Arg Val Glu Arg Gly Ser Tyr Val Arg Tyr
100 105 110

Asn Phe Met Asn Asp Gly Phe Phe Leu Lys Val Thr Ala Leu Thr Gln
115 120 125

Lys Pro Asp Val Tyr Ile Pro Glu Thr Leu Glu Pro Gly Gln Pro Val
130 135 140

Thr Val Ile Cys Val Phe Asn Trp Ala Phe Glu Glu Cys Pro Pro Pro
145 150 155 160

Ser Phe Ser Trp Thr Gly Ala Ala Leu Ser Ser Gln Gly Thr Lys Pro
165 170 175

Thr Thr Ser His Phe Ser Val Leu Ser Phe Thr Pro Arg Pro Gln Asp
180 185 190

His Asn Thr Asp Leu Thr Cys His Val Asp Phe Ser Arg Lys Gly Val
195 200 205

Ser Ala Gln Arg Thr Val Arg Leu Arg Val Ala Tyr Ala Pro Arg Asp
210 215 220

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

Pro Gln Gly Asn Val Pro Tyr Leu Glu Ala Gln Lys Gly Gln Phe Leu
245 250 255

Arg Leu Leu Cys Ala Ala Asp Ser Gln Pro Pro Ala Thr Leu Ser Trp
260 265 270

Val Leu Gln Asn Arg Val Leu Ser Ser Ser His Pro Trp Gly Pro Arg
275 280 285

Pro Leu Gly Leu Glu Leu Pro Gly Val Lys Ala Gly Asp Ser Gly Arg
290 295 300

Tyr Thr Cys Arg Ala Glu Asn Arg Leu Gly Ser Gln Gln Arg Ala Leu
305 310 315 320

Asp Leu Ser Val Gln Tyr Pro Pro Glu Asn Leu Arg Val Met Val Ser
325 330 335

Gln Ala Asn Arg Thr Val Leu Glu Asn Leu Gly Asn Gly Thr Ser Leu
340 345 350

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

Ser Pro Pro Ala Arg Leu Ser Trp Thr Gln Arg Gly Gln Val Leu Ser
370 375 380

Pro Ser Gln Pro Ser Asp Pro Gly Val Leu Glu Leu Pro Arg Val Gln
385 390 395 400

Val Glu His Glu Gly Glu Phe Thr Cys His Ala Arg His Pro Leu Gly
405 410 415

Ser Gln His Val Ser Leu Ser Leu Ser Val His Tyr Ser Pro Lys Leu
420 425 430

Leu Gly Pro Ser Cys Ser Trp Glu Ala Glu Gly Leu His Cys Ser Cys
435 440 445

Ser Ser Gln Ala Ser Pro Ala Pro Ser Leu Arg Trp Trp Leu Gly Glu
450 455 460

Glu Leu Leu Glu Gly Asn Ser Ser Gln Asp Ser Phe Glu Val Thr Pro
465 470 475 480

Ser Ser Ala Gly Pro Trp Ala Asn Ser Ser Leu Ser Leu His Gly Gly
485 490 495

Leu Ser Ser Gly Leu Arg Leu Arg Cys Glu Ala Trp Asn Val His Gly
500 505 510

Ala Gln Ser Gly Ser Ile Leu Gln Leu Pro Asp Lys Lys Gly Leu Ile
515 520 525

Ser Thr Ala Phe Ser Asn
530

<210> 130
<211> 112
<212> PRT
<213> Artificial sequence

<220>

<223> TIGIT, AA 22-134 NO MUTATIONS (Q495A1 Uniprot ID) AA SEQUENCE

<400> 130

Met Thr Gly Thr Ile Glu Thr Thr Gly Asn Ile Ser Ala Glu Lys Gly
1 5 10 15

Gly Ser Ile Ile Leu Gln Cys His Leu Ser Ser Thr Thr Ala Gln Val
20 25 30

Thr Gln Val Asn Trp Glu Gln Gln Asp Gln Leu Leu Ala Ile Cys Asn
35 40 45

Ala Asp Leu Gly Trp His Ile Ser Pro Ser Phe Lys Asp Arg Val Ala
50 55 60

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

Thr Gly Glu Tyr Phe Cys Ile Tyr His Thr Tyr Pro Asp Gly Thr Tyr
85 90 95

Thr Gly Arg Ile Phe Leu Glu Val Leu Glu Ser Ser Val Ala Glu His
100 105 110

<210> 131

<211> 336

<212> DNA

<213> Artificial sequence

<220>

<223> TIGIT, ECD AA 22-141 NO MUTATIONS (Q495A1 Uniprot ID) NA
SEQUENCE

<400> 131

atgaccggca caatcgagac aacaggcaac atctctgccg agaaggagg cagcatcatc 60
ctgcagtgcc acctgagcag caccacagcc caggtgaccc aggtgaactg ggagcagcag 120
gaccagctgc tggccatctg caatgccgat ctgggctggc acatcagccc ctcctttaag 180
gatagggtgg cacctggacc aggcctgggc ctgaccctgc agagcctgac cgtgaatgac 240
acaggcgagt acttctgtat ctaccacaca tctctgatg gcacctatac aggcagaatc 300
tttctggagg tgctggagtc tagcgtggcc gagcac 336

<210> 132
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> TIGIT, AA 22-134 plus I42A C69S (Q495A1 Uniprot ID) AA SEQUENCE

<400> 132

Met Thr Gly Thr Ile Glu Thr Thr Gly Asn Ile Ser Ala Glu Lys Gly
1 5 10 15

Gly Ser Ile Ala Leu Gln Cys His Leu Ser Ser Thr Thr Ala Gln Val
20 25 30

Thr Gln Val Asn Trp Glu Gln Gln Asp Gln Leu Leu Ala Ile Ser Asn
35 40 45

Ala Asp Leu Gly Trp His Ile Ser Pro Ser Phe Lys Asp Arg Val Ala
50 55 60

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

Thr Gly Glu Tyr Phe Cys Ile Tyr His Thr Tyr Pro Asp Gly Thr Tyr
85 90 95

Thr Gly Arg Ile Phe Leu Glu Val Leu Glu Ser Ser Val Ala Glu His
100 105 110

<210> 133
<211> 336
<212> DNA
<213> Artificial sequence

<220>
<223> TIGIT, AA 22-134 plus I42A C69S (Q495A1 Uniprot ID) NA SEQUENCE

<400> 133

atgaccggca caatcgagac aacaggcaac atctctgccg agaagggagg cagcatcgcc 60
ctgcagtgcc acctgagcag caccacagcc caggtgaccc aggtgaactg ggagcagcag 120
gaccagctgc tggccatctc caatgccgat ctgggctggc acatcagccc ctcctttaag 180

gatagggtgg cacctggacc aggcctgggc ctgaccctgc agagcctgac cgtgaatgac 240
acaggcgagt acttctgtat ctaccacaca tadcctgatg gcacctatac aggcagaatc 300
tttctggagg tgctggagtc tagcgtggcc gagcac 336

<210> 134
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> LINKER amino acid sequence

<400> 134

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

<210> 135
<211> 25
<212> PRT
<213> Artificial sequence

<220>
<223> LINKER amino acid sequence

<400> 135

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25

<210> 136
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> LINKER amino acid sequence

<400> 136

Gly Gly Gly Gly Gly Gly Gly Gly
1 5

<210> 137

<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> LINKER amino acid sequence

<400> 137

Gly Gly Gly Gly Gly Gly Gly Gly
1 5

<210> 138
<211> 642
<212> PRT
<213> Artificial sequence

<220>
<223> LILRB2 D1-4 Fc IgG4 Knob: in TSP 214 and 215 217 218 221 and
222 AA SEQUENCE

<400> 138

Gln Thr Gly Thr Ile Pro Lys Pro Thr Leu Trp Ala Glu Pro Asp Ser
1 5 10 15

Val Ile Thr Gln Gly Ser Pro Val Thr Leu Ser Cys Gln Gly Ser Leu
20 25 30

Glu Ala Gln Glu Tyr Arg Leu Tyr Arg Glu Lys Lys Ser Ala Ser Trp
35 40 45

Ile Thr Arg Ile Arg Pro Glu Leu Val Lys Asn Gly Gln Phe His Ile
50 55 60

Pro Ser Ile Thr Trp Glu His Thr Gly Arg Tyr Gly Cys Gln Tyr Tyr
65 70 75 80

Ser Arg Ala Arg Trp Ser Glu Leu Ser Asp Pro Leu Val Leu Val Met
85 90 95

Thr Gly Ala Tyr Pro Lys Pro Thr Leu Ser Ala Gln Pro Ser Pro Val
100 105 110

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

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

Cys Leu Asn Ser Gln Pro His Ala Arg Gly Ser Ser Arg Ala Ile Phe
145 150 155 160

Ser Val Gly Pro Val Ser Pro Asn Arg Arg Trp Ser His Arg Cys Tyr
165 170 175

Gly Tyr Asp Leu Asn Ser Pro Tyr Val Trp Ser Ser Pro Ser Asp Leu
180 185 190

Leu Glu Leu Leu Val Pro Gly Val Ser Lys Lys Pro Ser Leu Ser Val
195 200 205

Gln Pro Gly Pro Val Val Ala Pro Gly Glu Ser Leu Thr Leu Gln Cys
210 215 220

Val Ser Asp Val Gly Tyr Asp Arg Phe Val Leu Tyr Lys Glu Gly Glu
225 230 235 240

Arg Asp Leu Arg Gln Leu Pro Gly Arg Gln Pro Gln Ala Gly Leu Ser
245 250 255

Gln Ala Asn Phe Thr Leu Gly Pro Val Ser Arg Ser Tyr Gly Gly Gln
260 265 270

Tyr Arg Cys Tyr Gly Ala His Asn Leu Ser Ser Glu Cys Ser Ala Pro
275 280 285

Ser Asp Pro Leu Asp Ile Leu Ile Thr Gly Gln Ile Arg Gly Thr Pro
290 295 300

Phe Ile Ser Val Gln Pro Gly Pro Thr Val Ala Ser Gly Glu Asn Val
305 310 315 320

Thr Leu Leu Cys Gln Ser Trp Arg Gln Phe His Thr Phe Leu Leu Thr
325 330 335

Lys Ala Gly Ala Ala Asp Ala Pro Leu Arg Leu Arg Ser Ile His Glu
340 345 350

Tyr Pro Lys Tyr Gln Ala Glu Phe Pro Met Ser Pro Val Thr Ser Ala
355 360 365

His Ala Gly Thr Tyr Arg Cys Tyr Gly Ser Leu Asn Ser Asp Pro Tyr
370 375 380

Leu Leu Ser His Pro Ser Glu Pro Leu Glu Leu Val Val Ser Gly Gly
385 390 395 400

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ser Lys
405 410 415

Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly
420 425 430

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
435 440 445

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu
450 455 460

Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
465 470 475 480

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg
485 490 495

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
500 505 510

Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu
515 520 525

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys
530 535 540

Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu
545 550 555 560

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
565 570 575

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
580 585 590

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp
595 600 605

Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His
610 615 620

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu
625 630 635 640

Gly Lys

<210> 139
<211> 1926
<212> DNA
<213> Artificial sequence

<220>
<223> LILRB2 D1-4 Fc IgG4 Knob: in TSP 214 and 215 217 218 221 and
222 NA SEQUENCE

<400> 139
cagaccggca caatcccca gcctaccctg tgggccgagc cagatagcgt gatcaccag 60
ggctcccccg tgacactgtc ttgccagggc agcctggagg cacaggagta cggctgtat 120
agagagaaga agagcgcctc ctggatcacc cggatcagac ccgagctggt gaagaacggc 180
cagtttcaca tcccttccat cacctgggag cacacaggcc ggtacggatg ccagtactat 240
tctcgggcca gatggagcga gctgtccgac cccctggtgc tggatcatgac cggcgcctat 300
ccaaagccca cactgtccgc ccagccttct ccagtgggtga cctctggcgg cagagtgaca 360
ctgcagtgtg agagccagggt ggccttcggc ggctttatcc tgtgcaagga gggcgaggag 420
gagcaccccc agtgtctgaa tagccagcct cagccccggg gcagctccag agccatcttc 480
tctgtgggcc ctgtgagccc aaaccggaga tgggtcccaca ggtgctacgg ctatgacctg 540

aacagcccat acgtgtggtc tagccccctct gatctgctgg agctgctggt gcctggcgtg	600
agcaagaagc catctctgag cgtgcagcca ggccctgtgg tggcacctgg cgagtctctg	660
accctgcagt gcgtgagcga cgtgggctac gatcggttcg tgctgtataa ggaggagag	720
agggatctga ggcagctgcc aggcagacag cctcaggcag gactgtcca ggcaaacttt	780
acactgggcc ccgtgagccg gagctacggc ggacagtacc gctgctatgg agcacacaat	840
ctgtcctctg agtgttctgc cccagcgac cccctggaca tcctgatcac cggccagatc	900
aggggcacac cattcatcag cgtgcagcca ggaccaaccg tggcctccgg cgagaacgtg	960
acactgctgt gccagagctg gcgccagttc cacacctttc tgctgacaaa ggcaggagca	1020
gcagacgcac ctctgaggct gcgctccatc cagcagctacc caaagtatca ggccgagttt	1080
ccaatgagcc ccgtgacctc cgcccacgca ggcacataca gatgctatgg cagcctgaac	1140
agcgaccctt acctgctgag ccacccttcc gagccactgg agctggtggt gtccggcggc	1200
ggcggctctg gcggaggagg cagcggagga ggaggatccg agtctaagta cggaccacca	1260
tgccctccat gtcctgcacc agagtctgag ggaggacct ccgtgttcct gtttccacct	1320
aagcctaagg acaccctgat gatctccaga acccccgagg tgacatgcgt ggtggtggac	1380
gtgtctcagg aggatcctga ggtgcagttc aattggtacg tggatggcgt ggaggtgcac	1440
aacgccaaga caaagccccg ggaggagcag tttaatagca cctacagagt ggtgtccgtg	1500
ctgacagtgc tgcaccagga ttggctgaat ggcaaggagt ataagtgtaa ggtgagcaac	1560
aagggcctgc ctagctccat cgagaagacc atctccaagg ccaagggcca gccaaagagag	1620
ccacagggtg gcaccctgcc accaagccag gaggagatga caaagaatca ggtgtccctg	1680
tgggtgtctgg tgaagggtt ctacccttcc gacatcgccg tggagtggga gtctaacggc	1740
cagccagaga acaattacaa gaccacacct ccagtgtctgg actctgatgg cagcttcttt	1800
ctgtattctc ggctgaccgt ggataagagc agatggcagg agggcaacgt gttcagctgc	1860
tccgtgatgc acgaggccct gcacaaccac tatacacaga agtctctgag cctgtccctg	1920
ggcaag	1926

<210> 140
 <211> 442
 <212> PRT
 <213> Artificial sequence

<220>

<223> LILRB2 D1-2 Fc IgG4 Knob: in TSP 214 V1 and 215 V1 AA SEQUENCE

<400> 140

Gln Thr Gly Thr Ile Pro Lys Pro Thr Leu Trp Ala Glu Pro Asp Ser
1 5 10 15

Val Ile Thr Gln Gly Ser Pro Val Thr Leu Ser Cys Gln Gly Ser Leu
20 25 30

Glu Ala Gln Glu Tyr Arg Leu Tyr Arg Glu Lys Lys Ser Ala Ser Trp
35 40 45

Ile Thr Arg Ile Arg Pro Glu Leu Val Lys Asn Gly Gln Phe His Ile
50 55 60

Pro Ser Ile Thr Trp Glu His Thr Gly Arg Tyr Gly Cys Gln Tyr Tyr
65 70 75 80

Ser Arg Ala Arg Trp Ser Glu Leu Ser Asp Pro Leu Val Leu Val Met
85 90 95

Thr Gly Ala Tyr Pro Lys Pro Thr Leu Ser Ala Gln Pro Ser Pro Val
100 105 110

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

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

Cys Leu Asn Ser Gln Pro His Ala Arg Gly Ser Ser Arg Ala Ile Phe
145 150 155 160

Ser Val Gly Pro Val Ser Pro Asn Arg Arg Trp Ser His Arg Cys Tyr
165 170 175

Gly Tyr Asp Leu Asn Ser Pro Tyr Val Trp Ser Ser Pro Ser Asp Leu
180 185 190

Leu Glu Leu Leu Val Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

195

200

205

Gly Gly Gly Gly Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys
 210 215 220

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

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

Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp
 260 265 270

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

Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 290 295 300

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

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

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

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

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

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

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

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

Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440

<210> 141
<211> 1326
<212> DNA
<213> Artificial sequence

<220>
<223> LILRB2 D1-2 Fc IgG4 Knob: in TSP 214 V1 and 215 V1 NA SEQUENCE

<400> 141
cagaccggca caatcccaa gcctaccctg tgggccgagc cagatagcgt gatcaccag 60
ggctcccccg tgacactgtc ttgccagggc agcctggagg cacaggagta ccggctgtat 120
agagagaaga agagcgcctc ctggatcacc cggatcagac ccgagctggt gaagaacggc 180
cagtttcaca tcccttccat cacctgggag cacacaggcc ggtacggatg ccagtactat 240
tctcggggcca gatggagcga gctgtccgac cccctgggtgc tggatcatgac cggcgcctat 300
ccaaagccca cactgtccgc ccagccttct ccagtgggtga cctctggcgg cagagtgaca 360
ctgcagtgtg agagccaggt ggcccttcggc ggctttatcc tgtgcaagga gggcgaggag 420
gagcaccccc agtgtctgaa tagccagcct cagccccggg gcagctccag agccatcttc 480
tctgtggggc ctgtgagccc aaaccggaga tgggtcccaca ggtgctacgg ctatgacctg 540
aacagcccat acgtgtggtc tagccccctc gatctgctgg agctgctggt gcctggcggc 600
ggcgggctctg gcggaggagg cagcggagga ggaggatccg agtctaagta cggaccacca 660
tgccctccat gtcctgcacc agagttcgag ggaggaccat ccgtgttcct gtttccacct 720
aagcctaagg acaccctgat gatctccaga acccccaggg tgacatgcgt ggtggtggac 780
gtgtctcagg aggatcctga ggtgcagttc aattggtacg tggatggcgt ggaggtgcac 840
aacgccaaga caaagccccg ggaggagcag tttaatagca cctacagagt ggtgtccgtg 900
ctgacagtgc tgcaccagga ttggctgaat ggcaaggagt ataagtgtaa ggtgagcaac 960
aagggcctgc ctagctccat cgagaagacc atctccaagg ccaagggcca gccaaagagag 1020
ccacaggtgt gcaccctgcc accaagccag gaggagatga caaagaatca ggtgtccctg 1080

tggtgtctgg tgaagggtt ctacccttcc gacatcgccg tggagtggga gtctaacggc	1140
cagccagaga acaattacaa gaccacacct ccagtgtctg actctgatgg cagcttcttt	1200
ctgtattctc ggctgaccgt ggataagagc agatggcagg agggcaacgt gttcagctgc	1260
tccgtgatgc acgaggccct gcacaaccac tatacacaga agtctctgag cctgtccctg	1320
ggcaag	1326

<210> 142
<211> 1252
<212> PRT
<213> Artificial sequence

<220>
<223> LILRB2 D1-4 -Fc IgG4 Hole-sc3x41BBL: in DSP 214 AA SEQUENCE

Gln Thr Gly Thr Ile Pro Lys Pro Thr Leu Trp Ala Glu Pro Asp Ser
1 5 10 15

Glu Ala Gln Glu Tyr Arg Leu Tyr Arg Glu Lys Lys Ser Ala Ser Trp
35 40 45

Pro Ser Ile Thr Trp Glu His Thr Gly Arg Tyr Gly Cys Gln Tyr Tyr
65 70 75 80

Thr Gly Ala Tyr Pro Lys Pro Thr Leu Ser Ala Gln Pro Ser Pro Val
100 105 110

Phe Gly Gly Phe Ile Leu Cys Lys Glu Gly Glu Glu Glu His Pro Gln

130

135

140

Cys Leu Asn Ser Gln Pro His Ala Arg Gly Ser Ser Arg Ala Ile Phe
 145 150 155 160

Ser Val Gly Pro Val Ser Pro Asn Arg Arg Trp Ser His Arg Cys Tyr
 165 170 175

Gly Tyr Asp Leu Asn Ser Pro Tyr Val Trp Ser Ser Pro Ser Asp Leu
 180 185 190

Leu Glu Leu Leu Val Pro Gly Val Ser Lys Lys Pro Ser Leu Ser Val
 195 200 205

Gln Pro Gly Pro Val Val Ala Pro Gly Glu Ser Leu Thr Leu Gln Cys
 210 215 220

Val Ser Asp Val Gly Tyr Asp Arg Phe Val Leu Tyr Lys Glu Gly Glu
 225 230 235 240

Arg Asp Leu Arg Gln Leu Pro Gly Arg Gln Pro Gln Ala Gly Leu Ser
 245 250 255

Gln Ala Asn Phe Thr Leu Gly Pro Val Ser Arg Ser Tyr Gly Gly Gln
 260 265 270

Tyr Arg Cys Tyr Gly Ala His Asn Leu Ser Ser Glu Cys Ser Ala Pro
 275 280 285

Ser Asp Pro Leu Asp Ile Leu Ile Thr Gly Gln Ile Arg Gly Thr Pro
 290 295 300

Phe Ile Ser Val Gln Pro Gly Pro Thr Val Ala Ser Gly Glu Asn Val
 305 310 315 320

Thr Leu Leu Cys Gln Ser Trp Arg Gln Phe His Thr Phe Leu Leu Thr
 325 330 335

Lys Ala Gly Ala Ala Asp Ala Pro Leu Arg Leu Arg Ser Ile His Glu
 340 345 350

Tyr Pro Lys Tyr Gln Ala Glu Phe Pro Met Ser Pro Val Thr Ser Ala
355 360 365

His Ala Gly Thr Tyr Arg Cys Tyr Gly Ser Leu Asn Ser Asp Pro Tyr
370 375 380

Leu Leu Ser His Pro Ser Glu Pro Leu Glu Leu Val Val Ser Gly Gly
385 390 395 400

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ser Lys
405 410 415

Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly
420 425 430

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
435 440 445

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu
450 455 460

Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
465 470 475 480

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg
485 490 495

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
500 505 510

Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu
515 520 525

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
530 535 540

Thr Leu Pro Pro Ser Gln Cys Glu Met Thr Lys Asn Gln Val Ser Leu
545 550 555 560

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

565

570

575

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 580 585 590

Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Arg Leu Thr Val Asp
 595 600 605

Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His
 610 615 620

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu
 625 630 635 640

Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Ala Ser Pro
 645 650 655

Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu
 660 665 670

Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val
 675 680 685

Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala
 690 695 700

Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu
 705 710 715 720

Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu
 725 730 735

Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala
 740 745 750

Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala
 755 760 765

Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala
 770 775 780

Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu
785 790 795 800

Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu
805 810 815

Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile
820 825 830

Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly
835 840 845

Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Ala Ser Pro Arg Leu Arg
850 855 860

Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu
865 870 875 880

Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile
885 890 895

Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser
900 905 910

Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val
915 920 925

Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg
930 935 940

Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu
945 950 955 960

Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val
965 970 975

Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe
980 985 990

Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His

995

1000

1005

Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
 1010 1015 1020

Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro
 1025 1030 1035

Ala Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly
 1040 1045 1050

Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Ala Ser Pro Arg Leu
 1055 1060 1065

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu
 1070 1075 1080

Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val
 1085 1090 1095

Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu
 1100 1105 1110

Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr
 1115 1120 1125

Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe
 1130 1135 1140

Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser
 1145 1150 1155

Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
 1160 1165 1170

Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser
 1175 1180 1185

Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His
 1190 1195 1200

Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala
 1205 1210 1215

Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu
 1220 1225 1230

Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser
 1235 1240 1245

Pro Arg Ser Glu
 1250

<210> 143
 <211> 3756
 <212> DNA
 <213> Artificial sequence

<220>
 <223> LILRB2 D1-4 -Fc IgG4 Hole-sc3x41BBL: in DSP 214 AA SEQUENCE NA
 SEQUENCE

<400> 143
 cagaccggca caatcccaa gcctaccctg tgggccgagc cagatagcgt gatcaccag 60
 ggctcccccg tgacactgtc ttgccagggc agcctggagg cacaggagta ccggctgtat 120
 agagagaaga agagcgcctc ctggatcacc cggatcagac ccgagctggt gaagaacggc 180
 cagtttcaca tcccttccat cacctgggag cacacaggcc ggtacggatg ccagtactat 240
 tctcgggcca gatggagcga gctgtccgac cccctggtgc tggatcatgac cggcgcctat 300
 ccaaagccca cactgtccgc ccagccttct ccagtggatga cctctggcgg cagagtgaca 360
 ctgcagtgtg agagccaggt ggccttcggc ggctttatcc tgtgcaagga gggcgaggag 420
 gagcaccccc agtgtctgaa tagccagcct cagccccggg gcagctccag agccatcttc 480
 tctgtgggcc ctgtgagccc aaaccggaga tgggtcccaca ggtgctacgg ctatgacctg 540
 aacagcccat acgtgtgggtc tagcccctct gatctgctgg agctgctggt gcctggcgtg 600
 agcaagaagc catctctgag cgtgcagcca ggccctgtgg tggcacctgg cgagtctctg 660
 accctgcagt gcgtgagcga cgtgggctac gatcggttcg tgctgtataa ggaggagag 720
 agggatctga ggcagctgcc aggcagacag cctcaggcag gactgtcca ggcaaacttt 780
 aactgggcc ccgtgagccg gagctacggc ggacagtacc gctgctatgg agcacacaat 840

ctgtcctctg agtgttctgc ccccagcgac cccctggaca tcctgatcac cggccagatc	900
aggggcacac cattcatcag cgtgcagcca ggaccaaccg tggcctccgg cgagaacgtg	960
acactgctgt gccagagctg gcgccagttc cacacctttc tgctgacaaa ggcaggagca	1020
gcagacgcac ctctgaggct gcgctccatc cacgagtacc caaagtatca ggccgagttt	1080
ccaatgagcc ccgtgacctc cgcccacgca ggcacataca gatgctatgg cagcctgaac	1140
agcgaccctt acctgctgag ccacccttcc gagccactgg agctgggtggg gtccggcggc	1200
ggcgggtctg gaggaggagg atccggagga ggaggatccg agtctaagta tggaccacca	1260
tgccctccat gtccagcacc tgagtttgag ggaggacctt ccgtgttcct gtttccccct	1320
aagccaaagg acacactgat gatctccagg acaccagagg tgacctgcgt ggtggtggac	1380
gtgtctcagg aggatcccga ggtgcagttc aactggtacg tggatggcgt ggaggtgcac	1440
aatgccaaga ccaagcctag ggaggagcag tttaactcca cataccgcgt ggtgtctgtg	1500
ctgaccgtgc tgcaccagga ttggctgaac ggcaaggagt ataagtgtaa ggtgagcaat	1560
aagggcctgc caagctccat cgagaagacc atctccaagg caaagggaca gccaaaggag	1620
cctcaggtgt atacactgcc acccagccag tgcgagatga ccaagaacca ggtgagcctg	1680
tcctgtgccg tgaagggtt ctacccatct gacatcgccg tggagtggga gagcaatggc	1740
cagcccgaga acaattataa gaccacacct ccagtgtctg actccgatgg ctctttcttt	1800
ctggtgtcca ggctgacagt ggataagtct cgctggcagg agggcaacgt gttttcttgt	1860
agcgtgatgc acgaggccct gcacaatcac tacaccaga agtccctgtc tctgagcctg	1920
ggcaagggcg gcggcggctc cggaggagga ggaagcgccg cctcccctag gctgcgcgag	1980
ggaccagagc tgagcccaga cgatccagca ggactgctgg acctgaggca gggaatgttc	2040
gcacagctgg tggcccagaa cgtgctgctg atcgacggcc ctctgtcttg gtacagcgat	2100
ccaggactgg caggcgtgag cctgacaggc ggactgtcct ataaggagga taccaaggag	2160
ctggtggtgg caaaggcagg cgtgtactac gtgttcttcc agctggagct gaggagagtg	2220
gtggcaggag agggatccgg atctgtgagc ctggccctgc acctgcagcc actgcggagc	2280
gccgcaggag cagccgccct ggccctgacc gtggacctgc cacctgcatc tagcgaggca	2340
cggaattctg ccttcggctt tcagggcaga ctgctgcacc tgagcgccgg acagaggctg	2400
ggagtgcacc tgcacacaga ggcaagggca agacacgcat ggagctgac acagggagca	2460

accgtgctgg gactgttccg cgtgaccct gagatcccag caggactgcc atcccccg	2520
tctgagggcg gcggcgggtc cggaggagga ggatctggcg gcggcggcag cgccgcctcc	2580
cccaggctgc gcgagggacc tgagctgtcc ccagacgac ctgccggcct gctggacctg	2640
agacagggaa tgtttgccca gctggtcgct cagaacgtgc tgctgattga cggccccctg	2700
tcctggtata gcgacctgg actggcaggc gtgtctctga caggcggact gagttacaaa	2760
gaagacacta aagaactggt cgtcgccaaa gccggcgtgt actacgtgtt cttccaactg	2820
gagctgagga gggtcgtcgc cggcgaaggc agcggctctg tgagcctggc cctgcacctg	2880
caaccactga ggagcgccgc cggcgccgcc gccctggccc tgactgtgga cctgccacca	2940
gcatcctctg aggcaaggaa ttccgccttc ggcttccagg gccggctgct gcacctgtct	3000
gccggacaga gactgggcgt ccacctgcat accgaagcca gagccaggca tgcctggcag	3060
ctgaccagg gcgccaccgt gctgggcctg ttcagagtga cccagaaat tccagcagga	3120
ctgccttccc caaggtctga gggaggagga ggaagtggcg gaggaggatc cggaggggga	3180
gggagcgccg cctccccaag actgagagag ggaccagagc tgtcccctga tgaccctgcc	3240
gggctgctgg acctgagaca aggcattgtc gccagctgg tcgcacaaaa cgtgctgtta	3300
attgacggcc cactgtcctg gtattccgac cctggcctgg ccggcgtgtc cctgacaggc	3360
ggcctgtctt acaaagaaga cacaaaagaa ctggtcgtcg cttaaagctgg cgtgtactac	3420
gtgttcttcc aattagaact gagaagggtc gtcgccggcg agggcagcgg gtctgtgagc	3480
ctggccctgc acctgcaacc gctgcggagc gccgccggcg ctgccgccct ggccctgaca	3540
gtggacctgc ctccagcaag ctccaggga aggaatagcg ctttcggctt tcaaggccgc	3600
ctgctgcacc tgtccgccgg acagcggctg ggcgtccacc tgcacaccga agccagagcc	3660
cgccatgcct ggcagctgac tcagggcgct accgtgctgg gcctgttccg cgtgacccca	3720
gagatccctg ccggcctgcc ctcccctcg tctgag	3756

<210> 144
 <211> 1052
 <212> PRT
 <213> Artificial sequence

<220>
 <223> LILRB2 D1-2- Fc IgG4 Hole- sc3x41BBL: in DSP 214 V1 AA SEQUENCE

<400> 144

Gln Thr Gly Thr Ile Pro Lys Pro Thr Leu Trp Ala Glu Pro Asp Ser
1 5 10 15

Val Ile Thr Gln Gly Ser Pro Val Thr Leu Ser Cys Gln Gly Ser Leu
20 25 30

Glu Ala Gln Glu Tyr Arg Leu Tyr Arg Glu Lys Lys Ser Ala Ser Trp
35 40 45

Ile Thr Arg Ile Arg Pro Glu Leu Val Lys Asn Gly Gln Phe His Ile
50 55 60

Pro Ser Ile Thr Trp Glu His Thr Gly Arg Tyr Gly Cys Gln Tyr Tyr
65 70 75 80

Ser Arg Ala Arg Trp Ser Glu Leu Ser Asp Pro Leu Val Leu Val Met
85 90 95

Thr Gly Ala Tyr Pro Lys Pro Thr Leu Ser Ala Gln Pro Ser Pro Val
100 105 110

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

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

Cys Leu Asn Ser Gln Pro His Ala Arg Gly Ser Ser Arg Ala Ile Phe
145 150 155 160

Ser Val Gly Pro Val Ser Pro Asn Arg Arg Trp Ser His Arg Cys Tyr
165 170 175

Gly Tyr Asp Leu Asn Ser Pro Tyr Val Trp Ser Ser Pro Ser Asp Leu
180 185 190

Leu Glu Leu Leu Val Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
195 200 205

Gly Gly Gly Gly Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys
210 215 220

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

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

Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp
260 265 270

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

Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
290 295 300

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

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

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

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

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

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

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

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

Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Gly Gly Gly Gly Ser Gly
435 440 445

Gly Gly Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu
450 455 460

Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe
465 470 475 480

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

Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu
500 505 510

Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val
515 520 525

Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu
530 535 540

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

Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala
565 570 575

Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu
580 585 590

His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala
595 600 605

Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly
610 615 620

Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg
625 630 635 640

Ser Glu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
645 650 655

Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp
660 665 670

Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu
675 680 685

Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser
690 695 700

Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys
705 710 715 720

Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val
725 730 735

Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly
740 745 750

Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
755 760 765

Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu
770 775 780

Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
785 790 795 800

Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
805 810 815

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
820 825 830

Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu Gly
835 840 845

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Ala
850 855 860

Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala
865 870 875 880

Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln
885 890 895

Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly
900 905 910

Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr
915 920 925

Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln
930 935 940

Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser
945 950 955 960

Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala
965 970 975

Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn
980 985 990

Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln
995 1000 1005

Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala
1010 1015 1020

Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val
1025 1030 1035

Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
1040 1045 1050

<210> 145
<211> 3156
<212> DNA
<213> Artificial sequence

<220>

<223> LILRB2 D1-2- Fc IgG4 Hole- sc3x41BBL: in DSP 214 V1 NA SEQUENCE

<400> 145

cagaccggca caatcccaa gcctaccctg tgggccgagc cagatagcgt gatcaccag	60
ggctcccccg tgacactgtc ttgccagggc agcctggagg cacaggagta ccggctgtat	120
agagagaaga agagcgcctc ctggatcacc cggatcagac ccgagctggt gaagaacggc	180
cagtttcaca tcccttccat cacctgggag cacacaggcc ggtacggatg ccagtactat	240
tctcgggcca gatggagcga gctgtccgac cccctgggtg tggtcatgac cggcgcctat	300
ccaaagccca cactgtccgc ccagccttct ccagtggatga cctctggcgg cagagtgaca	360
ctgcagtgtg agagccaggt ggccttcggc ggctttatcc tgtgcaagga gggcgaggag	420
gagcaccccc agtgtctgaa tagccagcct cagccccggg gcagctccag agccatcttc	480
tctgtgggccc ctgtgagccc aaaccggaga tgggtcccaca ggtgctacgg ctatgacctg	540
aacagcccat acgtgtggtc tagccccctc gatctgctgg agctgctggt gcctggcggc	600
ggcggctctg gaggaggagg atccggagga ggaggatccg agtctaagta tggaccacca	660
tgccctccat gtccagcacc tgagtttgag ggaggacctt ccgtgttcct gtttccccct	720
aagccaaagg acacactgat gatctccagg acaccagagg tgacctgcgt ggtggtggac	780
gtgtctcagg aggatcccga ggtgcagttc aactggtacg tggatggcgt ggaggtgcac	840
aatgccaaaga ccaagcctag ggaggagcag tttaactcca cataccgcgt ggtgtctgtg	900
ctgaccgtgc tgcaccagga ttggctgaac ggcaaggagt ataagtgtaa ggtgagcaat	960
aagggcctgc caagctccat cgagaagacc atctccaagg caaagggaca gccaaaggag	1020
cctcaggtgt atacactgcc acccagccag tgcgagatga ccaagaacca ggtgagcctg	1080
tcctgtgccg tgaagggctt ctacccatct gacatcgccg tggagtggga gagcaatggc	1140
cagcccgaga acaattataa gaccacacct ccagtgtctg actccgatgg ctctttcttt	1200
ctggtgtcca ggctgacagt ggataagtct cgctggcagg agggcaacgt gttttcttgt	1260
agcgtgatgc acgaggccct gcacaatcac tacaccaga agtccctgtc tctgagcctg	1320
ggcaagggcg gcggcggctc cggaggagga ggaagcgccg cctcccctag gctgcgcgag	1380
ggaccagagc tgagcccaga cgatccagca ggactgctgg acctgaggca gggaatgttc	1440
gcacagctgg tggcccagaa cgtgctgctg atcgacggcc ctctgtcttg gtacagcgat	1500

ccaggactgg caggcgtgag cctgacaggc ggactgtcct ataaggagga taccaaggag	1560
ctggtggtgg caaaggcagg cgtgtactac gtgttcttcc agctggagct gaggagagtg	1620
gtggcaggag agggatccgg atctgtgagc ctggccctgc acctgcagcc actgcggagc	1680
gccgcaggag cagccgccct ggccctgacc gtggacctgc cacctgcatc tagcgaggca	1740
cgggaattctg ctttcggctt tcagggcaga ctgctgcacc tgagcgccgg acagaggctg	1800
ggagtgcacc tgcacacaga ggcaaggga agacacgcat ggagctgac acaggagca	1860
accgtgctgg gactgttccg cgtgaccct gagatcccag caggactgcc atcccccg	1920
tctgagggcg gcggcgggtc cggaggagga ggatctggcg gcggcggcag cgccgcctcc	1980
cccaggctgc gcgagggacc tgagctgtcc ccagacgac ctgccggcct gctggacctg	2040
agacaggga tgtttgcca gctggctgct cagaacgtgc tgctgattga cggccccctg	2100
tcctggtata gcgacctgg actggcaggc gtgtctctga caggcggact gagttacaaa	2160
gaagacacta aagaactggt cgtcgccaaa gccggcgtgt actacgtgtt cttccaaactg	2220
gagctgagga gggtcgtcgc cggcgaaggc agcggctctg tgagcctggc cctgcacctg	2280
caaccactga ggagcgccgc cggcgccgcc gccctggccc tgactgtgga cctgccacca	2340
gcatcctctg aggcaaggaa ttccgccttc ggcttccagg gccggctgct gcacctgtct	2400
gccggacaga gactgggctt ccacctgcat accgaagcca gagccaggca tgcctggcag	2460
ctgaccagg gcgccaccgt gctgggcctg ttcagagtga cccagaaat tccagcagga	2520
ctgccttccc caaggtctga gggaggagga ggaagtggcg gaggaggatc cggaggggga	2580
gggagcgccg cctccccaag actgagagag ggaccagagc tgtcccctga tgacctgcc	2640
gggctgctgg acctgagaca aggcattgtt gccagctgg tcgcacaaaa cgtgctgtta	2700
attgacggcc cactgtcctg gtattccgac cctggcctgg ccggcgtgtc cctgacaggc	2760
ggcctgtctt acaaagaaga cacaaaaga ctggtcgtcg cttaaagctgg cgtgtactac	2820
gtgttcttcc aattagaact gagaagggtc gtcgccggcg agggcagcgg gtctgtgagc	2880
ctggccctgc acctgcaacc gctgcggagc gccgccggcg ctgccgccct ggccctgaca	2940
gtggacctgc ctccagcaag ctccaggga aggaatagcg ctttcggctt tcaaggccgc	3000
ctgctgcacc tgtccgccgg acagcggctg ggcgtccacc tgcacaccga agccagagcc	3060
cgccatgcct ggagctgac tcagggcgct accgtgctgg gcctgttccg cgtgacccca	3120

gagatccctg ccggcctgcc ctcccctcgg tctgag

3156

<210> 146
<211> 1076
<212> PRT
<213> Artificial sequence

<220>
<223> SIRPa -Fc Hole IgG4- sc3xCD40L: in TSP 112 and 217 AA SEQUENCE

<400> 146

Glu Glu Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala
1 5 10 15

Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro
20 25 30

Val Gly Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu
35 40 45

Ile Tyr Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser
50 55 60

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

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

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

Ser Val Arg Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala
115 120 125

Arg Ala Thr Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly
130 135 140

Phe Ser Pro Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu
145 150 155 160

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

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

His Ser Gln Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp
195 200 205

Pro Leu Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro
210 215 220

Thr Leu Glu Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn
225 230 235 240

Val Thr Cys Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr
245 250 255

Trp Leu Glu Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val
260 265 270

Thr Glu Asn Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val
275 280 285

Asn Val Ser Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu
290 295 300

His Asp Gly Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser
305 310 315 320

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

Ser Asn Glu Arg Asn Ile Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly
340 345 350

Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu
355 360 365

Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
370 375 380

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
385 390 395 400

Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
405 410 415

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
420 425 430

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
435 440 445

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
450 455 460

Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
465 470 475 480

Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Cys Glu Met Thr Lys Asn
485 490 495

Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile
500 505 510

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
515 520 525

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Arg
530 535 540

Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys
545 550 555 560

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
565 570 575

Ser Leu Ser Leu Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
580 585 590

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Lys Gly Asp Gln Asn
595 600 605

Pro Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr
610 615 620

Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn
625 630 635 640

Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly
645 650 655

Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala
660 665 670

Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Ser Leu Lys Ser Pro Gly
675 680 685

Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala
690 695 700

Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu
705 710 715 720

Gln Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val
725 730 735

Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu Gly Gly
740 745 750

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Lys Gly
755 760 765

Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser
770 775 780

Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met
785 790 795 800

Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys
805 810 815

Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn
820 825 830

Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Ser Leu Lys
835 840 845

Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His
850 855 860

Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val
865 870 875 880

Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro
885 890 895

Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys
900 905 910

Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
915 920 925

Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser Glu
930 935 940

Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr
945 950 955 960

Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu
965 970 975

Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe
980 985 990

Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu
995 1000 1005

Ser Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala
1010 1015 1020

Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile
 1025 1030 1035

His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe
 1040 1045 1050

Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe
 1055 1060 1065

Thr Ser Phe Gly Leu Leu Lys Leu
 1070 1075

<210> 147
 <211> 3228
 <212> DNA
 <213> Artificial sequence

<220>
 <223> SIRPa -Fc Hole IgG4- sc3xCD40L: in TSP 112 and 217 NA SEQUENCE

<400> 147
 gaggaggagc tgcaggtcat ccagcctgat aagtctgtgc tgggtggcagc aggagagaca 60
 gccacactgc ggtgcaccgc cacaagcctg atcccagtg gcccacatcca gtggttcagg 120
 ggagcaggac ctggaaggga gctgatctac aaccagaagg agggccactt tccaagagtg 180
 accacagtgt ccgacctgac caagcggaac aatatggatt tctctatcag aatcggcaat 240
 atcacacctg ccgacgccgg cacctactat tgcgtgaagt tcaggaaggg ctccccagac 300
 gatgtggagt ttaagagcgg agcaggcacc gagctgtccg tgagggccaa gccttctgcc 360
 ccagtggatga gcggaccagc agccagagcc accccacagc acacagtgag cttcacctgt 420
 gagagccacg gcttttcccc ccgggacatc accctgaagt ggttcaagaa cggcaatgag 480
 ctgtccgact ttacagacaa cgtggacccc gtgggcgagt ctgtgagcta ttccatccac 540
 tctacagcca aggtgggtgct gacccgcgag gacgtgcaca gccaggtcat ctgagaggtg 600
 gcacacgtga ccctgcaggg cgatcccctg aggggcacag ccaatctgag cgagacaatc 660
 agagtgcccc ctacactgga ggtgaccag cagcccgtgc gcgcagagaa ccaagtgaat 720
 gtgacatgtc aggtgcggaa gttctaccct cagagactgc agctgacctg gctggagaac 780
 ggcaacgtga gccggaccga gacagccagc accgtgacag agaacaagga cggcacatat 840
 aattggatgt cttggctgct ggtgaacgtg agcgcgccaca gggacgatgt gaagctgacc 900

tgccaggtgg agcacgacgg acagccagcc gtgtctaaga gccacgatct gaaggtgagc	960
gcccacccta aggagcaggg ctccaacaca gccgccgaga ataccggcag caacgagcgg	1020
aatatctacg gaggaggagg ctccggagga ggaggctccg agtctaagta tggaccacca	1080
tgccctccat gtccagcacc tgagttcgag ggaggaccta gcgtgttcct gtttccccct	1140
aagccaaagg acaccctgat gatctccaga acaccagagg tgacctgcgt ggtggtggac	1200
gtgtctcagg aggaccccga ggtgcagttt aactggtacg tggatggcgt ggaggtgcac	1260
aatgccaaaga ccaagccccg ggaggagcag ttcaattcca cataccgcgt ggtgtctgtg	1320
ctgaccgtgc tgcaccagga ctggctgaac ggcaaggagt ataagtgtaa ggtgagcaat	1380
aagggcctgc caagctccat cgagaaaacc atcagcaagg caaagggaca gccccgggag	1440
cctcaggtgt atacactgcc accctcccag tgcgagatga ccaagaacca ggtgagcctg	1500
tcctgtgccg tgaagggctt ttacccatct gacatcgccg tggagtggga gagcaatggc	1560
cagcccgaga acaattataa gaccacacct ccagtgtctg actccgatgg ctctttcttt	1620
ctggtgtcca ggctgacagt ggataagtct cgctggcagg agggcaacgt gttctcttgt	1680
agcgtgatgc acgaggccct gcacaatcac tacacccaaa agtccctgtc tctgagcctg	1740
ggcaagggcg gcggcggctc cggcggagga ggctctggcg gcggcggcag cggaggcggc	1800
ggctcccaga agggcgatca gaacccccag atcgccgccc acgtgatctc cgaggcctct	1860
agcaagacca catctgtgct gcagtgggcc gagaagggt actatacaat gagcaacaat	1920
ctggtgacct tggagaacgg caagcagctg acagtgaagc ggcagggcct gtactatctc	1980
tatgcccagg tgaccttctg ctccaataga gaggcctcct ctgaggcccc ctttatcgcc	2040
tccctgtctc tgaagtctcc tggccggttc gagagaatcc tgctgagggc agcaaacaca	2100
cacagctccg ccaagccctg tggccagcag tctatccacc tgggcggcgt gttcgagctg	2160
cagccaggag ccagcgtggt tgtgaatgtg accgacccta gccaggtgtc ccacggcacc	2220
ggcttcacca gcttcggcct gctgaagctg ggcggcggcg gctctggcgg aggaggcagc	2280
ggaggaggag gctcccagaa aggcgatcag aaccctcaga ttgctgcccc cgtgatcagc	2340
gaggcctcta gcaagaccac atccgtgctg cagtgggctg aaaaaggata ctatacaatg	2400
tctaataatc tggtgaccct ggagaatggc aagcagctga ccgtcaagag acagggcctg	2460
tattatatct acgcccaggt gaccttttgc agcaatcgcg aggcctcctc tcaggctcca	2520

Ser Arg Ala Arg Trp Ser Glu Leu Ser Asp Pro Leu Val Leu Val Met
85 90 95

Thr Gly Ala Tyr Pro Lys Pro Thr Leu Ser Ala Gln Pro Ser Pro Val
100 105 110

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

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

Cys Leu Asn Ser Gln Pro His Ala Arg Gly Ser Ser Arg Ala Ile Phe
145 150 155 160

Ser Val Gly Pro Val Ser Pro Asn Arg Arg Trp Ser His Arg Cys Tyr
165 170 175

Gly Tyr Asp Leu Asn Ser Pro Tyr Val Trp Ser Ser Pro Ser Asp Leu
180 185 190

Leu Glu Leu Leu Val Pro Gly Val Ser Lys Lys Pro Ser Leu Ser Val
195 200 205

Gln Pro Gly Pro Val Val Ala Pro Gly Glu Ser Leu Thr Leu Gln Cys
210 215 220

Val Ser Asp Val Gly Tyr Asp Arg Phe Val Leu Tyr Lys Glu Gly Glu
225 230 235 240

Arg Asp Leu Arg Gln Leu Pro Gly Arg Gln Pro Gln Ala Gly Leu Ser
245 250 255

Gln Ala Asn Phe Thr Leu Gly Pro Val Ser Arg Ser Tyr Gly Gly Gln
260 265 270

Tyr Arg Cys Tyr Gly Ala His Asn Leu Ser Ser Glu Cys Ser Ala Pro
275 280 285

Ser Asp Pro Leu Asp Ile Leu Ile Thr Gly Gln Ile Arg Gly Thr Pro
290 295 300

Phe Ile Ser Val Gln Pro Gly Pro Thr Val Ala Ser Gly Glu Asn Val
305 310 315 320

Thr Leu Leu Cys Gln Ser Trp Arg Gln Phe His Thr Phe Leu Leu Thr
325 330 335

Lys Ala Gly Ala Ala Asp Ala Pro Leu Arg Leu Arg Ser Ile His Glu
340 345 350

Tyr Pro Lys Tyr Gln Ala Glu Phe Pro Met Ser Pro Val Thr Ser Ala
355 360 365

His Ala Gly Thr Tyr Arg Cys Tyr Gly Ser Leu Asn Ser Asp Pro Tyr
370 375 380

Leu Leu Ser His Pro Ser Glu Pro Leu Glu Leu Val Val Ser Gly Gly
385 390 395 400

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ser Lys
405 410 415

Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly
420 425 430

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
435 440 445

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu
450 455 460

Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
465 470 475 480

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg
485 490 495

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
500 505 510

Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu
515 520 525

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
530 535 540

Thr Leu Pro Pro Ser Gln Cys Glu Met Thr Lys Asn Gln Val Ser Leu
545 550 555 560

Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
565 570 575

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
580 585 590

Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Arg Leu Thr Val Asp
595 600 605

Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His
610 615 620

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu
625 630 635 640

Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
645 650 655

Ser Gly Gly Gly Gly Ser Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala
660 665 670

Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln
675 680 685

Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu
690 695 700

Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile
705 710 715 720

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

Pro Phe Ile Ala Ser Leu Ser Leu Lys Ser Pro Gly Arg Phe Glu Arg
740 745 750

Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly
755 760 765

Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala
770 775 780

Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr
785 790 795 800

Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu Gly Gly Gly Gly Ser Gly
805 810 815

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Lys Gly Asp Gln Asn Pro
820 825 830

Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser
835 840 845

Val Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu
850 855 860

Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu
865 870 875 880

Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser
885 890 895

Ser Gln Ala Pro Phe Ile Ala Ser Leu Ser Leu Lys Ser Pro Gly Arg
900 905 910

Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys
915 920 925

Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln
930 935 940

Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser
945 950 955 960

His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu Gly Gly Gly
965 970 975

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Lys Gly Asp
980 985 990

Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser Lys
995 1000 1005

Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met
1010 1015 1020

Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val
1025 1030 1035

Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys
1040 1045 1050

Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu
1055 1060 1065

Ser Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala
1070 1075 1080

Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile
1085 1090 1095

His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe
1100 1105 1110

Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe
1115 1120 1125

Thr Ser Phe Gly Leu Leu Lys Leu
1130 1135

<210> 149
<211> 3408
<212> DNA
<213> Artificial sequence

<220>

<223> LILRB2-Fc -Fc Hole IgG4- sc3xCD40L: in TSP 218 NA SEQUENCE

<400> 149

cagaccggca caatccctaa gccaaccctg tgggccgagc ctgatagcgt gatcaccag	60
ggctccccag tgacactgag ctgccagggc tccctggagg cacaggagta ccggctgtat	120
agagagaaga agtctgccag ctggatcacc cggatcagac ctgagctggt gaagaacggc	180
cagttccaca tcccatctat cacctgggag cacacaggcc ggtacggatg ccagtactat	240
agccggggcca gatggtctga gctgagcgac cccctggtgc tggatcatgac cggagcctat	300
cccaagccta cactgtctgc ccagccaagc ccagtgggtga cctctggcgg cagagtgaca	360
ctgcagtgtg agagccaggt ggccttcggc ggctttatcc tgtgcaagga gggcgaggag	420
gagcaccac agtgtctgaa tagccagcca cacgccaggg gcagctcccg cgccatcttc	480
agcgtgggac ccgtgagccc aaaccggaga tggctccacc gctgctacgg ctatgacctg	540
aacagccctt acgtgtgggtc tagcccaagc gatctgctgg agctgctggt gcccggcgtg	600
agcaagaagc cttccctgtc tgtgcagcct ggaccagtgg tggcacctgg agagtccttg	660
accctgcagt gcgtgagcga cgtgggctac gatcggtttg tgctgtataa ggaggagag	720
agggatctga ggcagctgcc aggcagacag ccacaggccg gcctgtcca ggccaacttc	780
accctgggcc cagtgagccg gtcctatggc ggccagtaca gatgctatgg cgcccacaat	840
ctgtcctctg agtgttccgc cccaagcgac cccctggaca tcctgatcac cggccagatc	900
aggggcacac cttttatcag cgtgcagcca ggacctaccg tggcctccgg cgagaacgtg	960
acactgctgt gccagagctg gcgccagttc cacacctttc tgctgacaaa ggcaggagca	1020
gcagacgcac cactgaggct gcgctccatc cacgagtacc ccaagtatca ggccgagttc	1080
ccaatgtccc cagtgacctc tgcccacgca ggcacataca ggtgttatgg cagcctgaac	1140
agcgacccct acctgctgtc tcaccctagc gagccactgg agctgggtgg gtctggagga	1200
ggaggcagcg gcggaggagg ctccggaggc ggcggctctg agagcaagta tggaccacct	1260
tgcccacat gtccagcacc agagttcgag ggaggaccaa gcgtgttcct gtttcctcca	1320
aagcctaagg acaccctgat gatctccgc acccctgagg tgacatgcgt ggtggtggac	1380

gtgtctcagg aggaccccg ggtgcagttt aactggtacg tggatggcgt ggaggtgcac	1440
aatgccaaaga ccaagccccg ggaggagcag ttcaactcta cctacagagt ggtgagcgtg	1500
ctgacagtgc tgcaccagga ctggctgaac ggcaaggagt ataagtgtaa ggtgagcaat	1560
aagggcctgc ctagctccat cgagaaaacc atcagcaagg caaagggaca gcccaggag	1620
cctcaggtgt ataccctgcc cccttcccag tgcgagatga caaagaacca ggtgtccctg	1680
tcttgtgccg tgaagggtt ttacccatcc gacatcgccg tggagtggga gtctaattggc	1740
cagcccgaga acaattataa gaccacacca cccgtgctgg actccgatgg ctctttcttt	1800
ctggtgagca ggctgaccgt ggataagtcc cgctggcagg agggcaacgt gttcagctgc	1860
tccgtgatgc acgaggccct gcacaatcac tacacacaga agtctctgag cctgtccctg	1920
ggcaagggcg gcggcggctc tggcggcggc ggacgcggcg gcggcggctc cggaggaggc	1980
ggctctcaga agggcgatca gaacccccag atcgccgcc acgtgatcag cgaggcctct	2040
agcaagacca catccgtgct gcagtgggcc gagaagggt actataccat gagcaacaat	2100
ctggtgacac tggagaacgg caagcagctg accgtgaaga ggacgggcct gtactatatc	2160
tacgcccagg tgacattctg ctccaatcgc gaggcctcct ctcaggcccc ttttatcgcc	2220
tctctgagcc tgaagtctcc aggccggtt gagagaatcc tgctgagggc agcaaacacc	2280
cacagctccg ccaagccttg tggccagcag tctatccacc tgggcggcgt gttcagctg	2340
cagccaggag ccagcgtgtt tgtgaatgtg acagacccta gccaggtgtc ccacggcacc	2400
ggcttcacca gcttcggcct gctgaagctg ggcgcgggcg gcagcggggg cggcggctcc	2460
ggagggggag gctctcagaa aggcgatcag aatccacaga ttgctgcca cgtgatctct	2520
gaggcctcta gcaagaccac aagcgtgctg cagtgggctg aaaaaggata ctataccatg	2580
tctaataatc tggtgacact ggagaatggc aagcagctga ctgtcaagag acagggcctg	2640
tattacatct acgctcaggt gacattttgc agcaatagag aggcctcctc tcaggctccc	2700
ttcatcgcct ccctgtctct gaagtcccct ggacaggttg agcgcatcct gctgagagcc	2760
gccaatactc acagctccgc caagccatgt ggacagcagt ccattcacct gggcggcgtg	2820
ttcagagtgc aaccaggagc cagcgtgttc gtgaatgtga cagaccctc tcaggtgagc	2880
cacggcaccg gcttcaccag cttcggcctg ctgaagctgg gtggcggcgg cagcggcggg	2940
ggcggctccg gaggcggagg ctctcagaag ggcgatcaga atcctcagat tgcagcccac	3000

gtgatctccg aggcctctag caagaccaca tctgtgctgc agtgggctga gaaaggctac 3060
 tataccatgt ctaacaatct ggtgacactg gagaacggca agcaactgac tgtcaaaaga 3120
 cagggcctgt attatatcta cgctcaagtg acattctgca gcaatcggga ggcctcctct 3180
 caggcaccct tcatcgccag cctgtccctg aagtcccctg gccggttcga gagaatcctg 3240
 ttaagagccg ccaatacaca cagctccgcc aaaccatgtg gacagcagag catacacctg 3300
 ggcggcgtgt tcgagctgca accgggagcc tccgtgtttg tcaatgtgac agacccatcc 3360
 caggtgtctc acggcaccgg cttcaccagc ttcggcctgc tgaagctg 3408

<210> 150
 <211> 367
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Siglec-Fc Knob IgG4: in TSP 401 and 403 AA SEQUENCE

<400> 150

Asp Gly Arg Phe Trp Ile Arg Val Gln Glu Ser Val Met Val Pro Glu
 1 5 10 15

Gly Leu Ser Ile Ser Val Pro Cys Ser Phe Ser Tyr Pro Arg Gln Asp
 20 25 30

Trp Thr Gly Ser Thr Pro Ala Tyr Gly Tyr Trp Phe Lys Ala Val Thr
 35 40 45

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

Val Glu Met Ser Thr Arg Gly Arg Phe Gln Leu Thr Gly Asp Pro Ala
 65 70 75 80

Lys Gly Asn Cys Ser Leu Val Ile Arg Asp Ala Gln Met Gln Asp Glu
 85 90 95

Ser Gln Tyr Phe Phe Arg Val Glu Arg Gly Ser Tyr Val Arg Tyr Asn
 100 105 110

Phe Met Asn Asp Gly Phe Phe Leu Lys Val Thr Ala Leu Thr Gln Lys
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ser Lys Tyr Gly Pro
130 135 140

Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val
145 150 155 160

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
165 170 175

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
180 185 190

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
195 200 205

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
210 215 220

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

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
245 250 255

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro
260 265 270

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp Cys Leu
275 280 285

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
290 295 300

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
305 310 315 320

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
325 330 335

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
340 345 350

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
355 360 365

<210> 151
<211> 1101
<212> DNA
<213> Artificial sequence

<220>
<223> Siglec-Fc Knob IgG4: in TSP 401 and 403 NA SEQUENCE

<400> 151
gatggccggt tttggatcag agtgcaggag tccgtgatgg tgcctgaggg cctgtctatc 60
agcgtgccat gtcctttctc ttaccccaga caggactgga ccggctctac acccgcttac 120
ggctatttgt ttaaggccgt gaccgagaca acaaagggcg cccctgtggc cacaaaccac 180
cagagcagag aggtggagat gtccacccgg ggcagattcc agctgacagg cgaccccgcc 240
aagggcaatt gtagcctggg catcaggagc gccagatgc aggatgagtc tcagtacttc 300
tttaggggtg agcgcggcag ctacgtgctc tataacttta tgaatgatgg cttctttctg 360
aaggtgaccg ccctgacaca gaaggaggga ggaggctccg gcggaggagg cagcgagtcc 420
aagtatggac caccttgccc accatgtcct gcaccagagt tcgaggaggagg acctagcgtg 480
ttcctgtttc ctcaaagcc aaaggacacc ctgatgatca gcaggactcc tgaggtgaca 540
tgcgtgggtg tggacgtgtc ccaggaggac cccgaggtgc agttcaactg gtatgtggat 600
ggcgtggagg tgcacaatgc caagacaaag ccacgggagg agcagtttaa ctctacctac 660
agagtgggtg gcgtgctgac agtgctgcac caggattggc tgaacggcaa ggagtataag 720
tgtaagggtg ctaataaggg cctgcccagc tccatcgaga aaaccatcag caaggcaaag 780
ggacagcccc gggagcctca ggtgtgcacc ctgccccctt cccaggaggga gatgacaaag 840
aaccaggtgt ctctgtgggt tctgggtgaag ggcttctacc caagcgacat cgccgtggag 900
tgggagtcca atggccagcc cgagaacaat tacaagacca caccaccgt gctggactcc 960
gatggctctt tctttctgta ttccaggctg accgtggata agtctcgctg gcaggagggc 1020
aacgtgtttt cttgcagcgt gatgcacgag gccctgcaca atcactatac acagaagtcc 1080

ctgtctctga gcctgggcaa g

1101

<210> 152

<211> 351

<212> PRT

<213> Artificial sequence

<220>

<223> TIGIT-Fc Knob IgG4: in TSP 501 and 503 AA SEQUENCE

<400> 152

Met Thr Gly Thr Ile Glu Thr Thr Gly Asn Ile Ser Ala Glu Lys Gly
1 5 10 15

Gly Ser Ile Ala Leu Gln Cys His Leu Ser Ser Thr Thr Ala Gln Val
20 25 30

Thr Gln Val Asn Trp Glu Gln Gln Asp Gln Leu Leu Ala Ile Ser Asn
35 40 45

Ala Asp Leu Gly Trp His Ile Ser Pro Ser Phe Lys Asp Arg Val Ala
50 55 60

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

Thr Gly Glu Tyr Phe Cys Ile Tyr His Thr Tyr Pro Asp Gly Thr Tyr
85 90 95

Thr Gly Arg Ile Phe Leu Glu Val Leu Glu Ser Ser Val Ala Glu His
100 105 110

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

Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val
130 135 140

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
145 150 155 160

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
165 170 175

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
180 185 190

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
195 200 205

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
210 215 220

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
225 230 235 240

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro
245 250 255

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp Cys Leu
260 265 270

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
275 280 285

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
290 295 300

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
305 310 315 320

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
325 330 335

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
340 345 350

<210> 153
<211> 1053
<212> DNA
<213> Artificial sequence

<220>

<223> TIGIT-Fc Knob IgG4: in TSP 501 and 503 NA SEQUENCE

<400> 153

```
atgaccggca caatcgagac aacaggcaac atctctgccg agaaggagg cagcatcgcc      60
ctgcagtgcc acctgagcag caccacagcc caggtgaccc aggtgaactg ggagcagcag      120
gaccagctgc tggccatctc caatgccgat ctgggctggc acatcagccc ctcctttaag      180
gatagggtgg cacctggacc aggcctgggc ctgaccctgc agagcctgac cgtgaatgac      240
acaggcgagt acttctgtat ctaccacaca tctcctgatg gcacctatac aggcagaatc      300
tttctggagg tgctggagtc tagcgtggcc gagcacggag gaggaggctc cggaggagga      360
ggctctgaga gcaagtacgg accaccttgc ccaccatgtc cagcacctga gttcgaggga      420
ggacctagcg tgttctgttt tcctccaaag ccaaaggaca ccctgatgat cagcaggacc      480
cctgagggtga catgcgtggt ggtggacgtg tcccaggagg accccgaggt gcagttcaac      540
tggtatgtgg atggcgtgga ggtgcacaat gccaaagaaa agcccaggga ggagcagttt      600
aactccacct accgctggtg gtctgtgctg acagtgtgtc accaggactg gctgaacggc      660
aaggagtata agtghtaagg gtctaataag ggcctgccct cctctatcga gaaaaccatc      720
agcaaggcca agggccagcc aagagagcca caggtgtgca ccctgccacc ttcccaggag      780
gagatgacaa agaaccaggt gtctctgtgg tgtctggtga agggcttcta cccatctgac      840
atcgccgtgg agtgggagag caatggccag cccgagaaca attacaagac cacaccaccc      900
gtgctggaca gcgatggctc cttctttctg tatagccggc tgaccgtgga taagtccaga      960
tggcaggagg gcaacgtgtt ttcctgtctt gtgatgcacg aggccctgca caatcactat     1020
acacagaaga gcctgtccct gtctctgggc aag                                     1053
```

<210> 154

<211> 873

<212> PRT

<213> Artificial sequence

<220>

<223> PD1- Fc Hole IgG4-sc3xCD40L: in TSP222 and 403 and 503 AA SEQUENCE

<400> 154

```
Asp Ser Pro Asp Arg Pro Trp Asn Pro Pro Thr Phe Ser Pro Ala Leu
1           5           10          15
```

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

Asn Thr Ser Glu Ser Phe Val Leu Asn Trp Tyr Arg Met Ser Pro Ser
35 40 45

Asn Gln Thr Asp Lys Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro
50 55 60

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

Phe His Met Ser Val Val Arg Ala Arg Arg Asn Asp Ser Gly Thr Tyr
85 90 95

Leu Cys Gly Ala Ile Ser Leu Ala Pro Lys Ala Gln Ile Lys Glu Ser
100 105 110

Leu Arg Ala Glu Leu Arg Val Thr Glu Arg Arg Ala Glu Val Pro Thr
115 120 125

Ala His Pro Ser Pro Ser Pro Arg Pro Ala Gly Gln Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
145 150 155 160

Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro
165 170 175

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
180 185 190

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

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
210 215 220

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val

225					230						235				240
Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser
				245					250					255	
Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys
			260					265					270		
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Cys
		275					280					285			
Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Ser	Cys	Ala	Val	Lys	Gly	Phe
	290					295					300				
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
305					310					315					320
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe
				325					330					335	
Phe	Leu	Val	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly
			340					345					350		
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
	355						360					365			
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Gly	Gly	Gly	Gly	Ser
	370					375					380				
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gln
385					390					395					400
Lys	Gly	Asp	Gln	Asn	Pro	Gln	Ile	Ala	Ala	His	Val	Ile	Ser	Glu	Ala
			405					410						415	
Ser	Ser	Lys	Thr	Thr	Ser	Val	Leu	Gln	Trp	Ala	Glu	Lys	Gly	Tyr	Tyr
			420					425					430		
Thr	Met	Ser	Asn	Asn	Leu	Val	Thr	Leu	Glu	Asn	Gly	Lys	Gln	Leu	Thr
	435						440					445			

Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys
450 455 460

Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Ser
465 470 475 480

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

Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly
500 505 510

Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn Val Thr
515 520 525

Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu
530 535 540

Leu Lys Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
545 550 555 560

Gly Ser Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile
565 570 575

Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys
580 585 590

Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys
595 600 605

Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val
610 615 620

Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala
625 630 635 640

Ser Leu Ser Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg
645 650 655

Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile

660

665

670

His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val
 675 680 685

Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser
 690 695 700

Phe Gly Leu Leu Lys Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 705 710 715 720

Gly Gly Gly Gly Ser Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala
 725 730 735

His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp
 740 745 750

Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu
 755 760 765

Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr
 770 775 780

Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro
 785 790 795 800

Phe Ile Ala Ser Leu Ser Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile
 805 810 815

Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln
 820 825 830

Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser
 835 840 845

Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly
 850 855 860

Phe Thr Ser Phe Gly Leu Leu Lys Leu
 865 870

<210> 155
<211> 2619
<212> DNA
<213> Artificial sequence

<220>

<223> PD1- Fc Hole IgG4-sc3xCD40L: in TSP222 and 403 and 503 AA
SEQUENCE

<400> 155

gacagcccag atagaccttg gaatccacct accttctccc ccgccctgct ggtggtgaca	60
gagggcgata acgccacctt cacatgctct tttagcaaca cctccgagtc ttttgtgctg	120
aattggtaca ggatgagccc ttccaaccag acagacaagc tggccgcatt ccctgaggac	180
cgctcccagc caggacagga ttctcggttc agagtgacct agctgcaaaa tggccgggac	240
tttcacatga gcgtgggtgag agcccggaga aacgattccg gcacatacct gtgcggagcc	300
atctctcttg ccccaaaggc acagatcaag gagtccctgc gggcagagct gagagtgacc	360
gagaggaggg cagaggtgcc cacagcacac ccatctccta gcccacggcc cgcaggacag	420
ggaggaggag gcagcggggg aggaggctcc gagtctaagt acggaccacc atgccctcca	480
tgtcctgcac cagagttcga gggaggacca tccgtgttcc tgtttccacc taagcctaag	540
gacaccctga tgatcagccg gaccccagag gtgacatgcg tgggtggtgga cgtgagccag	600
gaggaccccc aggtgcagtt taattggtat gtggatggcg tggaggtgca caacgccaag	660
accaagccca gggaggagca gttcaacagc acctaccgcg tgggtgtccgt gctgacagtg	720
ctgcaccagg actggctgaa tggcaaggag tataagtgta aggtgtccaa caagggcctg	780
cctagctcca tcgagaaaac catcagcaag gcaaagggac agccacggga gccacaggtg	840
tacaccctgc caccaagcca gtgcgagatg acaaagaatc aggtgagcct gtcctgtgcc	900
gtgaagggct tttacccttc cgacatcgcc gtggagtggg agtctaacgg ccagccagag	960
aacaattata agaccacacc tccagtgtcg gactccgatg gctctttctt tctggtgtct	1020
aggctgaccg tggataagag ccgctggcag gagggcaacg tgttcagctg cagcgtgatg	1080
cacgaggccc tgcacaacca ctatacaca aagtccctgt ctctgagcct gggcaagggc	1140
ggcggcggca gcggcggagg aggctccgga ggcggcggct ctggcggcgg cggcagccag	1200
aagggcgatc agaatcctca gatcgccgcc cacgtgatca gcgaggcctc tagcaagacc	1260
acatccgtgc tgcatgtggg cgagaagggc tactatacca tgagcaacaa tctggtgaca	1320

ctggagaatg gcaagcagct gaccgtgaag cggcagggcc tgtactatat ctacgcccag	1380
gtgacattct gcagcaacag agaggcctcc tctcaggccc cttttatcgc ctctctgagc	1440
ctgaagtctc caggccggtt cgagagaatc ctgctgaggg cagcaaacac ccacagctcc	1500
gccaagcctt gtggccagca gtctatccac ctgggcggcg tgttcgagct gcagccagga	1560
gccagcgtgt ttgtgaatgt gacagaccct agccaggtgt cccacggcac cggcttcacc	1620
agcttcggcc tgctgaagct gggcggcggc ggcagcgggg gcggcggctc cggaggggga	1680
ggctctcaga aaggcgatca gaatccacag attgctgccc acgtgatctc tgaggcctct	1740
agcaagacca caagcgtgct gcagtgggct gaaaaaggat actataccat gtctaataat	1800
ctggtgacac tggagaatgg caagcagctg actgtcaaga gacagggcct gtattacatc	1860
tacgctcagg tgacattttg cagcaataga gaggcctcct ctcaggctcc cttcatcgcc	1920
tccctgtctc tgaagtcccc tggcagggtt gagcgcattc tgctgagagc cgccaatact	1980
cacagctccg ccaagccatg tggacagcag tccattcacc tgggcggcgt gttcgagctg	2040
caaccaggag ccagcgtgtt cgtgaatgtg acagaccct ctcaggtgag ccacggcacc	2100
ggcttcacca gcttcggcct gctgaagctg ggtggcggcg gcagcggcgg gggcggctcc	2160
ggaggcggag gctctcagaa gggcgatcag aatcctcaga ttgcagcca cgtgatctcc	2220
gaggcctcta gcaagaccac atctgtgctg cagtgggctg agaaaggcta ctataccatg	2280
tctaacaatc tggtgacact ggagaacggc aagcaactga ctgtcaaaag acagggcctg	2340
tattatatct acgctcaagt gacattctgc agcaatcggg aggcctcctc tcaggcaccc	2400
ttcatcgcca gcctgtccct gaagtcccct ggccggttcg agagaatcct gttaagagcc	2460
gccaatacac acagctccgc caaacatgt ggacagcaga gcatacacct gggcggcgtg	2520
ttcgagctgc aaccgggagc ctccgtgttt gtcaatgtga cagacccatc ccaggtgtct	2580
cacggcaccg gcttcaccag cttcggcctg ctgaagctg	2619

<210> 156
 <211> 961
 <212> PRT
 <213> Artificial sequence

<220>
 <223> TIGIT-Fc Hole IgG4-sc3x4-1BBL: in TSP 501V1 AA SEQUENCE

<400> 156

Met Thr Gly Thr Ile Glu Thr Thr Gly Asn Ile Ser Ala Glu Lys Gly
1 5 10 15

Gly Ser Ile Ala Leu Gln Cys His Leu Ser Ser Thr Thr Ala Gln Val
20 25 30

Thr Gln Val Asn Trp Glu Gln Gln Asp Gln Leu Leu Ala Ile Ser Asn
35 40 45

Ala Asp Leu Gly Trp His Ile Ser Pro Ser Phe Lys Asp Arg Val Ala
50 55 60

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

Thr Gly Glu Tyr Phe Cys Ile Tyr His Thr Tyr Pro Asp Gly Thr Tyr
85 90 95

Thr Gly Arg Ile Phe Leu Glu Val Leu Glu Ser Ser Val Ala Glu His
100 105 110

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

Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val
130 135 140

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
145 150 155 160

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
165 170 175

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
180 185 190

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
195 200 205

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
210 215 220

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
225 230 235 240

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
245 250 255

Pro Ser Gln Cys Glu Met Thr Lys Asn Gln Val Ser Leu Ser Cys Ala
260 265 270

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
275 280 285

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
290 295 300

Asp Gly Ser Phe Phe Leu Val Ser Arg Leu Thr Val Asp Lys Ser Arg
305 310 315 320

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
325 330 335

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Gly
340 345 350

Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Ala Ser Pro Arg Leu Arg
355 360 365

Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu
370 375 380

Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile
385 390 395 400

Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser
405 410 415

Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val
420 425 430

Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg
435 440 445

Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu
450 455 460

Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val
465 470 475 480

Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe
485 490 495

Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His
500 505 510

Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly
515 520 525

Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly
530 535 540

Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly Gly Gly Gly
545 550 555 560

Ser Gly Gly Gly Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro
565 570 575

Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
580 585 590

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
595 600 605

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
610 615 620

Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala
625 630 635 640

Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala
645 650 655

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
660 665 670

Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro
675 680 685

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
690 695 700

Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr
705 710 715 720

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val
725 730 735

Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser
740 745 750

Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
755 760 765

Gly Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser
770 775 780

Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala
785 790 795 800

Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp
805 810 815

Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser
820 825 830

Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr
835 840 845

Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly
850 855 860

Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala
865 870 875 880

Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser
885 890 895

Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His
900 905 910

Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg
915 920 925

Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu
930 935 940

Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser
945 950 955 960

Glu

<210> 157
<211> 2883
<212> DNA
<213> Artificial sequence

<220>
<223> TIGIT-Fc Hole IgG4-sc3x4-1BBL: in TSP 501V1 NA SEQUENCE

<400> 157
atgaccggca caatcgagac aacaggcaac atctctgccg agaagggagg cagcatcgcc 60
ctgcagtgcc acctgagcag caccacagcc caggtgaccc aggtgaactg ggagcagcag 120
gaccagctgc tggccatctc caatgccgat ctgggctggc acatcagccc ctcctttaag 180
gatagggtgg cacctggacc aggcctgggc ctgaccctgc agagcctgac cgtgaatgac 240
acaggcgagt acttctgtat ctaccacaca tctcctgatg gcacctatac aggcagaatc 300
tttctggagg tgctggagtc tagcgtggcc gagcacggag gaggaggatc cggaggagga 360
ggatccgagt ctaagtatgg accacatgc cctccatgtc cagcacctga gtttgaggga 420
ggaccttccg tgttcctgtt tccccctaag ccaaaggaca cactgatgat ctccaggaca 480

ccagaggtga cctgcgtggt ggtggacgtg tctcaggagg atcccagaggt gcagttcaac	540
tggtacgtgg atggcgtgga ggtgcacaat gccaaagacca agcctaggga ggagcagttt	600
aactccacat accgcgtggt gtctgtgctg accgtgctgc accaggattg gctgaacggc	660
aaggagtata agtgtaaggt gagcaataag ggcctgcaa gctccatcga gaagaccatc	720
tccaaggcaa agggacagcc aaggagcct caggtgtata cactgccacc cagccagtgc	780
gagatgacca agaaccaggt gagcctgtcc tgtgccgtga agggcttcta cccatctgac	840
atgccgtgg agtgggagag caatggccag cccgagaaca attataagac cacacctcca	900
gtgctggact ccgatggctc tttctttctg gtgtccaggc tgacagtgga taagtctcgc	960
tggcaggagg gcaacgtgtt ttctttagtc gtgatgcacg agggcctgca caatcactac	1020
accagaagt ccctgtctct gagcctgggc aagggcggcg gcggctccgg aggaggagga	1080
agcgccgcct cccctaggct gcgcgaggga ccagagctga gccagacga tccagcagga	1140
ctgctggacc tgaggcaggg aatgttcgca cagctggtgg ccagaaacgt gctgctgac	1200
gacggccctc tgtcttggtg cagcgatcca ggactggcag gcgtgagcct gacaggcgga	1260
ctgtcctata aggaggatac caaggagctg gtggtggcaa aggcaggcgt gtactacgtg	1320
ttcttccagc tggagctgag gagagtgggt gcaggagagg gatccgcatc tgtgagcctg	1380
gccctgcacc tgcagccact gcggagcgcc gcaggagcag ccgccctggc cctgaccgtg	1440
gacctgccac ctgcatctag cgaggcacgg aattctgcct tcggctttca gggcagactg	1500
ctgcacctga gcgccggaca gaggctggga gtgcacctgc acacagaggc aagggaaga	1560
cacgcatggc agctgacaca gggagcaacc gtgctgggac tgttccgcgt gaccctgag	1620
atcccagcag gactgccatc cccccgtct gagggcggcg gcgggtccgg aggaggagga	1680
tctggcggcg gcggcagcgc cgcctcccc aggctgcgcg agggacctga gctgtccca	1740
gacgatcctg ccggcctgct ggacctgaga cagggaatgt ttgccagct ggtcgctcag	1800
aacgtgctgc tgattgacgg ccccctgtcc tggtatagcg atcctggact ggcaggcgtg	1860
tctctgacag gcggactgag ttacaaagaa gacactaaag aactggtcgt cgccaaagcc	1920
ggcgtgtact acgtgttctt ccaactggag ctgaggaggg tcgtcgccgg cgaaggcagc	1980
ggctctgtga gcctggccct gcacctgcaa cactgagga gcgccgccgg cgccgccgcc	2040
ctggccctga ctgtggacct gccaccagca tcctctgagg caaggaattc cgccttcggc	2100

ttccagggcc ggctgctgca cctgtctgcc ggacagagac tgggcgtcca cctgcataacc	2160
gaagccagag ccaggcatgc ctggcagctg acccagggcg ccaccgtgct gggcctgttc	2220
agagtgaccc cagaaattcc agcaggactg ccttcccaa ggtctgaggg aggaggagga	2280
agtggcggag gaggatccgg agggggaggg agcgccgcct cccaagact gagagaggga	2340
ccagagctgt cccctgatga ccctgccggg ctgctggacc tgagacaagg catgttcgcc	2400
cagctggctg caaaaacgt gctgttaatt gacggccac tgtcctggta ttccgacct	2460
ggcctggccg gcgtgtccct gacaggcggc ctgtcttaca aagaagacac aaaagaactg	2520
gtcgtcgcta aagctggcgt gtactacgtg ttcttccaat tagaactgag aagggtcgtc	2580
gccggcgagg gcagcgggtc tgtgagcctg gccctgcacc tgcaaccgct gcggagcgcc	2640
gccggcgctg ccgccctggc cctgacagtg gacctgcctc cagcaagctc cgaggcaagg	2700
aatagcgcct tcggctttca aggccgcctg ctgcacctgt ccgccggaca gcggctgggc	2760
gtccacctgc acaccgaagc cagagccgc catgcctggc agctgactca gggcgctacc	2820
gtgctgggcc tgttccgctg gacccagag atccctgccg gcctgcctc ccctcgtct	2880
gag	2883

<210> 158
 <211> 845
 <212> PRT
 <213> Artificial sequence

<220>
 <223> TIGIT-Fc Hole IgG4-sc3xCD40L: in TSP 503V1 AA SEQUENCE

<400> 158

Met	Thr	Gly	Thr	Ile	Glu	Thr	Thr	Gly	Asn	Ile	Ser	Ala	Glu	Lys	Gly
1				5				10						15	

Gly	Ser	Ile	Ala	Leu	Gln	Cys	His	Leu	Ser	Ser	Thr	Thr	Ala	Gln	Val
			20					25					30		

Thr	Gln	Val	Asn	Trp	Glu	Gln	Gln	Asp	Gln	Leu	Leu	Ala	Ile	Ser	Asn
		35					40					45			

Ala	Asp	Leu	Gly	Trp	His	Ile	Ser	Pro	Ser	Phe	Lys	Asp	Arg	Val	Ala
	50					55					60				

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

Thr Gly Glu Tyr Phe Cys Ile Tyr His Thr Tyr Pro Asp Gly Thr Tyr
85 90 95

Thr Gly Arg Ile Phe Leu Glu Val Leu Glu Ser Ser Val Ala Glu His
100 105 110

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

Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val
130 135 140

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
145 150 155 160

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
165 170 175

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
180 185 190

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
195 200 205

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
210 215 220

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
225 230 235 240

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
245 250 255

Pro Ser Gln Cys Glu Met Thr Lys Asn Gln Val Ser Leu Ser Cys Ala
260 265 270

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
275 280 285

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
290 295 300

Asp Gly Ser Phe Phe Leu Val Ser Arg Leu Thr Val Asp Lys Ser Arg
305 310 315 320

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
325 330 335

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Gly
340 345 350

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
355 360 365

Gly Gly Ser Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val
370 375 380

Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu
385 390 395 400

Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly
405 410 415

Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln
420 425 430

Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile
435 440 445

Ala Ser Leu Ser Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu
450 455 460

Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser
465 470 475 480

Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe
485 490 495

Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr
500 505 510

Ser Phe Gly Leu Leu Lys Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly
515 520 525

Ser Gly Gly Gly Gly Ser Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala
530 535 540

Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln
545 550 555 560

Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu
565 570 575

Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile
580 585 590

Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala
595 600 605

Pro Phe Ile Ala Ser Leu Ser Leu Lys Ser Pro Gly Arg Phe Glu Arg
610 615 620

Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly
625 630 635 640

Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala
645 650 655

Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr
660 665 670

Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu Gly Gly Gly Gly Ser Gly
675 680 685

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Lys Gly Asp Gln Asn Pro
690 695 700

Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser
705 710 715 720

Val Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu
725 730 735

Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu
740 745 750

Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser
755 760 765

Ser Gln Ala Pro Phe Ile Ala Ser Leu Ser Leu Lys Ser Pro Gly Arg
770 775 780

Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys
785 790 795 800

Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln
805 810 815

Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser
820 825 830

His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu
835 840 845

<210> 159
<211> 2535
<212> DNA
<213> Artificial sequence

<220>
<223> TIGIT-Fc Hole IgG4-sc3xCD40L: in TSP 503V1 AA SEQUENCE

<400> 159
atgaccggca caatcgagac aacaggcaac atctctgccg agaagggagg cagcatcgcc 60
ctgcagtgcc acctgagcag caccacagcc caggtgaccc aggtgaactg ggagcagcag 120
gaccagctgc tggccatctc caatgccgat ctgggctggc acatcagccc ctcctttaag 180
gataggggtgg cacctggacc aggcctgggc ctgaccctgc agagcctgac cgtgaatgac 240
acaggcgagt acttctgtat ctaccacaca tatcctgatg gcacctatac aggcagaatc 300

tttctggagg tgctggagtc tagcgtggcc gagcacggag gaggaggcag cgggggagga	360
ggctccgagt ctaagtacgg accaccatgc cctccatgtc ctgcaccaga gttcgaggga	420
ggaccatccg tgttcctggt tccacctaag cctaaggaca ccctgatgat cagccggacc	480
ccagaggtga catgcgtggt ggtggacgtg agccaggagg accccgaggt gcagtttaat	540
tggtatgtgg atggcgtgga ggtgcacaac gccaagacca agcccaggga ggagcagttc	600
aacagcacct accgcgtggt gtccgtgctg acagtgtgc accaggactg gctgaatggc	660
aaggagtata agtgtaaggt gtccaacaag ggcctgccta gctccatcga gaaaaccatc	720
agcaaggcaa agggacagcc acgggagcca caggtgtaca ccctgccacc aagccagtgc	780
gagatgacaa agaatcaggt gagcctgtcc tgtgccgtga agggctttta cccttcgcac	840
atcgccgtgg agtgggagtc taacggccag ccagagaaca attataagac cacacctcca	900
gtgctggact ccgatggctc tttctttctg gtgtctaggc tgaccgtgga taagagccgc	960
tggcaggagg gcaacgtggt cagctgcagc gtgatgcacg aggccctgca caaccactat	1020
acacaaaagt ccctgtctct gagcctgggc aagggcggcg gcggcagcgg cggaggaggc	1080
tccggaggcg gcggctctgg cggcggcggc agccagaagg gcgatcagaa tcctcagatc	1140
gccgcccacg tgatcagcga ggcctctagc aagaccacat ccgtgctgca gtgggcccag	1200
aagggtact ataccatgag caacaatctg gtgacactgg agaatggcaa gcagctgacc	1260
gtgaagcggc agggcctgta ctatatctac gcccagggtga cattctgcag caacagagag	1320
gcctcctctc agggcccttt tatcgcctct ctgagcctga agtctccagg ccggttcgag	1380
agaatcctgc tgagggcagc aaacaccac agctccgcca agccttgttg ccagcagtct	1440
atccacctgg gcggcgtggt cgagctgcag ccaggagcca gcgtgtttgt gaatgtgaca	1500
gaccctagcc aggtgtccca cggcaccggc ttcaccagct tcggcctgct gaagctgggc	1560
ggcggcggca gcggggggcg cggctccgga gggggaggct ctcagaaagg cgatcagaat	1620
ccacagattg ctgcccacgt gatctctgag gcctctagca agaccacaag cgtgctgcag	1680
tgggctgaaa aaggatacta taccatgtct aataatctgg tgacactgga gaatggcaag	1740
cagctgactg tcaagagaca gggcctgtat tacatctacg ctgaggtgac attttgcagc	1800
aatagagagg cctcctctca ggctcccttc atcgcctccc tgtctctgaa gtcccctggc	1860
aggtttgagc gcacctgct gagagccgcc aatactcaca gctccgcaa gccatgtgga	1920

cagcagtcca ttcacctggg cggcgtgttc gagctgcaac caggagccag cgtgttcgtg 1980
 aatgtgacag acccctctca ggtgagccac ggcaccggct tcaccagctt cggcctgctg 2040
 aagctgggtg gcggcggcag cggcgggggc ggctccggag gcggaggctc tcagaagggc 2100
 gatcagaatc ctcagattgc agcccacgtg atctccgagg cctctagcaa gaccacatct 2160
 gtgctgcagt gggctgagaa aggctactat accatgtcta acaatctggt gacactggag 2220
 aacggcaagc aactgactgt caaaagacag ggcctgtatt atatctacgc tcaagtgaca 2280
 ttctgcagca atcgggaggc ctctctcag gcacccttca tcgccagcct gtcctgaag 2340
 tcccctggcc ggttcgagag aatcctgtta agagccgcca atacacacag ctccgcaaaa 2400
 ccatgtggac agcagagcat acacctgggc ggcgtgttcg agctgcaacc gggagcctcc 2460
 gtgtttgtca atgtgacaga cccatcccag gtgtctcacg gcaccggctt caccagcttc 2520
 ggcctgctga agctg 2535

<210> 160
 <211> 244
 <212> PRT
 <213> Artificial sequence

<220>
 <223> TIGIT full length (Q495A1 Uniprot ID) AA SEQUENCE

<400> 160

Met Arg Trp Cys Leu Leu Leu Ile Trp Ala Gln Gly Leu Arg Gln Ala
 1 5 10 15

Pro Leu Ala Ser Gly Met Met Thr Gly Thr Ile Glu Thr Thr Gly Asn
 20 25 30

Ile Ser Ala Glu Lys Gly Gly Ser Ile Ile Leu Gln Cys His Leu Ser
 35 40 45

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

Leu Leu Ala Ile Cys Asn Ala Asp Leu Gly Trp His Ile Ser Pro Ser
 65 70 75 80

Phe Lys Asp Arg Val Ala Pro Gly Pro Gly Leu Gly Leu Thr Leu Gln
85 90 95

Ser Leu Thr Val Asn Asp Thr Gly Glu Tyr Phe Cys Ile Tyr His Thr
100 105 110

Tyr Pro Asp Gly Thr Tyr Thr Gly Arg Ile Phe Leu Glu Val Leu Glu
115 120 125

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

Ala Met Ala Ala Thr Leu Val Val Ile Cys Thr Ala Val Ile Val Val
145 150 155 160

Val Ala Leu Thr Arg Lys Lys Lys Ala Leu Arg Ile His Ser Val Glu
165 170 175

Gly Asp Leu Arg Arg Lys Ser Ala Gly Gln Glu Glu Trp Ser Pro Ser
180 185 190

Ala Pro Ser Pro Pro Gly Ser Cys Val Gln Ala Glu Ala Ala Pro Ala
195 200 205

Gly Leu Cys Gly Glu Gln Arg Gly Glu Asp Cys Ala Glu Leu His Asp
210 215 220

Tyr Phe Asn Val Leu Ser Tyr Arg Ser Leu Gly Asn Cys Ser Phe Phe
225 230 235 240

Thr Glu Thr Gly

<210> 161

<211> 598

<212> PRT

<213> Artificial sequence

<220>

<223> LILRB2 D1-4, full length (Q8N423-1 UniParc) AA SEQUENCE

<400> 161

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

Pro Arg Thr His Val Gln Thr Gly Thr Ile Pro Lys Pro Thr Leu Trp
20 25 30

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

Cys Gln Gly Ser Leu Glu Ala Gln Glu Tyr Arg Leu Tyr Arg Glu Lys
50 55 60

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

Gly Gln Phe His Ile Pro Ser Ile Thr Trp Glu His Thr Gly Arg Tyr
85 90 95

Gly Cys Gln Tyr Tyr Ser Arg Ala Arg Trp Ser Glu Leu Ser Asp Pro
100 105 110

Leu Val Leu Val Met Thr Gly Ala Tyr Pro Lys Pro Thr Leu Ser Ala
115 120 125

Gln Pro Ser Pro Val Val Thr Ser Gly Gly Arg Val Thr Leu Gln Cys
130 135 140

Glu Ser Gln Val Ala Phe Gly Gly Phe Ile Leu Cys Lys Glu Gly Glu
145 150 155 160

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

Ser Arg Ala Ile Phe Ser Val Gly Pro Val Ser Pro Asn Arg Arg Trp
180 185 190

Ser His Arg Cys Tyr Gly Tyr Asp Leu Asn Ser Pro Tyr Val Trp Ser
195 200 205

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

Pro Ser Leu Ser Val Gln Pro Gly Pro Val Val Ala Pro Gly Glu Ser
225 230 235 240

Leu Thr Leu Gln Cys Val Ser Asp Val Gly Tyr Asp Arg Phe Val Leu
245 250 255

Tyr Lys Glu Gly Glu Arg Asp Leu Arg Gln Leu Pro Gly Arg Gln Pro
260 265 270

Gln Ala Gly Leu Ser Gln Ala Asn Phe Thr Leu Gly Pro Val Ser Arg
275 280 285

Ser Tyr Gly Gly Gln Tyr Arg Cys Tyr Gly Ala His Asn Leu Ser Ser
290 295 300

Glu Cys Ser Ala Pro Ser Asp Pro Leu Asp Ile Leu Ile Thr Gly Gln
305 310 315 320

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

Ser Gly Glu Asn Val Thr Leu Leu Cys Gln Ser Trp Arg Gln Phe His
340 345 350

Thr Phe Leu Leu Thr Lys Ala Gly Ala Ala Asp Ala Pro Leu Arg Leu
355 360 365

Arg Ser Ile His Glu Tyr Pro Lys Tyr Gln Ala Glu Phe Pro Met Ser
370 375 380

Pro Val Thr Ser Ala His Ala Gly Thr Tyr Arg Cys Tyr Gly Ser Leu
385 390 395 400

Asn Ser Asp Pro Tyr Leu Leu Ser His Pro Ser Glu Pro Leu Glu Leu
405 410 415

Val Val Ser Gly Pro Ser Met Gly Ser Ser Pro Pro Pro Thr Gly Pro
420 425 430

Ile Ser Thr Pro Ala Gly Pro Glu Asp Gln Pro Leu Thr Pro Thr Gly
435 440 445

Ser Asp Pro Gln Ser Gly Leu Gly Arg His Leu Gly Val Val Ile Gly
450 455 460

Ile Leu Val Ala Val Val Leu Leu Leu Leu Leu Leu Leu Leu Phe
465 470 475 480

Leu Ile Leu Arg His Arg Arg Gln Gly Lys His Trp Thr Ser Thr Gln
485 490 495

Arg Lys Ala Asp Phe Gln His Pro Ala Gly Ala Val Gly Pro Glu Pro
500 505 510

Thr Asp Arg Gly Leu Gln Trp Arg Ser Ser Pro Ala Ala Asp Ala Gln
515 520 525

Glu Glu Asn Leu Tyr Ala Ala Val Lys Asp Thr Gln Pro Glu Asp Gly
530 535 540

Val Glu Met Asp Thr Arg Ala Ala Ala Ser Glu Ala Pro Gln Asp Val
545 550 555 560

Thr Tyr Ala Gln Leu His Ser Leu Thr Leu Arg Arg Lys Ala Thr Glu
565 570 575

Pro Pro Pro Ser Gln Glu Arg Glu Pro Pro Ala Glu Pro Ser Ile Tyr
580 585 590

Ala Thr Leu Ala Ile His
595

<210> 162
<211> 697
<212> PRT
<213> Artificial sequence

<220>
<223> Siglec 10 full length (Q96LC7-1 Uniprot) AA SEQUENCE

<400> 162

Met Leu Leu Pro Leu Leu Leu Ser Ser Leu Leu Gly Gly Ser Gln Ala
1 5 10 15

Met Asp Gly Arg Phe Trp Ile Arg Val Gln Glu Ser Val Met Val Pro
20 25 30

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

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

Thr Glu Thr Thr Lys Gly Ala Pro Val Ala Thr Asn His Gln Ser Arg
65 70 75 80

Glu Val Glu Met Ser Thr Arg Gly Arg Phe Gln Leu Thr Gly Asp Pro
85 90 95

Ala Lys Gly Asn Cys Ser Leu Val Ile Arg Asp Ala Gln Met Gln Asp
100 105 110

Glu Ser Gln Tyr Phe Phe Arg Val Glu Arg Gly Ser Tyr Val Arg Tyr
115 120 125

Asn Phe Met Asn Asp Gly Phe Phe Leu Lys Val Thr Ala Leu Thr Gln
130 135 140

Lys Pro Asp Val Tyr Ile Pro Glu Thr Leu Glu Pro Gly Gln Pro Val
145 150 155 160

Thr Val Ile Cys Val Phe Asn Trp Ala Phe Glu Glu Cys Pro Pro Pro
165 170 175

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

Thr Thr Ser His Phe Ser Val Leu Ser Phe Thr Pro Arg Pro Gln Asp
195 200 205

His Asn Thr Asp Leu Thr Cys His Val Asp Phe Ser Arg Lys Gly Val
210 215 220

Ser Ala Gln Arg Thr Val Arg Leu Arg Val Ala Tyr Ala Pro Arg Asp
225 230 235 240

Leu Val Ile Ser Ile Ser Arg Asp Asn Thr Pro Ala Leu Glu Pro Gln
245 250 255

Pro Gln Gly Asn Val Pro Tyr Leu Glu Ala Gln Lys Gly Gln Phe Leu
260 265 270

Arg Leu Leu Cys Ala Ala Asp Ser Gln Pro Pro Ala Thr Leu Ser Trp
275 280 285

Val Leu Gln Asn Arg Val Leu Ser Ser Ser His Pro Trp Gly Pro Arg
290 295 300

Pro Leu Gly Leu Glu Leu Pro Gly Val Lys Ala Gly Asp Ser Gly Arg
305 310 315 320

Tyr Thr Cys Arg Ala Glu Asn Arg Leu Gly Ser Gln Gln Arg Ala Leu
325 330 335

Asp Leu Ser Val Gln Tyr Pro Pro Glu Asn Leu Arg Val Met Val Ser
340 345 350

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

Pro Val Leu Glu Gly Gln Ser Leu Cys Leu Val Cys Val Thr His Ser
370 375 380

Ser Pro Pro Ala Arg Leu Ser Trp Thr Gln Arg Gly Gln Val Leu Ser
385 390 395 400

Pro Ser Gln Pro Ser Asp Pro Gly Val Leu Glu Leu Pro Arg Val Gln
405 410 415

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

Ser Gln His Val Ser Leu Ser Leu Ser Val His Tyr Ser Pro Lys Leu
435 440 445

Leu Gly Pro Ser Cys Ser Trp Glu Ala Glu Gly Leu His Cys Ser Cys
450 455 460

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

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

Ser Ser Ala Gly Pro Trp Ala Asn Ser Ser Leu Ser Leu His Gly Gly
500 505 510

Leu Ser Ser Gly Leu Arg Leu Arg Cys Glu Ala Trp Asn Val His Gly
515 520 525

Ala Gln Ser Gly Ser Ile Leu Gln Leu Pro Asp Lys Lys Gly Leu Ile
530 535 540

Ser Thr Ala Phe Ser Asn Gly Ala Phe Leu Gly Ile Gly Ile Thr Ala
545 550 555 560

Leu Leu Phe Leu Cys Leu Ala Leu Ile Ile Met Lys Ile Leu Pro Lys
565 570 575

Arg Arg Thr Gln Thr Glu Thr Pro Arg Pro Arg Phe Ser Arg His Ser
580 585 590

Thr Ile Leu Asp Tyr Ile Asn Val Val Pro Thr Ala Gly Pro Leu Ala
595 600 605

Gln Lys Arg Asn Gln Lys Ala Thr Pro Asn Ser Pro Arg Thr Pro Leu
610 615 620

Pro Pro Gly Ala Pro Ser Pro Glu Ser Lys Lys Asn Gln Lys Lys Gln
625 630 635 640

Tyr Gln Leu Pro Ser Phe Pro Glu Pro Lys Ser Ser Thr Gln Ala Pro
645 650 655

Glu Ser Gln Glu Ser Gln Glu Glu Leu His Tyr Ala Thr Leu Asn Phe
660 665 670

Pro Gly Val Arg Pro Arg Pro Glu Ala Arg Met Pro Lys Gly Thr Gln
675 680 685

Ala Asp Tyr Ala Glu Val Lys Phe Gln
690 695

<210> 163
<211> 261
<212> PRT
<213> Artificial sequence

<220>
<223> CD40L full length (P29965 Uniprot) AA SEQUENCE

<400> 163

Met Ile Glu Thr Tyr Asn Gln Thr Ser Pro Arg Ser Ala Ala Thr Gly
1 5 10 15

Leu Pro Ile Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu
20 25 30

Ile Thr Gln Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg
35 40 45

Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val
50 55 60

Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser
65 70 75 80

Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys
85 90 95

Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu
100 105 110

Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser
115 120 125

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

Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln
145 150 155 160

Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr
165 170 175

Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser
180 185 190

Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala
195 200 205

Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His
210 215 220

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

Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe
245 250 255

Gly Leu Leu Lys Leu
260

<210> 164
<211> 120
<212> PRT
<213> Artificial sequence

<220>
<223> TIGIT Full ECD AA SEQUENCE

<400> 164

Met Met Thr Gly Thr Ile Glu Thr Thr Gly Asn Ile Ser Ala Glu Lys
1 5 10 15

Gly Gly Ser Ile Ile Leu Gln Cys His Leu Ser Ser Thr Thr Ala Gln
20 25 30

Val Thr Gln Val Asn Trp Glu Gln Gln Asp Gln Leu Leu Ala Ile Cys
35 40 45

Asn Ala Asp Leu Gly Trp His Ile Ser Pro Ser Phe Lys Asp Arg Val
50 55 60

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

Asp Thr Gly Glu Tyr Phe Cys Ile Tyr His Thr Tyr Pro Asp Gly Thr
85 90 95

Tyr Thr Gly Arg Ile Phe Leu Glu Val Leu Glu Ser Ser Val Ala Glu
100 105 110

His Gly Ala Arg Phe Gln Ile Pro
115 120

<210> 165
<211> 440
<212> PRT
<213> Artificial sequence

<220>
<223> LILRB2 Full ECD AA SEQUENCE

<400> 165

Gln Thr Gly Thr Ile Pro Lys Pro Thr Leu Trp Ala Glu Pro Asp Ser
1 5 10 15

Val Ile Thr Gln Gly Ser Pro Val Thr Leu Ser Cys Gln Gly Ser Leu
20 25 30

Glu Ala Gln Glu Tyr Arg Leu Tyr Arg Glu Lys Lys Ser Ala Ser Trp
35 40 45

Ile Thr Arg Ile Arg Pro Glu Leu Val Lys Asn Gly Gln Phe His Ile
50 55 60

Pro Ser Ile Thr Trp Glu His Thr Gly Arg Tyr Gly Cys Gln Tyr Tyr
65 70 75 80

Ser Arg Ala Arg Trp Ser Glu Leu Ser Asp Pro Leu Val Leu Val Met
85 90 95

Thr Gly Ala Tyr Pro Lys Pro Thr Leu Ser Ala Gln Pro Ser Pro Val
100 105 110

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

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

Cys Leu Asn Ser Gln Pro His Ala Arg Gly Ser Ser Arg Ala Ile Phe
145 150 155 160

Ser Val Gly Pro Val Ser Pro Asn Arg Arg Trp Ser His Arg Cys Tyr
165 170 175

Gly Tyr Asp Leu Asn Ser Pro Tyr Val Trp Ser Ser Pro Ser Asp Leu
180 185 190

Leu Glu Leu Leu Val Pro Gly Val Ser Lys Lys Pro Ser Leu Ser Val
195 200 205

Gln Pro Gly Pro Val Val Ala Pro Gly Glu Ser Leu Thr Leu Gln Cys
210 215 220

Val Ser Asp Val Gly Tyr Asp Arg Phe Val Leu Tyr Lys Glu Gly Glu
225 230 235 240

Arg Asp Leu Arg Gln Leu Pro Gly Arg Gln Pro Gln Ala Gly Leu Ser
245 250 255

Gln Ala Asn Phe Thr Leu Gly Pro Val Ser Arg Ser Tyr Gly Gly Gln
260 265 270

Tyr Arg Cys Tyr Gly Ala His Asn Leu Ser Ser Glu Cys Ser Ala Pro
275 280 285

Ser Asp Pro Leu Asp Ile Leu Ile Thr Gly Gln Ile Arg Gly Thr Pro
290 295 300

Phe Ile Ser Val Gln Pro Gly Pro Thr Val Ala Ser Gly Glu Asn Val
305 310 315 320

Thr Leu Leu Cys Gln Ser Trp Arg Gln Phe His Thr Phe Leu Leu Thr
325 330 335

Lys Ala Gly Ala Ala Asp Ala Pro Leu Arg Leu Arg Ser Ile His Glu
340 345 350

Tyr Pro Lys Tyr Gln Ala Glu Phe Pro Met Ser Pro Val Thr Ser Ala
355 360 365

His Ala Gly Thr Tyr Arg Cys Tyr Gly Ser Leu Asn Ser Asp Pro Tyr
370 375 380

Leu Leu Ser His Pro Ser Glu Pro Leu Glu Leu Val Val Ser Gly Pro
385 390 395 400

Ser Met Gly Ser Ser Pro Pro Pro Thr Gly Pro Ile Ser Thr Pro Ala
405 410 415

Gly Pro Glu Asp Gln Pro Leu Thr Pro Thr Gly Ser Asp Pro Gln Ser
420 425 430

Gly Leu Gly Arg His Leu Gly Val
435 440

<210> 166
<211> 1422
<212> DNA
<213> Artificial sequence

<220>
<223> sc3xCD40L, AA 114-261 C194S (P29965 Uniprot) internal linker
3x(GGGGS) NA SEQUENCE

<400> 166
cagaagggcg atcagaaccc ccagatcgcc gccacgtga tctccgaggc ctctagcaag 60
accacatctg tgctgcagtg ggccgagaag ggctactata caatgagcaa caatctggtg 120

accctggaga acggcaagca gctgacagtg aagcggcagg gcctgtacta tatctatgcc	180
caggtgacct tctgctcaa tagagaggcc tcctctcagg cccctttat cgcctccctg	240
tctctgaagt ctctggccg gttcgagaga atcctgctga gggcagcaaa cacacacagc	300
tccgccaagc cctgtggcca gcagtctatc cacctgggcg gcgtgttcga gctgcagcca	360
ggagccagcg tgtttgtgaa tgtgaccgac cctagccagg tgtcccacgg caccggcttc	420
accagcttcg gcctgctgaa gctgggcggc ggaggctctg gcggaggagg cagcggagga	480
ggaggctccc agaaaggcga tcagaaccct cagattgctg cccacgtgat cagcagggcc	540
tctagcaaga ccacatccgt gctgcagtgg gctgaaaaag gatactatac aatgtctaata	600
aatctggtga ccctggagaa tggcaagcag ctgaccgtca agagacaggg cctgtattat	660
atctacgccc aggtgacctt ttgcagcaat cgcgaggcct cctctcaggc tccattcatc	720
gccagcctgt ccctgaagtc cccaggcagg tttagcgca tcctgctgag agccgccaat	780
accacagct ccgccaagcc atgtggacag cagtccattc acctgggagg cgtgttcgag	840
ctgcaaccag gagccagcgt gttcgtgaat gtgaccgacc cctctcaggc gagccacggc	900
accggcttca ccagcttcgg cctgctgaag ctgggtggag gaggctctgg cgggggcggc	960
agcggcggag gaggctccca gaaggcgat cagaatcctc agattgccgc ccacgtgac	1020
tctgaggcct ctagcaagac cacaagcgtg ctgcagtggg cagaaaaagg gtactataca	1080
atgtctaaca atctggtgac cctggagaac ggcaagcaac tgaccgtcaa aagacagggc	1140
ctgtactaca tctacgtca ggtgacctt tgcagcaata gggaggcctc ctctcaggca	1200
ccttttatcg cctctctgag cctgaagtcc ccaggccggt tcgagagaat cctgttaagg	1260
gcagcaaaca ctacagctc cgccaaacca tgtggacagc agagcataca cctgggcggc	1320
gtgttcgagc tgcaaccggg agcctccgtg tttgtcaatg tgaccgacc atcccaggtg	1380
tctcacggca ccggcttcac cagcttcggc ctgctgaagc tg	1422