

<110> Carsgen therapeutics Co.,Ltd

<130> P2018-0140

<150> 201710087299.2

<151> 2017-02-17

<150> 201810079015.X

<151> 2018-01-26

<160> 75

<170> PatentIn version 3.5

 $\langle 210 \rangle$ 1

363 <211>

⟨212⟩ DNA

⟨213⟩ Artificial sequence

 $\langle 220 \rangle$

<223> 31C2 VH

 $\langle 400 \rangle$ 1

gaggtgcaat	tgctggagtc	tgggggaggc	ttggtacagc	ctggggggtc	cctgagactc	60
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ccagggaagg	ggctggagtg	ggtctcagct	attagtggta	gtggtggtag	cacatactac	180
gcagactccg	tgaaggccg	gttcaccatc	tccagagaca	attccaagaa	cacgctgtat	240
ctgcagatga	acagcctgag	agccgaggac	acggccgtat	attactgtgc	gaaagttcgt	300
tacggttggg	gtgcaggtgc	attcgactac	tggggccaag	gaaccctggt	caccgtctcg	360
agt						363

 $\langle 210 \rangle$ 2 $\langle 211 \rangle$ 121

<212> PRT

⟨213⟩ Artificial sequence

 $\langle 220 \rangle$

<223> 31C2 VH

 $\langle 400 \rangle$ 2

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

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

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

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

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

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

Ala Lys Val Arg Tyr Gly Trp Gly Ala Gly Ala Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 3

<211> 324

<212> DNA

<213> Artifical sequence

<220>

<223> 31C2 VL

<400> 3

gacatccaga tgaccagtc tccttcacc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gtgccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgat gctccagtt tggaaagtgg ggtcccatca 180
cgtttcagcg gcagtggatc cgggacagaa ttcactctca ccatcagcag cttgcagcct 240
gatgattttg caacttatta ctgccaacag tacgatacct acccaccaat cacgtttggc 300
cagggcacca aagtcgagat caag 324

<210> 4

<211> 108

<212> PRT

<213> Artifical sequence

<220>

<223> 31C2VL

<400> 4

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

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

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

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly

50	55	60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro		
65	70	75 80
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Thr Tyr Pro Pro		
	85	90 95
Ile Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys		
	100	105

<210> 5
 <211> 354
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> 32H4 VH
 <400> 5

gaggtgcaat tgctggagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc	60
tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct	120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gcgtgttgca	300
ttctctggtt ctttcgacta ctggggccaa ggaacctgg tcaccgtctc gagt	354

<210> 6
 <211> 118
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> 32H4 VH
 <400> 6

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

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

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

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

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

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

Ala Arg Val Ala Phe Ser Gly Ser Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 7

<211> 321

<212> DNA

<213> Artifical sequence

<220>

<223> 32H4 VL

<400> 7

gacatccaga tgaccagtc tccttcacc ctgtctgcat ctgtaggaga ccgtgtcacc	60
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gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca	180
cgtttcagcg gcagtggatc cgggacagaa ttcactctca ccatcagcag cttgcagcct	240
gatgattttg caacttatta ctgccaacag agaaacagat accaccaac gtttggccag	300
ggcaccaaag tcgagatcaa g	321

<210> 8

<211> 107

<212> PRT

<213> Artifical sequence

<220>

<223> 32H4 VL

<400> 8

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

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

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

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

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

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Arg Asn Arg Tyr Pro Pro
85 90 95

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

<210> 9
<211> 5
<212> PRT
<213> Artifical sequence
<220>
<223> 31C2&32H4 HCDR1
<400> 9

Ser Tyr Ala Met Ser
1 5

<210> 10
<211> 17
<212> PRT
<213> Artifical sequence
<220>
<223> 31C2&32H4 HCDR2
<400> 10

Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 11
<211> 12
<212> PRT
<213> Artifical sequence
<220>
<223> 31C2 HCDR3
<400> 11

Val Arg Tyr Gly Trp Gly Ala Gly Ala Phe Asp Tyr
1 5 10

<210> 12

<211> 9
 <212> PRT
 <213> Artifical sequence
 <220>
 <223> 32H4 HCDR3
 <400> 12
 Val Ala Phe Ser Gly Ser Phe Asp Tyr
 1 5

<210> 13
 <211> 11
 <212> PRT
 <213> Artifical sequence
 <220>
 <223> 31C2&32H4 LCDR1
 <400> 13
 Arg Ala Ser Gln Ser Ile Ser Ser Trp Leu Ala
 1 5 10

<210> 14
 <211> 7
 <212> PRT
 <213> Artifical sequence
 <220>
 <223> 31C2&32H4 LCDR2
 <400> 14
 Asp Ala Ser Ser Leu Glu Ser
 1 5

<210> 15
 <211> 10
 <212> PRT
 <213> Artifical sequence
 <220>
 <223> 31C2 LCDR3
 <400> 15
 Gln Gln Tyr Asp Thr Tyr Pro Pro Ile Thr
 1 5 10

<210> 16
 <211> 9
 <212> PRT
 <213> Artifical sequence
 <220>

<223> 32H4 LCDR3

<400> 16

Gln Gln Arg Asn Arg Tyr Pro Pro Thr

1 5

<210> 17

<211> 951

<212> DNA

<213> Artifical sequence

<220>

<223> IL13Ra2 ECD

<400> 17

gacaccgaga	taaaagttaa	ccctcctcag	gattttgaga	tagtggatcc	cggatactta	60
ggttatctct	atttgcaatg	gcaaccccca	ctgtctctgg	atcattttta	ggaatgcaca	120
gtggaatatg	aactaaaata	ccgaaacatt	ggtagtgaaa	catggaagac	catcattact	180
aagaatctac	attacaaaga	tgggtttgat	cttaacaagg	gcattgaagc	gaagatacac	240
acgcttttac	catggcaatg	cacaaatgga	tcagaagttc	aaagttcctg	ggcagaaact	300
acttattgga	taccaccaca	aggaattcca	gaaactaaag	ttcaggatat	ggattgcgta	360
tattacaatt	ggcaatat	actctgttct	tggaaacctg	gcataggtgt	acttcttgat	420
accaattaca	acttgtttta	ctggtatgag	ggcttggatc	atgcattaca	gtgtgttgat	480
tacatcaagg	ctgatggaca	aaatatagga	tgcagatttc	cctatttgga	ggcatcagac	540
tataaagatt	tctatatttg	tgtaaatgga	tcatcagaga	acaagcctat	cagatccagt	600
tatttcactt	ttcagcttca	aaatatagtt	aaacctttgc	cgccagtcta	tcttactttt	660
actcgggaga	gttcatgtga	aattaagctg	aaatggagca	tacctttggg	acctattcca	720
gcaaggtggt	ttgattatga	aattgagatc	agagaagatg	atactacctt	ggtgactgct	780
acagttgaaa	atgaaacata	caccttgaaa	acaacaaatg	aaacccgaca	attatgcttt	840
gtagtaagaa	gcaaagtga	tattttattgc	tcagatgacg	gaatttggag	tgagtggagt	900
gataaacaat	gctgggaagg	tgaagaccta	tcgaagaaaa	ctttgctacg	t	951

<210> 18

<211> 317

<212> PRT

<213> Artifical sequence

<220>

<223> IL13Ra2 ECD

<400> 18

Asp Thr Glu Ile Lys Val Asn Pro Pro Gln Asp Phe Glu Ile Val Asp

1 5 10 15

Pro Gly Tyr Leu Gly Tyr Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser

20 25 30

Leu Asp His Phe Lys Glu Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg

35 40 45

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

275	280	285
Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys		
290	295	300

Trp Glu Gly Glu Asp Leu Ser Lys Lys Thr Leu Leu Arg
305 310 315

<210> 19
 <211> 964
 <212> DNA
 <213> Artifical sequence
 <220>
 <223> IL13Ra1 ECD
 <400> 19

gggcgggggc gccgcgccta cggaaactca gccacctgtg acaaatttga gtgtctctgt	60
tgaaaacctc tgcacagtaa tatggacatg gaatccaccc gagggagcca gctcaaattg	120
tagtctatgg tatttttagtc attttggcga caaacaagat aagaaaatag ctccggaaac	180
tcgtcgttca atagaagtac ccctgaatga gaggatttgt ctgcaagtgg ggtcccagtg	240
tagcaccaat gagagtgaga agcctagcat tttggttgaa aaatgcatct cacccccaga	300
aggtgatect gagtctgctg tgactgagct tcaatgcatt tggcacaacc tgagctacat	360
gaagtgttct tggctccctg gaaggaatac cagtcccgac actaactata ctctctacta	420
ttggcacaga agcctggaaa aaattcatca atgtgaaaac atcttttagag aaggccaata	480
ctttggttgt tcctttgatc tgaccaaagt gaaggattcc agttttgaac aacacagtg	540
ccaataaatg gtcaaggata atgcaggaaa aattaaacca tccttcaata tagtgccttt	600
aacttcccgt gtgaaacctg atcctccaca tattaaaaac ctctccttcc acaatgatga	660
cctatatgtg caatgggaga atccacagaa ttttattagc agatgcctat tttatgaagt	720
agaagtcaat aacagccaaa ctgagacaca taatgttttc tacgtccaag aggctaaatg	780
tgagaatcca gaatttgaga gaaatgtgga gaatacatct tgtttcatgg tccctggtgt	840
tcttcctgat actttgaaca cagtcagaat aagagtcaaa acaataaagt tatgctatga	900
ggatgacaaa ctctggagta attggagcca agaaatgagt ataggtaaga agcgcaattc	960
caca	964

<210> 20
 <211> 322
 <212> PRT
 <213> Artifical sequence
 <220>
 <223> IL13Ra1 ECD
 <400> 20

Gly Gly Gly Gly Ala Ala Pro Thr Glu Thr Gln Pro Pro Val Thr Asn
1 5 10 15

Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile Trp Thr Trp Asn

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

Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg Asn Val Glu Asn
260 265 270

Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp Thr Leu Asn Thr
275 280 285

Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr Glu Asp Asp Lys
290 295 300

Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly Lys Lys Arg Asn
305 310 315 320

Ser Thr

<210> 21

<211> 1638

<212> DNA

<213> Artificial sequence

<220>

<223> IL13Ra2 ECD_huFc

<400> 21

gacaccgaga	taaaagttaa	ccctcctcag	gattttgaga	tagtggatcc	cggatactta	60
ggttatctct	atttgcaatg	gcaaccccc	ctgtctctgg	atcattttta	ggaatgcaca	120
gtggaatatg	aactaaaata	ccgaaacatt	ggtagtgaaa	catggaagac	catcattact	180
aagaatctac	attacaaaga	tgggtttgat	cttaacaagg	gcattgaagc	gaagatacac	240
acgcttttac	catggcaatg	cacaaatgga	tcagaagttc	aaagttcctg	ggcagaaact	300
acttattgga	taccaccaca	aggaattcca	gaaactaaag	ttcaggatat	ggattgcgta	360
tattacaatt	ggcaatat	actctgttct	tggaaacctg	gcataggtgt	acttcttgat	420
accaattaca	acttgtttta	ctggtatgag	ggcttgatc	atgcattaca	gtgtgttgat	480
tacatcaagg	ctgatggaca	aaatatagga	tgcagatttc	cctatttgga	ggcatcagac	540
tataaagatt	tctatatttg	tgtaaatgga	tcatcagaga	acaagcctat	cagatccagt	600
tatttcactt	ttcagcttca	aaatatagtt	aaacctttgc	cgccagtcta	tcttactttt	660
actcgggaga	gttcatgtga	aattaagctg	aaatggagca	tacctttggg	acctattcca	720
gcaaggtggt	ttgattatga	aattgagatc	agagaagatg	atactacctt	ggtgactgct	780
acagttgaaa	atgaaacata	caccttgaaa	acaacaaatg	aaacccgaca	attatgcttt	840
gtagtaagaa	gcaaagtga	tatttattgc	tcagatgacg	gaatttggag	tgagtggagt	900
gataaacaat	gctgggaagg	tgaagacct	tcgaagaaaa	ctttgctacg	tgatccgac	960
aaaactcaca	catgcccacc	gtgcccagca	cctgaactcc	tggggggacc	gtcagtcctc	1020
ctcttcccc	caaaacccaa	ggacaccctc	atgatctccc	ggaccctga	ggtcacatgc	1080
gtggtggtgg	acgtgagcca	cgaagaccct	gaggtcaagt	tcaactggta	cgtggacggc	1140
gtggaggtgc	ataatgcaa	gacaaagccg	cgggaggagc	agtacaacag	cacgtaccgt	1200
gtggtcagcg	tcctcaccgt	cctgcaccag	gactggctga	atggcaagga	gtacaagtgc	1260
aaggtctcca	acaaagccct	cccagcccc	atcgagaaaa	ccatctccaa	agccaaaggg	1320

cagccccgag	aaccacaggt	gtacaccctg	cccccatccc	gggatgagct	gaccaagaac	1380
caggtcagcc	tgacctgcct	gtcaaaggc	ttctatccca	gcgacatcgc	cgtggagtgg	1440
gagagcaatg	ggcagccgga	gaacaactac	aagaccacgc	ctcccgtgct	ggactccgac	1500
ggctccttct	tcctctatag	caagctcacc	gtggacaaga	gcaggtggca	gcaggggaac	1560
gtcttctcat	gctccgtgat	gcatgaggct	ctgcacaacc	actacacgca	gaagagcctc	1620
tccctgtctc	cgggtaaa					1638

22

<211> 546

⟨212⟩ PRT

Artificial sequence

 $\langle 220 \rangle$

〈223〉 IL13Ra2 ECD huFc

<400> 22

Asp Thr Glu Ile Lys Val Asn Pro Pro Gln Asp Phe Glu Ile Val Asp
1 5 10 15

Pro Gly Tyr Leu Gly Tyr Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser
20 25 30

Leu Asp His Phe Lys Glu Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg
35 40 45

Asn Ile Gly Ser Glu Thr Trp Lys Thr Ile Ile Thr Lys Asn Leu His
50 55 60

Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile Glu Ala Lys Ile His
65 70 75 80

Thr Leu Leu Pro Trp Gln Cys Thr Asn Gly Ser Glu Val Gln Ser Ser
85 90 95

Trp Ala Glu Thr Thr Tyr Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr
100 105 110

Lys Val Gln Asp Met Asp Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu
115 120 125

Cys Ser Trp Lys Pro Gly Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn
130 135 140

Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ala Leu Gln Cys Val Asp
145 150 155 160

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

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

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
420 425 430

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
435 440 445

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
465 470 475 480

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
485 490 495

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
500 505 510

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
515 520 525

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
530 535 540

Gly Lys
545

<210> 23

<211> 1653

<212> DNA

<213> Artificial sequence

<220>

<223> IL13Ra1 ECD_huFc

<400> 23

gggggcgggg gcgccgcgcc tacggaaact cagccacctg tgacaaattt gagtgtctct	60
gttgaaaacc tctgcacagt aatatggaca tggaatccac ccgagggagc cagctcaaat	120
tgtagtctat ggtatttttag tcattttggc gacaaacaag ataagaaaat agctccggaa	180
actcgtcgtt caatagaagt acccctgaat gagaggattt gtctgcaagt ggggtcccag	240
tgtagcacca atgagagtga gaagcctagc attttggttg aaaaatgcat ctcaccccca	300
gaaggtgata ctgagtctgc tgtgactgag cttcaatgca tttggcacaa cctgagctac	360

atgaagtgtt	cttggtctcc	tggaaggaat	accagtcccg	acactaacta	tactctctac	420
tattggcaca	gaagcctgga	aaaaattcat	caatgtgaaa	acatctttag	agaaggccaa	480
tacttttggt	gttcctttga	tctgaccaaa	gtgaaggatt	ccagttttga	acaacacagt	540
gtccaaataa	tggtcaagga	taatgcagga	aaaattaaac	catccttcaa	tatagtgcct	600
ttaacttccc	gtgtgaaacc	tgatcctcca	catattaaaa	acctctcctt	ccacaatgat	660
gacctatatg	tgcaatggga	gaatccacag	aattttatta	gcagatgcct	attttatgaa	720
gtagaagtca	ataacagcca	aactgagaca	cataatgttt	tctacgtcca	agaggctaaa	780
tgtgagaatc	cagaatttga	gagaaatgtg	gagaatacat	cttgtttcat	ggtccctggt	840
gttcttctctg	atactttgaa	cacagtcaga	ataagagtca	aaacaaataa	gttatgctat	900
gaggatgaca	aactctggag	taattggagc	caagaaatga	gtataggtaa	gaagcgcaat	960
tccacaggat	ccgacaaaac	tcacacatgc	ccaccgtgcc	cagcacctga	actcctgggg	1020
ggaccgtcag	tcttctcttt	ccccccaaaa	cccaaggaca	ccctcatgat	ctccccggacc	1080
cctgaggtca	catgcgtggt	ggtggacgtg	agccacgaag	accctgaggt	caagttcaac	1140
tggtacgtgg	acggcgtgga	ggtgcataat	gccaaagaca	agccgcggga	ggagcagtac	1200
aacagcacgt	accgtgtggt	cagcgtcctc	accgtcctgc	accaggactg	gctgaatggc	1260
aaggagtaca	agtgaaggt	ctccaacaaa	gcctcccag	cccccatcga	gaaaaccatc	1320
tccaaagcca	aagggcagcc	ccgagaacca	caggtgtaca	ccctgcccc	atccccgggat	1380
gagctgacca	agaaccaggt	cagcctgacc	tgcttggtca	aaggcttcta	tcccagcgac	1440
atcgccgtgg	agtgggagag	caatgggcag	ccggagaaca	actacaagac	cacgcctccc	1500
gtgctggact	ccgacggctc	cttcttctctc	tatagcaagc	tcaccgtgga	caagagcagg	1560
tggcagcagg	ggaacgtctt	ctcatgctcc	gtgatgcatg	aggtcttgca	caaccactac	1620
acgcagaaga	gcctctccct	gtctccgggt	aaa			1653

<210> 24

<211> 551

<212> PRT

<213> Artifical sequence

<220>

<223> IL13Ra1 ECD_huFc

<400> 24

Gly	Gly	Gly	Gly	Ala	Ala	Pro	Thr	Glu	Thr	Gln	Pro	Pro	Val	Thr	Asn
1				5				10					15		

Leu	Ser	Val	Ser	Val	Glu	Asn	Leu	Cys	Thr	Val	Ile	Trp	Thr	Trp	Asn
		20					25					30			

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

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

Ile	Glu	Val	Pro	Leu	Asn	Glu	Arg	Ile	Cys	Leu	Gln	Val	Gly	Ser	Gln
65					70				75					80	

Cys	Ser	Thr	Asn	Glu	Ser	Glu	Lys	Pro	Ser	Ile	Leu	Val	Glu	Lys	Cys	85	90	95
Ile	Ser	Pro	Pro	Glu	Gly	Asp	Pro	Glu	Ser	Ala	Val	Thr	Glu	Leu	Gln	100	105	110
Cys	Ile	Trp	His	Asn	Leu	Ser	Tyr	Met	Lys	Cys	Ser	Trp	Leu	Pro	Gly	115	120	125
Arg	Asn	Thr	Ser	Pro	Asp	Thr	Asn	Tyr	Thr	Leu	Tyr	Tyr	Trp	His	Arg	130	135	140
Ser	Leu	Glu	Lys	Ile	His	Gln	Cys	Glu	Asn	Ile	Phe	Arg	Glu	Gly	Gln	145	150	155
Tyr	Phe	Gly	Cys	Ser	Phe	Asp	Leu	Thr	Lys	Val	Lys	Asp	Ser	Ser	Phe	165	170	175
Glu	Gln	His	Ser	Val	Gln	Ile	Met	Val	Lys	Asp	Asn	Ala	Gly	Lys	Ile	180	185	190
Lys	Pro	Ser	Phe	Asn	Ile	Val	Pro	Leu	Thr	Ser	Arg	Val	Lys	Pro	Asp	195	200	205
Pro	Pro	His	Ile	Lys	Asn	Leu	Ser	Phe	His	Asn	Asp	Asp	Leu	Tyr	Val	210	215	220
Gln	Trp	Glu	Asn	Pro	Gln	Asn	Phe	Ile	Ser	Arg	Cys	Leu	Phe	Tyr	Glu	225	230	235
Val	Glu	Val	Asn	Asn	Ser	Gln	Thr	Glu	Thr	His	Asn	Val	Phe	Tyr	Val	245	250	255
Gln	Glu	Ala	Lys	Cys	Glu	Asn	Pro	Glu	Phe	Glu	Arg	Asn	Val	Glu	Asn	260	265	270
Thr	Ser	Cys	Phe	Met	Val	Pro	Gly	Val	Leu	Pro	Asp	Thr	Leu	Asn	Thr	275	280	285
Val	Arg	Ile	Arg	Val	Lys	Thr	Asn	Lys	Leu	Cys	Tyr	Glu	Asp	Asp	Lys	290	295	300
Leu	Trp	Ser	Asn	Trp	Ser	Gln	Glu	Met	Ser	Ile	Gly	Lys	Lys	Arg	Asn			

305		310		315		320
Ser Thr Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro						
		325		330		335
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys						
		340		345		350
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val						
		355		360		365
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp						
		370		375		380
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr						
		385		390		395
						400
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp						
		405		410		415
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu						
		420		425		430
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg						
		435		440		445
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys						
		450		455		460
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp						
		465		470		475
						480
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys						
		485		490		495
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser						
		500		505		510
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser						
		515		520		525
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser						
		530		535		540

Leu Ser Leu Ser Pro Gly Lys
 545 550

<210> 25

<211> 245

<212> PRT

<213> Artificial sequence

<220>

<223> 31C2(scFv)

<400> 25

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

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

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

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

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

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

Ala Lys Val Arg Tyr Gly Trp Gly Ala Gly Ala Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
 115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
 130 135 140

Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
 145 150 155 160

Ala Ser Gln Ser Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu Glu Ser

180	185	190
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr		
195	200	205
Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys		
210	215	220
Gln Gln Tyr Asp Thr Tyr Pro Pro Ile Thr Phe Gly Gln Gly Thr Lys		
225	230	235
		240
Val Glu Ile Lys Arg		
245		

<210> 26
 <211> 735
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> 31C2(scFv)
 <400> 26

gaggtgcaat tgctggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc	60
tcctgtgcag cctccggatt caccttttagc agttatgcca tgagctgggt ccgccagget	120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagtctgt	300
tacggttggg gtgcaggtgc attcgactac tggggccaag gaaccctggt caccgtctcg	360
agtgggtggag gcggttcagg cggaggtggt tctggcggtg gcggatcgga catccagatg	420
accagtcctc cttccaccct gtctgcactt gtaggagacc gtgtcaccat cacttgccgt	480
gccagtcaga gtattagtag ctggttggcc tggtatcagc agaaaccagg gaaagccct	540
aagctcctga tctatgatgc ctccagtttg gaaagtgggg tcccatcacg tttcagcggc	600
agtggatccg ggacagaatt cactctcacc atcagcagct tgcagcctga tgattttgca	660
acttattact gccaacagta cgatacctac ccaccaatca cgtttggcca gggcaccaaaa	720
gtcgagatca agcgt	735

<210> 27
 <211> 241
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> 32H4(scFv)
 <400> 27

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

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

<210> 28
 <211> 723
 <212> DNA
 <213> Artifical sequence
 <220>
 <223> 32H4(scFv)
 <400> 28
 gaggtgcaat tgctggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctccggatt caccttttagc agttatgcca tgagctgggt ccgccagget 120
 ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gcgtgttgca 300
 ttctctggtt ctttcgacta ctggggccaa ggaaccctgg tcaccgtctc gagtggtgga 360
 ggcggttcag gcggaggtgg ttctggcggg ggccgatcgg acatccagat gaccagttct 420
 ccttcacccc tgtctgcac ttaggagac cgtgtcacca tcaactgccg tgccagtcag 480
 agtattagta gctggttggc ctggtatcag cagaaaccag ggaaagcccc taagctcctg 540
 atctatgatg cctccagttt ggaaagtggg gtcccatcac gtttcagcgg cagtggatcc 600
 gggacagaat tcaactctac catcagcagc ttgcagcctg atgattttgc aacttattac 660
 tgccaacaga gaaacagata cccaccaacg tttggccagg gcaccaaagt cgagatcaag 720
 cgt 723

<210> 29
 <211> 121
 <212> PRT
 <213> Artifical sequence
 <220>
 <223> 2C7 VH
 <400> 29
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Leu Pro
 20 25 30
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Thr Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

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

Ala Lys Val Arg Tyr Gly Trp Gly Ala Gly Ala Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 30

<211> 363

<212> DNA

<213> Artificial sequence

<220>

<223> 2C7 VH

<400> 30

gaggtgcaat tgctggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt cacctttaaa ctgccggcca tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcagca attactggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagttcgt 300
tacggttggg gtgcaggtgc attcgactac tggggccaag gaaccctggt caccgtctcg 360
agt 363

<210> 31

<211> 121

<212> PRT

<213> Artificial sequence

<220>

<223> 2D3 VH

<400> 31

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

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

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

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

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

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

Val Lys Val Arg Tyr Gly Trp Gly Ala Gly Ala Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 32

<211> 363

<212> DNA

<213> Artifical sequence

<220>

<223> 2D3 VH

<400> 32

gaggtgcaat tgctggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt cacctttcgc agacctgcca tgacatgggt ccgccagget 120
ccagggaagg ggctggagtg ggtctcagca attacaggta gtggtggtag tacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgt gaaagttcgt 300
tacggttggg gtgcaggtgc attcgactac tggggccaag gaaccctggt caccgtctcg 360
agt 363

<210> 33

<211> 121

<212> PRT

<213> Artifical sequence

<220>

<223> 1D11 VH

<400> 33

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

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

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

Ser Ser Ile Ser Gly Ser Ala Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50	55	60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr		
65	70	75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys		
	85	90 95
Ala Lys Val Arg Tyr Gly Trp Gly Ala Gly Ala Phe Asp Tyr Trp Gly		
	100	105 110
Gln Gly Thr Leu Val Thr Val Ser Ser		
	115	120

<210> 34

<211> 363

<212> DNA

<213> Artificial sequence

<220>

<223> 1D11 VH

<400> 34

gaggtgcaat tgctggagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc	60
tcctgtgcag cctccggatt cacctttgga acaattccca tgagctgggt ccgccagget	120
ccagggaagg ggctggagtg ggtctcatcc attagtggta gtgctggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagtctcg	300
tacggttggg gtgcaggtgc attcgactac tggggccaag gaaccctggt caccgtctcg	360
agt	363

<210> 35

<211> 121

<212> PRT

<213> Artificial sequence

<220>

<223> 1B11 VH

<400> 35

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

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

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

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

Ala Lys Val Arg Tyr Gly Trp Gly Ala Gly Ala Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 36

<211> 363

<212> DNA

<213> Artifical sequence

<220>

<223> 1B11 VH

<400> 36

gaggtgcaat tgctggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt caccttttagc agggatgctt tgaactgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacattttac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagtctcg 300
tacggttggg gtgcaggtgc attcgactac tggggccaag gaaccctggt caccgtctcg 360
agt 363

<210> 37

<211> 121

<212> PRT

<213> Artifical sequence

<220>

<223> 2A5 VH

<400> 37

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

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

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

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

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

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

Ala Lys Val Arg Tyr Gly Trp Gly Ala Gly Ala Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 38

<211> 363

<212> DNA

<213> Artificial sequence

<220>

<223> 2A5 VH

<400> 38

gaggtgcaat tgctggagtc tgggggaggc ttggtacagc ctgggggggc cctgagactc	60
tcctgtgcag cctccggatt cacctttagc aggtatgccca tgaactgggt ccgccaggct	120
ccagggaagg ggctggagtg ggtctcagct attagtgcta gtggtggtgg gacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagttcgt	300
tacggttggg gtgcaggtgc attcgactac tggggccaag gaaccctggt caccgtctcg	360
agt	363

<210> 39

<211> 121

<212> PRT

<213> Artificial sequence

<220>

<223> 2D4 VH

<400> 39

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Lys Tyr

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

<210> 40

<211> 363

<212> DNA

<213> Artifical sequence

<220>

<223> 2D4 VH

<400> 40

gaggtgcaat tgctggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc	60
tcctgtgcag cctccgatt cacctttcgc aagtatgcca tgggctgggt cgcaggct	120
ccagggaagg ggctggagt ggtctcaggt attagtggta gtgttgtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagttcgt	300
tacggttggg gtgcaggtgc attcgactac tggggccaag gaacctggt caccgtctcg	360
agt	363

<210> 41

<211> 121

<212> PRT

<213> Artifical sequence

<220>

<223> 1H7 VH

<400> 41

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

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

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

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

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

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

Ala Lys Val Arg Tyr Gly Trp Gly Ala Gly Ala Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 42

<211> 363

<212> DNA

<213> Artifical sequence

<220>

<223> 1H7 VH

<400> 42

gaggtgcaat tgctggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tctgtgcag cctccggatt caccttctgt cgctatgcc tgagctgggt cgcgcaggct 120
ccagggaagg ggctggagtg ggtctcaggt attagcggga gtggtggtgg gacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagttcgt 300
tacggttggg gtgcaggtgc attcgactac tggggccaag gaaccctggt caccgtctcg 360
agt 363

<210> 43

<211> 121

<212> PRT

<213> Artifical sequence

<220>

<223> 1D8 VH

<400> 43

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

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

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

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

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

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

Ala Lys Val Arg Tyr Gly Trp Gly Ala Gly Ala Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 44

<211> 363

<212> DNA

<213> Artifical sequence

<220>

<223> 1D8 VH

<400> 44

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 tcctgtgcag cctccggatt caccttttagc agatacgcca tgaactgggt ccgccagget 120
 ccaggggaagg ggctggagtg ggtctcagct attaatgcaa gtggaggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagtctcg 300
 tacggttggg gtgcaggtgc attcgactac tggggccaag gaaccctggt caccgtctcg 360
 agt 363

<210> 45

<211> 6

<212> PRT

<213> Artifical sequence

<220>

<223> 2C7 HCDR1
 <400> 45
 Lys Leu Pro Ala Met Ser
 1 5

<210> 46
 <211> 6
 <212> PRT
 <213> Artifical sequence
 <220>
 <223> 2D3 HCDR1
 <400> 46
 Arg Arg Pro Ala Met Thr
 1 5

<210> 47
 <211> 6
 <212> PRT
 <213> Artifical sequence
 <220>
 <223> 1D11 HCDR1
 <400> 47
 Gly Thr Ile Pro Met Ser
 1 5

<210> 48
 <211> 6
 <212> PRT
 <213> Artifical sequence
 <220>
 <223> 1B11 HCDR1
 <400> 48
 Ser Arg Asp Ala Leu Asn
 1 5

<210> 49
 <211> 6
 <212> PRT
 <213> Artifical sequence
 <220>
 <223> 2A5&1D8 HCDR1
 <400> 49
 Ser Arg Tyr Ala Met Asn
 1 5

<210> 50
 <211> 6
 <212> PRT
 <213> Artifical sequence
 <220>
 <223> 2D4 HCDR1
 <400> 50
 Arg Lys Tyr Ala Met Gly
 1 5

<210> 51
 <211> 6
 <212> PRT
 <213> Artifical sequence
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 <223> 1H7 HCDR1
 <400> 51
 Arg Arg Tyr Ala Met Ser
 1 5

<210> 52
 <211> 17
 <212> PRT
 <213> Artifical sequence
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 <223> 2C7&2D3 HCDR2
 <400> 52
 Ala Ile Thr Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
 1 5 10 15

Gly

<210> 53
 <211> 17
 <212> PRT
 <213> Artifical sequence
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 <223> 1D11 HCDR2
 <400> 53
 Ser Ile Ser Gly Ser Ala Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
 1 5 10 15

Gly

<210> 54

<211> 17

<212> PRT

<213> Artifical sequence

<220>

<223> 1B11 HCDR2

<400> 54

Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 55

<211> 17

<212> PRT

<213> Artifical sequence

<220>

<223> 2A5 HCDR2

<400> 55

Ala Ile Ser Ala Ser Gly Gly Gly Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 56

<211> 17

<212> PRT

<213> Artifical sequence

<220>

<223> 2D4 HCDR2

<400> 56

Gly Ile Ser Gly Ser Val Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 57

<211> 17

<212> PRT
 <213> Artificial sequence
 <220>
 <223> 1H7 HCDR2
 <400> 57
 Gly Ile Ser Gly Ser Gly Gly Gly Thr Tyr Tyr Ala Asp Ser Val Lys
 1 5 10 15

Gly

<210> 58
 <211> 17
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> 1D8 HCDR2
 <400> 58
 Ala Ile Asn Ala Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
 1 5 10 15

Gly

<210> 59
 <211> 118
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> 5G3 VH
 <400> 59
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Val Ala Phe Ser Gly Ser Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ser
 115

<210> 60
 <211> 354
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> 5G3 VH
 <400> 60
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 tcctgtgcag cctccggatt caccttttagc agttacgtcc tgagctgggt cgcgcaggct 120
 ccagggaagg ggctggagtg ggtctcagca attaggggta gtgctggtaa cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gcgtgttgca 300
 ttctctggtt ctttcgacta ctggggccaa ggaacctgg tcaccgtctc gagt 354

<210> 61
 <211> 118
 <212> PRT
 <213> Artificial sequence
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 <223> 5D7 VH
 <400> 61
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
 20 25 30
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Arg Ser Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Arg Val Ala Phe Ser Gly Ser Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 62

<211> 354

<212> DNA

<213> Artifical sequence

<220>

<223> 5D7 VH

<400> 62

gaggtgcaat tgctggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tctgtgcag cctccggatt caccttttagc aactatgcaa tgagctgggt ccgccagget 120
ccaggaagg ggctggagtg ggtctcaggc attcgtagta gtggtggtcg cacattctac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gcgtgttgca 300
ttctctgggt ctttcgacta ctggggccaa ggaaccctgg tcaccgtctc gagt 354

<210> 63

<211> 6

<212> PRT

<213> Artifical sequence

<220>

<223> 5G3 HCDR1

<400> 63

Ser Ser Tyr Val Leu Ser
1 5

<210> 64

<211> 6

<212> PRT

<213> Artifical sequence

<220>

<223> 5D7 HCDR1

<400> 64

Ser Asn Tyr Ala Met Ser

1 5

<210> 65

<211> 17

<212> PRT

<213> Artifical sequence

<220>

<223> 5G3 HCDR2

<400> 65

Ala Ile Arg Gly Ser Ala Gly Asn Thr Tyr Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 66

<211> 17

<212> PRT

<213> Artifical sequence

<220>

<223> 5D7 HCDR2

<400> 66

Gly Ile Arg Ser Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 67

<211> 245

<212> PRT

<213> Artifical sequence

<220>

<223> 2D4 scFv

<400> 67

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Lys Tyr

20 25 30

Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

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

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

Ala Lys Val Arg Tyr Gly Trp Gly Ala Gly Ala Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
130 135 140

Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145 150 155 160

Ala Ser Gln Ser Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu Glu Ser
180 185 190

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
195 200 205

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Tyr Asp Thr Tyr Pro Pro Ile Thr Phe Gly Gln Gly Thr Lys
225 230 235 240

Val Glu Ile Lys Arg
245

<210> 68

<211> 63

<212> DNA

<213> Artificial sequence

<220>

<223> CD8 α Signal peptide
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 ccg 63

<210> 69
 <211> 135
 <212> DNA
 <213> Artifical sequence
 <220>
 <223> CD8 hinge
 <400> 69
 accacgacgc cagcgccgcg accaccaaca ccggcgccca ccatcgcgtc gcagcccctg 60
 tccctgcgcc cagaggcgtg ccggccagcg gcggggggcg cagtgcacac gagggggctg 120
 gacttcgcct gtgat 135

<210> 70
 <211> 81
 <212> DNA
 <213> Artifical sequence
 <220>
 <223> CD28 transmembrane region
 <400> 70
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 gcctttatta ttttctgggt g 81

<210> 71
 <211> 123
 <212> DNA
 <213> Artifical sequence
 <220>
 <223> CD28 intracellular domain
 <400> 71
 aggagtaaga ggagcaggct cctgcacagt gactacatga acatgactcc ccgccgcccc 60
 gggccaaccc gcaagcatta ccagccctat gccccaccac gcgacttcgc agcctatcgc 120
 tcc 123

<210> 72
 <211> 339
 <212> DNA
 <213> Artifical sequence
 <220>
 <223> CD3Z domain
 <400> 72

agagtgaagt tcagcaggag cgcagacgcc cccgcgtacc agcagggcca gaaccagetc 60
tataacgagc tcaatctagg acgaagagag gagtacgatg ttttgacaa gagacgtggc 120
cgggaccctg agatgggggg aaagccgcag agaaggaaga accctcagga aggcctgtac 180
aatgaactgc agaaagataa gatggcggag gcctacagtg agattgggat gaaaggcgag 240
cgccggaggg gcaaggggca cgatggcctt taccagggtc tcagtacagc caccaaggac 300
acctacgacg cccttcacat gcaggccctg cccctcgc 339

<210> 73

<211> 63

<212> DNA

<213> Artificial sequence

<220>

<223> CD8 transmembrane

<400> 73

atctacatct gggcgccctt ggccgggact tgtggggctc ttctcctgtc actggttacc 60
acc 63

<210> 74

<211> 126

<212> DNA

<213> Artificial sequence

<220>

<223> CD137 intracellular signaling domain

<400> 74

aaacggggca gaaagaaact cctgtatata ttcaacaac catttatgag accagtacaa 60
actactcaag aggaagatgg ctgtagctgc cgatttcag aagaagaaga aggaggatgt 120
gaactg 126

<210> 75

<211> 241

<212> PRT

<213> Artificial sequence

<220>

<223> 5G3 scFv

<400> 75

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

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

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

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

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

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

Ala Arg Val Ala Phe Ser Gly Ser Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu
130 135 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
145 150 155 160

Ser Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala
165 170 175

Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro
180 185 190

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
195 200 205

Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Arg
210 215 220

Asn Arg Tyr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
225 230 235 240

Arg